(12) STANDARD PATENT APPLICATION (11) Application No. **AU 2026201462 A1**
(19) AUSTRALIAN PATENT OFFICE

(54) Title
Alphavirus neoantigen vectors

(51) International Patent Classification(s)
C12N 15/86 (2006.01) ***C07K 14/18*** (2006.01)
A61K 35/76 (2015.01) ***C07K 14/705*** (2006.01)
A61K 39/12 (2006.01)

(21) Application No: **2026201462** (22) Date of Filing: **2026.02.26**

(43) Publication Date: **2026.03.19**
(43) Publication Journal Date: **2026.03.19**

(62) Divisional of:
2023202423

(71) Applicant(s)
Seattle Project Corp.

(72) Inventor(s)
BLAIR, Wade;JOOSS, Karin;RAPPAPORT, Amy Rachel;SCALLAN, Ciaran Daniel;GITLIN, Leonid

(74) Agent / Attorney
FB Rice Pty Ltd, Level 29 126 Phillip Street, Sydney, NSW, 2000, AU

26 Feb 2026
2026201462

ABSTRACT

Disclosed herein are alphavirus vectors that include neoantigen-encoding nucleic acid sequences derived from a tumor of a subject. Also disclosed are nucleotides, cells, and methods associated with the vectors including their use as vaccines.

2026201462 26 Feb 2026

ALPHAVIRUS NEOANTIGEN VECTORS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a divisional application pursuant to Section 79B of the *Patents Act 1990* of Australian Patent Application No. 2023202423, which itself is a divisional application of Australian Patent Application No. 2018266705, which is an Australian national phase application derived from International Patent Application No. PCT/US2018/031696 filed 8 May 2018, which claims the benefit of priority of U.S. Provisional Patent Application No. 62/503,283 filed 8 May 2017, U.S. Provisional Patent Application No. 62/523,201 filed 21 June 2017, and U.S. Provisional Patent Application No. 62/590,163 filed 22 November 2017. The entire contents of each of the above-referenced disclosures are specifically incorporated herein by reference without disclaimer.

BACKGROUND

[0002] Therapeutic vaccines based on tumor-specific neoantigens hold great promise as a next-generation of personalized cancer immunotherapy. [1–3] Cancers with a high mutational burden, such as non-small cell lung cancer (NSCLC) and melanoma, are particularly attractive targets of such therapy given the relatively greater likelihood of neoantigen generation. [4,5] Early evidence shows that neoantigen-based vaccination can elicit T-cell responses[6] and that neoantigen targeted cell-therapy can cause tumor regression under certain circumstances in selected patients.[7]

[0003] One question for neoantigen vaccine design is which of the many coding mutations present in subject tumors can generate the "best" therapeutic neoantigens, e.g., antigens that can elicit anti-tumor immunity and cause tumor regression.

[0004] Initial methods have been proposed incorporating mutation-based analysis using next-generation sequencing, RNA gene expression, and prediction of MHC binding affinity of candidate neoantigen peptides [8]. However, these proposed methods can fail to model the entirety of the epitope generation process, which contains many steps (e.g., TAP transport, proteasomal cleavage, and/or TCR recognition) in addition to gene expression and MHC binding[9]. Consequently, existing methods are likely to suffer from reduced low positive predictive value (PPV). (Figure 1A)

2026201462 26 Feb 2026

[0005] Indeed, analyses of peptides presented by tumor cells performed by multiple groups have shown that <5% of peptides that are predicted to be presented using gene expression and MHC binding affinity can be found on the tumor surface MHC[10,11] (Figure 1B). This low correlation between binding prediction and MHC presentation was further reinforced by recent observations of the lack of predictive accuracy improvement of binding-restricted neoantigens for checkpoint inhibitor response over the number of mutations alone.[12]

[0006] This low positive predictive value (PPV) of existing methods for predicting presentation presents a problem for neoantigen-based vaccine design. If vaccines are designed using predictions with a low PPV, most patients are unlikely to receive a therapeutic neoantigen and fewer still are likely to receive more than one (even assuming all presented peptides are immunogenic). Thus, neoantigen vaccination with current methods is unlikely to succeed in a substantial number of subjects having tumors. (Figure 1C)

[0007] Additionally, previous approaches generated candidate neoantigens using only *cis*-acting mutations, and largely neglected to consider additional sources of neo-ORFs, including mutations in splicing factors, which occur in multiple tumor types and lead to aberrant splicing of many genes[13], and mutations that create or remove protease cleavage sites.

[0008] Finally, standard approaches to tumor genome and transcriptome analysis can miss somatic mutations that give rise to candidate neoantigens due to suboptimal conditions in library construction, exome and transcriptome capture, sequencing, or data analysis. Likewise, standard tumor analysis approaches can inadvertently promote sequence artifacts or germline polymorphisms as neoantigens, leading to inefficient use of vaccine capacity or auto-immunity risk, respectively.

[0009] In addition to the challenges of current neoantigen prediction methods certain challenges also exist with the available vector systems that can be used for neoantigen delivery in humans, many of which are derived from humans. For example, many humans have pre-existing immunity to human viruses as a result of previous natural exposure, and this immunity can be a major obstacle to the use of recombinant human viruses for neoantigen delivery for cancer treatment.

SUMMARY

[0010] Disclosed herein is a composition for delivery of a neoantigen expression system, comprising: the neoantigen expression system, wherein the neoantigen expression system

2026201462 26 Feb 2026

comprises one or more vectors, the one or more vectors comprising: (a) an RNA alphavirus backbone, wherein the RNA alphavirus backbone comprises: (i) at least one promoter nucleotide sequence, and (ii) at least one polyadenylation (poly(A)) sequence; and (b) a neoantigen cassette, wherein the neoantigen cassette comprises: (i) at least one neoantigen-encoding nucleic acid sequence derived from a tumor present within a subject, comprising: (I) at least one tumor-specific and subject-specific MHC class I neoantigen-encoding nucleic acid sequence derived from the tumor, and comprising: (A) a MHC class I epitope encoding nucleic acid sequence with at least one alteration that makes the encoded peptide sequence distinct from the corresponding peptide sequence encoded by a wild-type nucleic acid sequence, and (B) optionally, a 5' linker sequence, and (C) optionally, a 3' linker sequence; (ii) optionally, a second promoter nucleotide sequence operably linked to the neoantigen-encoding nucleic acid sequence; and (iii) optionally, at least one MHC class II antigen-encoding nucleic acid sequence; (iv) optionally, at least one nucleic acid sequence encoding a GPGPG amino acid linker sequence (SEQ ID NO:56); and (v) optionally, at least one second poly(A) sequence, wherein the second poly(A) sequence is a native poly(A) sequence or an exogenous poly(A) sequence to the alphavirus.

[0011] Also disclosed herein is a composition for delivery of a neoantigen expression system, comprising: the neoantigen expression system, wherein the neoantigen expression system comprises one or more vectors, the one or more vectors comprising: (a) an RNA alphavirus backbone, wherein the RNA alphavirus backbone comprises the nucleic acid sequence set forth in SEQ ID NO:6, wherein the RNA alphavirus backbone sequence comprises a 26S promoter nucleotide sequence and a poly(A) sequence, wherein the 26S promoter sequence is endogenous to the RNA alphavirus backbone, and wherein the poly(A) sequence is endogenous to the RNA alphavirus backbone; and (b) a neoantigen cassette integrated between the 26S promoter nucleotide sequence and the poly(A) sequence , wherein the neoantigen cassette comprises: (i) at least one neoantigen-encoding nucleic acid sequence derived from a tumor present within a subject, comprising: (I) at least 10 tumor-specific and subject-specific MHC class I neoantigen-encoding nucleic acid sequences linearly linked to each other and each comprising: (A) a MHC class I epitope encoding nucleic acid sequence with at least one alteration that makes the encoded peptide sequence distinct from the corresponding peptide sequence encoded by a wild-type nucleic acid sequence, wherein the MHC I epitope encoding nucleic acid sequence encodes a MHC class I epitope 7-15 amino acids in length, (B) a 5' linker sequence, wherein the 5' linker sequence encodes a native N-

2026201462 26 Feb 2026

terminal amino acid sequence of the MHC I epitope, and wherein the 5' linker sequence encodes a peptide that is at least 3 amino acids in length, (C) a 3' linker sequence, wherein the 3' linker sequence encodes a native N-terminal acid sequence of the MHC I epitope, and wherein the 3' linker sequence encodes a peptide that is at least 3 amino acids in length, and wherein the neoantigen cassette is operably linked to the 26S promoter nucleotide sequence, wherein each of the MHC class I neoantigen-encoding nucleic acid sequences encodes a polypeptide that is between 13 and 25 amino acids in length, and wherein each 3' end of each MHC class I neoantigen-encoding nucleic acid sequence is linked to the 5' end of the following MHC class I neoantigen-encoding nucleic acid sequence with the exception of the final MHC class I neoantigen-encoding nucleic acid sequence in the neoantigen cassette; and (ii) at least two MHC class II antigen-encoding nucleic acid sequences comprising: (I) a PADRE MHC class II sequence (SEQ ID NO:48), (II) a Tetanus toxoid MHC class II sequence (SEQ ID NO:46), (III) a first nucleic acid sequence encoding a GPGPG amino acid linker sequence linking the PADRE MHC class II sequence and the Tetanus toxoid MHC class II sequence, (IV) a second nucleic acid sequence encoding a GPGPG amino acid linker sequence linking the 5' end of the at least two MHC class II antigen-encoding nucleic acid sequences to the at least 20 tumor-specific and subject-specific MHC class I neoantigen-encoding nucleic acid sequences, (V) optionally, a third nucleic acid sequence encoding a GPGPG amino acid linker sequence at the 3' end of the at least two MHC class II antigen-encoding nucleic acid sequences.

[0012] In some aspects, an ordered sequence of each element of the neoantigen cassette is described in the formula, from 5' to 3', comprising:

Pa-(L5b-Nc-L3d)X-(G5e-Uf)Y-G3g

[0013] wherein P comprises the second promoter nucleotide sequence, where a = 0 or 1, N comprises one of the MHC class I epitope encoding nucleic acid sequences, where c = 1, L5 comprises the 5' linker sequence, where b = 0 or 1, L3 comprises the 3' linker sequence, where d = 0 or 1, G5 comprises one of the at least one nucleic acid sequences encoding a GPGPG amino acid linker, where e = 0 or 1, G3 comprises one of the at least one nucleic acid sequences encoding a GPGPG amino acid linker, where g = 0 or 1, U comprises one of the at least one MHC class II antigen-encoding nucleic acid sequence, where f = 1, X = 1 to 400, where for each X the corresponding Nc is a epitope encoding nucleic acid sequence, and Y = 0, 1, or 2, where for each Y the corresponding Uf is an antigen-encoding nucleic acid sequence. In some aspects, for each X the corresponding Nc is a distinct MHC class I epitope encoding

2026201462 26 Feb 2026

nucleic acid sequence. In some aspects, for each Y the corresponding Uf is a distinct MHC class II antigen-encoding nucleic acid sequence.

[0014] In some aspects, a = 0, b = 1, d = 1, e = 1, g = 1, h = 1, X = 20, Y = 2, the at least one promoter nucleotide sequence is a single 26S promoter nucleotide sequence provided by the RNA alphavirus backbone, the at least one polyadenylation poly(A) sequence is a poly(A) sequence of at least 100 consecutive A nucleotides provided by the RNA alphavirus backbone, each N encodes a MHC class I epitope 7-15 amino acids in length, L5 is a native 5' linker sequence that encodes a native N-terminal amino acid sequence of the MHC I epitope, and wherein the 5' linker sequence encodes a peptide that is at least 3 amino acids in length, L3 is a native 3' linker sequence that encodes a native nucleic-terminal acid sequence of the MHC I epitope, and wherein the 3' linker sequence encodes a peptide that is at least 3 amino acids in length, U is each of a PADRE class II sequence and a Tetanus toxoid MHC class II sequence, the RNA alphavirus backbone is the sequence set forth in SEQ ID NO:6, and each of the MHC class I neoantigen-encoding nucleic acid sequences encodes a polypeptide that is between 13 and 25 amino acids in length.

[0015] In some aspects, any of the above compositions further comprise a nanoparticulate delivery vehicle. The nanoparticulate delivery vehicle, in some aspects, may be a lipid nanoparticle (LNP). In some aspects, the LNP comprises ionizable amino lipids. In some aspects, the ionizable amino lipids comprise MC3-like (dilinoleylmethyl- 4-dimethylaminobutyrate) molecules. In some aspects, the nanoparticulate delivery vehicle encapsulates the neoantigen expression system.

[0016] In some aspects, any of the above compositions further comprise a plurality of LNPs, wherein the LNPs comprise: the neoantigen expression system; a cationic lipid; a non-cationic lipid; and a conjugated lipid that inhibits aggregation of the LNPs, wherein at least about 95% of the LNPs in the plurality of LNPs either: have a non-lamellar morphology; or are electron-dense.

[0017] In some aspects, the non-cationic lipid is a mixture of (1) a phospholipid and (2) cholesterol or a cholesterol derivative.

[0018] In some aspects, the conjugated lipid that inhibits aggregation of the LNPs is a polyethyleneglycol (PEG)-lipid conjugate. In some aspects, the PEG-lipid conjugate is selected from the group consisting of: a PEG-diacylglycerol (PEG-DAG) conjugate, a PEG dialkyloxypropyl (PEG-DAA) conjugate, a PEG-phospholipid conjugate, a PEG-ceramide (PEG-Cer) conjugate, and a mixture thereof. In some aspects the PEG-DAA conjugate is a

2026201462 26 Feb 2026

member selected from the group consisting of: a PEG-didecyloxypropyl (C_{10}) conjugate, a PEG-dilauryloxypropyl (C_{12}) conjugate, a PEG-dimyristyloxypropyl (C_{14}) conjugate, a PEG-dipalmityloxypropyl (C_{16}) conjugate, a PEG-distearyloxypropyl (C_{18}) conjugate, and a mixture thereof.

[0019] In some aspects, the neoantigen expression system is fully encapsulated in the LNPs.

[0020] In some aspects, the non-lamellar morphology of the LNPs comprises an inverse hexagonal (H_{II}) or cubic phase structure.

[0021] In some aspects, the cationic lipid comprises from about 10 mol % to about 50 mol % of the total lipid present in the LNPs. In some aspects, the cationic lipid comprises from about 20 mol % to about 50 mol % of the total lipid present in the LNPs. In some aspects, the cationic lipid comprises from about 20 mol % to about 40 mol % of the total lipid present in the LNPs.

[0022] In some aspects, the non-cationic lipid comprises from about 10 mol % to about 60 mol % of the total lipid present in the LNPs. In some aspects, the non-cationic lipid comprises from about 20 mol % to about 55 mol % of the total lipid present in the LNPs. In some aspects, the non-cationic lipid comprises from about 25 mol % to about 50 mol % of the total lipid present in the LNPs.

[0023] In some aspects, the conjugated lipid comprises from about 0.5 mol % to about 20 mol % of the total lipid present in the LNPs. In some aspects, the conjugated lipid comprises from about 2 mol % to about 20 mol % of the total lipid present in the LNPs. In some aspects, the conjugated lipid comprises from about 1.5 mol % to about 18 mol % of the total lipid present in the LNPs.

[0024] In some aspects, greater than 95% of the LNPs have a non-lamellar morphology. In some aspects, greater than 95% of the LNPs are electron dense.

[0025] In some aspects, any of the above compositions further comprise a plurality of LNPs, wherein the LNPs comprise: a cationic lipid comprising from 50 mol % to 65 mol % of the total lipid present in the LNPs; a conjugated lipid that inhibits aggregation of LNPs comprising from 0.5 mol % to 2 mol % of the total lipid present in the LNPs; and a non-cationic lipid comprising either: a mixture of a phospholipid and cholesterol or a derivative thereof, wherein the phospholipid comprises from 4 mol % to 10 mol % of the total lipid present in the LNPs and the cholesterol or derivative thereof comprises from 30 mol % to 40 mol % of the total lipid present in the LNPs; a mixture of a phospholipid and cholesterol or a

2026201462 26 Feb 2026

derivative thereof, wherein the phospholipid comprises from 3 mol % to 15 mol % of the total lipid present in the LNPs and the cholesterol or derivative thereof comprises from 30 mol % to 40 mol % of the total lipid present in the LNPs; or up to 49.5 mol % of the total lipid present in the LNPs and comprising a mixture of a phospholipid and cholesterol or a derivative thereof, wherein the cholesterol or derivative thereof comprises from 30 mol % to 40 mol % of the total lipid present in the LNPs.

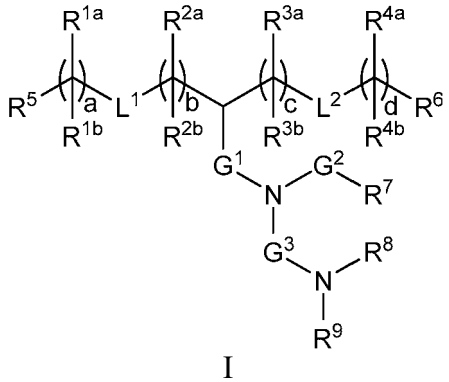
[0026] In some aspects, any of the above compositions further comprise a plurality of LNPs, wherein the LNPs comprise: a cationic lipid comprising from 50 mol % to 85 mol % of the total lipid present in the LNPs; a conjugated lipid that inhibits aggregation of LNPs comprising from 0.5 mol % to 2 mol % of the total lipid present in the LNPs; and a non-cationic lipid comprising from 13 mol % to 49.5 mol % of the total lipid present in the LNPs.

[0027] In some aspects, the phospholipid comprises dipalmitoylphosphatidylcholine (DPPC), distearoylphosphatidylcholine (DSPC), or a mixture thereof.

[0028] In some aspects, the conjugated lipid comprises a polyethyleneglycol (PEG)-lipid conjugate. In some aspects, the PEG-lipid conjugate comprises a PEG-diacylglycerol (PEG-DAG) conjugate, a PEG-dialkyloxypropyl (PEG-DAA) conjugate, or a mixture thereof. In some aspects, the PEG-DAA conjugate comprises a PEG-dimyristyloxypropyl (PEG-DMA) conjugate, a PEG-distearyloxypropyl (PEG-DSA) conjugate, or a mixture thereof. In some aspects, the PEG portion of the conjugate has an average molecular weight of about 2,000 daltons.

[0029] In some aspects, the conjugated lipid comprises from 1 mol % to 2 mol % of the total lipid present in the LNPs.

[0030] In some aspects, the LNP comprises a compound having a structure of Formula I:



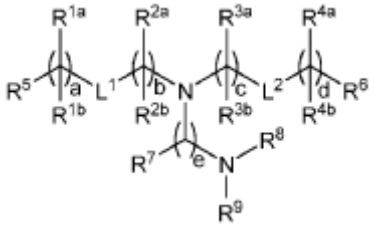
I

or a pharmaceutically acceptable salt, tautomer, prodrug or stereoisomer thereof, wherein:

L^1 and L^2 are each independently -0(C=0)-, -(C=0)0-, -C(=0)-, -0-, -$S(0)_x$-, -S-S-, -C(=0)S-, -SC(=0)-, - R^aC(=0)-, -C(=0) R^a-, - R^aC(=0) R^a-, -OC(=0) R^a-, - R^aC(=0)0- or a direct bond;

G^1 is Ci-C_2 alkylene, - (C=0)-, -0(C=0)-, -SC(=0)-, - R^aC(=0)- or a direct bond: -C(=0)-, -(C=0)0-, -C(=0)S-, -C(=0) R^a- or a direct bond; G is Ci-C_6 alkylene; R^a is H or C1-C12 alkyl; R^{1a} and R^{1b} are, at each occurrence, independently either: (a) H or C_1-C_{12} alkyl; or (b) R^{1a} is H or C_1-C_{12} alkyl, and R^{1b} together with the carbon atom to which it is bound is taken together with an adjacent R^{1b} and the carbon atom to which it is bound to form a carbon-carbon double bond; R^{2a} and R^{2b} are, at each occurrence, independently either: (a) H or C_1-C_{12} alkyl; or (b) R^{2a} is H or C_1-C_{12} alkyl, and R^{2b} together with the carbon atom to which it is bound is taken together with an adjacent R^{2b} and the carbon atom to which it is bound to form a carbon-carbon double bond; R^{3a} and R^{3b} are, at each occurrence, independently either (a): H or C_1-C_{12} alkyl; or (b) R^{3a} is H or C_1-C_{12} alkyl, and R^{3b} together with the carbon atom to which it is bound is taken together with an adjacent R and the carbon atom to which it is bound to form a carbon-carbon double bond; R^{4a} and R^{4b} are, at each occurrence, independently either: (a) H or C1-C12 alkyl; or (b) R^{4a} is H or C1-C12 alkyl, and R^{4b} together with the carbon atom to which it is bound is taken together with an adjacent R^{4b} and the carbon atom to which it is bound to form a carbon-carbon double bond; R^5 and R^6 are each independently H or methyl; R^7 is C4-C20 alkyl; R^8 and R^9 are each independently C1-C12 alkyl; or R^8 and R^9, together with the nitrogen atom to which they are attached, form a 5, 6 or 7-membered heterocyclic ring; a, b, c and d are each independently an integer from 1 to 24; and x is 0, 1 or 2.

[0031] In some aspects, the LNP comprises a compound having a structure of Formula II:



II

or a pharmaceutically acceptable salt, tautomer, prodrug or stereoisomer thereof, wherein: L^1 and L^2 are each independently -0(C=0)-, -(C=0)0- or a carbon-carbon double bond; R^{1a} and R^{1b} are, at each occurrence, independently either (a) H or C_1-C_{12} alkyl, or (b) R^{1a} is H or C_1-C_{12} alkyl, and R^{1b} together with the carbon atom to which it is bound is taken together with an adjacent R^{1b} and the carbon atom to which it is bound to form a carbon-carbon double bond; R^{2a} and R^{2b} are, at each occurrence, independently either (a) H or C_1-C_{12} alkyl, or (b) R^{2a} is H or C_1-C_{12} alkyl, and R^{2b} together with the carbon atom to which it is bound is taken together with an adjacent R^{2b} and the carbon atom to which it is bound to form a carbon-carbon double

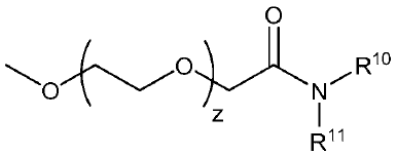
bond; R^{3a} and R^{3b} are, at each occurrence, independently either (a) H or C_1-C_{12} alkyl, or (b) R^{3a} is H or C_1-C_{12} alkyl, and R^{3b} together with the carbon atom to which it is bound is taken together with an adjacent R^{3b} and the carbon atom to which it is bound to form a carbon-carbon double bond; R^{4a} and R^{4b} are, at each occurrence, independently either (a) H or C_1-C_{12} alkyl, or (b) R^{4a} is H or C_1-C_{12} alkyl, and R^{4b} together with the carbon atom to which it is bound is taken together with an adjacent R^{4b} and the carbon atom to which it is bound to form a carbon-carbon double bond; R^5 and R^6 are each independently methyl or cycloalkyl; R^7 is, at each occurrence, independently H or C_1-C_{12} alkyl; R^8 and R^9 are each independently unsubstituted C1-C12 alkyl; or R^8 and R^9, together with the nitrogen atom to which they are attached, form a 5, 6 or 7-membered heterocyclic ring comprising one nitrogen atom; a and d are each independently an integer from 0 to 24; b and c are each independently an integer from 1 to 24; and e is 1 or 2, provided that: at least one of R^{la}, R^{2a}, R^{3a} or R^{4a} is C1-C12 alkyl, or at least one of L^1 or L^2 is -0(C=0)- or -(C=0)0-; and R^{la} and R^{lb} are not isopropyl when a is 6 or n-butyl when a is 8.

[0032] In some aspects, any of the above compositions further comprise one or more excipients comprising a neutral lipid, a steroid, and a polymer conjugated lipid. In some aspects, the neutral lipid comprises at least one of l,2-Distearoyl-*sn*-glycero-3-phosphocholine (DSPC), l,2-Dipalmitoyl-*sn*-glycero-3-phosphocholine (DPPC), l,2-Dimyristoyl-*sn*-glycero-3-phosphocholine (DMPC), 1-Palmitoyl-2-oleoyl-*sn*-glycero-3-phosphocholine (POPC), 1,2-dioleoyl-*sn*-glycero-3-phosphocholine (DOPC), and l,2-Dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE). In some aspects, the neutral lipid is DSPC.

[0033] In some aspects, the molar ratio of the compound to the neutral lipid ranges from about 2:1 to about 8:1.

[0034] In some aspects, the steroid is cholesterol. In some aspects, the molar ratio of the compound to cholesterol ranges from about 2:1 to 1:1.

[0035] In some aspects, the polymer conjugated lipid is a pegylated lipid. In some aspects, the molar ratio of the compound to the pegylated lipid ranges from about 100:1 to about 25:1. In some aspects, the pegylated lipid is PEG-DAG, a PEG polyethylene (PEG-PE), a PEG-succinoyl-diacylglycerol (PEG-S-DAG), PEG-cer or a PEG dialkyoxypropylcarbamate. In some aspects, the pegylated lipid has the following structure III:



III

2026201462 26 Feb 2026

or a pharmaceutically acceptable salt, tautomer or stereoisomer thereof, wherein: R^{10} and R^{11} are each independently a straight or branched, saturated or unsaturated alkyl chain containing from 10 to 30 carbon atoms, wherein the alkyl chain is optionally interrupted by one or more ester bonds; and z has a mean value ranging from 30 to 60. In some aspects, R^{10} and R^{11} are each independently straight, saturated alkyl chains having 12 to 16 carbon atoms. In some aspects, the average z is about 45.

start here

[0036] In some aspects, the LNP self-assembles into non-bilayer structures when mixed with polyanionic nucleic acid. In some aspects, the non-bilayer structures have a diameter between 60nm and 120nm. In some aspects, the non-bilayer structures have a diameter of about 70nm, about 80nm, about 90nm, or about 100nm. In some aspects, wherein the nanoparticulate delivery vehicle has a diameter of about 100nm.

[0037] In some aspects, the neoantigen cassette is integrated between the at least one promoter nucleotide sequence and the at least one poly(A) sequence. In some aspects, the at least one promoter nucleotide sequence is operably linked to the neoantigen-encoding nucleic acid sequence.

[0038] In some aspects, the one or more vectors comprise one or more +-stranded RNA vectors. In some aspects, the one or more +-stranded RNA vectors comprise a 5' 7-methylguanosine (m7g) cap. In some aspects, the one or more +-stranded RNA vectors are produced by *in vitro* transcription. In some aspects, the one or more vectors are self-replicating within a mammalian cell.

[0039] In some aspects, the RNA alphavirus backbone comprises at least one nucleotide sequence of an Aura virus, a Fort Morgan virus, a Venezuelan equine encephalitis virus, a Ross River virus, a Semliki Forest virus, a Sindbis virus, or a Mayaro virus. In some aspects, the RNA alphavirus backbone comprises at least one nucleotide sequence of a Venezuelan equine encephalitis virus. In some aspects, the RNA alphavirus backbone comprises at least sequences for nonstructural protein-mediated amplification, a 26S promoter sequence, a poly(A) sequence, a nonstructural protein 1 (nsP1) gene, a nsP2 gene, a nsP3 gene, and a nsP4 gene encoded by the nucleotide sequence of the Aura virus, the Fort Morgan virus, the Venezuelan equine encephalitis virus, the Ross River virus, the Semliki Forest virus, the Sindbis virus, or the Mayaro virus. In some aspects, the RNA alphavirus backbone comprises at least sequences for nonstructural protein-mediated amplification, a 26S promoter sequence, and a poly(A) sequence encoded by the nucleotide sequence of the Aura virus, the Fort Morgan virus, the

2026201462 26 Feb 2026

Venezuelan equine encephalitis virus, the Ross River virus, the Semliki Forest virus, the Sindbis virus, or the Mayaro virus. In some aspects, sequences for nonstructural protein-mediated amplification are selected from the group consisting of: an alphavirus 5' UTR, a 51-nt CSE, a 24-nt CSE, a 26S subgenomic promoter sequence, a 19-nt CSE, an alphavirus 3' UTR, or combinations thereof.

[0040] In some aspects, the RNA alphavirus backbone does not encode structural virion proteins capsid, E2 and E1. In some aspects, the neoantigen cassette is inserted in place of the structural virion proteins within the nucleotide sequence of the Aura virus, the Fort Morgan virus, the Venezuelan equine encephalitis virus, the Ross River virus, the Semliki Forest virus, the Sindbis virus, or the Mayaro virus.

[0041] In some aspects, the Venezuelan equine encephalitis virus (VEE) comprises the strain TC-83. In some aspects, the Venezuelan equine encephalitis virus comprises the sequence set forth in SEQ ID NO:3 or SEQ ID NO:5. In some aspects, the Venezuelan equine encephalitis virus comprises the sequence of SEQ ID NO:3 or SEQ ID NO:5 further comprising a deletion between base pair 7544 and 11175. In some aspects, the RNA alphavirus backbone is the sequence set forth in SEQ ID NO:6 or SEQ ID NO:7**.** In some aspects, the neoantigen cassette is inserted to replace the deletion between base pair 7544 and 11175 set forth in the sequence of SEQ ID NO:3 or SEQ ID NO:5.

[0042] In some aspects, the insertion of the neoantigen cassette provides for transcription of a polycistronic RNA comprising the nsP1-4 genes and the at least one of antigen-encoding nucleic acid sequences, wherein the nsP1-4 genes and the at least one of antigen-encoding nucleic acid sequences are in separate open reading frames.

[0043] In some aspects, the at least one promoter nucleotide sequence is the native 26S promoter nucleotide sequence encoded by the RNA alphavirus backbone. In some aspects, the at least one promoter nucleotide sequence is an exogenous RNA promoter. In some aspects, the second promoter nucleotide sequence is a 26S promoter nucleotide sequence. In some aspects, the second promoter nucleotide sequence comprises multiple 26S promoter nucleotide sequences, wherein each 26S promoter nucleotide sequence provides for transcription of one or more of the separate open reading frames.

[0044] In some aspects, the one or more neoantigen expression vectors are each at least 300nt in size. In some aspects, the one or more neoantigen expression vectors are each at least 1kb in size. In some aspects, the one or more neoantigen expression vectors are each 2kb in

2026201462 26 Feb 2026

size. In some aspects, the one or more neoantigen expression vectors are each less than 5kb in size.

[0045] In some aspects, at least one of the at least one neoantigen-encoding nucleic acid sequences encodes a polypeptide sequence or portion thereof that is presented by MHC class I on the tumor cell. In some aspects, each antigen-encoding nucleic acid sequence is linked directly to one another. In some aspects, at least one of the at least one antigen-encoding nucleic acid sequences is linked to a distinct antigen-encoding nucleic acid sequence with a nucleic acid sequence encoding a linker. In some aspects, the linker links two MHC class I sequences or an MHC class I sequence to an MHC class II sequence. In some aspects, the linker is selected from the group consisting of: (1) consecutive glycine residues, at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 residues in length; (2) consecutive alanine residues, at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 residues in length; (3) two arginine residues (RR); (4) alanine, alanine, tyrosine (AAY); (5) a consensus sequence at least 2, 3, 4, 5, 6, 7, 8 , 9, or 10 amino acid residues in length that is processed efficiently by a mammalian proteasome; and (6) one or more native sequences flanking the antigen derived from the cognate protein of origin and that is at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 2-20 amino acid residues in length. In some aspects, the linker links two MHC class II sequences or an MHC class II sequence to an MHC class I sequence. In some aspects, the linker comprises the sequence GPGPG.

[0046] In some aspects, at least one sequence of the at least one antigen-encoding nucleic acid sequences is linked, operably or directly, to a separate or contiguous sequence that enhances the expression, stability, cell trafficking, processing and presentation, and/or immunogenicity of the at least one antigen-encoding nucleic acid sequences. In some aspects, the separate or contiguous sequence comprises at least one of: a ubiquitin sequence, a ubiquitin sequence modified to increase proteasome targeting (e.g., the ubiquitin sequence contains a Gly to Ala substitution at position 76), an immunoglobulin signal sequence (e.g., IgK), a major histocompatibility class I sequence, lysosomal-associated membrane protein (LAMP)-1, human dendritic cell lysosomal-associated membrane protein, and a major histocompatibility class II sequence; optionally wherein the ubiquitin sequence modified to increase proteasome targeting is A76.

[0047] In some aspects, at least one of the at least one neoantigen-encoding nucleic acid sequences encodes a polypeptide sequence or portion thereof that has increased binding affinity to its corresponding MHC allele relative to the translated, corresponding wild-type, nucleic

2026201462 26 Feb 2026

acid sequence. In some aspects, at least one of the at least one neoantigen-encoding nucleic acid sequences in the plurality encodes a polypeptide sequence or portion thereof that has increased binding stability to its corresponding MHC allele relative to the translated, corresponding wild-type, nucleic acid sequence. In some aspects, at least one of the at least one neoantigen-encoding nucleic acid sequences in the plurality encodes a polypeptide sequence or portion thereof that has an increased likelihood of presentation on its corresponding MHC allele relative to the translated, corresponding wild-type, nucleic acid sequence.

[0048] In some aspects, at least one mutation comprises a point mutation, a frameshift mutation, a non-frameshift mutation, a deletion mutation, an insertion mutation, a splice variant, a genomic rearrangement, or a proteasome-generated spliced antigen.

[0049] In some aspects, the tumor is selected from the group consisting of: lung cancer, melanoma, breast cancer, ovarian cancer, prostate cancer, kidney cancer, gastric cancer, colon cancer, testicular cancer, head and neck cancer, pancreatic cancer, bladder cancer, brain cancer, B-cell lymphoma, acute myelogenous leukemia, adult acute lymphoblastic leukemia, chronic myelogenous leukemia, chronic lymphocytic leukemia, T cell lymphocytic leukemia, non-small cell lung cancer, and small cell lung cancer.

[0050] In some aspects, the at least one neoantigen-encoding nucleic acid sequence comprises at least 2-10, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleic acid sequences. In some aspects, the at least one neoantigen-encoding nucleic acid sequence comprises at least 11-20, 15-20, 11-100, 11-200, 11-300, 11-400, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or up to 400 nucleic acid sequences.

[0051] In some aspects, the at least one neoantigen-encoding nucleic acid sequence comprises at least 2-400 nucleic acid sequences and wherein at least two of the neoantigen-encoding nucleic acid sequences encode polypeptide sequences or portions thereof that are presented by MHC class I on the tumor cell surface. In some aspects, at least two of the neoantigen-encoding nucleic acid sequences encode polypeptide sequences or portions thereof that are presented by MHC class I on the tumor cell surface. In some aspects, when administered to the subject and translated, at least one of the neoantigens enocoded by the at least one neoantigen-encoding nucleic acid sequence are presented on antigen presenting cells resulting in an immune response targeting at least one of the neoantigens on the tumor cell surface. In some aspects, the at least one neoantigen-encoding nucleic acid sequences when administered to the subject and translated, at least one of the MHC class I or class II

2026201462 26 Feb 2026

neoantigens are presented on antigen presenting cells resulting in an immune response targeting at least one of the neoantigens on the tumor cell surface, and optionally wherein the expression of each of the at least one neoantigen-encoding nucleic acid sequences is driven by the at least one promoter nucleotide sequence.

[0052] In some aspects, each MHC class I neoantigen-encoding nucleic acid sequence encodes a polypeptide sequence between 8 and 35 amino acids in length, optionally 9-17, 9-25, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34 or 35 amino acids in length.

[0053] In some aspects, at least one MHC class II antigen-encoding nucleic acid sequence is present. In some aspects, at least one MHC class II antigen-encoding nucleic acid sequence is present and comprises at least one MHC class II neoantigen-encoding nucleic acid sequence that comprises at least one mutation that makes it distinct from the corresponding wild-type, parental nucleic acid sequence. In some aspects, the at least one MHC class II antigen-encoding nucleic acid sequence is 12-20, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 20-40 amino acids in length. In some aspects, the at least one MHC class II antigen-encoding nucleic acid sequence is present and comprises at least one universal MHC class II antigen-encoding nucleic acid sequence, optionally wherein the at least one universal sequence comprises at least one of Tetanus toxoid and PADRE.

[0054] In some aspects, the at least one promoter nucleotide sequence or the second promoter nucleotide sequence is inducible. In some aspects, the at least one promoter nucleotide sequence or the second promoter nucleotide sequence is non-inducible.

[0055] In some aspects, the at least one poly(A) sequence comprises a poly(A) sequence native to the alphavirus. In some aspects, the at least one poly(A) sequence comprises a poly(A) sequence exogenous to the alphavirus. In some aspects, the at least one poly(A) sequence is operably linked to at least one of the at least one antigen-encoding nucleic acid sequences. In some aspects, the at least one poly(A) sequence is at least 20 , at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, or at least 90 consecutive A nucleotides. In some aspects, the at least one poly(A) sequence is at least 100 consecutive A nucleotides.

[0056] In some aspects, the neoantigen cassette further comprises at least one of: an intron sequence, a woodchuck hepatitis virus posttranscriptional regulatory element (WPRE) sequence, an internal ribosome entry sequence (IRES) sequence, a nucleotide sequence encoding a 2A self cleaving peptide sequence, a nucleotide sequence encoding a Furin cleavage site, or a sequence in the 5’ or 3’ non-coding region known to enhance the nuclear export,

2026201462 26 Feb 2026

stability, or translation efficiency of mRNA that is operably linked to at least one of the at least one antigen-encoding nucleic acid sequences.

[0057] In some aspects, the neoantigen cassette further comprises a reporter gene, including but not limited to, green fluorescent protein (GFP), a GFP variant, secreted alkaline phosphatase, luciferase, a luciferase variant, or a detectable peptide or epitope. In some aspects, the detectable peptide or epitope is selected from the group consisting of an HA tag, a Flag tag, a His-tag, or a V5 tag.

[0058] In some aspects, the one or more vectors further comprise one or more nucleic acid sequences encoding at least one immune modulator. In some aspects, the immune modulator is an anti-CTLA4 antibody or an antigen-binding fragment thereof, an anti-PD-1 antibody or an antigen-binding fragment thereof, an anti-PD-L1 antibody or an antigen-binding fragment thereof, an anti-4-1BB antibody or an antigen-binding fragment thereof, or an anti-OX-40 antibody or an antigen-binding fragment thereof. In some aspects, the antibody or antigen-binding fragment thereof is a Fab fragment, a Fab' fragment, a single chain Fv (scFv), a single domain antibody (sdAb) either as single specific or multiple specificities linked together (e.g., camelid antibody domains), or full-length single-chain antibody (e.g., full-length IgG with heavy and light chains linked by a flexible linker). In some aspects, the heavy and light chain sequences of the antibody are a contiguous sequence separated by either a self-cleaving sequence such as 2A or IRES; or the heavy and light chain sequences of the antibody are linked by a flexible linker such as consecutive glycine residues.

[0059] In some aspects, the immune modulator is a cytokine. In some aspects, the cytokine is at least one of IL-2, IL-7, IL-12, IL-15, or IL-21 or variants thereof of each.

[0060] Also, disclosed herein is an adenovirus vector comprising a neoantigen cassette, the neoantigen cassette comprising: a plurality of antigen-encoding nucleic acid sequences derived from a tumor present within a subject, the plurality comprising: at least two MHC class I neoantigen-encoding nucleic acid sequences each comprising at least one alteration that makes it distinct from the corresponding wild-type, parental nucleic acid sequence, and optionally, at least one MHC class II antigen-encoding nucleic acid sequence; and at least one promoter sequence operably linked to at least one sequence of the plurality.

[0061] In some aspects, the adenovirus vector is a chimpanzee adenovirus (ChAd) vector, optionally a C68 vector. In some aspects, the adenovirus vector comprises the sequence set forth in SEQ ID NO:1. In some aspects, the adenovirus vector comprises the sequence set forth in SEQ ID NO:1, except that the sequence is fully deleted or functionally deleted in at least one

2026201462 26 Feb 2026

gene selected from the group consisting of the chimpanzee adenovirus E1A, E1B, E2A, E2B, E3, E4, L1, L2, L3, L4, and L5 genes of the sequence set forth in SEQ ID NO: 1, optionally wherein the sequence is fully deleted or functionally deleted in: (1) E1A and E1B; (2) E1A, E1B, and E3; or (3) E1A, E1B, E3, and E4 of the sequence set forth in SEQ ID NO: 1. In some aspects, the adenovirus vector comprises a gene or regulatory sequence obtained from the sequence of SEQ ID NO: 1, optionally wherein the gene is selected from the group consisting of the chimpanzee adenovirus inverted terminal repeat (ITR), E1A, E1B, E2A, E2B, E3, E4, L1, L2, L3, L4, and L5 genes of the sequence set forth in SEQ ID NO: 1.

[0062] In some aspects, the neoantigen cassette is inserted in the adenovirus vector at the E1 region, E3 region, and/or any deleted AdV region that allows incorporation of the neoantigen cassette.

[0063] In some aspects, the at least one promoter sequence of the adenovirus vector is inducible. In some aspects, the at least one promoter sequence of the adenovirus vector is non-inducible. In some aspects, the at least one promoter sequence of the adenovirus vector is a CMV, SV40, EF-1, RSV, PGK, or EBV promoter sequence.

[0064] In some aspects, the neoantigen cassette of the adenovirus vector further comprises at least one polyA sequence operably linked to at least one of the sequences in the plurality, optionally wherein the polyA sequence is located 3' of the at least one sequence in the plurality.

[0065] In some aspects, the adenovirus vector is generated from one of a first generation, a second generation, or a helper-dependent adenoviral vector.

[0066] In some aspects, the adenovirus vector comprises one or more deletions between base pair number 577 and 3407 and optionally wherein the adenovirus vector further comprises one or more deletions between base pair 27,141 and 32,022 or between base pair 27,816 and 31,332 of the sequence set forth in SEQ ID NO:1. In some aspects, the adenovirus vector further comprises one or more deletions between base pair number 3957 and 10346, base pair number 21787 and 23370, and base pair number 33486 and 36193 of the sequence set forth in SEQ ID NO:1.

[0067] In some aspects, the at least one MHC class I neoantigen-encoding nucleic acid sequence is selected by performing the steps of: (a) obtaining at least one of exome, transcriptome, or whole genome tumor nucleotide sequencing data from the tumor, wherein the tumor nucleotide sequencing data is used to obtain data representing peptide sequences of each of a set of neoantigens; (b) inputting the peptide sequence of each neoantigen into a

2026201462 26 Feb 2026

presentation model to generate a set of numerical likelihoods that each of the neoantigens is presented by one or more of the MHC alleles on the tumor cell surface of the tumor, the set of numerical likelihoods having been identified at least based on received mass spectrometry data; and (c) selecting a subset of the set of neoantigens based on the set of numerical likelihoods to generate a set of selected neoantigens which are used to generate the at least one MHC class I neoantigen-encoding nucleic acid sequence.

[0068] In some aspects, each of the at least one MHC class I neoantigen-encoding nucleic acid sequence is selected by performing the steps of: (a) obtaining at least one of exome, transcriptome, or whole genome tumor nucleotide sequencing data from the tumor, wherein the tumor nucleotide sequencing data is used to obtain data representing peptide sequences of each of a set of neoantigens; (b) inputting the peptide sequence of each neoantigen into a presentation model to generate a set of numerical likelihoods that each of the neoantigens is presented by one or more of the MHC alleles on the tumor cell surface of the tumor, the set of numerical likelihoods having been identified at least based on received mass spectrometry data; and (c) selecting a subset of the set of neoantigens based on the set of numerical likelihoods to generate a set of selected neoantigens which are used to generate the at least one MHC class I neoantigen-encoding nucleic acid sequence.

[0069] In some aspects, a number of the set of selected neoantigens is 2-20.

[0070] In some aspects, the presentation model represents dependence between: presence of a pair of a particular one of the MHC alleles and a particular amino acid at a particular position of a peptide sequence; and likelihood of presentation on the tumor cell surface, by the particular one of the MHC alleles of the pair, of such a peptide sequence comprising the particular amino acid at the particular position.

[0071] In some aspects, selecting the set of selected neoantigens comprises selecting neoantigens that have an increased likelihood of being presented on the tumor cell surface relative to unselected neoantigens based on the presentation model. In some aspects, selecting the set of selected neoantigens comprises selecting neoantigens that have an increased likelihood of being capable of inducing a tumor-specific immune response in the subject relative to unselected neoantigens based on the presentation model. In some aspects, selecting the set of selected neoantigens comprises selecting neoantigens that have an increased likelihood of being capable of being presented to naïve T cells by professional antigen presenting cells (APCs) relative to unselected neoantigens based on the presentation model, optionally wherein the APC is a dendritic cell (DC). In some aspects, selecting the set of

2026201462 26 Feb 2026

selected neoantigens comprises selecting neoantigens that have a decreased likelihood of being subject to inhibition via central or peripheral tolerance relative to unselected neoantigens based on the presentation model. In some aspects, selecting the set of selected neoantigens comprises selecting neoantigens that have a decreased likelihood of being capable of inducing an autoimmune response to normal tissue in the subject relative to unselected neoantigens based on the presentation model. In some aspects, exome or transcriptome nucleotide sequencing data is obtained by performing sequencing on the tumor tissue. In some aspects, the sequencing is next generation sequencing (NGS) or any massively parallel sequencing approach.

[0072] In some aspects, the neoantigen cassette comprises junctional epitope sequences formed by adjacent sequences in the neoantigen cassette. In some aspects, at least one or each junctional epitope sequence has an affinity of greater than 500 nM for MHC. In some aspects, each junctional epitope sequence is non-self. In some aspects, the neoantigen cassette does not encode a non-therapeutic MHC class I or class II epitope nucleic acid sequence comprising a translated, wild-type nucleic acid sequence, wherein the non-therapeutic epitope is predicted to be displayed on an MHC allele of the subject. In some aspects, the non-therapeutic predicted MHC class I or class II epitope sequence is a junctional epitope sequence formed by adjacent sequences in the neoantigen cassette. In some aspects, the prediction is based on presentation likelihoods generated by inputting sequences of the non-therapeutic epitopes into a presentation model. In some aspects, an order of the at least one antigen-encoding nucleic acid sequences in the neoantigen cassette is determined by a series of steps comprising: (a) generating a set of candidate neoantigen cassette sequences corresponding to different orders of the at least one antigen-encoding nucleic acid sequences; (b) determining, for each candidate neoantigen cassette sequence, a presentation score based on presentation of non-therapeutic epitopes in the candidate neoantigen cassette sequence; and (c) selecting a candidate cassette sequence associated with a presentation score below a predetermined threshold as the neoantigen cassette sequence for a neoantigen vaccine.

[0073] Also disclosed herein is a pharmaceutical composition comprising any of the compositions disclosed herein (such as an alphavirus-based or ChAd-based vector disclosed herein) and a pharmaceutically acceptable carrier. In some aspects, the pharmaceutical composition further comprises an adjuvant. In some aspects, the pharmaceutical composition further comprises an immune modulator. In some aspects, the immune modulator is an anti-CTLA4 antibody or an antigen-binding fragment thereof, an anti-PD-1 antibody or an antigen-binding fragment thereof, an anti-PD-L1 antibody or an antigen-binding fragment thereof, an

2026201462 26 Feb 2026

anti-4-1BB antibody or an antigen-binding fragment thereof, or an anti-OX-40 antibody or an antigen-binding fragment thereof.

[0074] Also disclosed herein is an isolated nucleotide sequence or set of isolated nucleotide sequences comprising the neoantigen cassette of any of the above composition claims and one or more elements obtained from the sequence of SEQ ID NO:3 or SEQ ID NO:5,optionally wherein the one or more elements are selected from the group consisting of the sequences necessary for nonstructural protein-mediated amplification, the 26S promoter nucleotide sequence, the poly(A) sequence, and the nsP1-4 genes of the sequence set forth in SEQ ID NO:3 or SEQ ID NO:5,and optionally wherein the nucleotide sequence is cDNA. In some aspects, the sequence or set of isolated nucleotide sequences comprises a neoantigen cassette disclosed herein inserted at position 7544 of the sequence set forth in SEQ ID NO:6 or SEQ ID NO:7.. In some aspects, the isolated nucleotide sequence further comprises a T7 or SP6 RNA polymerase promoter nucleotide sequence 5' of the one or more elements obtained from the sequence of SEQ ID NO:3 or SEQ ID NO:5, and optionally one or more restriction sites 3' of the poly(A) sequence. In some aspects, the the neoantigen cassette disclosed herein is inserted at position 7563 of SEQ ID NO:8 or SEQ ID NO:9. In another aspect, the sequences set forth in SEQ ID NO:8 or SEQ ID NO:9 further comprise an additional adenine nucleotide inserted at position 17.

[0075] Also disclosed herein is an isolated nucleotide sequence comprising a neoantigen cassette disclosed herein and at least one promoter disclosed herein. In some aspects, the isolated nucleotide sequence further comprises a ChAd-based gene. In some aspects, the ChAd-based gene is obtained from the sequence of SEQ ID NO: 1, optionally wherein the gene is selected from the group consisting of the chimpanzee adenovirus ITR, E1A, E1B, E2A, E2B, E3, E4, L1, L2, L3, L4, and L5 genes of the sequence set forth in SEQ ID NO: 1, and optionally wherein the nucleotide sequence is cDNA.

[0076] Also disclosed herein is an isolated cell comprising an isolated nucleotide sequence disclosed herein, optionally wherein the cell is a BHK-21, CHO, HEK293 or variants thereof, 911, HeLa, A549, LP-293, PER.C6, or AE1-2a cell.

[0077] Also disclosed herein is a vector comprising an isolated nucleotide sequence disclosed herein.

[0078] Also disclosed herein is a kit comprising a vector or a composition disclosed herein and instructions for use.

2026201462 26 Feb 2026

[0079] Also disclosed herein is a method for treating a subject with cancer, the method comprising administering to the subject a vector disclosed herein or a pharmaceutical composition disclosed herein. In some aspects, the at least one MHC class I neoantigen-encoding nucleic acid sequence derived from a tumor are derived from the tumor of the subject with cancer. In some aspects, the at least one MHC class I neoantigen-encoding nucleic acid sequence are not derived from the tumor of the subject with cancer.

[0080] Also disclosed herein is a method for inducing an immune response in a subject, the method comprising administering to the subject any of the compositions, vectors, or pharmaceutical compositions described herein.

[0081] In some aspects, the vector or composition is administered intramuscularly (IM), intradermally (ID), or subcutaneously (SC), or intravenously (IV).

[0082] In some aspects, the methods described herein further comprise administration of one or more immune modulators, optionally wherein the immune modulator is administered before, concurrently with, or after administration of the composition or pharmaceutical composition. In some aspects, the one or more immune modulators are selected from the group consisting of: an anti-CTLA4 antibody or an antigen-binding fragment thereof, an anti-PD-1 antibody or an antigen-binding fragment thereof, an anti-PD-L1 antibody or an antigen-binding fragment thereof, an anti-4-1BB antibody or an antigen-binding fragment thereof, or an anti-OX-40 antibody or an antigen-binding fragment thereof. In some aspects, the immune modulator is administered intravenously (IV), intramuscularly (IM), intradermally (ID), or subcutaneously (SC). In some aspects, the subcutaneous administration is near the site of the composition or pharmaceutical composition administration or in close proximity to one or more vector or composition draining lymph nodes.

[0083] In some aspects, the methods described herein further comprise administering to the subject a second vaccine composition. In some aspects, the second vaccine composition is administered prior to the administration of the composition or the pharmaceutical composition described above. In some aspects, the second vaccine composition is administered subsequent to the administration of the composition or the pharmaceutical compositions described above. In some aspects, the second vaccine composition is the same as the composition or the pharmaceutical compositions described above. In some aspects, the second vaccine composition is different from the composition or the pharmaceutical compositions described above. In some aspects, the second vaccine composition comprises a chimpanzee adenovirus vector encoding at least one antigen-encoding nucleic acid sequence. In some aspects, the at

2026201462 26 Feb 2026

least one antigen-encoding nucleic acid sequence encoded by the chimpanzee adenovirus vector is the same as the at least one antigen-encoding nucleic acid sequence of any of the above compositions or vectors.

[0084] Also disclosed herein is a method of manufacturing the one or more vectors of any of the above compositions, the method comprising: obtaining a linearized DNA sequence comprising the RNA alphavirus backbone and the neoantigen cassette; *in vitro* transcribing the linearized DNA sequence by addition of the linearized DNA sequence to a *in vitro* transcription reaction containing all the necessary components to trancribe the linearized DNA sequence into RNA, optionally further comprising *in vitro* addition of the m7g cap to the resulting RNA; and isolating the one or more vectors from the *in vitro* transcription reaction. In some aspects, the linearized DNA sequence is generated by linearizing a DNA plasmid sequence or by amplification using PCR. In some aspects, the DNA plasmid sequence is generated using one of bacterial recombination or full genome DNA synthesis or full genome DNA synthesis with amplification of synthesized DNA in bacterial cells. In some aspects, the isolating the one or more vectors from the *in vitro* transcription reaction involves one or more of phenol chloroform extraction, silica column based purification, or similar RNA purification methods.

[0085] Also disclosed herein is a method of manufacturing any of the compositions disclosed herein, the method comprising: providing components for the nanoparticulate delivery vehicle; providing the neoantigen expression system; and providing conditions sufficient for the nanoparticulate delivery vehicle and the neoantigen expression system to produce the composition for delivery of the neoantigen expression system. In some aspects, the conditions are provided by microfluidic mixing.

[0086] Also disclosed herein is a method of manufacturing a adenovirus vector disclosed herein, the method comprising: obtaining a plasmid sequence comprising the at least one promoter sequence and the neoantigen cassette; transfecting the plasmid sequence into one or more host cells; and isolating the adenovirus vector from the one or more host cells.

[0087] In some aspects, isolating comprises: lysing the host cell to obtain a cell lysate comprising the adenovirus vector; and purifying the adenovirus vector from the cell lysate.

[0088] In some aspects, the plasmid sequence is generated using one of bacterial recombination or full genome DNA synthesis or full genome DNA synthesis with amplification of synthesized DNA in bacterial cells. In some aspects, the one or more host cells are at least one of CHO, HEK293 or variants thereof, 911, HeLa, A549, LP-293, PER.C6, and AE1-2a

2026201462 26 Feb 2026

cells. In some aspects, purifying the adenovirus vector from the cell lysate involves one or more of chromatographic separation, centrifugation, virus precipitation, and filtration.

BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWINGS

[0089] These and other features, aspects, and advantages of the present invention will become better understood with regard to the following description, and accompanying drawings, where:

[0090] **Figure (FIG.) 1A** shows current clinical approaches to neoantigen identification.

[0091] **FIG. 1B** shows that <5% of predicted bound peptides are presented on tumor cells.

[0092] **FIG. 1C** shows the impact of the neoantigen prediction specificity problem.

[0093] **FIG. 1D** shows that binding prediction is not sufficient for neoantigen identification.

[0094] **FIG. 1E** shows probability of MHC-I presentation as a function of peptide length.

[0095] **FIG. 1F** shows an example peptide spectrum generated from Promega's dynamic range standard.

[0096] **FIG. 1G** shows how the addition of features increases the model positive predictive value.

[0097] **FIG. 2A** is an overview of an environment for identifying likelihoods of peptide presentation in patients, in accordance with an embodiment.

[0098] **FIG. 2B** and **FIG. 2C** illustrate a method of obtaining presentation information, in accordance with an embodiment.

[0099] **FIG. 3** is a high-level block diagram illustrating the computer logic components of the presentation identification system, according to one embodiment.

[00100] **FIG. 4A** illustrates an example set of training data, according to one embodiment related to MHC class I alleles. **FIG. 4B** illustrates an example set of training data, according to one embodiment related to an MHC class II allele.

[00101] **FIG. 5** illustrates an example network model in association with an MHC allele.

[00102] **FIG. 6A** illustrates an example network model NNH(·) shared by MHC alleles, according to one embodiment. **FIG. 6B** illustrates an example network model $NN_H(\cdot)$ shared by MHC alleles, according to another embodiment.

[00103] **FIG. 7** illustrates generating a presentation likelihood for a peptide in association with an MHC allele using an example network model.

2026201462 26 Feb 2026

[00104] **FIG. 8** illustrates generating a presentation likelihood for a peptide in association with a MHC allele using example network models.

[00105] **FIG. 9** illustrates generating a presentation likelihood for a peptide in association with MHC alleles using example network models.

[00106] **FIG. 10** illustrates generating a presentation likelihood for a peptide in association with MHC alleles using example network models.

[00107] **FIG. 11** illustrates generating a presentation likelihood for a peptide in association with MHC alleles using example network models.

[00108] **FIG. 12** illustrates generating a presentation likelihood for a peptide in association with MHC alleles using example network models.

[00109] **FIG. 13A** shows performance results for peptide presentation determined by mass-spectrometry comparing various peptide presentation models. Shown are result for the maximum of per-alleles presentation model shown in equation (12) using the affine dependency function $g_h(\cdot)$ and the expit function $f(\cdot)$ and trained on a subset of mass spectrometry data for HLA-A*02:01 and HLA-B*07:02 ("MS"). Also shown are state-of-the-art models based on affinity predictions NETMHCpan "Affinity" and based on stability predictions NETMHCstab "Stability." The data shows the positive predictive value (PPV) at a 10% recall rate, and error bars (as indicated in solid lines) show 95% confidence intervals.

[00110] **FIG. 13B** shows performance results for peptide presentation determined by T-cell epitopes comparing various peptide presentation models. Shown are results for the maximum of per-alleles presentation model shown in equation (12) using the affine dependency function $g_h(\cdot)$ and the expit function $f(\cdot)$ and trained on a subset of mass spectrometry data for HLA-A*02:01. Also shown are state-of-the-art models based on affinity predictions NETMHCpan "Affinity" and based on stability predictions NETMHCstab "Stability." The data shows the positive predictive value (PPV) at a 10% recall rate, and error bars (as indicated in solid lines) show 95% confidence intervals.

[00111] **FIG. 13C** shows performance results for peptide presentation determined by mass-spectrometry for an example function-of-sums model (equation (13)), an example sum-of-functions model (equation (19)), and an example second order model (equation (23)) for predicting peptide presentation. The first column refers to the the area-under-curve (AUC) of the receiver operating characteristic (ROC) when each presentation model was applied to the test set, the second column refers to the value of the negative log likelihood loss, and the third column refers to the the positive predictive value (PPV) at a 10% recall rate.

2026201462 26 Feb 2026

[00112] **FIG. 13D** shows performance results for peptide presentation determined by mass-spectrometry for two example presentation models that are trained with and without single-allele mass spectrometry data. The first column refers to the the area-under-curve (AUC) of the receiver operating characteristic (ROC) when each presentation model was applied to the test set, the second column refers to the value of the negative log likelihood loss, and the third column refers to the the positive predictive value (PPV) at a 10% recall rate.

[00113] **FIG. 13E** shows performance results for peptide presentation determined by mass-spectrometry for two example presentation models that are trained with and without single-allele mass spectrometry data. "Correlation" refers to the correlation between the actual labels that indicate whether the peptide was presented on the corresponding allele in the test data, and the label for prediction.

[00114] **FIG. 13F** shows the frequency of common anchor residues at positions 2 (P2) and 9 (P9) among nonamers predicted by a presentation model trained without single-allele mass spectrometry data.

[00115] **FIG. 13G** shows performance results for peptide presentation determined by mass-spectrometry for an example presentation model that incorporated C- and N-terminal flanking sequences as allele-interacting variables, and an example presentation model that incorporated C- and N-terminal flanking sequences as allele-noninteracting variables. The first column refers to the the area-under-curve (AUC) of the receiver operating characteristic (ROC) when each presentation model was applied to the test set, the second column refers to the value of the negative log likelihood loss, and the third column refers to the the positive predictive value (PPV) at a 10% recall rate.

[00116] **FIG. 13H** shows the dependency between mRNA abundance and the frequency of peptides presented on a tumor cell as determined by mass-spectrometry. The horizontal axis indicates mRNA expression in terms of transcripts per million (TPM) quartiles. The vertical axis indicates fraction of presented epitopes from genes in corresponding mRNA expression quartiles. Each solid line is a plot relating the two measurements from a tumor sample that is associated with corresponding mass spectrometry data and mRNA expression measurements.

[00117] **FIG. 13I** shows performance performance results for peptide presentation determined by mass-spectrometry for example presentation models"MHCflurry + RNA filter" iss a model similar to the current state-of-the-art model that predicts peptide presentation based on affinity predictions with a standard gene expression filter that removed all peptides from proteins with mRNA quantification measurements that were less than 3.2 FPKM. The

2026201462 26 Feb 2026

"Example Model, no RNA" model is the "sum-of-sigmoids" example presentation model shown in equation (21). The "Example Model, with RNA" model is the "sum-of-sigmoids" presentation model shown in equation (19) incorporating mRNA quantification data through a log function. The data shows the positive predictive value (PPV) at a 20% recall rate.

[00118] **FIG. 13J** shows the probability of peptide presentation for different peptide lengths for presentation models that take peptide length into account and state-of-the-art models that do not account for peptide length when predicting peptide presentation. The plot "Truth (Blind Test Data)" showed the proportion of presented peptides according to the length of the peptide in a sample test data set. The plot "Models Ignoring Length" indicated predicted measurements if state-of-the-art models that ignore peptide length applied to the same test data set for presentation prediction. The "Example Model, with RNA" model is the "sum-of-sigmoids" presentation model shown in equation (19) incorporating mRNA quantification data through a log function.

[00119] **FIG. 13K** is a histogram of lengths of peptides eluted from class II MHC alleles on human tumor cells and tumor infiltrating lymphocytes (TIL) using mass spectrometry.

[00120] **FIG. 13L** illustrates the dependency between mRNA quantification and presented peptides per residue for two example datasets.

[00121] **FIG. 13M** compares performance results for example presentation models trained and tested using two example datasets.

[00122] **FIG. 13N** is a histogram that depicts the quantity of peptides sequenced using mass spectrometry for each sample of a total of 39 samples comprising HLA class II molecules.

[00123] **FIG. 13-O** is a histogram that depicts the quantity of samples in which a particular MHC class II molecule allele was identified.

[00124] **FIG. 13P** is a histogram that depicts the proportion of peptides presented by the MHC class II molecules in the 39 total samples, for each peptide length of a range of peptide lengths.

[00125] **FIG. 13Q** is a line graph that depicts the relationship between gene expression and prevalence of presenation of the gene expression product by a MHC class II molecule, for genes present in the 39 samples.

[00126] **FIG. 13R** is a line graph that compares the performance of identical models with varying inputs, at predicting the likelihood that peptides in a testing dataset of peptides will be presented by a MHC class II molecule.

2026201462 26 Feb 2026

[00127] **FIG. 13S** is a line graph that compares the performance of four different models at predicting the likelihood that peptides in a testing dataset of peptides will be presented by a MHC class II molecule.

[00128] **FIG. 13T** is a line graph that compares the performance of a best-in-class prior art model using two different criteria and the presentation model disclosed herein with two different inputs, at predicting the likelihood that peptides in a testing dataset of peptides will be presented by a MHC class II molecule.

[00129] **FIG. 14** illustrates an example computer for implementing the entities shown in FIGS. 1 and 3.

[00130] **FIG. 15** illustrates development of an *in vitro* T cell activation assay. Schematic of the assay in which the delivery of a vaccine cassette to antigen presenting cells, leads to expression, processing and MHC-restricted presentation of distinct peptide antigens. Reporter T cells engineered with T cell receptors that match the specific peptide-MHC combination become activated resulting in luciferase expression.

[00131] **FIG 16A** illustrates evaluation of linker sequences in short cassettes and shows five class I MHC restricted epitopes (epitopes 1 through 5) concatenated in the same position relative to each other followed by two universal class II MHC epitopes (MHC-II). Various iterations were generated using different linkers. In some cases the T cell epitopes are directly linked to each other. In others, the T cell epitopes are flanked on one or both sides by its natural sequence. In other iterations, the T cell epitopes are linked by the non-natural sequences AAY, RR, and DPP.

[00132] **FIG 16B** illustrates evaluation of linker sequences in short cassettes and shows sequence information on the T cell epitopes embedded in the short cassettes.

[00133] **FIG. 17** illustrates evaluation of cellular targeting sequences added to model vaccine cassettes. The targeting cassettes extend the short cassette designs with ubiquitin (Ub), signal peptides (SP) and/or transmembrane (TM) domains, feature next to the five marker human T cell epitopes (epitopes 1 through 5) also two mouse T cell epitopes SIINFEKL (SII) and SPSYAYHQF (A5), and use either the non natural linker AAY- or natural linkers flanking the T cell epitopes on both sides (25mer) .

[00134] **FIG. 18** illustrates *in vivo* evaluation of linker sequences in short cassettes. A) Experimental design of the *in vivo* evaluation of vaccine cassettes using HLA-A2 transgenic mice.

2026201462 26 Feb 2026

[00135] **FIG. 19A** illustrates *in vivo* evaluation of the impact of epitope position in long 21-mer cassettes and shows the design of long cassettes entails five marker class I epitopes (epitopes 1 through 5) contained in their 25-mer natural sequence (linker = natural flanking sequences), spaced with additional well-known T cell class I epitopes (epitopes 6 through 21) contained in their 25-mer natural sequence, and two universal class II epitopes (MHC-II0, with only the relative position of the class I epitopes varied.

[00136] **FIG. 19B** illustrates *in vivo* evaluation of the impact of epitope position in long 21-mer cassettes and shows the sequence information on the T cell epitopes used.

[00137] **FIG. 20A** illustrates final cassette design for preclinical IND-enabling studies and shows the design of the final cassettes comprises 20 MHC I epitopes contained in their 25-mer natural sequence (linker = natural flanking sequences), composed of 6 non-human primate (NHP) epitopes, 5 human epitopes, 9 murine epitopes, as well as 2 universal MHC class II epitopes.

[00138] **FIG. 20B** illustrates final cassette design for preclinical IND-enabling studies and shows the sequence information for the T cell epitopes used that are presented on class I MHC of non-human primate, mouse and human origin, as well as sequences of 2 universal MHC class II epitopes PADRE and Tetanus toxoid.

[00139] **FIG. 21A** illustrates ChAdV68.4WTnt.GFP virus production after transfection. HEK293A cells were transfected with ChAdV68.4WTnt.GFP DNA using the calcium phosphate protocol. Viral replication was observed 10 days after transfection and ChAdV68.4WTnt.GFP viral plaques were visualized using light microscopy (40x magnification).

[00140] **FIG. 21B** illustrates ChAdV68.4WTnt.GFP virus production after transfection. HEK293A cells were transfected with ChAdV68.4WTnt.GFP DNA using the calcium phosphate protocol. Viral replication was observed 10 days after transfection and ChAdV68.4WTnt.GFP viral plaques were visualized using fluorescent microscopy at 40x magnification.

[00141] **FIG. 21C** illustrates ChAdV68.4WTnt.GFP virus production after transfection. HEK293A cells were transfected with ChAdV68.4WTnt.GFP DNA using the calcium phosphate protocol. Viral replication was observed 10 days after transfection and ChAdV68.4WTnt.GFP viral plaques were visualized using fluorescent microscopy at 100x magnification.

2026201462 26 Feb 2026

[00142] **FIG. 22A** illustrates ChAdV68.5WTnt.GFP virus production after transfection. HEK293A cells were transfected with ChAdV68.5WTnt.GFP DNA using the lipofectamine protocol. Viral replication (plaques) was observed 10 days after transfection. A lysate was made and used to reinfect a T25 flask of 293A cells. ChAdV68.5WTnt.GFP viral plaques were visualized and photographed 3 days later using light microscopy (40x magnification)

[00143] **FIG. 22B** illustrates ChAdV68.5WTnt.GFP virus production after transfection. HEK293A cells were transfected with ChAdV68.5WTnt.GFP DNA using the lipofectamine protocol. Viral replication (plaques) was observed 10 days after transfection. A lysate was made and used to reinfect a T25 flask of 293A cells. ChAdV68.5WTnt.GFP viral plaques were visualized and photographed 3 days later using fluorescent microscopy at 40x magnification.

[00144] **FIG. 22C** illustrates ChAdV68.5WTnt.GFP virus production after transfection. HEK293A cells were transfected with ChAdV68.5WTnt.GFP DNA using the lipofectamine protocol. Viral replication (plaques) was observed 10 days after transfection. A lysate was made and used to reinfect a T25 flask of 293A cells. ChAdV68.5WTnt.GFP viral plaques were visualized and photographed 3 days later using fluorescent microscopy at 100x magnification.

[00145] **FIG. 23** illustrates the viral particle production scheme.

[00146] **FIG. 24** illustrates the alphavirus derived VEE self-replicating RNA (srRNA) vector.

[00147] **FIG. 25** illustrates *in vivo* reporter expression after inoculation of C57BL/6J mice with VEE-Luciferase srRNA. Shown are representative images of luciferase signal following immunization of C57BL/6J mice with VEE-Luciferase srRNA (10 ug per mouse, bilateral intramuscular injection, MC3 encapsulated) at various timepoints.

[00148] **FIG. 26A** illustrates T-cell responses measured 14 days after immunization with VEE srRNA formulated with MC3 LNP in B16-OVA tumor bearing mice. B16-OVA tumor bearing C57BL/6J mice were injected with 10 ug of VEE-Luciferase srRNA (control), VEE-UbAAY srRNA (Vax), VEE-Luciferase srRNA and anti-CTLA-4 (aCTLA-4) or VEE-UbAAY srRNA and anti-CTLA-4 (Vax + aCTLA-4). In addition, all mice were treated with anti-PD1 mAb starting at day 7. Each group consisted of 8 mice. Mice were sacrificed and spleens and lymph nodes were collected 14 days after immunization. SIINFEKL-specific T-cell responses were assessed by IFN-gamma ELISPOT and are reported as spot-forming cells (SFC) per 106 splenocytes. Lines represent medians.

[00149] **FIG. 26B** illustrates T-cell responses measured 14 days after immunization with VEE srRNA formulated with MC3 LNP in B16-OVA tumor bearing mice. B16-OVA tumor

2026201462 26 Feb 2026

bearing C57BL/6J mice were injected with 10 ug of VEE-Luciferase srRNA (control), VEE-UbAAY srRNA (Vax), VEE-Luciferase srRNA and anti-CTLA-4 (aCTLA-4) or VEE-UbAAY srRNA and anti-CTLA-4 (Vax + aCTLA-4). In addition, all mice were treated with anti-PD1 mAb starting at day 7. Each group consisted of 8 mice. Mice were sacrificed and spleens and lymph nodes were collected 14 days after immunization. SIINFEKL-specific T-cell responses were assessed by MHCI-pentamer staining, reported as pentamer positive cells as a percent of CD8 positive cells. Lines represent medians.

[00150] **FIG. 27A** illustrates antigen-specific T-cell responses following heterologous prime/boost in B16-OVA tumor bearing mice. B16-OVA tumor bearing C57BL/6J mice were injected with adenovirus expressing GFP (Ad5-GFP) and boosted with VEE-Luciferase srRNA formulated with MC3 LNP (Control) or Ad5-UbAAY and boosted with VEE-UbAAY srRNA (Vax). Both the Control and Vax groups were also treated with an IgG control mAb. A third group was treated with the Ad5-GFP prime/VEE-Luciferase srRNA boost in combination with anti-CTLA-4 (aCTLA-4), while the fourth group was treated with the Ad5-UbAAY prime/VEE-UbAAY boost in combination with anti-CTLA-4 (Vax + aCTLA-4). In addition, all mice were treated with anti-PD-1 mAb starting at day 21. T-cell responses were measured by IFN-gamma ELISPOT. Mice were sacrificed and spleens and lymph nodes collected at 14 days post immunization with adenovirus.

[00151] **FIG. 27B** illustrates antigen-specific T-cell responses following heterologous prime/boost in B16-OVA tumor bearing mice. B16-OVA tumor bearing C57BL/6J mice were injected with adenovirus expressing GFP (Ad5-GFP) and boosted with VEE-Luciferase srRNA formulated with MC3 LNP (Control) or Ad5-UbAAY and boosted with VEE-UbAAY srRNA (Vax). Both the Control and Vax groups were also treated with an IgG control mAb. A third group was treated with the Ad5-GFP prime/VEE-Luciferase srRNA boost in combination with anti-CTLA-4 (aCTLA-4), while the fourth group was treated with the Ad5-UbAAY prime/VEE-UbAAY boost in combination with anti-CTLA-4 (Vax + aCTLA-4). In addition, all mice were treated with anti-PD-1 mAb starting at day 21. T-cell responses were measured by IFN-gamma ELISPOT. Mice were sacrificed and spleens and lymph nodes collected at 14 days post immunization with adenovirus and 14 days post boost with srRNA (day 28 after prime).

[00152] **FIG. 27C** illustrates antigen-specific T-cell responses following heterologous prime/boost in B16-OVA tumor bearing mice. B16-OVA tumor bearing C57BL/6J mice were injected with adenovirus expressing GFP (Ad5-GFP) and boosted with VEE-Luciferase srRNA

2026201462 26 Feb 2026

formulated with MC3 LNP (Control) or Ad5-UbAAY and boosted with VEE-UbAAY srRNA (Vax). Both the Control and Vax groups were also treated with an IgG control mAb. A third group was treated with the Ad5-GFP prime/VEE-Luciferase srRNA boost in combination with anti-CTLA-4 (aCTLA-4), while the fourth group was treated with the Ad5-UbAAY prime/VEE-UbAAY boost in combination with anti-CTLA-4 (Vax + aCTLA-4). In addition, all mice were treated with anti-PD-1 mAb starting at day 21. T-cell responses were measured by MHC class I pentamer staining. Mice were sacrificed and spleens and lymph nodes collected at 14 days post immunization with adenovirus.

[00153] **FIG. 27D** illustrates antigen-specific T-cell responses following heterologous prime/boost in B16-OVA tumor bearing mice. B16-OVA tumor bearing C57BL/6J mice were injected with adenovirus expressing GFP (Ad5-GFP) and boosted with VEE-Luciferase srRNA formulated with MC3 LNP (Control) or Ad5-UbAAY and boosted with VEE-UbAAY srRNA (Vax). Both the Control and Vax groups were also treated with an IgG control mAb. A third group was treated with the Ad5-GFP prime/VEE-Luciferase srRNA boost in combination with anti-CTLA-4 (aCTLA-4), while the fourth group was treated with the Ad5-UbAAY prime/VEE-UbAAY boost in combination with anti-CTLA-4 (Vax + aCTLA-4). In addition, all mice were treated with anti-PD-1 mAb starting at day 21. T-cell responses were measured by MHC class I pentamer staining. Mice were sacrificed and spleens and lymph nodes collected at 14 days post immunization with adenovirus and 14 days post boost with srRNA (day 28 after prime).

[00154] **FIG. 28A** illustrates antigen-specific T-cell responses following heterologous prime/boost in CT26 (Balb/c) tumor bearing mice. Mice were immunized with Ad5-GFP and boosted 15 days after the adenovirus prime with VEE-Luciferase srRNA formulated with MC3 LNP (Control) or primed with Ad5-UbAAY and boosted with VEE-UbAAY srRNA (Vax). Both the Control and Vax groups were also treated with an IgG control mAb. A separate group was administered the Ad5-GFP/VEE-Luciferase srRNA prime/boost in combination with anti-PD-1 (aPD1), while a fourth group received the Ad5-UbAAY/VEE-UbAAY srRNA prime/boost in combination with an anti-PD-1 mAb (Vax + aPD1). T-cell responses to the AH1 peptide were measured using IFN-gamma ELISPOT. Mice were sacrificed and spleens and lymph nodes collected at 12 days post immunization with adenovirus.

[00155] **FIG. 28B** illustrates antigen-specific T-cell responses following heterologous prime/boost in CT26 (Balb/c) tumor bearing mice. Mice were immunized with Ad5-GFP and boosted 15 days after the adenovirus prime with VEE-Luciferase srRNA formulated with MC3

2026201462 26 Feb 2026

LNP (Control) or primed with Ad5-UbAAY and boosted with VEE-UbAAY srRNA (Vax). Both the Control and Vax groups were also treated with an IgG control mAb. A separate group was administered the Ad5-GFP/VEE-Luciferase srRNA prime/boost in combination with anti-PD-1 (aPD1), while a fourth group received the Ad5-UbAAY/VEE-UbAAY srRNA prime/boost in combination with an anti-PD-1 mAb (Vax + aPD1). T-cell responses to the AH1 peptide were measured using IFN-gamma ELISPOT. Mice were sacrificed and spleens and lymph nodes collected at 12 days post immunization with adenovirus and 6 days post boost with srRNA (day 21 after prime).

[00156] **FIG. 29** illustrates ChAdV68 eliciting T-Cell responses to mouse tumor antigens in mice. Mice were immunized with ChAdV68.5WTnt.MAG25mer, and T-cell responses to the MHC class I epitope SIINFEKL (OVA) were measured in C57BL/6J female mice and the MHC class I epitope AH1-A5 measured in Balb/c mice. Mean spot forming cells (SFCs) per 10^6 splenocytes measured in ELISpot assays presented. Error bars represent standard deviation.

[00157] **FIG. 30** illustrates cellular immune responses in a CT26 tumor model following a single immunization with either ChAdV6, ChAdV + anti-PD-1, srRNA, srRNA + anti-PD-1, or anti-PD-1 alone. Antigen-specific IFN-gamma production was measured in splenocytes for 6 mice from each group using ELISpot. Results are presented as spot forming cells (SFC) per 10^6 splenocytes. Median for each group indicated by horizontal line. P values determined using the Dunnett's multiple comparison test; *** P<0.0001, **P<0.001, *P<0.05. ChAdV= ChAdV68.5WTnt.MAG25mer; srRNA= VEE-MAG25mer srRNA.

[00158] **FIG. 31** illustrates CD8 T-Cell responses in a CT26 tumor model following a single immunization with either ChAdV6, ChAdV + anti-PD-1, srRNA, srRNA + anti-PD-1, or anti-PD-1 alone. Antigen-specific IFN-gamma production in CD8 T cells measured using ICS and results presented as antigen-specific CD8 T cells as a percentage of total CD8 T cells. Median for each group indicated by horizontal line. P values determined using the Dunnett's multiple comparison test; *** P<0.0001, **P<0.001, *P<0.05. ChAdV= ChAdV68.5WTnt.MAG25mer; srRNA= VEE-MAG25mer srRNA.

[00159] **FIG. 32** illustrates tumor growth in a CT26 tumor model following immunization with a ChAdV/srRNA heterologous prime/boost, a srRNA/ChAdV heterologous prime/boost, or a srRNA/srRNA homologous primer/boost. Also illustrated in a comparison of the prime/boost immunizations with or without administration of anti-PD1 during prime and boost. Tumor volumes measured twice per week and mean tumor volumes presented for the first 21

2026201462 26 Feb 2026

days of the study. 22-28 mice per group at study initiation. Error bars represent standard error of the mean (SEM). P values determined using the Dunnett's test; *** P<0.0001, **P<0.001, *P<0.05. ChAdV= ChAdV68.5WTnt.MAG25mer; srRNA= VEE-MAG25mer srRNA.

[00160] **FIG. 33** illustrates survival in a CT26 tumor model following immunization with a ChAdV/srRNA heterologous prime/boost, a srRNA/ChAdV heterologous prime/boost, or a srRNA/srRNA homologous primer/boost. Also illustrated in a comparison of the prime/boost immunizations with or without administration of anti-PD1 during prime and boost. P values determined using the log-rank test; *** P<0.0001, **P<0.001, *P<0.01. ChAdV= ChAdV68.5WTnt.MAG25mer; srRNA= VEE-MAG25mer srRNA.

[00161] **FIG. 34** illustrates antigen-specific cellular immune responses measured using ELISpot. Antigen-specific IFN-gamma production to six different mamu A01 restricted epitopes was measured in PBMCs for the VEE-MAG25mer srRNA-LNP1(30 μg) (**FIG. 34A**), VEE-MAG25mer srRNA-LNP1(100 μg) (**FIG. 34B**), or VEE-MAG25mer srRNA-LNP2(100 μg) (**FIG. 34C**) homologous prime/boost or the ChAdV68.5WTnt.MAG25mer /VEE-MAG25mer srRNA heterologous prime/boost group (**FIG. 34D**) using ELISpot 1, 2, 3, 4, 5, 6, 8, 9, or 10 weeks after the first boost immunization (6 rhesus macaques per group). Results are presented as mean spot forming cells (SFC) per 10^6 PBMCs for each epitope in a stacked bar graph format. Values for each animal were normalized to the levels at pre-bleed (week 0).

[00162] **FIG. 35** shows antigen-specific cellular immune response measured using ELISpot. Antigen-specific IFN-gamma production to six different mamu A01 restricted epitopes was measured in PBMCs after immunization with the ChAdV68.5WTnt.MAG25mer /VEE-MAG25mer srRNA heterologous prime/boost regimen using ELISpot prior to immunization and 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 or 24 weeks after the initial immunization. Results are presented as mean spot forming cells (SFC) per 10^6 PBMCs for each epitope (6 rhesus macaques per group) in a stacked bar graph format.

[00163] **FIG. 36** shows antigen-specific cellular immune response measured using ELISpot. Antigen-specific IFN-gamma production to six different mamu A01 restricted epitopes was measured in PBMCs after immunization with the VEE-MAG25mer srRNA LNP2 homologous prime/boost regimen using ELISpot prior to immunization and 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, or 15 weeks after the initial immunization. Results are presented as mean spot forming cells (SFC) per 10^6 PBMCs for each epitope (6 rhesus macaques per group) in a stacked bar graph format.

2026201462 26 Feb 2026

[00164] **FIG. 37** shows antigen-specific cellular immune response measured using ELISpot. Antigen-specific IFN-gamma production to six different mamu A01 restricted epitopes was measured in PBMCs after immunization with the VEE-MAG25mer srRNA LNP1 homologous prime/boost regimen using ELISpot prior to immunization and 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, or 15 weeks after the initial immunization. Results are presented as mean spot forming cells (SFC) per 10^6 PBMCs for each epitope (6 rhesus macaques per group) in a stacked bar graph format.

[00165] **FIG. 38** illustrates determining distance metrics for two example cassette sequences.

DETAILED DESCRIPTION

I. Definitions

[00166] In general, terms used in the claims and the specification are intended to be construed as having the plain meaning understood by a person of ordinary skill in the art. Certain terms are defined below to provide additional clarity. In case of conflict between the plain meaning and the provided definitions, the provided definitions are to be used.

[00167] As used herein the term "antigen" is a substance that induces an immune response.

[00168] As used herein the term "neoantigen" is an antigen that has at least one alteration that makes it distinct from the corresponding wild-type antigen, e.g., via mutation in a tumor cell or post-translational modification specific to a tumor cell. A neoantigen can include a polypeptide sequence or a nucleotide sequence. A mutation can include a frameshift or nonframeshift indel, missense or nonsense substitution, splice site alteration, genomic rearrangement or gene fusion, or any genomic or expression alteration giving rise to a neoORF. A mutations can also include a splice variant. Post-translational modifications specific to a tumor cell can include aberrant phosphorylation. Post-translational modifications specific to a tumor cell can also include a proteasome-generated spliced antigen. *See* Liepe et al., A large fraction of HLA class I ligands are proteasome-generated spliced peptides; Science. 2016 Oct 21;354(6310):354-358.

[00169] As used herein the term "tumor neoantigen" is a neoantigen present in a subject's tumor cell or tissue but not in the subject's corresponding normal cell or tissue.

[00170] As used herein the term "neoantigen-based vaccine" is a vaccine construct based on one or more neoantigens, e.g., a plurality of neoantigens.

2026201462 26 Feb 2026

[00171] As used herein the term “candidate neoantigen” is a mutation or other aberration giving rise to a new sequence that may represent a neoantigen.

[00172] As used herein the term “coding region” is the portion(s) of a gene that encode protein.

[00173] As used herein the term “coding mutation” is a mutation occurring in a coding region.

[00174] As used herein the term “ORF” means open reading frame.

[00175] As used herein the term “NEO-ORF” is a tumor-specific ORF arising from a mutation or other aberration such as splicing.

[00176] As used herein the term “missense mutation” is a mutation causing a substitution from one amino acid to another.

[00177] As used herein the term “nonsense mutation” is a mutation causing a substitution from an amino acid to a stop codon or causing removal of a canonical start codon.

[00178] As used herein the term “frameshift mutation” is a mutation causing a change in the frame of the protein.

[00179] As used herein the term “indel” is an insertion or deletion of one or more nucleic acids.

[00180] As used herein, the term percent "identity," in the context of two or more nucleic acid or polypeptide sequences, refer to two or more sequences or subsequences that have a specified percentage of nucleotides or amino acid residues that are the same, when compared and aligned for maximum correspondence, as measured using one of the sequence comparison algorithms described below (e.g., BLASTP and BLASTN or other algorithms available to persons of skill) or by visual inspection. Depending on the application, the percent "identity" can exist over a region of the sequence being compared, e.g., over a functional domain, or, alternatively, exist over the full length of the two sequences to be compared.

[00181] For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters. Alternatively, sequence similarity or dissimilarity can be established by the combined presence or absence of

2026201462 26 Feb 2026

particular nucleotides, or, for translated sequences, amino acids at selected sequence positions (e.g., sequence motifs).

[00182] Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by visual inspection (see generally Ausubel et al., infra).

[00183] One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al., J. Mol. Biol. 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information.

[00184] As used herein the term “non-stop or read-through” is a mutation causing the removal of the natural stop codon.

[00185] As used herein the term “epitope” is the specific portion of an antigen typically bound by an antibody or T cell receptor.

[00186] As used herein the term “immunogenic” is the ability to elicit an immune response, e.g., via T cells, B cells, or both.

[00187] As used herein the term “HLA binding affinity” “MHC binding affinity” means affinity of binding between a specific antigen and a specific MHC allele.

[00188] As used herein the term “bait” is a nucleic acid probe used to enrich a specific sequence of DNA or RNA from a sample.

[00189] As used herein the term “variant” is a difference between a subject’s nucleic acids and the reference human genome used as a control.

[00190] As used herein the term “variant call” is an algorithmic determination of the presence of a variant, typically from sequencing.

[00191] As used herein the term “polymorphism” is a germline variant, i.e., a variant found in all DNA-bearing cells of an individual.

[00192] As used herein the term “somatic variant” is a variant arising in non-germline cells of an individual.

[00193] As used herein the term “allele” is a version of a gene or a version of a genetic sequence or a version of a protein.

2026201462 26 Feb 2026

[00194] As used herein the term “HLA type” is the complement of HLA gene alleles.

[00195] As used herein the term “nonsense-mediated decay” or “NMD” is a degradation of an mRNA by a cell due to a premature stop codon.

[00196] As used herein the term “truncal mutation” is a mutation originating early in the development of a tumor and present in a substantial portion of the tumor’s cells.

[00197] As used herein the term “subclonal mutation” is a mutation originating later in the development of a tumor and present in only a subset of the tumor’s cells.

[00198] As used herein the term “exome” is a subset of the genome that codes for proteins. An exome can be the collective exons of a genome.

[00199] As used herein the term “logistic regression” is a regression model for binary data from statistics where the logit of the probability that the dependent variable is equal to one is modeled as a linear function of the dependent variables.

[00200] As used herein the term “neural network” is a machine learning model for classification or regression consisting of multiple layers of linear transformations followed by element-wise nonlinearities typically trained via stochastic gradient descent and back-propagation.

[00201] As used herein the term “proteome” is the set of all proteins expressed and/or translated by a cell, group of cells, or individual.

[00202] As used herein the term “peptidome” is the set of all peptides presented by MHC-I or MHC-II on the cell surface. The peptidome may refer to a property of a cell or a collection of cells (e.g., the tumor peptidome, meaning the union of the peptidomes of all cells that comprise the tumor).

[00203] As used herein the term “ELISPOT” means Enzyme-linked immunosorbent spot assay – which is a common method for monitoring immune responses in humans and animals.

[00204] As used herein the term “dextramers” is a dextran-based peptide-MHC multimers used for antigen-specific T-cell staining in flow cytometry.

[00205] As used herein the term “tolerance or immune tolerance” is a state of immune non-responsiveness to one or more antigens, e.g. self-antigens.

[00206] As used herein the term “central tolerance” is a tolerance affected in the thymus, either by deleting self-reactive T-cell clones or by promoting self-reactive T-cell clones to differentiate into immunosuppressive regulatory T-cells (Tregs).

2026201462 26 Feb 2026

[00207] As used herein the term "peripheral tolerance" is a tolerance affected in the periphery by downregulating or anergizing self-reactive T-cells that survive central tolerance or promoting these T cells to differentiate into Tregs.

[00208] The term "sample" can include a single cell or multiple cells or fragments of cells or an aliquot of body fluid, taken from a subject, by means including venipuncture, excretion, ejaculation, massage, biopsy, needle aspirate, lavage sample, scraping, surgical incision, or intervention or other means known in the art.

[00209] The term "subject" encompasses a cell, tissue, or organism, human or non-human, whether in vivo, ex vivo, or in vitro, male or female. The term subject is inclusive of mammals including humans.

[00210] The term "mammal" encompasses both humans and non-humans and includes but is not limited to humans, non-human primates, canines, felines, murines, bovines, equines, and porcines.

[00211] The term "clinical factor" refers to a measure of a condition of a subject, e.g., disease activity or severity. "Clinical factor" encompasses all markers of a subject's health status, including non-sample markers, and/or other characteristics of a subject, such as, without limitation, age and gender. A clinical factor can be a score, a value, or a set of values that can be obtained from evaluation of a sample (or population of samples) from a subject or a subject under a determined condition. A clinical factor can also be predicted by markers and/or other parameters such as gene expression surrogates. Clinical factors can include tumor type, tumor sub-type, and smoking history.

[00212] The term "antigen-encoding nucleic acid sequences derived from a tumor" refers to nucleic acid sequences directly extracted from the tumor, e.g. via RT-PCR; or sequence data obtained by sequencing the tumor and then synthesizing the nucleic acid sequences using the sequencing data, e.g., via various synthetic or PCR-based methods known in the art.

[00213] The term "alphavirus" refers to members of the family *Togaviridae*, and are positive-sense single-stranded RNA viruses. Alphaviruses are typically classified as either Old World, such as Sindbis, Ross River, Mayaro, Chikungunya, and Semliki Forest viruses, or New World, such as eastern equine encephalitis, Aura, Fort Morgan, or Venezuelan equine encephalitis and its derivative strain TC-83. Alphaviruses are typically self-replicating RNA viruses.

[00214] The term "alphavirus backbone" refers to minimal sequence(s) of an alphavirus that allow for self-replication of the viral genome. Minimal sequences can include conserved

2026201462 26 Feb 2026

sequences for nonstructural protein-mediated amplification, a nonstructural protein 1 (nsP1) gene, a nsP2 gene, a nsP3 gene, a nsP4 gene, and a polyA sequence, as well as sequences for expression of subgenomic viral RNA including a 26S promoter element.

[00215] The term "sequences for nonstructural protein-mediated amplification" includes alphavirus conserved sequence elements (CSE) well known to those in the art. CSEs include, but are not limited to, an alphavirus 5' UTR, a 51-nt CSE, a 24-nt CSE, or other 26S subgenomic promoter sequence, a 19-nt CSE, and an alphavirus 3' UTR.

[00216] The term "RNA polymerase" includes polymerases that catalyze the production of RNA polynucleotides from a DNA template. RNA polymerases include, but are not limited to, bacteriophage derived polymerases including T3, T7, and SP6.

[00217] The term "lipid" includes hydrophobic and/or amphiphilic molecules. Lipids can be cationic, anionic, or neutral. Lipids can be synthetic or naturally derived, and in some instances biodegradable. Lipids can include cholesterol, phospholipids, lipid conjugates including, but not limited to, polyethyleneglycol (PEG) conjugates (PEGylated lipids), waxes, oils, glycerides, fats, and fat-soluble vitamins. Lipids can also include dilinoleylmethyl- 4-dimethylaminobutyrate (MC3) and MC3-like molecules.

[00218] The term "lipid nanoparticle" or "LNP" includes vesicle like structures formed using a lipid containing membrane surrounding an aqueous interior, also referred to as liposomes. Lipid nanoparticles includes lipid-based compositions with a solid lipid core stabilized by a surfactant. The core lipids can be fatty acids, acylglycerols, waxes, and mixtures of these surfactants. Biological membrane lipids such as phospholipids, sphingomyelins, bile salts (sodium taurocholate), and sterols (cholesterol) can be utilized as stabilizers. Lipid nanoparticles can be formed using defined ratios of different lipid molecules, including, but not limited to, defined ratios of one or more cationic, anionic, or neutral lipids. Lipid nanoparticles can encapsulate molecules within an outer-membrane shell and subsequently can be contacted with target cells to deliver the encapsulated molecules to the host cell cytosol. Lipid nanoparticles can be modified or functionalized with non-lipid molecules, including on their surface. Lipid nanoparticles can be single-layered (unilamellar) or multi-layered (multilamellar). Lipid nanoparticles can be complexed with nucleic acid. Unilamellar lipid nanoparticles can be complexed with nucleic acid, wherein the nucleic acid is in the aqueous interior. Multilamellar lipid nanoparticles can be complexed with nucleic acid, wherein the nucleic acid is in the aqueous interior, or to form or sandwiched between

2026201462 26 Feb 2026

[00219] Abbreviations: MHC: major histocompatibility complex; HLA: human leukocyte antigen, or the human MHC gene locus; NGS: next-generation sequencing; PPV: positive predictive value; TSNA: tumor-specific neoantigen; FFPE: formalin-fixed, paraffin-embedded; NMD: nonsense-mediated decay; NSCLC: non-small-cell lung cancer; DC: dendritic cell.

[00220] It should be noted that, as used in the specification and the appended claims, the singular forms "a," "an," and "the" include plural referents unless the context clearly dictates otherwise.

[00221] Unless specifically stated or otherwise apparent from context, as used herein the term "about" is understood as within a range of normal tolerance in the art, for example within 2 standard deviations of the mean. About can be understood as within 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, 0.05%, or 0.01% of the stated value. Unless otherwise clear from context, all numerical values provided herein are modified by the term about.

[00222] Any terms not directly defined herein shall be understood to have the meanings commonly associated with them as understood within the art of the invention. Certain terms are discussed herein to provide additional guidance to the practitioner in describing the compositions, devices, methods and the like of aspects of the invention, and how to make or use them. It will be appreciated that the same thing may be said in more than one way. Consequently, alternative language and synonyms may be used for any one or more of the terms discussed herein. No significance is to be placed upon whether or not a term is elaborated or discussed herein. Some synonyms or substitutable methods, materials and the like are provided. Recital of one or a few synonyms or equivalents does not exclude use of other synonyms or equivalents, unless it is explicitly stated. Use of examples, including examples of terms, is for illustrative purposes only and does not limit the scope and meaning of the aspects of the invention herein.

[00223] All references, issued patents and patent applications cited within the body of the specification are hereby incorporated by reference in their entirety, for all purposes.

II. Methods of Identifying Neoantigens

[00224] Disclosed herein are methods for identifying neoantigens from a tumor of a subject that are likely to be presented on the cell surface of the tumor or immune cells, including professional antigen presenting cells such as dendritic cells, and/or are likely to be immunogenic. As an example, one such method may comprise the steps of: obtaining at least one of exome, transcriptome or whole genome tumor nucleotide sequencing data from the

2026201462 26 Feb 2026

tumor cell of the subject, wherein the tumor nucleotide sequencing data is used to obtain data representing peptide sequences of each of a set of neoantigens, and wherein the peptide sequence of each neoantigen comprises at least one alteration that makes it distinct from the corresponding wild-type peptide sequence; inputting the peptide sequence of each neoantigen into one or more presentation models to generate a set of numerical likelihoods that each of the neoantigens is presented by one or more MHC alleles on the tumor cell surface of the tumor cell of the subject or cells present in the tumor, the set of numerical likelihoods having been identified at least based on received mass spectrometry data; and selecting a subset of the set of neoantigens based on the set of numerical likelihoods to generate a set of selected neoantigens.

[00225] The presentation model can comprise a statistical regression or a machine learning (e.g., deep learning) model trained on a set of reference data (also referred to as a training data set) comprising a set of corresponding labels, wherein the set of reference data is obtained from each of a plurality of distinct subjects where optionally some subjects can have a tumor, and wherein the set of reference data comprises at least one of: data representing exome nucleotide sequences from tumor tissue, data representing exome nucleotide sequences from normal tissue, data representing transcriptome nucleotide sequences from tumor tissue, data representing proteome sequences from tumor tissue, and data representing MHC peptidome sequences from tumor tissue, and data representing MHC peptidome sequences from normal tissue. The reference data can further comprise mass spectrometry data, sequencing data, RNA sequencing data, and proteomics data for single-allele cell lines engineered to express a predetermined MHC allele that are subsequently exposed to synthetic protein, normal and tumor human cell lines, and fresh and frozen primary samples, and T cell assays (e.g., ELISPOT). In certain aspects, the set of reference data includes each form of reference data.

[00226] The presentation model can comprise a set of features derived at least in part from the set of reference data, and wherein the set of features comprises at least one of allele dependent-features and allele-independent features. In certain aspects each feature is included.

[00227] Also disclosed herein are methods for generating an output for constructing a personalized cancer vaccine by identifying one or more neoantigens from one or more tumor cells of a subject that are likely to be presented on a surface of the tumor cells. As an example, one such method may comprise the steps of: obtaining at least one of exome, transcriptome, or whole genome nucleotide sequencing data from the tumor cells and normal cells of the subject, wherein the nucleotide sequencing data is used to obtain data representing peptide sequences of each of a set of neoantigens identified by comparing the nucleotide sequencing data from the

2026201462 26 Feb 2026

tumor cells and the nucleotide sequencing data from the normal cells, and wherein the peptide sequence of each neoantigen comprises at least one alteration that makes it distinct from the corresponding wild-type, peptide sequence identified from the normal cells of the subject; encoding the peptide sequences of each of the neoantigens into a corresponding numerical vector, each numerical vector including information regarding a plurality of amino acids that make up the peptide sequence and a set of positions of the amino acids in the peptide sequence; inputting the numerical vectors, using a computer processor, into a deep learning presentation model to generate a set of presentation likelihoods for the set of neoantigens, each presentation likelihood in the set representing the likelihood that a corresponding neoantigen is presented by one or more class II MHC alleles on the surface of the tumor cells of the subject, the deep learning presentation model; selecting a subset of the set of neoantigens based on the set of presentation likelihoods to generate a set of selected neoantigens; and generating the output for constructing the personalized cancer vaccine based on the set of selected neoantigens.

[00228] In some embodiments, the presentation model comprises a plurality of parameters identified at least based on a training data set and a function representing a relation between the numerical vector received as an input and the presentation likelihood generated as output based on the numerical vector and the parameters. In certain embodiments, the training data set comprises labels obtained by mass spectrometry measuring presence of peptides bound to at least one class II MHC allele identified as present in at least one of a plurality of samples, training peptide sequences encoded as numerical vectors including information regarding a plurality of amino acids that make up the peptide sequence and a set of positions of the amino acids in the peptide sequence, and at least one HLA allele associated with the training peptide sequences.

[00229] Dendritic cell presentation to naïve T cell features can comprise at least one of: A feature described above. The dose and type of antigen in the vaccine. (e.g., peptide, mRNA, virus, etc.): (1) The route by which dendritic cells (DCs) take up the antigen type (e.g., endocytosis, micropinocytosis); and/or (2) The efficacy with which the antigen is taken up by DCs. The dose and type of adjuvant in the vaccine. The length of the vaccine antigen sequence. The number and sites of vaccine administration. Baseline patient immune functioning (e.g., as measured by history of recent infections, blood counts, etc). For RNA vaccines: (1) the turnover rate of the mRNA protein product in the dendritic cell; (2) the rate of translation of the mRNA after uptake by dendritic cells as measured in in vitro or in vivo experiments; and/or (3) the number or rounds of translation of the mRNA after uptake by dendritic cells as measured

2026201462 26 Feb 2026

by in vivo or in vitro experiments. The presence of protease cleavage motifs in the peptide, optionally giving additional weight to proteases typically expressed in dendritic cells (as measured by RNA-seq or mass spectrometry). The level of expression of the proteasome and immunoproteasome in typical activated dendritic cells (which may be measured by RNA-seq, mass spectrometry, immunohistochemistry, or other standard techniques). The expression levels of the particular MHC allele in the individual in question (e.g., as measured by RNA-seq or mass spectrometry), optionally measured specifically in activated dendritic cells or other immune cells. The probability of peptide presentation by the particular MHC allele in other individuals who express the particular MHC allele, optionally measured specifically in activated dendritic cells or other immune cells. The probability of peptide presentation by MHC alleles in the same family of molecules (e.g., HLA-A, HLA-B, HLA-C, HLA-DQ, HLA-DR, HLA-DP) in other individuals, optionally measured specifically in activated dendritic cells or other immune cells.

[00230] Immune tolerance escape features can comprise at least one of: Direct measurement of the self-peptidome via protein mass spectrometry performed on one or several cell types. Estimation of the self-peptidome by taking the union of all k-mer (e.g. 5-25) substrings of self-proteins. Estimation of the self-peptidome using a model of presentation similar to the presentation model described above applied to all non-mutation self-proteins, optionally accounting for germline variants.

[00231] Ranking can be performed using the plurality of neoantigens provided by at least one model based at least in part on the numerical likelihoods. Following the ranking a selecting can be performed to select a subset of the ranked neoantigens according to a selection criteria. After selecting a subset of the ranked peptides can be provided as an output.

[00232] A number of the set of selected neoantigens may be 20.

[00233] The presentation model may represent dependence between presence of a pair of a particular one of the MHC alleles and a particular amino acid at a particular position of a peptide sequence; and likelihood of presentation on the tumor cell surface, by the particular one of the MHC alleles of the pair, of such a peptide sequence comprising the particular amino acid at the particular position.

[00234] A method disclosed herein can also include applying the one or more presentation models to the peptide sequence of the corresponding neoantigen to generate a dependency score for each of the one or more MHC alleles indicating whether the MHC allele will present

2026201462 26 Feb 2026

the corresponding neoantigen based on at least positions of amino acids of the peptide sequence of the corresponding neoantigen.

[00235] A method disclosed herein can also include transforming the dependency scores to generate a corresponding per-allele likelihood for each MHC allele indicating a likelihood that the corresponding MHC allele will present the corresponding neoantigen; and combining the per-allele likelihoods to generate the numerical likelihood.

[00236] The step of transforming the dependency scores can model the presentation of the peptide sequence of the corresponding neoantigen as mutually exclusive.

[00237] A method disclosed herein can also include transforming a combination of the dependency scores to generate the numerical likelihood.

[00238] The step of transforming the combination of the dependency scores can model the presentation of the peptide sequence of the corresponding neoantigen as interfering between MHC alleles.

[00239] The set of numerical likelihoods can be further identified by at least an allele noninteracting feature, and a method disclosed herein can also include applying an allele noninteracting one of the one or more presentation models to the allele noninteracting features to generate a dependency score for the allele noninteracting features indicating whether the peptide sequence of the corresponding neoantigen will be presented based on the allele noninteracting features.

[00240] A method disclosed herein can also include combining the dependency score for each MHC allele in the one or more MHC alleles with the dependency score for the allele noninteracting feature; transforming the combined dependency scores for each MHC allele to generate a corresponding per-allele likelihood for the MHC allele indicating a likelihood that the corresponding MHC allele will present the corresponding neoantigen; and combining the per-allele likelihoods to generate the numerical likelihood.

[00241] A method disclosed herein can also include transforming a combination of the dependency scores for each of the MHC alleles and the dependency score for the allele noninteracting features to generate the numerical likelihood.

[00242] A set of numerical parameters for the presentation model can be trained based on a training data set including at least a set of training peptide sequences identified as present in a plurality of samples and one or more MHC alleles associated with each training peptide sequence, wherein the training peptide sequences are identified through mass spectrometry on isolated peptides eluted from MHC alleles derived from the plurality of samples.

2026201462 26 Feb 2026

[00243] The samples can also include cell lines engineered to express a single MHC class I or class II allele.

[00244] The samples can also include cell lines engineered to express a plurality of MHC class I or class II alleles.

[00245] The samples can also include human cell lines obtained or derived from a plurality of patients.

[00246] The samples can also include fresh or frozen tumor samples obtained from a plurality of patients.

[00247] The samples can also include fresh or frozen tissue samples obtained from a plurality of patients.

[00248] The samples can also include peptides identified using T-cell assays.

[00249] The training data set can further include data associated with: peptide abundance of the set of training peptides present in the samples; peptide length of the set of training peptides in the samples.

[00250] The training data set may be generated by comparing the set of training peptide sequences via alignment to a database comprising a set of known protein sequences, wherein the set of training protein sequences are longer than and include the training peptide sequences.

[00251] The training data set may be generated based on performing or having performed nucleotide sequencing on a cell line to obtain at least one of exome, transcriptome, or whole genome sequencing data from the cell line, the sequencing data including at least one nucleotide sequence including an alteration.

[00252] The training data set may be generated based on obtaining at least one of exome, transcriptome, and whole genome normal nucleotide sequencing data from normal tissue samples.

[00253] The training data set may further include data associated with proteome sequences associated with the samples.

[00254] The training data set may further include data associated with MHC peptidome sequences associated with the samples.

[00255] The training data set may further include data associated with peptide-MHC binding affinity measurements for at least one of the isolated peptides.

[00256] The training data set may further include data associated with peptide-MHC binding stability measurements for at least one of the isolated peptides.

2026201462 26 Feb 2026

[00257] The training data set may further include data associated with transcriptomes associated with the samples.

[00258] The training data set may further include data associated with genomes associated with the samples.

[00259] The training peptide sequences may be of lengths within a range of k-mers where k is between 8-15, inclusive for MHC class I or 6-30 inclusive for MHC class II.

[00260] A method disclosed herein can also include encoding the peptide sequence using a one-hot encoding scheme.

[00261] A method disclosed herein can also include encoding the training peptide sequences using a left-padded one-hot encoding scheme.

[00262] A method of treating a subject having a tumor, comprising performing the steps of any of the neoantigen identification methods described herein, and further comprising obtaining a tumor vaccine comprising the set of selected neoantigens, and administering the tumor vaccine to the subject.

[00263] A method dislocsed herein can also include identifying one or more T cells that are antigen-specific for at least one of the neoantigens in the subset. In some emobodiments, the identification comprises co-culturing the one or more T cells with one or more of the neoantigens in the subset under conditions that expand the one or more antigen-specific T cells. In further embodiments, the identification comprises contacting the one or more T cells with a tetramer comprising one or more of the neoantigens in the subset under conditions that allow binding between the T cell and the tetramer. In even further embodiments, the method disclosed herein can also include identifying one or more T cell receptors (TCR) of the one or more identified T cells. In certain embodiments, identifying the one or more T cell receptors comprises sequencing the T cell receptor sequences of the one or more identified T cells. The method disclosed herein can further comprise genetically engineering a plurality of T cells to express at least one of the one or more identified T cell receptors; culturing the plurality of T cells under conditions that expand the plurality of T cells; and infusing the expanded T cells into the subject. In some embodiments, genetically engineering the plurality of T cells to express at least one of the one or more identified T cell receptors comprises cloning the T cell receptor sequences of the one or more identified T cells into an expression vector; and transfecting each of the plurality of T cells with the expression vector. In some embodiments, the method disclosed herein further comprises culturing the one or more identified T cells

2026201462 26 Feb 2026

under conditions that expand the one or more identified T cells; and infusing the expanded T cells into the subject.

[00264] Also disclosed herein is an isolated T cell that is antigen-specific for at least one selected neoantigen in the subset.

[00265] Also disclosed herein is a methods for manufacturing a tumor vaccine, comprising the steps of: obtaining at least one of exome, transcriptome or whole genome tumor nucleotide sequencing data from the tumor cell of the subject, wherein the tumor nucleotide sequencing data is used to obtain data representing peptide sequences of each of a set of neoantigens, and wherein the peptide sequence of each neoantigen comprises at least one alteration that makes it distinct from the corresponding wild-type peptide sequence; inputting the peptide sequence of each neoantigen into one or more presentation models to generate a set of numerical likelihoods that each of the neoantigens is presented by one or more MHC alleles on the tumor cell surface of the tumor cell of the subject, the set of numerical likelihoods having been identified at least based on received mass spectrometry data; and selecting a subset of the set of neoantigens based on the set of numerical likelihoods to generate a set of selected neoantigens; and producing or having produced a tumor vaccine comprising the set of selected neoantigens.

[00266] Also disclosed herein is a tumor vaccine including a set of selected neoantigens selected by performing the method comprising the steps of: obtaining at least one of exome, transcriptome or whole genome tumor nucleotide sequencing data from the tumor cell of the subject, wherein the tumor nucleotide sequencing data is used to obtain data representing peptide sequences of each of a set of neoantigens, and wherein the peptide sequence of each neoantigen comprises at least one alteration that makes it distinct from the corresponding wild-type peptide sequence; inputting the peptide sequence of each neoantigen into one or more presentation models to generate a set of numerical likelihoods that each of the neoantigens is presented by one or more MHC alleles on the tumor cell surface of the tumor cell of the subject, the set of numerical likelihoods having been identified at least based on received mass spectrometry data; and selecting a subset of the set of neoantigens based on the set of numerical likelihoods to generate a set of selected neoantigens; and producing or having produced a tumor vaccine comprising the set of selected neoantigens.

[00267] The tumor vaccine may include one or more of a nucleotide sequence, a polypeptide sequence, RNA, DNA, a cell, a plasmid, or a vector.

[00268] The tumor vaccine may include one or more neoantigens presented on the tumor cell surface.

2026201462 26 Feb 2026

[00269] The tumor vaccine may include one or more neoantigens that is immunogenic in the subject.

[00270] The tumor vaccine may not include one or more neoantigens that induce an autoimmune response against normal tissue in the subject.

[00271] The tumor vaccine may include an adjuvant.

[00272] The tumor vaccine may include an excipient.

[00273] A method disclosed herein may also include selecting neoantigens that have an increased likelihood of being presented on the tumor cell surface relative to unselected neoantigens based on the presentation model.

[00274] A method disclosed herein may also include selecting neoantigens that have an increased likelihood of being capable of inducing a tumor-specific immune response in the subject relative to unselected neoantigens based on the presentation model.

[00275] A method disclosed herein may also include selecting neoantigens that have an increased likelihood of being capable of being presented to naïve T cells by professional antigen presenting cells (APCs) relative to unselected neoantigens based on the presentation model, optionally wherein the APC is a dendritic cell (DC).

[00276] A method disclosed herein may also include selecting neoantigens that have a decreased likelihood of being subject to inhibition via central or peripheral tolerance relative to unselected neoantigens based on the presentation model.

[00277] A method disclosed herein may also include selecting neoantigens that have a decreased likelihood of being capable of inducing an autoimmune response to normal tissue in the subject relative to unselected neoantigens based on the presentation model.

[00278] The exome or transcriptome nucleotide sequencing data may be obtained by performing sequencing on the tumor tissue.

[00279] The sequencing may be next generation sequencing (NGS) or any massively parallel sequencing approach.

[00280] The set of numerical likelihoods may be further identified by at least MHC-allele interacting features comprising at least one of: the predicted affinity with which the MHC allele and the neoantigen encoded peptide bind; the predicted stability of the neoantigen encoded peptide-MHC complex; the sequence and length of the neoantigen encoded peptide; the probability of presentation of neoantigen encoded peptides with similar sequence in cells from other individuals expressing the particular MHC allele as assessed by mass-spectrometry proteomics or other means; the expression levels of the particular MHC allele in the subject in

2026201462 26 Feb 2026

question (e.g. as measured by RNA-seq or mass spectrometry); the overall neoantigen encoded peptide-sequence-independent probability of presentation by the particular MHC allele in other distinct subjects who express the particular MHC allele; the overall neoantigen encoded peptide-sequence-independent probability of presentation by MHC alleles in the same family of molecules (e.g., HLA-A, HLA-B, HLA-C, HLA-DQ, HLA-DR, HLA-DP) in other distinct subjects.

[00281] The set of numerical likelihoods are further identified by at least MHC-allele noninteracting features comprising at least one of: the C- and N-terminal sequences flanking the neoantigen encoded peptide within its source protein sequence; the presence of protease cleavage motifs in the neoantigen encoded peptide, optionally weighted according to the expression of corresponding proteases in the tumor cells (as measured by RNA-seq or mass spectrometry); the turnover rate of the source protein as measured in the appropriate cell type; the length of the source protein, optionally considering the specific splice variants ("isoforms") most highly expressed in the tumor cells as measured by RNA-seq or proteome mass spectrometry, or as predicted from the annotation of germline or somatic splicing mutations detected in DNA or RNA sequence data; the level of expression of the proteasome, immunoproteasome, thymoproteasome, or other proteases in the tumor cells (which may be measured by RNA-seq, proteome mass spectrometry, or immunohistochemistry); the expression of the source gene of the neoantigen encoded peptide (e.g., as measured by RNA-seq or mass spectrometry); the typical tissue-specific expression of the source gene of the neoantigen encoded peptide during various stages of the cell cycle; a comprehensive catalog of features of the source protein and/or its domains as can be found in e.g. uniProt or PDB http://www.rcsb.org/pdb/home/home.do; features describing the properties of the domain of the source protein containing the peptide, for example: secondary or tertiary structure (e.g., alpha helix vs beta sheet); alternative splicing; the probability of presentation of peptides from the source protein of the neoantigen encoded peptide in question in other distinct subjects; the probability that the peptide will not be detected or over-represented by mass spectrometry due to technical biases; the expression of various gene modules/pathways as measured by RNASeq (which need not contain the source protein of the peptide) that are informative about the state of the tumor cells, stroma, or tumor-infiltrating lymphocytes (TILs); the copy number of the source gene of the neoantigen encoded peptide in the tumor cells; the probability that the peptide binds to the TAP or the measured or predicted binding affinity of the peptide to the TAP; the expression level of TAP in the tumor cells (which may be measured by RNA-seq,

2026201462 26 Feb 2026

proteome mass spectrometry, immunohistochemistry); presence or absence of tumor mutations, including, but not limited to: driver mutations in known cancer driver genes such as EGFR, KRAS, ALK, RET, ROS1, TP53, CDKN2A, CDKN2B, NTRK1, NTRK2, NTRK3, and in genes encoding the proteins involved in the antigen presentation machinery (e.g., B2M, HLA-A, HLA-B, HLA-C, TAP-1, TAP-2, TAPBP, CALR, CNX, ERP57, HLA-DM, HLA-DMA, HLA-DMB, HLA-DO, HLA-DOA, HLA-DOB, HLA-DP, HLA-DPA1, HLA-DPB1, HLA-DQ, HLA-DQA1, HLA-DQA2, HLA-DQB1, HLA-DQB2, HLA-DR, HLA-DRA, HLA-DRB1, HLA-DRB3, HLA-DRB4, HLA-DRB5 or any of the genes coding for components of the proteasome or immunoproteasome). Peptides whose presentation relies on a component of the antigen-presentation machinery that is subject to loss-of-function mutation in the tumor have reduced probability of presentation; presence or absence of functional germline polymorphisms, including, but not limited to: in genes encoding the proteins involved in the antigen presentation machinery (e.g., B2M, HLA-A, HLA-B, HLA-C, TAP-1, TAP-2, TAPBP, CALR, CNX, ERP57, HLA-DM, HLA-DMA, HLA-DMB, HLA-DO, HLA-DOA, HLA-DOB, HLA-DP, HLA-DPA1, HLA-DPB1, HLA-DQ, HLA-DQA1, HLA-DQA2, HLA-DQB1, HLA-DQB2, HLA-DR, HLA-DRA, HLA-DRB1, HLA-DRB3, HLA-DRB4, HLA-DRB5 or any of the genes coding for components of the proteasome or immunoproteasome); tumor type (e.g., NSCLC, melanoma); clinical tumor subtype (e.g., squamous lung cancer vs. non-squamous); smoking history; the typical expression of the source gene of the peptide in the relevant tumor type or clinical subtype, optionally stratified by driver mutation.

[00282] The at least one alteration may be a frameshift or nonframeshift indel, missense or nonsense substitution, splice site alteration, genomic rearrangement or gene fusion, or any genomic or expression alteration giving rise to a neoORF.

[00283] The tumor cell may be selected from the group consisting of: lung cancer, melanoma, breast cancer, ovarian cancer, prostate cancer, kidney cancer, gastric cancer, colon cancer, testicular cancer, head and neck cancer, pancreatic cancer, brain cancer, B-cell lymphoma, acute myelogenous leukemia, chronic myelogenous leukemia, chronic lymphocytic leukemia, and T cell lymphocytic leukemia, non-small cell lung cancer, and small cell lung cancer.

[00284] A method disclosed herein may also include obtaining a tumor vaccine comprising the set of selected neoantigens or a subset thereof, optionally further comprising administering the tumor vaccine to the subject.

2026201462 26 Feb 2026

[00285] At least one of neoantigens in the set of selected neoantigens, when in polypeptide form, may include at least one of: a binding affinity with MHC with an IC50 value of less than 1000nM, for MHC Class I polypeptides a length of 8-15, 8, 9, 10, 11, 12, 13, 14, or 15 amino acids, for MHC Class II polypeptides a length of 6-30, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18,19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 amino acids, presence of sequence motifs within or near the polypeptide in the parent protein sequence promoting proteasome cleavage, and presence of sequence motifs promoting TAP transport. For MHC Class II, presence of sequence motifs within or near the peptide promoting cleavage by extracellular or lysosomal proteases (e.g., cathepsins) or HLA-DM catalyzed HLA binding.

[00286] Also disclosed herein is a methods for generating a model for identifying one or more neoantigens that are likely to be presented on a tumor cell surface of a tumor cell, comprising the steps of: receiving mass spectrometry data comprising data associated with a plurality of isolated peptides eluted from major histocompatibility complex (MHC) derived from a plurality of samples; obtaining a training data set by at least identifying a set of training peptide sequences present in the samples and one or more MHCs associated with each training peptide sequence; training a set of numerical parameters of a presentation model using the training data set comprising the training peptide sequences, the presentation model providing a plurality of numerical likelihoods that peptide sequences from the tumor cell are presented by one or more MHC alleles on the tumor cell surface.

[00287] The presentation model may represent dependence between: presence of a particular amino acid at a particular position of a peptide sequence; and likelihood of presentation, by one of the MHC alleles on the tumor cell, of the peptide sequence containing the particular amino acid at the particular position.

[00288] The samples can also include cell lines engineered to express a single MHC class I or class II allele.

[00289] The samples can also include cell lines engineered to express a plurality of MHC class I or class II alleles.

[00290] The samples can also include human cell lines obtained or derived from a plurality of patients.

[00291] The samples can also include fresh or frozen tumor samples obtained from a plurality of patients.

[00292] The samples can also include peptides identified using T-cell assays.

2026201462 26 Feb 2026

[00293] The training data set may further include data associated with: peptide abundance of the set of training peptides present in the samples; peptide length of the set of training peptides in the samples.

[00294] A method disclosed herein can also include obtaining a set of training protein sequences based on the training peptide sequences by comparing the set of training peptide sequences via alignment to a database comprising a set of known protein sequences, wherein the set of training protein sequences are longer than and include the training peptide sequences.

[00295] A method disclosed herein can also include performing or having performed mass spectrometry on a cell line to obtain at least one of exome, transcriptome, or whole genome nucleotide sequencing data from the cell line, the nucelotide sequencing data including at least one protein sequence including a mutation.

[00296] A method disclosed herein can also include: encoding the training peptide sequences using a one-hot encoding scheme.

[00297] A method disclosed herein can also include obtaining at least one of exome, transcriptome, and whole genome normal nucleotide sequencing data from normal tissue samples; and training the set of parameters of the presentation model using the normal nucleotide sequencing data.

[00298] The training data set may further include data associated with proteome sequences associated with the samples.

[00299] The training data set may further include data associated with MHC peptidome sequences associated with the samples.

[00300] The training data set may further include data associated with peptide-MHC binding affinity measurements for at least one of the isolated peptides.

[00301] The training data set may further include data associated with peptide-MHC binding stability measurements for at least one of the isolated peptides.

[00302] The training data set may further include data associated with transcriptomes associated with the samples.

[00303] The training data set may further include data associated with genomes associated with the samples.

[00304] A method disclosed herein may also include logistically regressing the set of parameters.

[00305] The training peptide sequences may be lengths within a range of k-mers where k is between 8-15, inclusive for MHC class I or 6-30, inclusive for MHC class II.

2026201462 26 Feb 2026

[00306] A method disclosed herein may also include encoding the training peptide sequences using a left-padded one-hot encoding scheme.

[00307] A method disclosed herein may also include determining values for the set of parameters using a deep learning algorithm.

[00308] Disclosed herein is are methods for identifying one or more neoantigens that are likely to be presented on a tumor cell surface of a tumor cell, comprising executing the steps of: receiving mass spectrometry data comprising data associated with a plurality of isolated peptides eluted from major histocompatibility complex (MHC) derived from a plurality of fresh or frozen tumor samples; obtaining a training data set by at least identifying a set of training peptide sequences present in the tumor samples and presented on one or more MHC alleles associated with each training peptide sequence; obtaining a set of training protein sequences based on the training peptide sequences; and training a set of numerical parameters of a presentation model using the training protein sequences and the training peptide sequences, the presentation model providing a plurality of numerical likelihoods that peptide sequences from the tumor cell are presented by one or more MHC alleles on the tumor cell surface.

[00309] The presentation model may represent dependence between: presence of a pair of a particular one of the MHC alleles and a particular amino acid at a particular position of a peptide sequence; and likelihood of presentation on the tumor cell surface, by the particular one of the MHC alleles of the pair, of such a peptide sequence comprising the particular amino acid at the particular position.

[00310] A method disclosed herein can also include selecting a subset of neoantigens, wherein the subset of neoantigens is selected because each has an increased likelihood that it is presented on the cell surface of the tumor relative to one or more distinct tumor neoantigens.

[00311] A method disclosed herein can also include selecting a subset of neoantigens, wherein the subset of neoantigens is selected because each has an increased likelihood that it is capable of inducing a tumor-specific immune response in the subject relative to one or more distinct tumor neoantigens.

[00312] A method disclosed herein can also include selecting a subset of neoantigens, wherein the subset of neoantigens is selected because each has an increased likelihood that it is capable of being presented to naïve T cells by professional antigen presenting cells (APCs) relative to one or more distinct tumor neoantigens, optionally wherein the APC is a dendritic cell (DC).

2026201462 26 Feb 2026

[00313] A method disclosed herein can also include selecting a subset of neoantigens, wherein the subset of neoantigens is selected because each has a decreased likelihood that it is subject to inhibition via central or peripheral tolerance relative to one or more distinct tumor neoantigens.

[00314] A method disclosed herein can also include selecting a subset of neoantigens, wherein the subset of neoantigens is selected because each has a decreased likelihood that it is capable of inducing an autoimmune response to normal tissue in the subject relative to one or more distinct tumor neoantigens.

[00315] A method disclosed herein can also include selecting a subset of neoantigens, wherein the subset of neoantigens is selected because each has a decreased likelihood that it will be differentially post-translationally modified in tumor cells versus APCs, optionally wherein the APC is a dendritic cell (DC).

[00316] The practice of the methods herein will employ, unless otherwise indicated, conventional methods of protein chemistry, biochemistry, recombinant DNA techniques and pharmacology, within the skill of the art. Such techniques are explained fully in the literature. See, e.g., T.E. Creighton, *Proteins: Structures and Molecular Properties* (W.H. Freeman and Company, 1993); A.L. Lehninger, *Biochemistry* (Worth Publishers, Inc., current addition); Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); *Methods In Enzymology* (S. Colowick and N. Kaplan eds., Academic Press, Inc.); *Remington's Pharmaceutical Sciences*, 18th Edition (Easton, Pennsylvania: Mack Publishing Company, 1990); Carey and Sundberg *Advanced Organic Chemistry 3rd Ed.* (Plenum Press) Vols A and B(1992).

III. Identification of Tumor Specific Mutations in Neoantigens

[00317] Also disclosed herein are methods for the identification of certain mutations (e.g., the variants or alleles that are present in cancer cells). In particular, these mutations can be present in the genome, transcriptome, proteome, or exome of cancer cells of a subject having cancer but not in normal tissue from the subject.

[00318] Genetic mutations in tumors can be considered useful for the immunological targeting of tumors if they lead to changes in the amino acid sequence of a protein exclusively in the tumor. Useful mutations include: (1) non-synonymous mutations leading to different amino acids in the protein; (2) read-through mutations in which a stop codon is modified or deleted, leading to translation of a longer protein with a novel tumor-specific sequence at the

2026201462 26 Feb 2026

C-terminus; (3) splice site mutations that lead to the inclusion of an intron in the mature mRNA and thus a unique tumor-specific protein sequence; (4) chromosomal rearrangements that give rise to a chimeric protein with tumor-specific sequences at the junction of 2 proteins (i.e., gene fusion); (5) frameshift mutations or deletions that lead to a new open reading frame with a novel tumor-specific protein sequence. Mutations can also include one or more of nonframeshift indel, missense or nonsense substitution, splice site alteration, genomic rearrangement or gene fusion, or any genomic or expression alteration giving rise to a neoORF.

[00319] Peptides with mutations or mutated polypeptides arising from for example, splice-site, frameshift, readthrough, or gene fusion mutations in tumor cells can be identified by sequencing DNA, RNA or protein in tumor versus normal cells.

[00320] Also mutations can include previously identified tumor specific mutations. Known tumor mutations can be found at the Catalogue of Somatic Mutations in Cancer (COSMIC) database.

[00321] A variety of methods are available for detecting the presence of a particular mutation or allele in an individual's DNA or RNA. Advancements in this field have provided accurate, easy, and inexpensive large-scale SNP genotyping. For example, several techniques have been described including dynamic allele-specific hybridization (DASH), microplate array diagonal gel electrophoresis (MADGE), pyrosequencing, oligonucleotide-specific ligation, the TaqMan system as well as various DNA "chip" technologies such as the Affymetrix SNP chips. These methods utilize amplification of a target genetic region, typically by PCR. Still other methods, based on the generation of small signal molecules by invasive cleavage followed by mass spectrometry or immobilized padlock probes and rolling-circle amplification. Several of the methods known in the art for detecting specific mutations are summarized below.

[00322] PCR based detection means can include multiplex amplification of a plurality of markers simultaneously. For example, it is well known in the art to select PCR primers to generate PCR products that do not overlap in size and can be analyzed simultaneously. Alternatively, it is possible to amplify different markers with primers that are differentially labeled and thus can each be differentially detected. Of course, hybridization based detection means allow the differential detection of multiple PCR products in a sample. Other techniques are known in the art to allow multiplex analyses of a plurality of markers.

[00323] Several methods have been developed to facilitate analysis of single nucleotide polymorphisms in genomic DNA or cellular RNA. For example, a single base polymorphism can be detected by using a specialized exonuclease-resistant nucleotide, as disclosed, e.g., in

2026201462 26 Feb 2026

Mundy, C. R. (U.S. Pat. No. 4,656,127). According to the method, a primer complementary to the allelic sequence immediately 3' to the polymorphic site is permitted to hybridize to a target molecule obtained from a particular animal or human. If the polymorphic site on the target molecule contains a nucleotide that is complementary to the particular exonuclease-resistant nucleotide derivative present, then that derivative will be incorporated onto the end of the hybridized primer. Such incorporation renders the primer resistant to exonuclease, and thereby permits its detection. Since the identity of the exonuclease-resistant derivative of the sample is known, a finding that the primer has become resistant to exonucleases reveals that the nucleotide(s) present in the polymorphic site of the target molecule is complementary to that of the nucleotide derivative used in the reaction. This method has the advantage that it does not require the determination of large amounts of extraneous sequence data.

[00324] A solution-based method can be used for determining the identity of a nucleotide of a polymorphic site. Cohen, D. et al. (French Patent 2,650,840; PCT Appln. No. WO91/02087). As in the Mundy method of U.S. Pat. No. 4,656,127, a primer is employed that is complementary to allelic sequences immediately 3' to a polymorphic site. The method determines the identity of the nucleotide of that site using labeled dideoxynucleotide derivatives, which, if complementary to the nucleotide of the polymorphic site will become incorporated onto the terminus of the primer.

[00325] An alternative method, known as Genetic Bit Analysis or GBA is described by Goelet, P. et al. (PCT Appln. No. 92/15712). The method of Goelet, P. et al. uses mixtures of labeled terminators and a primer that is complementary to the sequence 3' to a polymorphic site. The labeled terminator that is incorporated is thus determined by, and complementary to, the nucleotide present in the polymorphic site of the target molecule being evaluated. In contrast to the method of Cohen et al. (French Patent 2,650,840; PCT Appln. No. WO91/02087) the method of Goelet, P. et al. can be a heterogeneous phase assay, in which the primer or the target molecule is immobilized to a solid phase.

[00326] Several primer-guided nucleotide incorporation procedures for assaying polymorphic sites in DNA have been described (Komher, J. S. et al., Nucl. Acids. Res. 17:7779-7784 (1989); Sokolov, B. P., Nucl. Acids Res. 18:3671 (1990); Syvanen, A.-C., et al., Genomics 8:684-692 (1990); Kuppuswamy, M. N. et al., Proc. Natl. Acad. Sci. (U.S.A.) 88:1143-1147 (1991); Prezant, T. R. et al., Hum. Mutat. 1:159-164 (1992); Ugozzoli, L. et al., GATA 9:107-112 (1992); Nyren, P. et al., Anal. Biochem. 208:171-175 (1993)). These methods differ from GBA in that they utilize incorporation of labeled deoxynucleotides to

2026201462 26 Feb 2026

discriminate between bases at a polymorphic site. In such a format, since the signal is proportional to the number of deoxynucleotides incorporated, polymorphisms that occur in runs of the same nucleotide can result in signals that are proportional to the length of the run (Syvanen, A.-C., et al., Amer. J. Hum. Genet. 52:46-59 (1993)).

[00327] A number of initiatives obtain sequence information directly from millions of individual molecules of DNA or RNA in parallel. Real-time single molecule sequencing-by-synthesis technologies rely on the detection of fluorescent nucleotides as they are incorporated into a nascent strand of DNA that is complementary to the template being sequenced. In one method, oligonucleotides 30-50 bases in length are covalently anchored at the 5' end to glass cover slips. These anchored strands perform two functions. First, they act as capture sites for the target template strands if the templates are configured with capture tails complementary to the surface-bound oligonucleotides. They also act as primers for the template directed primer extension that forms the basis of the sequence reading. The capture primers function as a fixed position site for sequence determination using multiple cycles of synthesis, detection, and chemical cleavage of the dye-linker to remove the dye. Each cycle consists of adding the polymerase/labeled nucleotide mixture, rinsing, imaging and cleavage of dye. In an alternative method, polymerase is modified with a fluorescent donor molecule and immobilized on a glass slide, while each nucleotide is color-coded with an acceptor fluorescent moiety attached to a gamma-phosphate. The system detects the interaction between a fluorescently-tagged polymerase and a fluorescently modified nucleotide as the nucleotide becomes incorporated into the de novo chain. Other sequencing-by-synthesis technologies also exist.

[00328] Any suitable sequencing-by-synthesis platform can be used to identify mutations. As described above, four major sequencing-by-synthesis platforms are currently available: the Genome Sequencers from Roche/454 Life Sciences, the 1G Analyzer from Illumina/Solexa, the SOLiD system from Applied BioSystems, and the Heliscope system from Helicos Biosciences. Sequencing-by-synthesis platforms have also been described by Pacific BioSciences and VisiGen Biotechnologies. In some embodiments, a plurality of nucleic acid molecules being sequenced is bound to a support (e.g., solid support). To immobilize the nucleic acid on a support, a capture sequence/universal priming site can be added at the 3' and/or 5' end of the template. The nucleic acids can be bound to the support by hybridizing the capture sequence to a complementary sequence covalently attached to the support. The capture sequence (also referred to as a universal capture sequence) is a nucleic acid sequence complementary to a sequence attached to a support that may dually serve as a universal primer.

2026201462 26 Feb 2026

[00329] As an alternative to a capture sequence, a member of a coupling pair (such as, e.g., antibody/antigen, receptor/ligand, or the avidin-biotin pair as described in, e.g., US Patent Application No. 2006/0252077) can be linked to each fragment to be captured on a surface coated with a respective second member of that coupling pair.

[00330] Subsequent to the capture, the sequence can be analyzed, for example, by single molecule detection/sequencing, e.g., as described in the Examples and in U.S. Pat. No. 7,283,337, including template-dependent sequencing-by-synthesis. In sequencing-by-synthesis, the surface-bound molecule is exposed to a plurality of labeled nucleotide triphosphates in the presence of polymerase. The sequence of the template is determined by the order of labeled nucleotides incorporated into the 3' end of the growing chain. This can be done in real time or can be done in a step-and-repeat mode. For real-time analysis, different optical labels to each nucleotide can be incorporated and multiple lasers can be utilized for stimulation of incorporated nucleotides.

[00331] Sequencing can also include other massively parallel sequencing or next generation sequencing (NGS) techniques and platforms. Additional examples of massively parallel sequencing techniques and platforms are the Illumina HiSeq or MiSeq, Thermo PGM or Proton, the Pac Bio RS II or Sequel, Qiagen's Gene Reader, and the Oxford Nanopore MinION. Additional similar current massively parallel sequencing technologies can be used, as well as future generations of these technologies.

[00332] Any cell type or tissue can be utilized to obtain nucleic acid samples for use in methods described herein. For example, a DNA or RNA sample can be obtained from a tumor or a bodily fluid, e.g., blood, obtained by known techniques (e.g. venipuncture) or saliva. Alternatively, nucleic acid tests can be performed on dry samples (e.g. hair or skin). In addition, a sample can be obtained for sequencing from a tumor and another sample can be obtained from normal tissue for sequencing where the normal tissue is of the same tissue type as the tumor. A sample can be obtained for sequencing from a tumor and another sample can be obtained from normal tissue for sequencing where the normal tissue is of a distinct tissue type relative to the tumor.

[00333] Tumors can include one or more of lung cancer, melanoma, breast cancer, ovarian cancer, prostate cancer, kidney cancer, gastric cancer, colon cancer, testicular cancer, head and neck cancer, pancreatic cancer, brain cancer, B-cell lymphoma, acute myelogenous leukemia, chronic myelogenous leukemia, chronic lymphocytic leukemia, and T cell lymphocytic leukemia, non-small cell lung cancer, and small cell lung cancer.

2026201462 26 Feb 2026

[00334] Alternatively, protein mass spectrometry can be used to identify or validate the presence of mutated peptides bound to MHC proteins on tumor cells. Peptides can be acid-eluted from tumor cells or from HLA molecules that are immunoprecipitated from tumor, and then identified using mass spectrometry.

IV. Neoantigens

[00335] Neoantigens can include nucleotides or polypeptides. For example, a neoantigen can be an RNA sequence that encodes for a polypeptide sequence. Neoantigens useful in vaccines can therefore include nucleotide sequences or polypeptide sequences.

[00336] Disclosed herein are isolated peptides that comprise tumor specific mutations identified by the methods disclosed herein, peptides that comprise known tumor specific mutations, and mutant polypeptides or fragments thereof identified by methods disclosed herein. Neoantigen peptides can be described in the context of their coding sequence where a neoantigen includes the nucleotide sequence (e.g., DNA or RNA) that codes for the related polypeptide sequence.

[00337] One or more polypeptides encoded by a neoantigen nucleotide sequence can comprise at least one of: a binding affinity with MHC with an IC50 value of less than 1000nM, for MHC Class I peptides a length of 8-15, 8, 9, 10, 11, 12, 13, 14, or 15 amino acids, presence of sequence motifs within or near the peptide promoting proteasome cleavage, and presence or sequence motifs promoting TAP transport. For MHC Class II peptides a length 6-30, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18,19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 amino acids, presence of sequence motifs within or near the peptide promoting cleavage by extracellular or lysosomal proteases (e.g., cathepsins) or HLA-DM catalyzed HLA binding.

[00338] One or more neoantigens can be presented on the surface of a tumor.

[00339] One or more neoantigens can be is immunogenic in a subject having a tumor, e.g., capable of eliciting a T cell response or a B cell response in the subject.

[00340] One or more neoantigens that induce an autoimmune response in a subject can be excluded from consideration in the context of vaccine generation for a subject having a tumor.

[00341] The size of at least one neoantigenic peptide molecule can comprise, but is not limited to, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 31, about 32, about 33, about 34, about 35, about 36, about 37, about 38, about 39, about 40, about 41, about

2026201462 26 Feb 2026

42, about 43, about 44, about 45, about 46, about 47, about 48, about 49, about 50, about 60, about 70, about 80, about 90, about 100, about 110, about 120 or greater amino molecule residues, and any range derivable therein. In specific embodiments the neoantigenic peptide molecules are equal to or less than 50 amino acids.

[00342] Neoantigenic peptides and polypeptides can be: for MHC Class I 15 residues or less in length and usually consist of between about 8 and about 11 residues, particularly 9 or 10 residues; for MHC Class II, 6-30 residues, inclusive.

[00343] If desirable, a longer peptide can be designed in several ways. In one case, when presentation likelihoods of peptides on HLA alleles are predicted or known, a longer peptide could consist of either: (1) individual presented peptides with an extensions of 2-5 amino acids toward the N- and C-terminus of each corresponding gene product; (2) a concatenation of some or all of the presented peptides with extended sequences for each. In another case, when sequencing reveals a long (>10 residues) neoepitope sequence present in the tumor (e.g. due to a frameshift, read-through or intron inclusion that leads to a novel peptide sequence), a longer peptide would consist of: (3) the entire stretch of novel tumor-specific amino acids--thus bypassing the need for computational or in vitro test-based selection of the strongest HLA-presented shorter peptide. In both cases, use of a longer peptide allows endogenous processing by patient cells and may lead to more effective antigen presentation and induction of T cell responses.

[00344] Neoantigenic peptides and polypeptides can be presented on an HLA protein. In some aspects neoantigenic peptides and polypeptides are presented on an HLA protein with greater affinity than a wild-type peptide. In some aspects, a neoantigenic peptide or polypeptide can have an IC50 of at least less than 5000 nM, at least less than 1000 nM, at least less than 500 nM, at least less than 250 nM, at least less than 200 nM, at least less than 150 nM, at least less than 100 nM, at least less than 50 nM or less.

[00345] In some aspects, neoantigenic peptides and polypeptides do not induce an autoimmune response and/or invoke immunological tolerance when administered to a subject.

[00346] Also provided are compositions comprising at least two or more neoantigenic peptides. In some embodiments the composition contains at least two distinct peptides. At least two distinct peptides can be derived from the same polypeptide. By distinct polypeptides is meant that the peptide vary by length, amino acid sequence, or both. The peptides are derived from any polypeptide known to or have been found to contain a tumor specific mutation. Suitable polypeptides from which the neoantigenic peptides can be derived can be found for

2026201462 26 Feb 2026

example in the COSMIC database. COSMIC curates comprehensive information on somatic mutations in human cancer. The peptide contains the tumor specific mutation. In some aspects the tumor specific mutation is a driver mutation for a particular cancer type.

[00347] Neoantigenic peptides and polypeptides having a desired activity or property can be modified to provide certain desired attributes, e.g., improved pharmacological characteristics, while increasing or at least retaining substantially all of the biological activity of the unmodified peptide to bind the desired MHC molecule and activate the appropriate T cell. For instance, neoantigenic peptide and polypeptides can be subject to various changes, such as substitutions, either conservative or non-conservative, where such changes might provide for certain advantages in their use, such as improved MHC binding, stability or presentation. By conservative substitutions is meant replacing an amino acid residue with another which is biologically and/or chemically similar, e.g., one hydrophobic residue for another, or one polar residue for another. The substitutions include combinations such as Gly, Ala; Val, Ile, Leu, Met; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr. The effect of single amino acid substitutions may also be probed using D-amino acids. Such modifications can be made using well known peptide synthesis procedures, as described in e.g., Merrifield, Science 232:341-347 (1986), Barany & Merrifield, The Peptides, Gross & Meienhofer, eds. (N.Y., Academic Press), pp. 1-284 (1979); and Stewart & Young, Solid Phase Peptide Synthesis, (Rockford, Ill., Pierce), 2d Ed. (1984).

[00348] Modifications of peptides and polypeptides with various amino acid mimetics or unnatural amino acids can be particularly useful in increasing the stability of the peptide and polypeptide in vivo. Stability can be assayed in a number of ways. For instance, peptidases and various biological media, such as human plasma and serum, have been used to test stability. See, e.g., Verhoef et al., Eur. J. Drug Metab Pharmacokin. 11:291-302 (1986). Half-life of the peptides can be conveniently determined using a 25% human serum (v/v) assay. The protocol is generally as follows. Pooled human serum (Type AB, non-heat inactivated) is delipidated by centrifugation before use. The serum is then diluted to 25% with RPMI tissue culture media and used to test peptide stability. At predetermined time intervals a small amount of reaction solution is removed and added to either 6% aqueous trichloracetic acid or ethanol. The cloudy reaction sample is cooled (4 degrees C) for 15 minutes and then spun to pellet the precipitated serum proteins. The presence of the peptides is then determined by reversed-phase HPLC using stability-specific chromatography conditions.

2026201462 26 Feb 2026

[00349] The peptides and polypeptides can be modified to provide desired attributes other than improved serum half-life. For instance, the ability of the peptides to induce CTL activity can be enhanced by linkage to a sequence which contains at least one epitope that is capable of inducing a T helper cell response. Immunogenic peptides/T helper conjugates can be linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, e.g., Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus can be a hetero- or homo-oligomer. When present, the spacer will usually be at least one or two residues, more usually three to six residues. Alternatively, the peptide can be linked to the T helper peptide without a spacer.

[00350] A neoantigenic peptide can be linked to the T helper peptide either directly or via a spacer either at the amino or carboxy terminus of the peptide. The amino terminus of either the neoantigenic peptide or the T helper peptide can be acylated. Exemplary T helper peptides include tetanus toxoid 830-843, influenza 307-319, malaria circumsporozoite 382-398 and 378-389.

[00351] Proteins or peptides can be made by any technique known to those of skill in the art, including the expression of proteins, polypeptides or peptides through standard molecular biological techniques, the isolation of proteins or peptides from natural sources, or the chemical synthesis of proteins or peptides. The nucleotide and protein, polypeptide and peptide sequences corresponding to various genes have been previously disclosed, and can be found at computerized databases known to those of ordinary skill in the art. One such database is the National Center for Biotechnology Information's Genbank and GenPept databases located at the National Institutes of Health website. The coding regions for known genes can be amplified and/or expressed using the techniques disclosed herein or as would be known to those of ordinary skill in the art. Alternatively, various commercial preparations of proteins, polypeptides and peptides are known to those of skill in the art.

[00352] In a further aspect a neoantigen includes a nucleic acid (e.g. polynucleotide) that encodes a neoantigenic peptide or portion thereof. The polynucleotide can be, e.g., DNA, cDNA, PNA, CNA, RNA (e.g., mRNA), either single- and/or double-stranded, or native or stabilized forms of polynucleotides, such as, e.g., polynucleotides with a phosphorothiate backbone, or combinations thereof and it may or may not contain introns. A still further aspect

2026201462 26 Feb 2026

provides an expression vector capable of expressing a polypeptide or portion thereof. Expression vectors for different cell types are well known in the art and can be selected without undue experimentation. Generally, DNA is inserted into an expression vector, such as a plasmid, in proper orientation and correct reading frame for expression. If necessary, DNA can be linked to the appropriate transcriptional and translational regulatory control nucleotide sequences recognized by the desired host, although such controls are generally available in the expression vector. The vector is then introduced into the host through standard techniques. Guidance can be found e.g. in Sambrook et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.

V. Vaccine Compositions

[00353] Also disclosed herein is an immunogenic composition, e.g., a vaccine composition, capable of raising a specific immune response, e.g., a tumor-specific immune response. Vaccine compositions typically comprise a plurality of neoantigens, e.g., selected using a method described herein. Vaccine compositions can also be referred to as vaccines.

[00354] A vaccine can contain between 1 and 30 peptides, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 different peptides, 6, 7, 8, 9, 10 11, 12, 13, or 14 different peptides, or 12, 13 or 14 different peptides. Peptides can include post-translational modifications. A vaccine can contain between 1 and 100 or more nucleotide sequences, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94,95, 96, 97, 98, 99, 100 or more different nucleotide sequences, 6, 7, 8, 9, 10 11, 12, 13, or 14 different nucleotide sequences, or 12, 13 or 14 different nucleotide sequences. A vaccine can contain between 1 and 30 neoantigen sequences, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94,95, 96, 97, 98, 99, 100 or more different neoantigen sequences, 6, 7, 8, 9, 10 11, 12, 13, or 14 different neoantigen sequences, or 12, 13 or 14 different neoantigen sequences.

[00355] In one embodiment, different peptides and/or polypeptides or nucleotide sequences encoding them are selected so that the peptides and/or polypeptides capable of associating with

2026201462 26 Feb 2026

different MHC molecules, such as different MHC class I molecules and/or different MHC class II molecules. In some aspects, one vaccine composition comprises coding sequence for peptides and/or polypeptides capable of associating with the most frequently occurring MHC class I molecules and/or different MHC class II molecules. Hence, vaccine compositions can comprise different fragments capable of associating with at least 2 preferred, at least 3 preferred, or at least 4 preferred MHC class I molecules and/or different MHC class II molecules.

[00356] The vaccine composition can be capable of raising a specific cytotoxic T-cells response and/or a specific helper T-cell response.

[00357] A vaccine composition can further comprise an adjuvant and/or a carrier. Examples of useful adjuvants and carriers are given herein below. A composition can be associated with a carrier such as e.g. a protein or an antigen-presenting cell such as e.g. a dendritic cell (DC) capable of presenting the peptide to a T-cell.

[00358] Adjuvants are any substance whose admixture into a vaccine composition increases or otherwise modifies the immune response to a neoantigen. Carriers can be scaffold structures, for example a polypeptide or a polysaccharide, to which a neoantigen, is capable of being associated. Optionally, adjuvants are conjugated covalently or non-covalently.

[00359] The ability of an adjuvant to increase an immune response to an antigen is typically manifested by a significant or substantial increase in an immune-mediated reaction, or reduction in disease symptoms. For example, an increase in humoral immunity is typically manifested by a significant increase in the titer of antibodies raised to the antigen, and an increase in T-cell activity is typically manifested in increased cell proliferation, or cellular cytotoxicity, or cytokine secretion. An adjuvant may also alter an immune response, for example, by changing a primarily humoral or Th response into a primarily cellular, or Th response.

[00360] Suitable adjuvants include, but are not limited to 1018 ISS, alum, aluminium salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, JuvImmune, LipoVac, MF59, monophosphoryl lipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PepTel vector system, PLG microparticles, resiquimod, SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, Aquila's QS21 stimulon (Aquila Biotech, Worcester, Mass., USA) which is derived from saponin, mycobacterial extracts and synthetic bacterial cell wall

2026201462 26 Feb 2026

mimics, and other proprietary adjuvants such as Ribi's Detox. Quil or Superfos. Adjuvants such as incomplete Freund's or GM-CSF are useful. Several immunological adjuvants (e.g., MF59) specific for dendritic cells and their preparation have been described previously (Dupuis M, et al., Cell Immunol. 1998; 186(1):18-27; Allison A C; Dev Biol Stand. 1998; 92:3-11). Also cytokines can be used. Several cytokines have been directly linked to influencing dendritic cell migration to lymphoid tissues (e.g., TNF-alpha), accelerating the maturation of dendritic cells into efficient antigen-presenting cells for T-lymphocytes (e.g., GM-CSF, IL-1 and IL-4) (U.S. Pat. No. 5,849,589, specifically incorporated herein by reference in its entirety) and acting as immunoadjuvants (e.g., IL-12) (Gabrilovich D I, et al., J Immunother Emphasis Tumor Immunol. 1996 (6):414-418).

[00361] CpG immunostimulatory oligonucleotides have also been reported to enhance the effects of adjuvants in a vaccine setting. Other TLR binding molecules such as RNA binding TLR 7, TLR 8 and/or TLR 9 may also be used.

[00362] Other examples of useful adjuvants include, but are not limited to, chemically modified CpGs (e.g. CpR, Idera), Poly(I:C)(e.g. polyi:CI2U), non-CpG bacterial DNA or RNA as well as immunoactive small molecules and antibodies such as cyclophosphamide, sunitinib, bevacizumab, celebrex, NCX-4016, sildenafil, tadalafil, vardenafil, sorafinib, XL-999, CP-547632, pazopanib, ZD2171, AZD2171, ipilimumab, tremelimumab, and SC58175, which may act therapeutically and/or as an adjuvant. The amounts and concentrations of adjuvants and additives can readily be determined by the skilled artisan without undue experimentation. Additional adjuvants include colony-stimulating factors, such as Granulocyte Macrophage Colony Stimulating Factor (GM-CSF, sargramostim).

[00363] A vaccine composition can comprise more than one different adjuvant. Furthermore, a therapeutic composition can comprise any adjuvant substance including any of the above or combinations thereof. It is also contemplated that a vaccine and an adjuvant can be administered together or separately in any appropriate sequence.

[00364] A carrier (or excipient) can be present independently of an adjuvant. The function of a carrier can for example be to increase the molecular weight of in particular mutant to increase activity or immunogenicity, to confer stability, to increase the biological activity, or to increase serum half-life. Furthermore, a carrier can aid presenting peptides to T-cells. A carrier can be any suitable carrier known to the person skilled in the art, for example a protein or an antigen presenting cell. A carrier protein could be but is not limited to keyhole limpet hemocyanin, serum proteins such as transferrin, bovine serum albumin, human serum albumin, thyroglobulin

2026201462 26 Feb 2026

or ovalbumin, immunoglobulins, or hormones, such as insulin or palmitic acid. For immunization of humans, the carrier is generally a physiologically acceptable carrier acceptable to humans and safe. However, tetanus toxoid and/or diptheria toxoid are suitable carriers. Alternatively, the carrier can be dextrans for example sepharose.

[00365] Cytotoxic T-cells (CTLs) recognize an antigen in the form of a peptide bound to an MHC molecule rather than the intact foreign antigen itself. The MHC molecule itself is located at the cell surface of an antigen presenting cell. Thus, an activation of CTLs is possible if a trimeric complex of peptide antigen, MHC molecule, and APC is present. Correspondingly, it may enhance the immune response if not only the peptide is used for activation of CTLs, but if additionally APCs with the respective MHC molecule are added. Therefore, in some embodiments a vaccine composition additionally contains at least one antigen presenting cell.

[00366] Neoantigens can also be included in viral vector-based vaccine platforms, such as vaccinia, fowlpox, self-replicating alphavirus, marabavirus, adenovirus (*See, e.g.,* Tatsis et al., Adenoviruses, *Molecular Therapy* (2004) 10, 616—629), or lentivirus, including but not limited to second, third or hybrid second/third generation lentivirus and recombinant lentivirus of any generation designed to target specific cell types or receptors (*See, e.g.,* Hu et al., Immunization Delivered by Lentiviral Vectors for Cancer and Infectious Diseases, *Immunol Rev.* (2011) 239(1): 45-61, Sakuma et al., Lentiviral vectors: basic to translational, *Biochem J.* (2012) 443(3):603-18, Cooper et al., Rescue of splicing-mediated intron loss maximizes expression in lentiviral vectors containing the human ubiquitin C promoter, *Nucl. Acids Res.* (2015) 43 (1): 682-690, Zufferey et al., Self-Inactivating Lentivirus Vector for Safe and Efficient In Vivo Gene Delivery, *J. Virol.* (1998) 72 (12): 9873-9880). Dependent on the packaging capacity of the above mentioned viral vector-based vaccine platforms, this approach can deliver one or more nucleotide sequences that encode one or more neoantigen peptides. The sequences may be flanked by non-mutated sequences, may be separated by linkers or may be preceded with one or more sequences targeting a subcellular compartment (See, e.g., Gros et al., Prospective identification of neoantigen-specific lymphocytes in the peripheral blood of melanoma patients, *Nat Med.* (2016) 22 (4):433-8, Stronen et al., Targeting of cancer neoantigens with donor-derived T cell receptor repertoires, *Science.* (2016) 352 (6291):1337-41, Lu et al., Efficient identification of mutated cancer antigens recognized by T cells associated with durable tumor regressions, *Clin Cancer Res.* (2014) 20(13):3401-10). Upon introduction into a host, infected cells express the neoantigens, and thereby elicit a host immune (e.g., CTL) response against the peptide(s). Vaccinia vectors and methods useful in

26 Feb 2026
2026201462

immunization protocols are described in, e.g., U.S. Pat. No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover et al. (Nature 351:456-460 (1991)). A wide variety of other vaccine vectors useful for therapeutic administration or immunization of neoantigens, e.g., Salmonella typhi vectors, and the like will be apparent to those skilled in the art from the description herein.

V.A. Neoantigen Cassette

[00367] The methods employed for the selection of one or more neoantigens, the cloning and construction of a “cassette” and its insertion into a viral vector are within the skill in the art given the teachings provided herein. By "neoantigen cassette" is meant the combination of a selected neoantigen or plurality of neoantigens and the other regulatory elements necessary to transcribe the neoantigen(s) and express the transcribed product. A neoantigen or plurality of neoantigens can be operatively linked to regulatory components in a manner which permits transcription. Such components include conventional regulatory elements that can drive expression of the neoantigen(s) in a cell transfected with the viral vector. Thus the neoantigen cassette can also contain a selected promoter which is linked to the neoantigen(s) and located, with other, optional regulatory elements, within the selected viral sequences of the recombinant vector.

[00368] Useful promoters can be constitutive promoters or regulated (inducible) promoters, which will enable control of the amount of neoantigen(s) to be expressed. For example, a desirable promoter is that of the cytomegalovirus immediate early promoter/enhancer [see, e.g., Boshart et al, Cell, 41:521-530 (1985)]. Another desirable promoter includes the Rous sarcoma virus LTR promoter/enhancer. Still another promoter/enhancer sequence is the chicken cytoplasmic beta-actin promoter [T. A. Kost et al, Nucl. Acids Res., 11(23):8287 (1983)]. Other suitable or desirable promoters can be selected by one of skill in the art.

[00369] The neoantigen cassette can also include nucleic acid sequences heterologous to the viral vector sequences including sequences providing signals for efficient polyadenylation of the transcript (poly(A), poly-A or pA) and introns with functional splice donor and acceptor sites. A common poly-A sequence which is employed in the exemplary vectors of this invention is that derived from the papovavirus SV-40. The poly-A sequence generally can be inserted in the cassette following the neoantigen-based sequences and before the viral vector sequences. A common intron sequence can also be derived from SV-40, and is referred to as the SV-40 T intron sequence. A neoantigen cassette can also contain such an intron, located

2026201462 26 Feb 2026

between the promoter/enhancer sequence and the neoantigen(s). Selection of these and other common vector elements are conventional [see, e.g., Sambrook et al, "Molecular Cloning. A Laboratory Manual.", 2d edit., Cold Spring Harbor Laboratory, New York (1989) and references cited therein] and many such sequences are available from commercial and industrial sources as well as from Genbank.

[00370] A neoantigen cassette can have one or more neoantigens. For example, a given cassette can include 1-10, 1-20, 1-30, 10-20, 15-25, 15-20, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more neoantigens. Neoantigens can be linked directly to one another. Neoantigens can also be linked to one another with linkers. Neoantigens can be in any orientation relative to one another including N to C or C to N.

[00371] As above stated, the neoantigen cassette can be located in the site of any selected deletion in the viral vector, such as the site of the E1 gene region deletion or E3 gene region deletion, among others which may be selected.

[00372] The neoantigen cassette can be described using the following formula to describe the ordered sequence of each element, from 5' to 3':

$$(P_a\text{-}(L5_b\text{-}N_c\text{-}L3_d)_X)_Z\text{-}(P2_h\text{-}(G5_e\text{-}U_f)_Y)_W\text{-}G3_g$$

[00373] wherein P and P2 comprise promoter nucleotide sequences, N comprises an MHC class I epitope encoding nucleic acid sequence, L5 comprises a 5' linker sequence, L3 comprises a 3' linker sequence, G5 comprises a nucleic acid sequences encoding an amino acid linker, G3 comprises one of the at least one nucleic acid sequences encoding an amino acid linker, U comprises an MHC class II antigen-encoding nucleic acid sequence, where for each X the corresponding Nc is a epitope encoding nucleic acid sequence, where for each Y the corresponding Uf is an antigen-encoding nucleic acid sequence. The composition and ordered sequence can be further defined by selecting the number of elements present, for example where a = 0 or 1, where b = 0 or 1, where c = 1, where d = 0 or 1, where e = 0 or 1, where f = 1, where g = 0 or 1, where h = 0 or 1, X = 1 to 400, Y = 0, 1, 2, 3, 4 or 5, Z = 1 to 400, and W = 0, 1, 2, 3, 4 or 5.

[00374] In one example, elements present include where a = 0, b = 1, d = 1, e = 1, g = 1, h = 0, X = 10, Y = 2, Z = 1, and W = 1, describing where no additional promoter is present (*i.e.* only the promoter nucleotide sequence provided by the RNA alphavirus backbone is present), 20 MHC class I epitope are present, a 5' linker is present for each N, a 3' linker is present for each N, 2 MHC class II epitopes are present, a linker is present linking the two MHC class II

2026201462 26 Feb 2026

epitopes, a linker is present linking the 5’ end of the two MHC class II epitopes to the 3’ linker of the final MHC class I epitope, and a linker is present linking the 3’ end of the two MHC class II epitopes to the to the RNA alphavirus backbone. Examples of linking the 3’ end of the neoantigen cassette to the RNA alphavirus backbone include linking directly to the 3’ UTR elements provided by the RNA alphavirus backbone, such as a 3’ 19-nt CSE. Examples of linking the 5’ end of the neoantigen cassette to the RNA alphavirus backbone include linking directly to a 26S promoter sequence, an alphavirus 5’ UTR, a 51-nt CSE, or a 24-nt CSE.

[00375] Other examples include: where a = 1 describing where a promoter other than the promoter nucleotide sequence provided by the RNA alphavirus backbone is present; where a = 1 and Z is greater than 1 where multiple promoters other than the promoter nucleotide sequence provided by the RNA alphavirus backbone are present each driving expression of 1 or more distinct MHC class I epitope encoding nucleic acid sequences; where h = 1 describing where a separate promoter is present to drive expression of the MHC class II antigen-encoding nucleic acid sequences; and where g = 0 describing the MHC class II antigen-encoding nucleic acid sequence, if present, is directly linked to the RNA alphavirus backbone.

[00376] Other examples include where each MHC class I epitope that is present can have a 5’ linker, a 3’ linker, neither, or both. In examples where more than one MHC class I epitope is present in the same neoantigen cassette, some MHC class I epitopes may have both a 5’ linker and a 3’ linker, while other MHC class I epitopes may have either a 5’ linker, a 3’ linker, or neither. In other examples where more than one MHC class I epitope is present in the same neoantigen cassette, some MHC class I epitopes may have either a 5’ linker or a 3’ linker, while other MHC class I epitopes may have either a 5’ linker, a 3’ linker, or neither.

[00377] In examples where more than one MHC class II epitope is present in the same neoantigen cassette, some MHC class II epitopes may have both a 5’ linker and a 3’ linker, while other MHC class II epitopes may have either a 5’ linker, a 3’ linker, or neither. In other examples where more than one MHC class II epitope is present in the same neoantigen cassette, some MHC class II epitopes may have either a 5’ linker or a 3’ linker, while other MHC class II epitopes may have either a 5’ linker, a 3’ linker, or neither.

[00378] The promoter nucleotide sequences P and/or P2 can be the same as a promoter nucleotide sequence provided by the RNA alphavirus backbone. For example, the promoter sequence provided by the RNA alphavirus backbone, Pn and P2, can each comprise a 26S subgenomic promoter. The promoter nucleotide sequences P and/or P2 can be different from

2026201462 26 Feb 2026

the promoter nucleotide sequence provided by the RNA alphavirus backbone, as well as can be different from each other.

[00379] The 5' linker L5 can be a native sequence or a non-natural sequence. Non-natural sequence include, but are not limited to, AAY, RR, and DPP. The 3' linker L3 can also be a native sequence or a non-natural sequence. Additionally, L5 and L3 can both be native sequences, both be non-natural sequences, or one can be native and the other non-natural. For each X, the amino acid linkers can be 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94,95, 96, 97, 98, 99, 100 or more amino acids in length. For each X, the amino acid linkers can be also be at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, or at least 30 amino acids in length.

[00380] The amino acid linker G5, for each Y, can be 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94,95, 96, 97, 98, 99, 100 or more amino acids in length. For each Y, the amino acid linkers can be also be at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, or at least 30 amino acids in length.

[00381] The amino acid linker G3 can be 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94,95, 96, 97, 98, 99, 100 or more amino acids in length. G3 can be also be at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, or at least 30 amino acids in length.

2026201462 26 Feb 2026

[00382] For each X, each N can encodes a MHC class I epitope 7-15 amino acids in length. For each X, each N can also encodes a MHC class I epitope 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 amino acids in length. For each X, each N can also encodes a MHC class I epitope at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, or at least 30 amino acids in length.

V.B. Immune Checkpoints

[00383] Vectors described herein, such as C68 vectors described herein or alphavirus vectors described herein, can comprise a nucleic acid which encodes at least one neoantigen and the same or a separate vector can comprise a nucleic acid which encodes at least one immune modulator (e.g., an antibody such as an scFv) which binds to and blocks the activity of an immune checkpoint molecule. Vectors can comprise a neoantigen cassette and one or more nucleic acid molecules encoding a checkpoint inhibitor.

[00384] Illustrative immune checkpoint molecules that can be targeted for blocking or inhibition include, but are not limited to, CTLA-4, 4-1BB (CD137), 4-1BBL (CD137L), PDL1, PDL2, PD1, B7-H3, B7-H4, BTLA, HVEM, TIM3, GAL9, LAG3, TIM3, B7H3, B7H4, VISTA, KIR, 2B4 (belongs to the CD2 family of molecules and is expressed on all NK, γδ, and memory CD8+ (αβ) T cells), CD160 (also referred to as BY55), and CGEN-15049. Immune checkpoint inhibitors include antibodies, or antigen binding fragments thereof, or other binding proteins, that bind to and block or inhibit the activity of one or more of CTLA-4, PDL1, PDL2, PD1, B7-H3, B7-H4, BTLA, HVEM, TIM3, GAL9, LAG3, TIM3, B7H3, B7H4, VISTA, KIR, 2B4, CD160, and CGEN-15049. Illustrative immune checkpoint inhibitors include Tremelimumab (CTLA-4 blocking antibody), anti-OX40, PD-L1 monoclonal Antibody (Anti-B7-H1; MEDI4736), ipilimumab, MK-3475 (PD-1 blocker), Nivolumamb (anti-PD1 antibody), CT-011 (anti-PD1 antibody), BY55 monoclonal antibody, AMP224 (anti-PDL1 antibody), BMS-936559 (anti-PDL1 antibody), MPLDL3280A (anti-PDL1 antibody), MSB0010718C (anti-PDL1 antibody) and Yervoy/ipilimumab (anti-CTLA-4 checkpoint inhibitor). Antibody-encoding sequences can be engineered into vectors such as C68 using ordinary skill in the art. An exemplary method is described in Fang et al., Stable antibody expression at therapeutic

2026201462 26 Feb 2026

levels using the 2A peptide. *Nat Biotechnol.* 2005 May;23(5):584-90. Epub 2005 Apr 17; herein incorporated by reference for all purposes.

V.C. Additional Considerations for Vaccine Design and Manufacture

V.C.1. Determination of a Set of Peptides that Cover All Tumor Subclones

[00385] Truncal peptides, meaning those presented by all or most tumor subclones, can be prioritized for inclusion into the vaccine.[53] Optionally, if there are no truncal peptides predicted to be presented and immunogenic with high probability, or if the number of truncal peptides predicted to be presented and immunogenic with high probability is small enough that additional non-truncal peptides can be included in the vaccine, then further peptides can be prioritized by estimating the number and identity of tumor subclones and choosing peptides so as to maximize the number of tumor subclones covered by the vaccine.[54]

V.C.2. Neoantigen Prioritization

[00386] After all of the above above neoantigen filters are applied, more candidate neoantigens may still be available for vaccine inclusion than the vaccine technology can support. Additionally, uncertainty about various aspects of the neoantigen analysis may remain and tradeoffs may exist between different properties of candidate vaccine neoantigens. Thus, in place of predetermined filters at each step of the selection process, an integrated multi-dimensional model can be considered that places candidate neoantigens in a space with at least the following axes and optimizes selection using an integrative approach.

1. Risk of auto-immunity or tolerance (risk of germline) (lower risk of auto-immunity is typically preferred)
2. Probability of sequencing artifact (lower probability of artifact is typically preferred)
3. Probability of immunogenicity (higher probability of immunogenicity is typically preferred)
4. Probability of presentation (higher probability of presentation is typically preferred)
5. Gene expression (higher expression is typically preferred)
6. Coverage of HLA genes (larger number of HLA molecules involved in the presentation of a set of neoantigens may lower the probability that a tumor will escape immune attack via downregulation or mutation of HLA molecules)
7. Coverage of HLA classes (covering both HLA-I and HLA-II may increase the probability of therapeutic response and decrease the probability of tumor escape)

[00387] Additionally, optionally, neoantigens can be deprioritized (e.g., excluded) from the vaccination if they are predicted to be presented by HLA alleles lost or inactivated in either all or part of the patient's tumor. HLA allele loss can occur by either somatic mutation, loss of

2026201462 26 Feb 2026

heterozygosity, or homozygous deletion of the locus. Methods for detection of HLA allele somatic mutation are well known in the art, e.g. (Shukla et al., 2015). Methods for detection of somatic LOH and homozygous deletion (including for HLA locus) are likewise well described. (Carter et al., 2012; McGranahan et al., 2017; Van Loo et al., 2010).

V.D. Alphavirus

V.D.1. Alphavirus Biology

[00388] Alphaviruses are members of the family *Togaviridae*, and are positive-sense single stranded RNA viruses. Alphaviruses can also be referred to as self-replicating RNA or srRNA. Members are typically classified as either Old World, such as Sindbis, Ross River, Mayaro, Chikungunya, and Semliki Forest viruses, or New World, such as eastern equine encephalitis, Aura, Fort Morgan, or Venezuelan equine encephalitis virus and its derivative strain TC-83 (Strauss Microbrial Review 1994). A natural alphavirus genome is typically around 12kb in length, the first two-thirds of which contain genes encoding non-structural proteins (nsPs) that form RNA replication complexes for self-replication of the viral genome, and the last third of which contains a subgenomic expression cassette encoding structural proteins for virion production (Frolov RNA 2001).

[00389] A model lifecycle of an alphavirus involves several distinct steps (Strauss Microbrial Review 1994, Jose Future Microbiol 2009). Following virus attachment to a host cell, the virion fuses with membranes within endocytic compartments resulting in the eventual release of genomic RNA into the cytosol. The genomic RNA, which is in a plus-strand orientation and comprises a 5' methylguanylate cap and 3' polyA tail, is translated to produce non-structural proteins nsP1-4 that form the replication complex. Early in infection, the plus-strand is then replicated by the complex into a minus-stand template. In the current model, the replication complex is further processed as infection progresses, with the resulting processed complex switching to transcription of the minus-strand into both full-length positive-strand genomic RNA, as well as the 26S subgenomic positive-strand RNA containing the structural genes. Several conserved sequence elements (CSEs) of alphavirus have been identified to potentially play a role in the various RNA replication steps including; a complement of the 5' UTR in the replication of plus-strand RNAs from a minus-strand template, a 51-nt CSE in the replication of minus-strand synthesis from the genomic template, a 24-nt CSE in the junction

2026201462 26 Feb 2026

region between the nsPs and the 26S RNA in the transcription of the subgenomic RNA from the minus-strand, and a 3' 19-nt CSE in minus-strand synthesis from the plus-strand template.

[00390] Following the replication of the various RNA species, virus particles are then typically assembled in the natural lifecycle of the virus. The 26S RNA is translated and the resulting proteins further processed to produce the structural proteins including capsid protein, glycoproteins E1 and E2, and two small polypeptides E3 and 6K (Strauss 1994). Encapsidation of viral RNA occurs, with capsid proteins normally specific for only genomic RNA being packaged, followed by virion assembly and budding at the membrane surface.

V.D.2. Alphavirus as a delivery vector

[00391] Alphaviruses have previously been engineered for use as expression vector systems (Pushko 1997, Rheme 2004). Alphaviruses offer several advantages, particularly in a vaccine setting where heterologous antigen expression can be desired. Due to its ability to self-replicate in the host cytosol, alphavirus vectors are generally able to produce high copy numbers of the expression cassette within a cell resulting in a high level of heterologous antigen production. Additionally, the vectors are generally transient, resulting in improved biosafety as well as reduced induction of immunological tolerance to the vector. The public, in general, also lacks pre-existing immunity to alphavirus vectors as compared to other standard viral vectors, such as human adenovirus. Alphavirus based vectors also generally result in cytotoxic responses to infected cells. Cytotoxicity, to a certain degree, can be important in a vaccine setting to properly illicit an immune response to the heterologous antigen expressed. However, the degree of desired cytotoxicity can be a balancing act, and thus several attenuated alphaviruses have been developed, including the TC-83 strain of VEE. Thus, an example of a neoantigen expression vector described herein can utilize an alphavirus backbone that allows for a high level of neoantigen expression, elicits a robust immune response to neoantigen, does not elicit an immune response to the vector itself, and can be used in a safe manner. Furthermore, the neoantigen expression cassette can be designed to elicit different levels of an immune response through optimization of which alphavirus sequences the vector uses, including, but not limited to, sequences derived from VEEor its attenuated derivative TC-83.

[00392] Several expression vector design strategies have been engineered using alphavirus sequences (Pushko 1997). In one strategy, a alphavirus vector design includes inserting a second copy of the 26S promoter sequence elements downstream of the structural protein genes, followed by a heterologous gene (Frolov 1993). Thus, in addition to the natural non-structural and structural proteins, an additional subgenomic RNA is produced that expresses the

2026201462 26 Feb 2026

heterologous protein. In this system, all the elements for production of infectious virions are present and, therefore, repeated rounds of infection of the expression vector in non-infected cells can occur.

[00393] Another expression vector design makes use of helper virus systems (Pushko 1997). In this strategy, the structural proteins are replaced by a heterologous gene. Thus, following self-replication of viral RNA mediated by still intact non-structural genes, the 26S subgenomic RNA provides for expression of the heterologous protein. Traditionally, additional vectors that expresses the structural proteins are then supplied *in trans,* such as by co-transfection of a cell line, to produce infectious virus. A system is described in detail in USPN 8,093,021, which is herein incorporated by reference in its entirety, for all purposes. The helper vector system provides the benefit of limiting the possibility of forming infectious particles and, therefore, improves biosafety. In addition, the helper vector system reduces the total vector length, potentially improving the replication and expression efficiency. Thus, an example of a neoantigen expression vector described herein can utilize an alphavirus backbone wherein the structural proteins are replaced by a neoantigen cassette, the resulting vector both reducing biosafety concerns, while at the same time promoting efficient expression due to the reduction in overall expression vector size.

V.D.3. Alphavirus production *in vitro*

[00394] Alphavirus delivery vectors are generally positive-sense RNA polynucleotides. A convenient technique well-known in the art for RNA production is *in vitro* transcription IVT. In this technique, a DNA template of the desired vector is first produced by techniques well-known to those in the art, including standard molecular biology techniques such as cloning, restriction digestion, ligation, gene synthesis, and polymerase chain reaction (PCR). The DNA template contains a RNA polymerase promoter at the 5’ end of the sequence desired to be transcribed into RNA. Promoters include, but are not limited to, bacteriophage polymerase promoters such as T3, T7, or SP6. The DNA template is then incubated with the appropriate RNA polymerase enzyme, buffer agents, and nucleotides (NTPs). The resulting RNA polynucleotide can optionally be further modified including, but limited to, addition of a 5’ cap structure such as 7-methylguanosine or a related structure, and optionally modifying the 3’ end to include a polyadenylate (polyA) tail. The RNA can then be purified using techniques well-known in the field, such as phenol-chloroform extraction.

V.D.4. Delivery via lipid nanoparticle

2026201462 26 Feb 2026

[00395] An important aspect to consider in vaccine vector design is immunity against the vector itself (Riley 2017). This may be in the form of preexisting immunity to the vector itself, such as with certain human adenovirus systems, or in the form of developing immunity to the vector following administration of the vaccine. The latter is an important consideration if multiple administrations of the same vaccine are performed, such as separate priming and boosting doses, or if the same vaccine vector system is to be used to deliver different neoantigen cassettes.

[00396] In the case of alphavirus vectors, the standard delivery method is the previously discussed helper virus system that provides capsid, E1, and E2 proteins *in trans* to produce infectious viral particles. However, it is important to note that the E1 and E2 proteins are often major targets of neutralizing antibodies (Strauss 1994). Thus, the efficacy of using alphavirus vectors to deliver neoantigens of interest to target cells may be reduced if infectious particles are targeted by neutralizing antibodies.

[00397] An alternative to viral particle mediated gene delivery is the use of nanomaterials to deliver expression vectors (Riley 2017). Nanomaterial vehicles, importantly, can be made of non-immunogenic materials and generally avoid eliciting immunity to the delivery vector itself. These materials can include, but are not limited to, lipids, inorganic nanomaterials, and other polymeric materials. Lipids can be cationic, anionic, or neutral. The materials can be synthetic or naturally derived, and in some instances biodegradable. Lipids can include fats, cholesterol, phospholipids, lipid conjugates including, but not limited to, polyethyleneglycol (PEG) conjugates (PEGylated lipids), waxes, oils, glycerides, and fat soulable vitamins.

[00398] Lipid nanoparticles (LNPs) are an attractive delivery system due to the amphiphilic nature of lipids enabling formation of membranes and vesicle like structures (Riley 2017). In general, these vesicles deliver the expression vector by absorbing into the membrane of target cells and releasing nucleic acid into the cytosol. In addition, LNPs can be further modified or functionalized to facilitate targeting of specific cell types. Another consideration in LNP design is the balance between targeting efficiency and cytotoxicity. Lipid compositions generally include defined mixtures of cationic, neutral, anionic, and amphipathic lipids. In some instances, specific lipids are included to prevent LNP aggregation, prevent lipid oxidation, or provide functional chemical groups that facilitate attachment of additional moieties. Lipid composition can influence overall LNP size and stability. In an example, the lipid composition comprises dilinoleylmethyl- 4-dimethylaminobutyrate (MC3) or MC3-like molecules. MC3

2026201462 26 Feb 2026

and MC3-like lipid compositions can be formulated to include one or more other lipids, such as a PEG or PEG-conjugated lipid, a sterol, or neutral lipids.

[00399] Nucleic-acid vectors, such as expression vectors, exposed directly to serum can have several undesirable consequences, including degradation of the nucleic acid by serum nucleases or off-target stimulation of the immune system by the free nucleic acids. Therefore, encapsulation of the alphavirus vector can be used to avoid degradation, while also avoiding potential off-target affects. In certain examples, an alphavirus vector is fully encapsulated within the delivery vehicle, such as within the aqueous interior of an LNP. Encapsulation of the alphavirus vector within an LNP can be carried out by techniques well-known to those skilled in the art, such as microfluidic mixing and droplet generation carried out on a microfluidic droplet generating device. Such devices include, but are not limited to, standard T-junction devices or flow-focusing devices. In an example, the desired lipid formulation, such as MC3 or MC3-like containing compositions, is provided to the droplet generating device in parallel with the alphavirus delivery vector and other desired agents, such that the delivery vector and desired agents are fully encapsulated within the interior of the MC3 or MC3-like based LNP. In an example, the droplet generating device can control the size range and size distribution of the LNPs produced. For example, the LNP can have a size ranging from 1 to 1000 nanometers in diameter, e.g., 1, 10, 50, 100, 500, or 1000 nanometers. Following droplet generation, the delivery vehicles encapsulating the expression vectors can be further treated or modified to prepare them for administration.

V.E. Chimpanzee adenovirus (ChAd)

V.E.1. Viral delivery with chimpanzee adenovirus

[00400] Vaccine compositions for delivery of one or more neoantigens (e.g., via a neoantigen cassette) can be created by providing adenovirus nucleotide sequences of chimpanzee origin, a variety of novel vectors, and cell lines expressing chimpanzee adenovirus genes. A nucleotide sequence of a chimpanzee C68 adenovirus (also referred to herein as ChAdV68) can be used in a vaccine composition for neoantigen delivery (*See* SEQ ID NO: 1). Use of C68 adenovirus derived vectors is described in further detail in USPN 6,083,716, which is herein incorporated by reference in its entirety, for all purposes.

[00401] In a further aspect, provided herein is a recombinant adenovirus comprising the DNA sequence of a chimpanzee adenovirus such as C68 and a neoantigen cassette operatively linked to regulatory sequences directing its expression. The recombinant virus is capable of

2026201462 26 Feb 2026

infecting a mammalian, preferably a human, cell and capable of expressing the neoantigen cassette product in the cell. In this vector, the native chimpanzee E1 gene, and/or E3 gene, and/or E4 gene can be deleted. A neoantigen cassette can be inserted into any of these sites of gene deletion. The neoantigen cassette can include a neoantigen against which a primed immune response is desired.

[00402] In another aspect, provided herein is a mammalian cell infected with a chimpanzee adenovirus such as C68.

[00403] In still a further aspect, a novel mammalian cell line is provided which expresses a chimpanzee adenovirus gene (e.g., from C68) or functional fragment thereof.

[00404] In still a further aspect, provided herein is a method for delivering a neoantigen cassette into a mammalian cell comprising the step of introducing into the cell an effective amount of a chimpanzee adenovirus, such as C68, that has been engineered to express the neoantigen cassette.

[00405] Still another aspect provides a method for eliciting an immune response in a mammalian host to treat cancer. The method can comprise the step of administering to the host an effective amount of a recombinant chimpanzee adenovirus, such as C68, comprising a neoantigen cassette that encodes one or more neoantigens from the tumor against which the immune response is targeted.

[00406] Also disclosed is a non-simian mammalian cell that expresses a chimpanzee adenovirus gene obtained from the sequence of SEQ ID NO: 1. The gene can be selected from the group consisting of the adenovirus E1A, E1B, E2A, E2B, E3, E4, L1, L2, L3, L4 and L5 of SEQ ID NO: 1.

[00407] Also disclosed is a nucleic acid molecule comprising a chimpanzee adenovirus DNA sequence comprising a gene obtained from the sequence of SEQ ID NO: 1. The gene can be selected from the group consisting of said chimpanzee adenovirus E1A, E1B, E2A, E2B, E3, E4, L1, L2, L3, L4 and L5 genes of SEQ ID NO: 1. In some aspects the nucleic acid molecule comprises SEQ ID NO: 1. In some aspects the nucleic acid molecule comprises the sequence of SEQ ID NO: 1, lacking at least one gene selected from the group consisting of E1A, E1B, E2A, E2B, E3, E4, L1, L2, L3, L4 and L5 genes of SEQ ID NO: 1.

[00408] Also disclosed is a vector comprising a chimpanzee adenovirus DNA sequence obtained from SEQ ID NO: 1 and a neoantigen cassette operatively linked to one or more regulatory sequences which direct expression of the cassette in a heterologous host cell,

2026201462 26 Feb 2026

optionally wherein the chimpanzee adenovirus DNA sequence comprises at least the *cis*-elements necessary for replication and virion encapsidation, the *cis*-elements flanking the neoantigen cassette and regulatory sequences. In some aspects, the chimpanzee adenovirus DNA sequence comprises a gene selected from the group consisting of E1A, E1B, E2A, E2B, E3, E4, L1, L2, L3, L4 and L5 gene sequences of SEQ ID NO: 1. In some aspects the vector can lack the E1A and/or E1B gene.

[00409] Also disclosed herein is a host cell transfected with a vector disclosed herein such as a C68 vector engineered to expression a neoantigen cassette. Also disclosed herein is a human cell that expresses a selected gene introduced therein through introduction of a vector disclosed herein into the cell.

[00410] Also disclosed herein is a method for delivering a neoantigen cassette to a mammalian cell comprising introducing into said cell an effective amount of a vector disclosed herein such as a C68 vector engineered to expression the neoantigen cassette.

[00411] Also disclosed herein is a method for producing a neoantigen comprising introducing a vector disclosed herein into a mammalian cell, culturing the cell under suitable conditions and producing the neoantigen.

2026201462 26 Feb 2026

V.E.2. E1-Expressing Complementation Cell Lines

[00412] To generate recombinant chimpanzee adenoviruses (Ad) deleted in any of the genes described herein, the function of the deleted gene region, if essential to the replication and infectivity of the virus, can be supplied to the recombinant virus by a helper virus or cell line, i.e., a complementation or packaging cell line. For example, to generate a replication-defective chimpanzee adenovirus vector, a cell line can be used which expresses the E1 gene products of the human or chimpanzee adenovirus; such a cell line can include HEK293 or variants thereof. The protocol for the generation of the cell lines expressing the chimpanzee E1 gene products (Examples 3 and 4 of USPN 6,083,716) can be followed to generate a cell line which expresses any selected chimpanzee adenovirus gene.

[00413] An AAV augmentation assay can be used to identify a chimpanzee adenovirus E1-expressing cell line. This assay is useful to identify E1 function in cell lines made by using the E1 genes of other uncharacterized adenoviruses, e.g., from other species. That assay is described in Example 4B of USPN 6,083,716.

[00414] A selected chimpanzee adenovirus gene, e.g., E1, can be under the transcriptional control of a promoter for expression in a selected parent cell line. Inducible or constitutive promoters can be employed for this purpose. Among inducible promoters are included the sheep metallothionine promoter, inducible by zinc, or the mouse mammary tumor virus (MMTV) promoter, inducible by a glucocorticoid, particularly, dexamethasone. Other inducible promoters, such as those identified in International patent application WO95/13392, incorporated by reference herein can also be used in the production of packaging cell lines. Constitutive promoters in control of the expression of the chimpanzee adenovirus gene can be employed also.

[00415] A parent cell can be selected for the generation of a novel cell line expressing any desired C68 gene. Without limitation, such a parent cell line can be HeLa [ATCC Accession No. CCL 2], A549 [ATCC Accession No. CCL 185], KB [CCL 17], Detroit [e.g., Detroit 510, CCL 72] and WI-38 [CCL 75] cells. Other suitable parent cell lines can be obtained from other sources. Parent cell lines can include CHO, HEK293 or variants thereof, 911, HeLa, A549, LP-293, PER.C6, or AE1-2a.

[00416] An E1-expressing cell line can be useful in the generation of recombinant chimpanzee adenovirus E1 deleted vectors. Cell lines constructed using essentially the same procedures that express one or more other chimpanzee adenoviral gene products are useful in

2026201462 26 Feb 2026

the generation of recombinant chimpanzee adenovirus vectors deleted in the genes that encode those products. Further, cell lines which express other human Ad E1 gene products are also useful in generating chimpanzee recombinant Ads.

V.E.3. Recombinant Viral Particles as Vectors

[00417] The compositions disclosed herein can comprise viral vectors, that deliver at least one neoantigen to cells. Such vectors comprise a chimpanzee adenovirus DNA sequence such as C68 and a neoantigen cassette operatively linked to regulatory sequences which direct expression of the cassette. The C68 vector is capable of expressing the cassette in an infected mammalian cell. The C68 vector can be functionally deleted in one or more viral genes. A neoantigen cassette comprises at least one neoantigen under the control of one or more regulatory sequences such as a promoter. Optional helper viruses and/or packaging cell lines can supply to the chimpanzee viral vector any necessary products of deleted adenoviral genes.

[00418] The term "functionally deleted" means that a sufficient amount of the gene region is removed or otherwise altered, e.g., by mutation or modification, so that the gene region is no longer capable of producing one or more functional products of gene expression. Mutations or modifications that can result in functional deletions include, but are not limited to, nonsense mutations such as introduction of premature stop codons and removal of canonical and non-canonical start codons, mutations that alter mRNA splicing or other transcriptional processing, or combinations thereof. If desired, the entire gene region can be removed.

[00419] Modifications of the nucleic acid sequences forming the vectors disclosed herein, including sequence deletions, insertions, and other mutations may be generated using standard molecular biological techniques and are within the scope of this invention.

V.E.4. Construction of The Viral Plasmid Vector

[00420] The chimpanzee adenovirus C68 vectors useful in this invention include recombinant, defective adenoviruses, that is, chimpanzee adenovirus sequences functionally deleted in the E1a or E1b genes, and optionally bearing other mutations, e.g., temperature-sensitive mutations or deletions in other genes. It is anticipated that these chimpanzee sequences are also useful in forming hybrid vectors from other adenovirus and/or adeno-associated virus sequences. Homologous adenovirus vectors prepared from human adenoviruses are described in the published literature [see, for example, Kozarsky I and II, cited above, and references cited therein, U.S. Pat. No. 5,240,846].

2026201462 26 Feb 2026

[00421] In the construction of useful chimpanzee adenovirus C68 vectors for delivery of a neoantigen cassette to a human (or other mammalian) cell, a range of adenovirus nucleic acid sequences can be employed in the vectors. A vector comprising minimal chimpanzee C68 adenovirus sequences can be used in conjunction with a helper virus to produce an infectious recombinant virus particle. The helper virus provides essential gene products required for viral infectivity and propagation of the minimal chimpanzee adenoviral vector. When only one or more selected deletions of chimpanzee adenovirus genes are made in an otherwise functional viral vector, the deleted gene products can be supplied in the viral vector production process by propagating the virus in a selected packaging cell line that provides the deleted gene functions in trans.

V.E.5. Recombinant Minimal Adenovirus

[00422] A minimal chimpanzee Ad C68 virus is a viral particle containing just the adenovirus cis-elements necessary for replication and virion encapsidation. That is, the vector contains the cis-acting 5' and 3' inverted terminal repeat (ITR) sequences of the adenoviruses (which function as origins of replication) and the native 5' packaging/enhancer domains (that contain sequences necessary for packaging linear Ad genomes and enhancer elements for the E1 promoter). See, for example, the techniques described for preparation of a "minimal" human Ad vector in International Patent Application WO96/13597 and incorporated herein by reference.

V.E.6. Other Defective Adenoviruses

[00423] Recombinant, replication-deficient adenoviruses can also contain more than the minimal chimpanzee adenovirus sequences. These other Ad vectors can be characterized by deletions of various portions of gene regions of the virus, and infectious virus particles formed by the optional use of helper viruses and/or packaging cell lines.

[00424] As one example, suitable vectors may be formed by deleting all or a sufficient portion of the C68 adenoviral immediate early gene E1a and delayed early gene E1b, so as to eliminate their normal biological functions. Replication-defective E1-deleted viruses are capable of replicating and producing infectious virus when grown on a chimpanzee adenovirus-transformed, complementation cell line containing functional adenovirus E1a and E1b genes which provide the corresponding gene products in trans. Based on the homologies to known adenovirus sequences, it is anticipated that, as is true for the human recombinant E1-deleted adenoviruses of the art, the resulting recombinant chimpanzee adenovirus is capable of

2026201462 26 Feb 2026

infecting many cell types and can express neoantigen(s), but cannot replicate in most cells that do not carry the chimpanzee E1 region DNA unless the cell is infected at a very high multiplicity of infection.

[00425] As another example, all or a portion of the C68 adenovirus delayed early gene E3 can be eliminated from the chimpanzee adenovirus sequence which forms a part of the recombinant virus.

[00426] Chimpanzee adenovirus C68 vectors can also be constructed having a deletion of the E4 gene. Still another vector can contain a deletion in the delayed early gene E2a.

[00427] Deletions can also be made in any of the late genes L1 through L5 of the chimpanzee C68 adenovirus genome. Similarly, deletions in the intermediate genes IX and IVa2 can be useful for some purposes. Other deletions may be made in the other structural or non-structural adenovirus genes.

[00428] The above discussed deletions can be used individually, i.e., an adenovirus sequence can contain deletions of E1 only. Alternatively, deletions of entire genes or portions thereof effective to destroy or reduce their biological activity can be used in any combination. For example, in one exemplary vector, the adenovirus C68 sequence can have deletions of the E1 genes and the E4 gene, or of the E1, E2a and E3 genes, or of the E1 and E3 genes, or of E1, E2a and E4 genes, with or without deletion of E3, and so on. As discussed above, such deletions can be used in combination with other mutations, such as temperature-sensitive mutations, to achieve a desired result.

[00429] The cassette comprising neoantigen(s) be inserted optionally into any deleted region of the chimpanzee C68 Ad virus. Alternatively, the cassette can be inserted into an existing gene region to disrupt the function of that region, if desired.

V.E.7. Helper Viruses

[00430] Depending upon the chimpanzee adenovirus gene content of the viral vectors employed to carry the neoantigen cassette, a helper adenovirus or non-replicating virus fragment can be used to provide sufficient chimpanzee adenovirus gene sequences to produce an infective recombinant viral particle containing the cassette.

[00431] Useful helper viruses contain selected adenovirus gene sequences not present in the adenovirus vector construct and/or not expressed by the packaging cell line in which the vector is transfected. A helper virus can be replication-defective and contain a variety of adenovirus

2026201462 26 Feb 2026

genes in addition to the sequences described above. The helper virus can be used in combination with the E1-expressing cell lines described herein.

[00432] For C68, the "helper" virus can be a fragment formed by clipping the C terminal end of the C68 genome with SspI, which removes about 1300 bp from the left end of the virus. This clipped virus is then co-transfected into an E1-expressing cell line with the plasmid DNA, thereby forming the recombinant virus by homologous recombination with the C68 sequences in the plasmid.

[00433] Helper viruses can also be formed into poly-cation conjugates as described in Wu et al, J. Biol. Chem., 264:16985-16987 (1989); K. J. Fisher and J. M. Wilson, Biochem. J., 299:49 (Apr. 1, 1994). Helper virus can optionally contain a reporter gene. A number of such reporter genes are known to the art. The presence of a reporter gene on the helper virus which is different from the neoantigen cassette on the adenovirus vector allows both the Ad vector and the helper virus to be independently monitored. This second reporter is used to enable separation between the resulting recombinant virus and the helper virus upon purification.

V.E.8. Assembly of Viral Particle and Infection of a Cell Line

[00434] Assembly of the selected DNA sequences of the adenovirus, the neoantigen cassette, and other vector elements into various intermediate plasmids and shuttle vectors, and the use of the plasmids and vectors to produce a recombinant viral particle can all be achieved using conventional techniques. Such techniques include conventional cloning techniques of cDNA, in vitro recombination techniques (e.g., Gibson assembly), use of overlapping oligonucleotide sequences of the adenovirus genomes, polymerase chain reaction, and any suitable method which provides the desired nucleotide sequence. Standard transfection and co-transfection techniques are employed, e.g., CaPO4 precipitation techniques or liposome-mediated transfection methods such as lipofectamine. Other conventional methods employed include homologous recombination of the viral genomes, plaquing of viruses in agar overlay, methods of measuring signal generation, and the like.

[00435] For example, following the construction and assembly of the desired neoantigen cassette-containing viral vector, the vector can be transfected in vitro in the presence of a helper virus into the packaging cell line. Homologous recombination occurs between the helper and the vector sequences, which permits the adenovirus-neoantigen sequences in the vector to be replicated and packaged into virion capsids, resulting in the recombinant viral vector particles.

2026201462 26 Feb 2026

[00436] The resulting recombinant chimpanzee C68 adenoviruses are useful in transferring a neoantigen cassette to a selected cell. In in vivo experiments with the recombinant virus grown in the packaging cell lines, the E1-deleted recombinant chimpanzee adenovirus demonstrates utility in transferring a cassette to a non-chimpanzee, preferably a human, cell.

V.E.9. Use of the Recombinant Virus Vectors

[00437] The resulting recombinant chimpanzee C68 adenovirus containing the neoantigen cassette (produced by cooperation of the adenovirus vector and helper virus or adenoviral vector and packaging cell line, as described above) thus provides an efficient gene transfer vehicle which can deliver neoantigen(s) to a subject in vivo or ex vivo.

[00438] The above-described recombinant vectors are administered to humans according to published methods for gene therapy. A chimpanzee viral vector bearing a neoantigen cassette can be administered to a patient, preferably suspended in a biologically compatible solution or pharmaceutically acceptable delivery vehicle. A suitable vehicle includes sterile saline. Other aqueous and non-aqueous isotonic sterile injection solutions and aqueous and non-aqueous sterile suspensions known to be pharmaceutically acceptable carriers and well known to those of skill in the art may be employed for this purpose.

[00439] The chimpanzee adenoviral vectors are administered in sufficient amounts to transduce the human cells and to provide sufficient levels of neoantigen transfer and expression to provide a therapeutic benefit without undue adverse or with medically acceptable physiological effects, which can be determined by those skilled in the medical arts. Conventional and pharmaceutically acceptable routes of administration include, but are not limited to, direct delivery to the liver, intranasal, intravenous, intramuscular, subcutaneous, intradermal, oral and other parental routes of administration. Routes of administration may be combined, if desired.

[00440] Dosages of the viral vector will depend primarily on factors such as the condition being treated, the age, weight and health of the patient, and may thus vary among patients. The dosage will be adjusted to balance the therapeutic benefit against any side effects and such dosages may vary depending upon the therapeutic application for which the recombinant vector is employed. The levels of expression of neoantigen(s) can be monitored to determine the frequency of dosage administration.

[00441] Recombinant, replication defective adenoviruses can be administered in a "pharmaceutically effective amount", that is, an amount of recombinant adenovirus that is

2026201462 26 Feb 2026

effective in a route of administration to transfect the desired cells and provide sufficient levels of expression of the selected gene to provide a vaccinal benefit, i.e., some measurable level of protective immunity. C68 vectors comprising a neoantigen cassette can be co-administered with adjuvant. Adjuvant can be separate from the vector (e.g., alum) or encoded within the vector, in particular if the adjuvant is a protein. Adjuvants are well known in the art.

[00442] Conventional and pharmaceutically acceptable routes of administration include, but are not limited to, intranasal, intramuscular, intratracheal, subcutaneous, intradermal, rectal, oral and other parental routes of administration. Routes of administration may be combined, if desired, or adjusted depending upon the immunogen or the disease. For example, in prophylaxis of rabies, the subcutaneous, intratracheal and intranasal routes are preferred. The route of administration primarily will depend on the nature of the disease being treated.

[00443] The levels of immunity to neoantigen(s) can be monitored to determine the need, if any, for boosters. Following an assessment of antibody titers in the serum, for example, optional booster immunizations may be desired

VI. Therapeutic and Manufacturing Methods

[00444] Also provided is a method of inducing a tumor specific immune response in a subject, vaccinating against a tumor, treating and or alleviating a symptom of cancer in a subject by administering to the subject one or more neoantigens such as a plurality of neoantigens identified using methods disclosed herein.

[00445] In some aspects, a subject has been diagnosed with cancer or is at risk of developing cancer. A subject can be a human, dog, cat, horse or any animal in which a tumor specific immune response is desired. A tumor can be any solid tumor such as breast, ovarian, prostate, lung, kidney, gastric, colon, testicular, head and neck, pancreas, brain, melanoma, and other tumors of tissue organs and hematological tumors, such as lymphomas and leukemias, including acute myelogenous leukemia, chronic myelogenous leukemia, chronic lymphocytic leukemia, T cell lymphocytic leukemia, and B cell lymphomas.

[00446] A neoantigen can be administered in an amount sufficient to induce a CTL response.

[00447] A neoantigen can be administered alone or in combination with other therapeutic agents. The therapeutic agent is for example, a chemotherapeutic agent, radiation, or immunotherapy. Any suitable therapeutic treatment for a particular cancer can be administered.

2026201462 26 Feb 2026

[00448] In addition, a subject can be further administered an anti-immunosuppressive/immunostimulatory agent such as a checkpoint inhibitor. For example, the subject can be further administered an anti-CTLA antibody or anti-PD-1 or anti-PD-L1. Blockade of CTLA-4 or PD-L1 by antibodies can enhance the immune response to cancerous cells in the patient. In particular, CTLA-4 blockade has been shown effective when following a vaccination protocol.

[00449] The optimum amount of each neoantigen to be included in a vaccine composition and the optimum dosing regimen can be determined. For example, a neoantigen or its variant can be prepared for intravenous (i.v.) injection, sub-cutaneous (s.c.) injection, intradermal (i.d.) injection, intraperitoneal (i.p.) injection, intramuscular (i.m.) injection. Methods of injection include s.c., i.d., i.p., i.m., and i.v. Methods of DNA or RNA injection include i.d., i.m., s.c., i.p. and i.v. Other methods of administration of the vaccine composition are known to those skilled in the art.

[00450] A vaccine can be compiled so that the selection, number and/or amount of neoantigens present in the composition is/are tissue, cancer, and/or patient-specific. For instance, the exact selection of peptides can be guided by expression patterns of the parent proteins in a given tissue. The selection can be dependent on the specific type of cancer, the status of the disease, earlier treatment regimens, the immune status of the patient, and, of course, the HLA-haplotype of the patient. Furthermore, a vaccine can contain individualized components, according to personal needs of the particular patient. Examples include varying the selection of neoantigens according to the expression of the neoantigen in the particular patient or adjustments for secondary treatments following a first round or scheme of treatment.

[00451] For a composition to be used as a vaccine for cancer, neoantigens with similar normal self-peptides that are expressed in high amounts in normal tissues can be avoided or be present in low amounts in a composition described herein. On the other hand, if it is known that the tumor of a patient expresses high amounts of a certain neoantigen, the respective pharmaceutical composition for treatment of this cancer can be present in high amounts and/or more than one neoantigen specific for this particularly neoantigen or pathway of this neoantigen can be included.

[00452] Compositions comprising a neoantigen can be administered to an individual already suffering from cancer. In therapeutic applications, compositions are administered to a patient in an amount sufficient to elicit an effective CTL response to the tumor antigen and to cure or at least partially arrest symptoms and/or complications. An amount adequate to accomplish this is

2026201462 26 Feb 2026

defined as "therapeutically effective dose." Amounts effective for this use will depend on, e.g., the composition, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician. It should be kept in mind that compositions can generally be employed in serious disease states, that is, life-threatening or potentially life threatening situations, especially when the cancer has metastasized. In such cases, in view of the minimization of extraneous substances and the relative nontoxic nature of a neoantigen, it is possible and can be felt desirable by the treating physician to administer substantial excesses of these compositions.

[00453] For therapeutic use, administration can begin at the detection or surgical removal of tumors. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter.

[00454] The pharmaceutical compositions (e.g., vaccine compositions) for therapeutic treatment are intended for parenteral, topical, nasal, oral or local administration. A pharmaceutical compositions can be administered parenterally, e.g., intravenously, subcutaneously, intradermally, or intramuscularly. The compositions can be administered at the site of surgical exiscion to induce a local immune response to the tumor. Disclosed herein are compositions for parenteral administration which comprise a solution of the neoantigen and vaccine compositions are dissolved or suspended in an acceptable carrier, e.g., an aqueous carrier. A variety of aqueous carriers can be used, e.g., water, buffered water, 0.9% saline, 0.3% glycine, hyaluronic acid and the like. These compositions can be sterilized by conventional, well known sterilization techniques, or can be sterile filtered. The resulting aqueous solutions can be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents, wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

[00455] Neoantigens can also be administered via liposomes, which target them to a particular cells tissue, such as lymphoid tissue. Liposomes are also useful in increasing half-life. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations the neoantigen to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule

2026201462 26 Feb 2026

which binds to, e.g., a receptor prevalent among lymphoid cells, such as monoclonal antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic compositions. Thus, liposomes filled with a desired neoantigen can be directed to the site of lymphoid cells, where the liposomes then deliver the selected therapeutic/immunogenic compositions. Liposomes can be formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, e.g., liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, e.g., Szoka et al., Ann. Rev. Biophys. Bioeng. 9; 467 (1980), U.S. Pat. Nos. 4,235,871, 4,501,728, 4,501,728, 4,837,028, and 5,019,369.

[00456] For targeting to the immune cells, a ligand to be incorporated into the liposome can include, e.g., antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension can be administered intravenously, locally, topically, etc. in a dose which varies according to, inter alia, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

[00457] For therapeutic or immunization purposes, nucleic acids encoding a peptide and optionally one or more of the peptides described herein can also be administered to the patient. A number of methods are conveniently used to deliver the nucleic acids to the patient. For instance, the nucleic acid can be delivered directly, as "naked DNA". This approach is described, for instance, in Wolff et al., Science 247: 1465-1468 (1990) as well as U.S. Pat. Nos. 5,580,859 and 5,589,466. The nucleic acids can also be administered using ballistic delivery as described, for instance, in U.S. Pat. No. 5,204,253. Particles comprised solely of DNA can be administered. Alternatively, DNA can be adhered to particles, such as gold particles. Approaches for delivering nucleic acid sequences can include viral vectors, mRNA vectors, and DNA vectors with or without electroporation.

[00458] The nucleic acids can also be delivered complexed to cationic compounds, such as cationic lipids. Lipid-mediated gene delivery methods are described, for instance, in 9618372WOAWO 96/18372; 9324640WOAWO 93/24640; Mannino & Gould-Fogerite, BioTechniques 6(7): 682-691 (1988); U.S. Pat. No. 5,279,833 Rose U.S. Pat. No. 5,279,833; 9106309WOAWO 91/06309; and Felgner et al., Proc. Natl. Acad. Sci. USA 84: 7413-7414 (1987).

[00459] Neoantigens can also be included in viral vector-based vaccine platforms, such as vaccinia, fowlpox, self-replicating alphavirus, marabavirus, adenovirus (*See, e.g.,* Tatsis et al.,

2026201462 26 Feb 2026

Adenoviruses, *Molecular Therapy* (2004) 10, 616—629), or lentivirus, including but not limited to second, third or hybrid second/third generation lentivirus and recombinant lentivirus of any generation designed to target specific cell types or receptors (*See, e.g.,* Hu et al., Immunization Delivered by Lentiviral Vectors for Cancer and Infectious Diseases, *Immunol Rev.* (2011) 239(1): 45-61, Sakuma et al., Lentiviral vectors: basic to translational, *Biochem J.* (2012) 443(3):603-18, Cooper et al., Rescue of splicing-mediated intron loss maximizes expression in lentiviral vectors containing the human ubiquitin C promoter, *Nucl. Acids Res.* (2015) 43 (1): 682-690, Zufferey et al., Self-Inactivating Lentivirus Vector for Safe and Efficient In Vivo Gene Delivery, *J. Virol.* (1998) 72 (12): 9873-9880). Dependent on the packaging capacity of the above mentioned viral vector-based vaccine platforms, this approach can deliver one or more nucleotide sequences that encode one or more neoantigen peptides. The sequences may be flanked by non-mutated sequences, may be separated by linkers or may be preceded with one or more sequences targeting a subcellular compartment (See, e.g., Gros et al., Prospective identification of neoantigen-specific lymphocytes in the peripheral blood of melanoma patients, *Nat Med.* (2016) 22 (4):433-8, Stronen et al., Targeting of cancer neoantigens with donor-derived T cell receptor repertoires, *Science.* (2016) 352 (6291):1337-41, Lu et al., Efficient identification of mutated cancer antigens recognized by T cells associated with durable tumor regressions, *Clin Cancer Res.* (2014) 20(13):3401-10). Upon introduction into a host, infected cells express the neoantigens, and thereby elicit a host immune (e.g., CTL) response against the peptide(s). Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Pat. No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover et al. (Nature 351:456-460 (1991)). A wide variety of other vaccine vectors useful for therapeutic administration or immunization of neoantigens, e.g., Salmonella typhi vectors, and the like will be apparent to those skilled in the art from the description herein.

[00460] A means of administering nucleic acids uses minigene constructs encoding one or multiple epitopes. To create a DNA sequence encoding the selected CTL epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes are reverse translated. A human codon usage table is used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences are directly adjoined, creating a continuous polypeptide sequence. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequence that could be reverse translated and included in the minigene sequence include: helper T lymphocyte, epitopes, a

2026201462 26 Feb 2026

leader (signal) sequence, and an endoplasmic reticulum retention signal. In addition, MHC presentation of CTL epitopes can be improved by including synthetic (e.g. poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL epitopes. The minigene sequence is converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) are synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides are joined using T4 DNA ligase. This synthetic minigene, encoding the CTL epitope polypeptide, can then cloned into a desired expression vector.

[00461] Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). A variety of methods have been described, and new techniques can become available. As noted above, nucleic acids are conveniently formulated with cationic lipids. In addition, glycolipids, fusogenic liposomes, peptides and compounds referred to collectively as protective, interactive, non-condensing (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

[00462] Also disclosed is a method of manufacturing a tumor vaccine, comprising performing the steps of a method disclosed herein; and producing a tumor vaccine comprising a plurality of neoantigens or a subset of the plurality of neoantigens.

[00463] Neoantigens disclosed herein can be manufactured using methods known in the art. For example, a method of producing a neoantigen or a vector (e.g., a vector including at least one sequence encoding one or more neoantigens) disclosed herein can include culturing a host cell under conditions suitable for expressing the neoantigen or vector wherein the host cell comprises at least one polynucleotide encoding the neoantigen or vector, and purifying the neoantigen or vector. Standard purification methods include chromatographic techniques, electrophoretic, immunological, precipitation, dialysis, filtration, concentration, and chromatofocusing techniques.

[00464] Host cells can include a Chinese Hamster Ovary (CHO) cell, NS0 cell, yeast, or a HEK293 cell. Host cells can be transformed with one or more polynucleotides comprising at least one nucleic acid sequence that encodes a neoantigen or vector disclosed herein, optionally wherein the isolated polynucleotide further comprises a promoter sequence operably linked to

2026201462 26 Feb 2026

the at least one nucleic acid sequence that encodes the neoantigen or vector. In certain embodiments the isolated polynucleotide can be cDNA.

VII. Neoantigen Use and Administration

[00465] A vaccination protocol can be used to dose a subject with one or more neoantigens. A priming vaccine and a boosting vaccine can be used to dose the subject. The priming vaccine can be based on C68 (e.g., the sequences shown in SEQ ID NO:1 or 2) or srRNA (e.g., the sequences shown in SEQ ID NO:3 or 4) and the boosting vaccine can be based on C68 (e.g., the sequences shown in SEQ ID NO:1 or 2) or srRNA (e.g., the sequences shown in SEQ ID NO:3 or 4). Each vector typically includes a cassette that includes neoantigens. Cassettes can include about 20 neoantigens, separated by spacers such as the natural sequence that normally surrounds each antigen or other non-natural spacer sequences such as AAY. Cassettes can also include MHCII antigens such a tetanus toxoid antigen and PADRE antigen, which can be considered universal class II antigens. Cassettes can also include a targeting sequence such as a ubiquitin targeting sequence. In addition, each vaccine dose can be administered to the subject in conjunction with (e.g., concurrently, before, or after) a checkpoint inhibitor (CPI). CPI's can include those that inhibit CTLA4, PD1, and/or PDL1 such as antibodies or antigen-binding portions thereof. Such antibodies can include tremelimumab or durvalumab.

[00466] A priming vaccine can be injected (e.g., intramuscularly) in a subject. Bilateral injections per dose can be used. For example, one or more injections of ChAdV68 (C68) can be used (e.g., total dose $1x10^{12}$ viral particles); one or more injections of self-replicating RNA (srRNA) at low vaccine dose selected from the range 0.001 to 1 ug RNA, in particular 0.1 or 1 ug can be used; or one or more injections of srRNA at high vaccine dose selected from the range 1 to 100 ug RNA, in particular 10 or 100 ug can be used.

[00467] A vaccine boost (boosting vaccine) can be injected (e.g., intramuscularly) after prime vaccination. A boosting vaccine can be administered about every 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 weeks, e.g., every 4 weeks and/or 8 weeks after the prime. Bilateral injections per dose can be used. For example, one or more injections of ChAdV68 (C68) can be used (e.g., total dose $1x10^{12}$ viral particles); one or more injections of self-replicating RNA (srRNA) at low vaccine dose selected from the range 0.001 to 1 ug RNA, in particular 0.1 or 1 ug can be used; or one or more injections of srRNA at high vaccine dose selected from the range 1 to 100 ug RNA, in particular 10 or 100 ug can be used.

2026201462 26 Feb 2026

[00468] Anti-CTLA-4 (e.g., tremelimumab) can also be administered to the subject. For example, anti-CTLA4 can be administered subcutaneously near the site of the intramuscular vaccine injection (ChAdV68 prime or srRNA low doses) to ensure drainage into the same lymph node. Tremelimumab is a selective human IgG2 mAb inhibitor of CTLA-4. Target Anti-CTLA-4 (tremelimumab) subcutaneous dose is typically 70-75 mg (in particular 75 mg) with a dose range of, e.g., 1-100 mg or 5-420 mg.

[00469] In certain instances an anti-PD-L1 antibody can be used such as durvalumab (MEDI 4736). Durvalumab is a selective, high affinity human IgG1 mAb that blocks PD-L1 binding to PD-1 and CD80. Durvalumab is generally administered at 20 mg/kg i.v. every 4 weeks.

[00470] Immune monitoring can be performed before, during, and/or after vaccine administration. Such monitoring can inform safety and efficacy, among other parameters.

[00471] To perform immune monitoring, PBMCs are commonly used. PBMCs can be isolated before prime vaccination, and after prime vaccination (e.g. 4 weeks and 8 weeks). PBMCs can be harvested just prior to boost vaccinations and after each boost vaccination (e.g. 4 weeks and 8 weeks).

[00472] T cell responses can be assessed as part of an immune monitoring protocol. T cell responses can be measured using one or more methods known in the art such as ELISpot, intracellular cytokine staining, cytokine secretion and cell surface capture, T cell proliferation, MHC multimer staining, or by cytotoxicity assay. T cell responses to epitopes encoded in vaccines can be monitored from PBMCs by measuring induction of cytokines, such as IFN-gamma, using an ELISpot assay. Specific CD4 or CD8 T cell responses to epitopes encoded in vaccines can be monitored from PBMCs by measuring induction of cytokines captured intracellularly or extracellularly, such as IFN-gamma, using flow cytometry. Specific CD4 or CD8 T cell responses to epitopes encoded in the vaccines can be monitored from PBMCs by measuring T cell populations expressing T cell receptors specific for epitope/MHC class I complexes using MHC multimer staining. Specific CD4 or CD8 T cell responses to epitopes encoded in the vaccines can be monitored from PBMCs by measuring the ex vivo expansion of T cell populations following 3H-thymidine, bromodeoxyuridine and carboxyfluoresceine-diacetate– succinimidylester (CFSE) incorporation. The antigen recognition capacity and lytic activity of PBMC-derived T cells that are specific for epitopes encoded in vaccines can be assessed functionally by chromium release assay or alternative colorimetric cytotoxicity assays.

2026201462 26 Feb 2026

VIII. Neoantigen Identification

VIII.A. Neoantigen Candidate Identification

[00473] Research methods for NGS analysis of tumor and normal exome and transcriptomes have been described and applied in the neoantigen identification space. [6,14,15] The example below considers certain optimizations for greater sensitivity and specificity for neoantigen identification in the clinical setting. These optimizations can be grouped into two areas, those related to laboratory processes and those related to the NGS data analysis.

VIII.A.1. Laboratory process optimizations

[00474] The process improvements presented here address challenges in high-accuracy neoantigen discovery from clinical specimens with low tumor content and small volumes by extending concepts developed for reliable cancer driver gene assessment in targeted cancer panels[16] to the whole- exome and -transcriptome setting necessary for neoantigen identification. Specifically, these improvements include:

1. Targeting deep (>500x) unique average coverage across the tumor exome to detect mutations present at low mutant allele frequency due to either low tumor content or subclonal state.
2. Targeting uniform coverage across the tumor exome, with <5% of bases covered at <100x, so that the fewest possible neoantigens are missed, by, for instance:
    a. Employing DNA-based capture probes with individual probe QC[17]
    b. Including additional baits for poorly covered regions
3. Targeting uniform coverage across the normal exome, where <5% of bases are covered at <20x so that the fewest neoantigens possible remain unclassified for somatic/germline status (and thus not usable as TSNAs)
4. To minimize the total amount of sequencing required, sequence capture probes will be designed for coding regions of genes only, as non-coding RNA cannot give rise to neoantigens. Additional optimizations include:
    a. supplementary probes for HLA genes, which are GC-rich and poorly captured by standard exome sequencing[18]
    b. exclusion of genes predicted to generate few or no candidate neoantigens, due to factors such as insufficient expression, suboptimal digestion by the proteasome, or unusual sequence features.

2026201462 26 Feb 2026

5. Tumor RNA will likewise be sequenced at high depth (>100M reads) in order to enable variant detection, quantification of gene and splice-variant ("isoform") expression, and fusion detection. RNA from FFPE samples will be extracted using probe-based enrichment[19], with the same or similar probes used to capture exomes in DNA.

2026201462 26 Feb 2026

VIII.A.2. NGS data analysis optimizations

[00475] Improvements in analysis methods address the suboptimal sensitivity and specificity of common research mutation calling approaches, and specifically consider customizations relevant for neoantigen identification in the clinical setting. These include:

1. Using the HG38 reference human genome or a later version for alignment, as it contains multiple MHC regions assemblies better reflective of population polymorphism, in contrast to previous genome releases.
2. Overcoming the limitations of single variant callers [20] by merging results from different programs.[5]
    a. Single-nucleotide variants and indels will be detected from tumor DNA, tumor RNA and normal DNA with a suite of tools including: programs based on comparisons of tumor and normal DNA, such as Strelka [21] and Mutect [22]; and programs that incorporate tumor DNA, tumor RNA and normal DNA, such as UNCeqR, which is particularly advantageous in low-purity samples [23].
    b. Indels will be determined with programs that perform local re-assembly, such as Strelka and ABRA [24].
    c. Structural rearrangements will be determined using dedicated tools such as Pindel [25] or Breakseq [26].
3. In order to detect and prevent sample swaps, variant calls from samples for the same patient will be compared at a chosen number of polymorphic sites.
4. Extensive filtering of artefactual calls will be performed, for instance, by:
    a. Removal of variants found in normal DNA, potentially with relaxed detection parameters in cases of low coverage, and with a permissive proximity criterion in case of indels
    b. Removal of variants due to low mapping quality or low base quality[27].
    c. Removal of variants stemming from recurrent sequencing artifacts, even if not observed in the corresponding normal[27]. Examples include variants primarily detected on one strand.
    d. Removal of variants detected in an unrelated set of controls[27]
5. Accurate HLA calling from normal exome using one of seq2HLA [28], ATHLATES [29] or Optitype and also combining exome and RNA sequencing data [28]. Additional potential optimizations include the adoption of a dedicated assay for HLA typing such as long-

2026201462 26 Feb 2026

read DNA sequencing[30], or the adaptation of a method for joining RNA fragments to retain continuity [31].

6. Robust detection of neo-ORFs arising from tumor-specific splice variants will be performed by assembling transcripts from RNA-seq data using CLASS [32], Bayesembler [33], StringTie [34] or a similar program in its reference-guided mode (i.e., using known transcript structures rather than attempting to recreate transcripts in their entirety from each experiment). While Cufflinks [35] is commonly used for this purpose, it frequently produces implausibly large numbers of splice variants, many of them far shorter than the full-length gene, and can fail to recover simple positive controls. Coding sequences and nonsense-mediated decay potential will be determined with tools such as SpliceR[36] and MAMBA[37], with mutant sequences re-introduced. Gene expression will be determined with a tool such as Cufflinks[35] or Express (Roberts and Pachter, 2013). Wild-type and mutant-specific expression counts and/or relative levels will be determined with tools developed for these purposes, such as ASE[38] or HTSeq[39]. Potential filtering steps include:
    a. Removal of candidate neo-ORFs deemed to be insufficiently expressed.
    b. Removal of candidate neo-ORFs predicted to trigger non-sense mediated decay (NMD).
7. Candidate neoantigens observed only in RNA (e.g., neoORFs) that cannot directly be verified as tumor-specific will be categorized as likely tumor-specific according to additional parameters, for instance by considering:
    a. Presence of supporting tumor DNA-only *cis*-acting frameshift or splice-site mutations
    b. Presence of corroborating tumor DNA-only trans-acting mutation in a splicing factor. For instance, in three independently published experiments with R625-mutant SF3B1, the genes exhibiting the most differentially splicing were concordant even though one experiment examined uveal melanoma patients [40], the second a uveal melanoma cell line [41], and the third breast cancer patients [42].
    c. For novel splicing isoforms, presence of corroborating “novel” splice-junction reads in the RNASeq data.
    d. For novel re-arrangements, presence of corroborating juxta-exon reads in tumor DNA that are absent from normal DNA

26 Feb 2026
2026201462

e. Absence from gene expression compendium such as GTEx[43] (i.e. making germline origin less likely)

8. Complementing the reference genome alignment-based analysis by comparing assembled DNA tumor and normal reads (or k-mers from such reads) directly to avoid alignment and annotation based errors and artifacts. (e.g. for somatic variants arising near germline variants or repeat-context indels)

[00476] In samples with poly-adenylated RNA, the presence of viral and microbial RNA in the RNA-seq data will be assessed using RNA CoMPASS[44] or a similar method, toward the identification of additional factors that may predict patient response.

VIII.B. Isolation and Detection of HLA Peptides

[00477] Isolation of HLA-peptide molecules was performed using classic immunoprecipitation (IP) methods after lysis and solubilization of the tissue sample (55-58). A clarified lysate was used for HLA specific IP.

[00478] Immunoprecipitation was performed using antibodies coupled to beads where the antibody is specific for HLA molecules. For a pan-Class I HLA immunoprecipitation, a pan-Class I CR antibody is used, for Class II HLA – DR, an HLA-DR antibody is used. Antibody is covalently attached to NHS-sepharose beads during overnight incubation. After covalent attachment, the beads were washed and aliquoted for IP. (59, 60) Immunoprecipitations can also be performed with antibodies that are not covalently attached to beads. Typically this is done using sepharose or magnetic beads coated with Protein A and/or Protein G to hold the antibody to the column. Some antibodies that can be used to selectively enrich MHC/peptide complex are listed below.

Antibody Name	Specificity
W6/32	Class I HLA-A, B, C
L243	Class II – HLA-DR
Tu36	Class II – HLA-DR
LN3	Class II – HLA-DR
Tu39	Class II – HLA-DR, DP, DQ

[00479] The clarified tissue lysate is added to the antibody beads for the immunoprecipitation. After immunoprecipitation, the beads are removed from the lysate and the lysate stored for additional experiments, including additional IPs. The IP beads are washed to remove non-specific binding and the HLA/peptide complex is eluted from the beads using

2026201462 26 Feb 2026

standard techniques. The protein components are removed from the peptides using a molecular weight spin column or C18 fractionation. The resultant peptides are taken to dryness by SpeedVac evaporation and in some instances are stored at -20C prior to MS analysis.

[00480] Dried peptides are reconstituted in an HPLC buffer suitable for reverse phase chromatography and loaded onto a C-18 microcapillary HPLC column for gradient elution in a Fusion Lumos mass spectrometer (Thermo). MS1 spectra of peptide mass/charge (m/z) were collected in the Orbitrap detector at high resolution followed by MS2 low resolution scans collected in the ion trap detector after HCD fragmentation of the selected ion. Additionally, MS2 spectra can be obtained using either CID or ETD fragmentation methods or any combination of the three techniques to attain greater amino acid coverage of the peptide. MS2 spectra can also be measured with high resolution mass accuracy in the Orbitrap detector.

[00481] MS2 spectra from each analysis are searched against a protein database using Comet (61, 62) and the peptide identification are scored using Percolator (63-65). Additional sequencing is performed using PEAKS studio (Bioinformatics Solutions Inc.) and other search engines or sequencing methods can be used including spectral matching and *de novo* sequencing (97).

VIII.B.1. MS limit of detection studies in support of comprehensive HLA peptide sequencing.

[00482] Using the peptide YVYVADVAAK it was determined what the limits of detection are using different amounts of peptide loaded onto the LC column. The amounts of peptide tested were 1 pmol, 100fmol, 10 fmol, 1 fmol, and 100amol. (Table 1) The results are shown in Figure 1F. These results indicate that the lowest limit of detection (LoD) is in the attomol range (10^{-18}), that the dynamic range spans five orders of magnitude, and that the signal to noise appears sufficient for sequencing at low femtomol ranges (10^{-15}).

Table 1

Peptide m/z	Loaded on Column	Copies/Cell in 1e9cells
566.830	1 pmol	600
562.823	100 fmol	60
559.816	10 fmol	6
556.810	1 fmol	0.6

26 Feb 2026
2026201462

553.802	100 amol	0.06

IX. Presentation Model

IX.A. System Overview

[00483] FIG. 2A is an overview of an environment 100 for identifying likelihoods of peptide presentation in patients, in accordance with an embodiment. The environment 100 provides context in order to introduce a presentation identification system 160, itself including a presentation information store 165.

[00484] The presentation identification system 160 is one or computer models, embodied in a computing system as discussed below with respect to FIG. 14, that receives peptide sequences associated with a set of MHC alleles and determines likelihoods that the peptide sequences will be presented by one or more of the set of associated MHC alleles. The presentation identification system 160 may be applied to both class I and class II MHC alleles. This is useful in a variety of contexts. One specific use case for the presentation identification system 160 is that it is able to receive nucleotide sequences of candidate neoantigens associated with a set of MHC alleles from tumor cells of a patient 110 and determine likelihoods that the candidate neoantigens will be presented by one or more of the associated MHC alleles of the tumor and/or induce immunogenic responses in the immune system of the patient 110. Those candidate neoantigens with high likelihoods as determined by system 160 can be selected for inclusion in a vaccine 118, such an anti-tumor immune response can be elicited from the immune system of the patient 110 providing the tumor cells.

[00485] The presentation identification system 160 determines presentation likelihoods through one or more presentation models. Specifically, the presentation models generate likelihoods of whether given peptide sequences will be presented for a set of associated MHC alleles, and are generated based on presentation information stored in store 165. For example, the presentation models may generate likelihoods of whether a peptide sequence "YVYVADVAAK" will be presented for the set of alleles HLA-A*02:01, HLA- A*03:01, HLA-B*07:02, HLA-B*08:03, HLA-C*01:04, HLA-A*06:03, HLA-B*01:04 on the cell surface of the sample. The presentation information 165 contains information on whether peptides bind to different types of MHC alleles such that those peptides are presented by MHC alleles, which in the models is determined depending on positions of amino acids in the peptide sequences. The presentation model can predict whether an unrecognized peptide sequence will be presented in association with an associated set of MHC alleles based on the presentation

2026201462 26 Feb 2026

information 165. As previously mentioned, the presentation models may be applied to both class I and class II MHC alleles.

IX.B. Presentation Information

[00486] FIG. 2 illustrates a method of obtaining presentation information, in accordance with an embodiment. The presentation information 165 includes two general categories of information: allele-interacting information and allele-noninteracting information. Allele-interacting information includes information that influence presentation of peptide sequences that are dependent on the type of MHC allele. Allele-noninteracting information includes information that influence presentation of peptide sequences that are independent on the type of MHC allele.

IX.B.1. Allele-interacting Information

[00487] Allele-interacting information primarily includes identified peptide sequences that are known to have been presented by one or more identified MHC molecules from humans, mice, etc. Notably, this may or may not include data obtained from tumor samples. The presented peptide sequences may be identified from cells that express a single MHC allele. In this case the presented peptide sequences are generally collected from single-allele cell lines that are engineered to express a predetermined MHC allele and that are subsequently exposed to synthetic protein. Peptides presented on the MHC allele are isolated by techniques such as acid-elution and identified through mass spectrometry. FIG. 2B shows an example of this, where the example peptide YEMFNDKS, presented on the predetermined MHC allele HLA-A*01:01, is isolated and identified through mass spectrometry. FIG. 2D shows another example of this, where the example peptide YEMFNDKSQRAPDDKMF, presented on the predetermined MHC allele HLA-DRB1*12:01, is isolated and identified through mass spectrometry.Since in these situations peptides are identified through cells engineered to express a single predetermined MHC protein, the direct association between a presented peptide and the MHC protein to which it was bound to is definitively known.

[00488] The presented peptide sequences may also be collected from cells that express multiple MHC alleles. Typically in humans, 6 different types of MHC-I and up to 12 different types of MHC-II molecules are expressed for a cell. Such presented peptide sequences may be identified from multiple-allele cell lines that are engineered to express multiple predetermined MHC alleles. Such presented peptide sequences may also be identified from tissue samples, either from normal tissue samples or tumor tissue samples. In this case particularly, the MHC

2026201462 26 Feb 2026

molecules can be immunoprecipitated from normal or tumor tissue. Peptides presented on the multiple MHC alleles can similarly be isolated by techniques such as acid-elution and identified through mass spectrometry. FIG. 2C shows an example of this, where the six example peptides, YEMFNDKSF, HROEIFSHDFJ, FJIEJFOESS, NEIOREIREI, JFKSIFEMMSJDSSU, and KNFLENFIESOFI, are presented on identified MHC alleles HLA-A*01:01, HLA-A*02:01, HLA-B*07:02, HLA-B*08:01, HLA-C*01:03, and HLA-C*01:04 and are isolated and identified through mass spectrometry. In another example, FIG. 2C shows where the six example peptides, YEMFNDKSF, HROEIFSHDFJ, FJIEJFOESS, NEIOREIREI, JFKSIFEMMSJDSSUIFLKSJFIEIFJ, and KNFLENFIESOFI, are presented on identified class I MHC alleles HLA-A*01:01, HLA-A*02:01, HLA-B*07:02, HLA-B*08:01, and class II MHC alleles HLA-DRB1*10:01, HLA-DRB1:11:01and are isolated and identified through mass spectrometry. In contrast to single-allele cell lines, in these examples the direct association between a presented peptide and the MHC protein to which it was bound to may be unknown since the bound peptides are isolated from the MHC molecules before being identified.

[00489] Allele-interacting information can also include mass spectrometry ion current which depends on both the concentration of peptide-MHC molecule complexes, and the ionization efficiency of peptides. The ionization efficiency varies from peptide to peptide in a sequence-dependent manner. Generally, ionization efficiency varies from peptide to peptide over approximately two orders of magnitude, while the concentration of peptide-MHC complexes varies over a larger range than that.

[00490] Allele-interacting information can also include measurements or predictions of binding affinity between a given MHC allele and a given peptide (94, 95, 96). One or more affinity models can generate such predictions. For example, going back to the example shown in FIG. 1D, presentation information 165 may include a binding affinity prediction of 1000nM between the peptide YEMFNDKSF and the class I allele HLA-A*01:01. Few peptides with IC50 > 1000nm are presented by the MHC, and lower IC50 values increase the probability of presentation. Presentation information 165 may include a binding affinity prediction between the peptide KNFLENFIESOFI and the class II allele HLA-DRB1:11:01.

[00491] Allele-interacting information can also include measurements or predictions of stability of the MHC complex. One or more stability models that can generate such predictions. More stable peptide-MHC complexes (i.e., complexes with longer half-lives) are more likely to be presented at high copy number on tumor cells and on antigen-presenting cells that encounter

2026201462 26 Feb 2026

vaccine antigen. For example, going back to the example shown in FIG. 2C, presentation information 165 may include a stability prediction of a half-life of 1h for the class I molecule HLA-A*01:01. Presentation information 165 may also include a stability prediction of a half-life for the class II molecule HLA-DRB1:11:01.

[00492] Allele-interacting information can also include the measured or predicted rate of the formation reaction for the peptide-MHC complex. Complexes that form at a higher rate are more likely to be presented on the cell surface at high concentration.

[00493] Allele-interacting information can also include the sequence and length of the peptide. MHC class I molecules typically prefer to present peptides with lengths between 8 and 15 peptides. 60-80% of presented peptides have length 9. Histograms of presented peptide lengths from several cell lines are shown in Figure 5. MHC class II molecules typically prefer to present peptides with lengths between 6-30 peptides.

[00494] Allele-interacting information can also include the presence of kinase sequence motifs on the neoantigen encoded peptide, and the absence or presence of specific post-translational modifications on the neoantigen encoded peptide. The presence of kinase motifs affects the probability of post-translational modification, which may enhance or interfere with MHC binding.

[00495] Allele-interacting information can also include the expression or activity levels of proteins involved in the process of post-translational modification, e.g., kinases (as measured or predicted from RNA seq, mass spectrometry, or other methods).

[00496] Allele-interacting information can also include the probability of presentation of peptides with similar sequence in cells from other individuals expressing the particular MHC allele as assessed by mass-spectrometry proteomics or other means.

[00497] Allele-interacting information can also include the expression levels of the particular MHC allele in the individual in question (e.g. as measured by RNA-seq or mass spectrometry). Peptides that bind most strongly to an MHC allele that is expressed at high levels are more likely to be presented than peptides that bind most strongly to an MHC allele that is expressed at a low level.

[00498] Allele-interacting information can also include the overall neoantigen encoded peptide-sequence-independent probability of presentation by the particular MHC allele in other individuals who express the particular MHC allele.

[00499] Allele-interacting information can also include the overall peptide-sequence-independent probability of presentation by MHC alleles in the same family of molecules (e.g.,

2026201462 26 Feb 2026

HLA-A, HLA-B, HLA-C, HLA-DQ, HLA-DR, HLA-DP) in other individuals. For example, HLA-C molecules are typically expressed at lower levels than HLA-A or HLA-B molecules, and consequently, presentation of a peptide by HLA-C is a priori less probable than presentation by HLA-A or HLA-B. For another example, HLA-DP is typically expressed at lower levels than HLA-DR or HLA-DQ; consequently, presentation of a peptide by HLA-DP is a prior less probable than presentation by HLA-DR or HLA-DQ.

[00500] Allele-interacting information can also include the protein sequence of the particular MHC allele.

[00501] Any MHC allele-noninteracting information listed in the below section can also be modeled as an MHC allele-interacting information.

IX.B.2. Allele-noninteracting Information

[00502] Allele-noninteracting information can include C-terminal sequences flanking the neoantigen encoded peptide within its source protein sequence. For MHC-I, C-terminal flanking sequences may impact proteasomal processing of peptides. However, the C-terminal flanking sequence is cleaved from the peptide by the proteasome before the peptide is transported to the endoplasmic reticulum and encounters MHC alleles on the surfaces of cells. Consequently, MHC molecules receive no information about the C-terminal flanking sequence, and thus, the effect of the C-terminal flanking sequence cannot vary depending on MHC allele type. For example, going back to the example shown in FIG. 2C, presentation information 165 may include the C-terminal flanking sequence FOEIFNDKSLDKFJI of the presented peptide FJIEJFOESS identified from the source protein of the peptide.

[00503] Allele-noninteracting information can also include mRNA quantification measurements. For example, mRNA quantification data can be obtained for the same samples that provide the mass spectrometry training data. As later described in reference to FIG. 13H, RNA expression was identified to be a strong predictor of peptide presentation. In one embodiment, the mRNA quantification measurements are identified from software tool RSEM. Detailed implementation of the RSEM software tool can be found at Bo Li and Colin N. Dewey. *RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome*. **BMC Bioinformatics**, 12:323, August 2011. In one embodiment, the mRNA quantification is measured in units of fragments per kilobase of transcript per Million mapped reads (FPKM).

[00504] Allele-noninteracting information can also include the N-terminal sequences flanking the peptide within its source protein sequence.

2026201462 26 Feb 2026

[00505] Allele-noninteracting information can also include the source gene of the peptide sequence. The source gene may be defined as the Ensembl protein family of the peptide sequence. In other examples, the source gene may be defined as the source DNA or the source RNA of the peptide sequence. The source gene can, for example, be represented as a string of nucleotides that encode for a protein, or alternatively be more categorically represented based on a named set of known DNA or RNA sequences that are known to encode specific proteins. In another example, allele-noninteracting information can also include the source transcript or isoform or set of potential source transcripts or isoforms of the peptide sequence drawn from a database such as Ensembl or RefSeq.

[00506] Allele-noninteracting information can also include the presence of protease cleavage motifs in the peptide, optionally weighted according to the expression of corresponding proteases in the tumor cells (as measured by RNA-seq or mass spectrometry). Peptides that contain protease cleavage motifs are less likely to be presented, because they will be more readily degraded by proteases, and will therefore be less stable within the cell.

[00507] Allele-noninteracting information can also include the turnover rate of the source protein as measured in the appropriate cell type. Faster turnover rate (i.e., lower half-life) increases the probability of presentation; however, the predictive power of this feature is low if measured in a dissimilar cell type.

[00508] Allele-noninteracting information can also include the length of the source protein, optionally considering the specific splice variants ("isoforms") most highly expressed in the tumor cells as measured by RNA-seq or proteome mass spectrometry, or as predicted from the annotation of germline or somatic splicing mutations detected in DNA or RNA sequence data.

[00509] Allele-noninteracting information can also include the level of expression of the proteasome, immunoproteasome, thymoproteasome, or other proteases in the tumor cells (which may be measured by RNA-seq, proteome mass spectrometry, or immunohistochemistry). Different proteasomes have different cleavage site preferences. More weight will be given to the cleavage preferences of each type of proteasome in proportion to its expression level.

[00510] Allele-noninteracting information can also include the expression of the source gene of the peptide (e.g., as measured by RNA-seq or mass spectrometry). Possible optimizations include adjusting the measured expression to account for the presence of stromal cells and tumor-infiltrating lymphocytes within the tumor sample. Peptides from more highly expressed

2026201462 26 Feb 2026

genes are more likely to be presented. Peptides from genes with undetectable levels of expression can be excluded from consideration.

[00511] Allele-noninteracting information can also include the probability that the source mRNA of the neoantigen encoded peptide will be subject to nonsense-mediated decay as predicted by a model of nonsense-mediated decay, for example, the model from Rivas et al, Science 2015.

[00512] Allele-noninteracting information can also include the typical tissue-specific expression of the source gene of the peptide during various stages of the cell cycle. Genes that are expressed at a low level overall (as measured by RNA-seq or mass spectrometry proteomics) but that are known to be expressed at a high level during specific stages of the cell cycle are likely to produce more presented peptides than genes that are stably expressed at very low levels.

[00513] Allele-noninteracting information can also include a comprehensive catalog of features of the source protein as given in e.g. uniProt or PDB http://www.rcsb.org/pdb/home/home.do. These features may include, among others: the secondary and tertiary structures of the protein, subcellular localization 11, Gene ontology (GO) terms. Specifically, this information may contain annotations that act at the level of the protein, e.g., 5' UTR length, and annotations that act at the level of specific residues, e.g., helix motif between residues 300 and 310. These features can also include turn motifs, sheet motifs, and disordered residues.

[00514] Allele-noninteracting information can also include features describing the properties of the domain of the source protein containing the peptide, for example: secondary or tertiary structure (e.g., alpha helix vs beta sheet); Alternative splicing.

[00515] Allele-noninteracting information can also include features describing the presence or absence of a presentation hotspot at the position of the peptide in the source protein of the peptide.

[00516] Allele-noninteracting information can also include the probability of presentation of peptides from the source protein of the peptide in question in other individuals (after adjusting for the expression level of the source protein in those individuals and the influence of the different HLA types of those individuals).

[00517] Allele-noninteracting information can also include the probability that the peptide will not be detected or over-represented by mass spectrometry due to technical biases.

2026201462 26 Feb 2026

[00518] The expression of various gene modules/pathways as measured by a gene expression assay such as RNASeq, microarray(s), targeted panel(s) such as Nanostring, or single/multi- gene representatives of gene modules measured by assays such as RT-PCR (which need not contain the source protein of the peptide) that are informative about the state of the tumor cells, stroma, or tumor-infiltrating lymphocytes (TILs).

[00519] Allele-noninteracting information can also include the copy number of the source gene of the peptide in the tumor cells. For example, peptides from genes that are subject to homozygous deletion in tumor cells can be assigned a probability of presentation of zero.

[00520] Allele-noninteracting information can also include the probability that the peptide binds to the TAP or the measured or predicted binding affinity of the peptide to the TAP. Peptides that are more likely to bind to the TAP, or peptides that bind the TAP with higher affinity are more likely to be presented by MHC-I.

[00521] Allele-noninteracting information can also include the expression level of TAP in the tumor cells (which may be measured by RNA-seq, proteome mass spectrometry, immunohistochemistry). For MHC-I, higher TAP expression levels increase the probability of presentation of all peptides.

[00522] Allele-noninteracting information can also include the presence or absence of tumor mutations, including, but not limited to:

i. Driver mutations in known cancer driver genes such as EGFR, KRAS, ALK, RET, ROS1, TP53, CDKN2A, CDKN2B, NTRK1, NTRK2, NTRK3

ii. In genes encoding the proteins involved in the antigen presentation machinery (e.g., B2M, HLA-A, HLA-B, HLA-C, TAP-1, TAP-2, TAPBP, CALR, CNX, ERP57, HLA-DM, HLA-DMA, HLA-DMB, HLA-DO, HLA-DOA, HLA-DOB, HLA-DP, HLA-DPA1, HLA-DPB1, HLA-DQ, HLA-DQA1, HLA-DQA2, HLA-DQB1, HLA-DQB2, HLA-DR, HLA-DRA, HLA-DRB1, HLA-DRB3, HLA-DRB4, HLA-DRB5 or any of the genes coding for components of the proteasome or immunoproteasome). Peptides whose presentation relies on a component of the antigen-presentation machinery that is subject to loss-of-function mutation in the tumor have reduced probability of presentation.

[00523] Presence or absence of functional germline polymorphisms, including, but not limited to:

i. In genes encoding the proteins involved in the antigen presentation machinery (e.g., B2M, HLA-A, HLA-B, HLA-C, TAP-1, TAP-2, TAPBP, CALR, CNX, ERP57, HLA-DM, HLA-

2026201462 26 Feb 2026

DMA, HLA-DMB, HLA-DO, HLA-DOA, HLA-DOB, HLA-DP, HLA-DPA1, HLA-DPB1, HLA-DQ, HLA-DQA1, HLA-DQA2, HLA-DQB1, HLA-DQB2, HLA-DR, HLA-DRA, HLA-DRB1, HLA-DRB3, HLA-DRB4, HLA-DRB5 or any of the genes coding for components of the proteasome or immunoproteasome)

[00524] Allele-noninteracting information can also include tumor type (e.g., NSCLC, melanoma).

[00525] Allele-noninteracting information can also include known functionality of HLA alleles, as reflected by, for instance HLA allele suffixes. For example, the N suffix in the allele name HLA-A*24:09N indicates a null allele that is not expressed and is therefore unlikely to present epitopes; the full HLA allele suffix nomenclature is described at https://www.ebi.ac.uk/ipd/imgt/hla/nomenclature/suffixes.html.

[00526] Allele-noninteracting information can also include clinical tumor subtype (e.g., squamous lung cancer vs. non-squamous).

[00527] Allele-noninteracting information can also include smoking history.

[00528] Allele-noninteracting information can also include history of sunburn, sun exposure, or exposure to other mutagens.

[00529] Allele-noninteracting information can also include the typical expression of the source gene of the peptide in the relevant tumor type or clinical subtype, optionally stratified by driver mutation. Genes that are typically expressed at high levels in the relevant tumor type are more likely to be presented.

[00530] Allele-noninteracting information can also include the frequency of the mutation in all tumors, or in tumors of the same type, or in tumors from individuals with at least one shared MHC allele, or in tumors of the same type in individuals with at least one shared MHC allele.

[00531] In the case of a mutated tumor-specific peptide, the list of features used to predict a probability of presentation may also include the annotation of the mutation (e.g., missense, read-through, frameshift, fusion, etc.) or whether the mutation is predicted to result in nonsense-mediated decay (NMD). For example, peptides from protein segments that are not translated in tumor cells due to homozygous early-stop mutations can be assigned a probability of presentation of zero. NMD results in decreased mRNA translation, which decreases the probability of presentation.

2026201462 26 Feb 2026

IX.C. Presentation Identification System

[00532] FIG. 3 is a high-level block diagram illustrating the computer logic components of the presentation identification system 160, according to one embodiment. In this example embodiment, the presentation identification system 160 includes a data management module 312, an encoding module 314, a training module 316, and a prediction module 320. The presentation identification system 160 is also comprised of a training data store 170 and a presentation models store 175. Some embodiments of the model management system 160 have different modules than those described here. Similarly, the functions can be distributed among the modules in a different manner than is described here.

IX.C.1. Data Management Module

[00533] The data management module 312 generates sets of training data 170 from the presentation information 165. Each set of training data contains a plurality of data instances, in which each data instance i contains a set of independent variables $\boldsymbol{z}^i$ that include at least a presented or non-presented peptide sequence $\boldsymbol{p}^i$, one or more associated MHC alleles $\boldsymbol{a}^i$ associated with the peptide sequence $\boldsymbol{p}^i$, and a dependent variable y^i that represents information that the presentation identification system 160 is interested in predicting for new values of independent variables.

[00534] In one particular implementation referred throughout the remainder of the specification, the dependent variable y^i is a binary label indicating whether peptide $\boldsymbol{p}^i$ was presented by the one or more associated MHC alleles $\boldsymbol{a}^i$. However, it is appreciated that in other implementations, the dependent variable $\boldsymbol{y}^i$ can represent any other kind of information that the presentation identification system 160 is interested in predicting dependent on the independent variables $\boldsymbol{z}^i$. For example, in another implementation, the dependent variable $\boldsymbol{y}^i$ may also be a numerical value indicating the mass spectrometry ion current identified for the data instance.

[00535] The peptide sequence $\boldsymbol{p}^i$ for data instance $\boldsymbol{i}$ is a sequence of k_i amino acids, in which k_i may vary between data instances i within a range. For example, that range may be 8-15 for MHC class I or 6-30 for MHC class II. In one specific implementation of system 160, all peptide sequences $\boldsymbol{p}^i$ in a training data set may have the same length, e.g. 9. The number of amino acids in a peptide sequence may vary depending on the type of MHC alleles (e.g., MHC alleles in humans, etc.). The MHC alleles $\boldsymbol{a}^i$ for data instance i indicate which MHC alleles were present in association with the corresponding peptide sequence $\boldsymbol{p}^i$.

2026201462 26 Feb 2026

[00536] The data management module 312 may also include additional allele-interacting variables, such as binding affinity b^i and stability s^i predictions in conjunction with the peptide sequences p^i and associated MHC alleles a^i contained in the training data 170. For example, the training data 170 may contain binding affinity predictions b^i between a peptide p^i and each of the associated MHC molecules indicated in a^i. As another example, the training data 170 may contain stability predictions s^i for each of the MHC alleles indicated in a^i.

[00537] The data management module 312 may also include allele-noninteracting variables w^i, such as C-terminal flanking sequences and mRNA quantification measurements in conjunction with the peptide sequences p^i.

[00538] The data management module 312 also identifies peptide sequences that are not presented by MHC alleles to generate the training data 170. Generally, this involves identifying the "longer" sequences of source protein that include presented peptide sequences prior to presentation. When the presentation information contains engineered cell lines, the data management module 312 identifies a series of peptide sequences in the synthetic protein to which the cells were exposed to that were not presented on MHC alleles of the cells. When the presentation information contains tissue samples, the data management module 312 identifies source proteins from which presented peptide sequences originated from, and identifies a series of peptide sequences in the source protein that were not presented on MHC alleles of the tissue sample cells.

[00539] The data management module 312 may also artificially generate peptides with random sequences of amino acids and identify the generated sequences as peptides not presented on MHC alleles. This can be accomplished by randomly generating peptide sequences allows the data management module 312 to easily generate large amounts of synthetic data for peptides not presented on MHC alleles. Since in reality, a small percentage of peptide sequences are presented by MHC alleles, the synthetically generated peptide sequences are highly likely not to have been presented by MHC alleles even if they were included in proteins processed by cells.

[00540] FIG. 4A illustrates an example set of training data 170A, according to one embodiment. Specifically, the first 3 data instances in the training data 170A indicate peptide presentation information from a single-allele cell line involving the allele HLA-C*01:03 and 3 peptide sequences QCEIOWARE, FIEUHFWI, and FEWRHRJTRUJR. The fourth data instance in the training data 170A indicates peptide information from a multiple-allele cell line involving the alleles HLA-B*07:02, HLA-C*01:03, HLA-A*01:01and a peptide sequence

2026201462 26 Feb 2026

QIEJOEIJE. The first data instance indicates that peptide sequence QCEIOWARE was not presented by the allele HLA-C*01:03. As discussed in the prior two paragraphs, the peptide sequence may be randomly generated by the data management module 312 or identified from source protein of presented peptides. The training data 170A also includes a binding affinity prediction of 1000nM and a stability prediction of a half-life of 1h for the peptide sequence-allele pair. The training data 170A also includes allele-noninteracting variables, such as the C-terminal flanking sequence of the peptide FJELFISBOSJFIE, and a mRNA quantification measurement of 10^2 TPM. The fourth data instance indicates that peptide sequence QIEJOEIJE was presented by one of the alleles HLA-B*07:02, HLA-C*01:03, or HLA-A*01:01. The training data 170A also includes binding affinity predictions and stability predictions for each of the alleles, as well as the C-terminal flanking sequence of the peptide and the mRNA quantification measurement for the peptide.

[00541] FIG. 4B illustrates another example set of training data 170A, according to one embodiment. Specifically, the first data instances in the training data 170A indicate peptide presentation information from a single-allele cell line involving the class II allele HLA-DRB3:01:01 and the peptide sequence QCEIOWAREFLKEIGJ. The first data instance indicates that peptide sequence QCEIOWAREFLKEIGJ was not presented by the allele HLA-DRB3:01:01.

IX.C.2. Encoding Module

[00542] The encoding module 314 encodes information contained in the training data 170 into a numerical representation that can be used to generate the one or more presentation models. In one implementation, the encoding module 314 one-hot encodes sequences (e.g., peptide sequences or C-terminal flanking sequences) over a predetermined 20-letter amino acid alphabet. Specifically, a peptide sequence $\boldsymbol{p^i}$ with k_i amino acids is represented as a row vector of $20 \cdot k_i$ elements, where a single element among $p^i_{20\cdot(j-1)+1}$, $p^i_{20\cdot(j-1)+2}$, …, $p^i_{20\cdot j}$ that corresponds to the alphabet of the amino acid at the *j-th* position of the peptide sequence has a value of 1. Otherwise, the remaining elements have a value of 0. As an example, for a given alphabet {A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y}, the peptide sequence EAF of 3 amino acids for data instance *i* may be represented by the row vector of 60 elements $\boldsymbol{p^i}$ =[0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

2026201462 26 Feb 2026

[00543] When the training data 170 contains sequences of differing lengths of amino acids, the encoding module 314 may further encode the peptides into equal-length vectors by adding a PAD character to extend the predetermined alphabet. For example, this may be performed by left-padding the peptide sequences with the PAD character until the length of the peptide sequence reaches the peptide sequence with the greatest length in the training data 170. Thus, when the peptide sequence with the greatest length has k_{max} amino acids, the encoding module 314 numerically represents each sequence as a row vector of $(20+1)\cdot k_{max}$ elements. As an example, for the extended alphabet {PAD, A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y} and a maximum amino acid length of $k_{max}=5$, the same example peptide sequence EAF of 3 amino acids may be represented by the row vector of 105 elements $\boldsymbol{p^i}$=[1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

2026201462 26 Feb 2026

discussed, each data instance i typically contains at most 6 different MHC class I allele types in association with the peptide sequence $\boldsymbol{p_i}$, and/or at most 4 different MHC class II DR allele types in association with the peptide sequence $\boldsymbol{p_i}$, and/or at most 12 different MHC class II allele types in association with the peptide sequence $\boldsymbol{p_i}$.

[00546] The encoding module 314 also encodes the label y_i for each data instance i as a binary variable having values from the set of {0, 1}, in which a value of 1 indicates that peptide $\boldsymbol{x^i}$ was presented by one of the associated MHC alleles $\boldsymbol{a^i}$, and a value of 0 indicates that peptide $\boldsymbol{x^i}$ was not presented by any of the associated MHC alleles $\boldsymbol{a^i}$. When the dependent variable y_i represents the mass spectrometry ion current, the encoding module 314 may additionally scale the values using various functions, such as the log function having a range of $[-\infty, \infty]$ for ion current values between $[0, \infty]$.

[00547] The encoding module 314 may represent a pair of allele-interacting variables $\boldsymbol{x_h^i}$ for peptide p_i and an associated MHC allele h as a row vector in which numerical representations of allele-interacting variables are concatenated one after the other. For example, the encoding module 314 may represent $\boldsymbol{x_h^i}$ as a row vector equal to $\boldsymbol{[p^i]}$, $\boldsymbol{[p^i}\ b_h^i\boldsymbol{]}$, $\boldsymbol{[p^i}\ s_h^i\boldsymbol{]}$, or $\boldsymbol{[p^i}\ b_h^i\ s_h^i\boldsymbol{]}$, where b_h^i is the binding affinity prediction for peptide p_i and associated MHC allele h, and similarly for s_h^i for stability. Alternatively, one or more combination of allele-interacting variables may be stored individually (e.g., as individual vectors or matrices).

[00548] In one instance, the encoding module 314 represents binding affinity information by incorporating measured or predicted values for binding affinity in the allele-interacting variables $\boldsymbol{x_h^i}$.

[00549] In one instance, the encoding module 314 represents binding stability information by incorporating measured or predicted values for binding stability in the allele-interacting variables $\boldsymbol{x_h^i}$,

[00550] In one instance, the encoding module 314 represents binding on-rate information by incorporating measured or predicted values for binding on-rate in the allele-interacting variables $\boldsymbol{x_h^i}$.

[00551] In one instance, for peptides presented by class I MHC molecules, the encoding module 314 represents peptide length as a vector $\boldsymbol{T_k}$=[$\mathbb{1}(L_k$=8) $\mathbb{1}(L_k$=9) $\mathbb{1}(L_k$=10) $\mathbb{1}(L_k$=11) $\mathbb{1}(L_k$=12) $\mathbb{1}(L_k$=13) $\mathbb{1}(L_k$=14) $\mathbb{1}(L_k$=15)] where $\mathbb{1}$ is the indicator function, and L_k denotes the length of peptide $\boldsymbol{p_k}$. The vector $\boldsymbol{T_k}$ can be included in the allele-interacting variables $\boldsymbol{x_h^i}$. In another instance, for peptides presented by class II MHC molecules, the encoding module 314 represents peptide length as a vector $\boldsymbol{T_k}$=[$\mathbb{1}(L_k$=6) $\mathbb{1}(L_k$=7) $\mathbb{1}(L_k$=8) $\mathbb{1}(L_k$=9) $\mathbb{1}(L_k$=10) $\mathbb{1}(L_k$=11)

2026201462 26 Feb 2026

$\mathbb{1}(L_k=12)$ $\mathbb{1}(L_k=13)$ $\mathbb{1}(L_k=14)$ $\mathbb{1}(L_k=15)$ $\mathbb{1}(L_k=16)$ $\mathbb{1}(L_k=17)$ $\mathbb{1}(L_k=18)$ $\mathbb{1}(L_k=19)$ $\mathbb{1}(L_k=20)$ $\mathbb{1}(L_k=21)$ $\mathbb{1}(L_k=22)$ $\mathbb{1}(L_k=23)$ $\mathbb{1}(L_k=24)$ $\mathbb{1}(L_k=25)$ $\mathbb{1}(L_k=26)$ $\mathbb{1}(L_k=27)$ $\mathbb{1}(L_k=28)$ $\mathbb{1}(L_k=29)$ $\mathbb{1}(L_k=30)$] where $\mathbb{1}$ is the indicator function, and L_k denotes the length of peptide $\boldsymbol{p_k}$. The vector $\boldsymbol{T_k}$ can be included in the allele-interacting variables $\boldsymbol{x_h^i}$.

[00552] In one instance, the encoding module 314 represents RNA expression information of MHC alleles by incorporating RNA-seq based expression levels of MHC alleles in the allele-interacting variables $\boldsymbol{x_h^i}$.

[00553] Similarly, the encoding module 314 may represent the allele-noninteracting variables $\boldsymbol{w^i}$ as a row vector in which numerical representations of allele-noninteracting variables are concatenated one after the other. For example, $\boldsymbol{w^i}$ may be a row vector equal to $\boldsymbol{[c^i]}$ or $\boldsymbol{[c^i\ m^i\ w^i]}$ in which $\boldsymbol{w^i}$ is a row vector representing any other allele-noninteracting variables in addition to the C-terminal flanking sequence of peptide $\boldsymbol{p^i}$ and the mRNA quantification measurement $\boldsymbol{m^i}$ associated with the peptide. Alternatively, one or more combination of allele-noninteracting variables may be stored individually (e.g., as individual vectors or matrices).

[00554] In one instance, the encoding module 314 represents turnover rate of source protein for a peptide sequence by incorporating the turnover rate or half-life in the allele-noninteracting variables $\boldsymbol{w^i}$.

[00555] In one instance, the encoding module 314 represents length of source protein or isoform by incorporating the protein length in the allele-noninteracting variables $\boldsymbol{w^i}$.

[00556] In one instance, the encoding module 314 represents activation of immunoproteasome by incorporating the mean expression of the immunoproteasome-specific proteasome subunits including the $\beta 1_\mathrm{i}$, $\beta 2_\mathrm{i}$, $\beta 5_\mathrm{i}$ subunits in the allele-noninteracting variables $\boldsymbol{w^i}$.

[00557] In one instance, the encoding module 314 represents the RNA-seq abundance of the source protein of the peptide or gene or transcript of a peptide (quantified in units of FPKM, TPM by techniques such as RSEM) can be incorporating the abundance of the source protein in the allele-noninteracting variables $\boldsymbol{w^i}$.

[00558] In one instance, the encoding module 314 represents the probability that the transcript of origin of a peptide will undergo nonsense-mediated decay (NMD) as estimated by the model in, for example, Rivas et. al. *Science,* 2015 by incorporating this probability in the allele-noninteracting variables $\boldsymbol{w^i}$.

[00559] In one instance, the encoding module 314 represents the activation status of a gene module or pathway assessed via RNA-seq by, for example, quantifying expression of the genes

2026201462 26 Feb 2026

in the pathway in units of TPM using e.g., RSEM for each of the genes in the pathway then computing a summary statistics, e.g., the mean, across genes in the pathway. The mean can be incorporated in the allele-noninteracting variables $\boldsymbol{w}^i$.

[00560] In one instance, the encoding module 314 represents the copy number of the source gene by incorporating the copy number in the allele-noninteracting variables $\boldsymbol{w}^i$.

[00561] In one instance, the encoding module 314 represents the TAP binding affinity by including the measured or predicted TAP binding affinity (e.g., in nanomolar units) in the allele-noninteracting variables $\boldsymbol{w}^i$.

[00562] In one instance, the encoding module 314 represents TAP expression levels by including TAP expression levels measured by RNA-seq (and quantified in units of TPM by e.g., RSEM) in the allele-noninteracting variables $\boldsymbol{w}^i$.

[00563] In one instance, the encoding module 314 represents tumor mutations as a vector of indicator variables (i.e., $\boldsymbol{d}^k = 1$ if peptide $\boldsymbol{p}^k$ comes from a sample with a KRAS G12D mutation and 0 otherwise) in the allele-noninteracting variables $\boldsymbol{w}^i$.

[00564] In one instance, the encoding module 314 represents germline polymorphisms in antigen presentation genes as a vector of indicator variables (i.e., $\boldsymbol{d}^k = 1$ if peptide $\boldsymbol{p}^k$ comes from a sample with a specific germline polymorphism in the TAP). These indicator variables can be included in the allele-noninteracting variables $\boldsymbol{w}^i$.

[00565] In one instance, the encoding module 314 represents tumor type as a length-one one-hot encoded vector over the alphabet of tumor types (e.g., NSCLC, melanoma, colorectal cancer, etc). These one-hot-encoded variables can be included in the allele-noninteracting variables $\boldsymbol{w}^i$.

[00566] In one instance, the encoding module 314 represents MHC allele suffixes by treating 4-digit HLA alleles with different suffixes. For example, HLA-A*24:09N is considered a different allele from HLA-A*24:09 for the purpose of the model. Alternatively, the probability of presentation by an N-suffixed MHC allele can be set to zero for all peptides, because HLA alleles ending in the N suffix are not expressed.

[00567] In one instance, the encoding module 314 represents tumor subtype as a length-one one-hot encoded vector over the alphabet of tumor subtypes (e.g., lung adenocarcinoma, lung squamous cell carcinoma, etc). These onehot-encoded variables can be included in the allele-noninteracting variables $\boldsymbol{w}^i$.

[00568] In one instance, the encoding module 314 represents smoking history as a binary indicator variable ($\boldsymbol{d}^k = 1$ if the patient has a smoking history, and 0 otherwise), that can be

2026201462 26 Feb 2026

included in the allele-noninteracting variables $\boldsymbol{w^i}$. Alternatively, smoking history can be encoded as a length-one one-hot-enocded variable over an alphabet of smoking severity. For example, smoking status can be rated on a 1-5 scale, where 1 indicates nonsmokers, and 5 indicates current heavy smokers. Because smoking history is primarily relevant to lung tumors, when training a model on multiple tumor types, this variable can also be defined to be equal to 1 if the patient has a history of smoking and the tumor type is lung tumors and zero otherwise.

[00569] In one instance, the encoding module 314 represents sunburn history as a binary indicator variable ($\boldsymbol{d^k} = 1$ if the patient has a history of severe sunburn, and 0 otherwise), which can be included in the allele-noninteracting variables $\boldsymbol{w^i}$. Because severe sunburn is primarily relevant to melanomas, when training a model on multiple tumor types, this variable can also be defined to be equal to 1 if the patient has a history of severe sunburn and the tumor type is melanoma and zero otherwise.

[00570] In one instance, the encoding module 314 represents distribution of expression levels of a particular gene or transcript for each gene or transcript in the human genome as summary statistics (e,g., mean, median) of distribution of expression levels by using reference databases such as TCGA. Specifically, for a peptide $\boldsymbol{p^k}$ in a sample with tumor type melanoma, we can include not only the measured gene or transcript expression level of the gene or transcript of origin of peptide $\boldsymbol{p^k}$ in the allele-noninteracting variables $\boldsymbol{w^i}$, but also the mean and/or median gene or transcript expression of the gene or transcript of origin of peptide $\boldsymbol{p^k}$ in melanomas as measured by TCGA.

[00571] In one instance, the encoding module 314 represents mutation type as a length-one one-hot-encoded variable over the alphabet of mutation types (e.g., missense, frameshift, NMD-inducing, etc). These onehot-encoded variables can be included in the allele-noninteracting variables $\boldsymbol{w^i}$.

[00572] In one instance, the encoding module 314 represents protein-level features of protein as the value of the annotation (e.g., 5' UTR length) of the source protein in the allele-noninteracting variables $\boldsymbol{w^i}$. In another instance, the encoding module 314 represents residue-level annotations of the source protein for peptide $\boldsymbol{p^i}$ by including an indicator variable, that is equal to 1 if peptide $\boldsymbol{p^i}$ overlaps with a helix motif and 0 otherwise, or that is equal to 1 if peptide $\boldsymbol{p^i}$ is completely contained with within a helix motif in the allele-noninteracting variables $\boldsymbol{w^i}$. In another instance, a feature representing proportion of residues in peptide $\boldsymbol{p^i}$ that are contained within a helix motif annotation can be included in the allele-noninteracting variables $\boldsymbol{w^i}$.

2026201462 26 Feb 2026

[00573] In one instance, the encoding module 314 represents type of proteins or isoforms in the human proteome as an indicator vector $\boldsymbol{o}^k$ that has a length equal to the number of proteins or isoforms in the human proteome, and the corresponding element $o^k{}_i$ is 1 if peptide $\boldsymbol{p}^k$ comes from protein i and 0 otherwise.

[00574] In one instance, the encoding module 314 represents the source gene G=gene($\boldsymbol{p}^i$) of peptide $\boldsymbol{p}^i$ as a categorical variable with L possible categories, where L denotes the upper limit of the number of indexed source genes 1, 2, …, L.

[00575] The encoding module 314 may also represent the overall set of variables $\boldsymbol{z}^i$ for peptide $\boldsymbol{p}^i$ and an associated MHC allele h as a row vector in which numerical representations of the allele-interacting variables $\boldsymbol{x}^i$ and the allele-noninteracting variables $\boldsymbol{w}^i$ are concatenated one after the other. For example, the encoding module 314 may represent $\boldsymbol{z}_h{}^i$ as a row vector equal to $[\boldsymbol{x}_h{}^i\ \boldsymbol{w}^i]$ or $[\boldsymbol{w}_i\ \boldsymbol{x}_h{}^i]$.

X. Training Module

[00576] The training module 316 constructs one or more presentation models that generate likelihoods of whether peptide sequences will be presented by MHC alleles associated with the peptide sequences. Specifically, given a peptide sequence $\boldsymbol{p}^k$ and a set of MHC alleles $\boldsymbol{a}^k$ associated with the peptide sequence $\boldsymbol{p}^k$, each presentation model generates an estimate u_k indicating a likelihood that the peptide sequence $\boldsymbol{p}^k$ will be presented by one or more of the associated MHC alleles $\boldsymbol{a}^k$.

X.A. Overview

[00577] The training module 316 constructs the one more presentation models based on the training data sets stored in store 170 generated from the presentation information stored in 165. Generally, regardless of the specific type of presentation model, all of the presentation models capture the dependence between independent variables and dependent variables in the training data 170 such that a loss function is minimized. Specifically, the loss function $\ell(y_{i\in S}, u_{i\in S}; \boldsymbol{\theta})$ represents discrepancies between values of dependent variables $y_{i\in S}$ for one or more data instances S in the training data 170 and the estimated likelihoods $u_{i\in S}$ for the data instances S generated by the presentation model. In one particular implementation referred throughout the remainder of the specification, the loss function ($y_{i\in S}$, $u_{i\in S}$; $\boldsymbol{\theta}$) is the negative log likelihood function given by equation (1a) as follows:

$$\ell(y_{i\in S}, u_{i\in S}; \boldsymbol{\theta}) = \sum_{i\in S} (y_i \log u_i + (1 - y_i) \log(1 - u_i)). \tag{1a}$$

2026201462 26 Feb 2026

However, in practice, another loss function may be used. For example, when predictions are made for the mass spectrometry ion current, the loss function is the mean squared loss given by equation 1b as follows:

$$\ell(y_{i\in S}, u_{i\in S}; \theta) = \sum_{i\in S} (\|y_i - u_i\|_2^2). \quad (1b)$$

[00578] The presentation model may be a parametric model in which one or more parameters $\boldsymbol{\theta}$ mathematically specify the dependence between the independent variables and dependent variables. Typically, various parameters of parametric-type presentation models that minimize the loss function ($y_{i\in S}$, $u_{i\in S}$; $\boldsymbol{\theta}$) are determined through gradient-based numerical optimization algorithms, such as batch gradient algorithms, stochastic gradient algorithms, and the like. Alternatively, the presentation model may be a non-parametric model in which the model structure is determined from the training data 170 and is not strictly based on a fixed set of parameters.

X.B. Per-Allele Models

[00579] The training module 316 may construct the presentation models to predict presentation likelihoods of peptides on a per-allele basis. In this case, the training module 316 may train the presentation models based on data instances S in the training data 170 generated from cells expressing single MHC alleles.

[00580] In one implementation, the training module 316 models the estimated presentation likelihood u_k for peptide $\boldsymbol{p^k}$ for a specific allele h by:

$$u_k^h = \Pr(\boldsymbol{p^k} \text{ presented; MHC allele } h) = f\left(g_h(\boldsymbol{x_h^k}; \boldsymbol{\theta_h})\right), \quad (2)$$

where peptide sequence $\boldsymbol{x_h^k}$ denotes the encoded allele-interacting variables for peptide $\boldsymbol{p^k}$ and corresponding MHC allele h, $f(\cdot)$ is any function, and is herein throughout is referred to as a transformation function for convenience of description. Further, $g_h(\cdot)$ is any function, is herein throughout referred to as a dependency function for convenience of description, and generates dependency scores for the allele-interacting variables $\boldsymbol{x_h^k}$ based on a set of parameters $\boldsymbol{\theta_h}$ determined for MHC allele h. The values for the set of parameters $\boldsymbol{\theta_h}$ for each MHC allele h can be determined by minimizing the loss function with respect to $\boldsymbol{\theta_h}$, where i is each instance in the subset S of training data 170 generated from cells expressing the single MHC allele h.

[00581] The output of the dependency function $g_h(\boldsymbol{x_h^k}; \boldsymbol{\theta_h})$ represents a dependency score for the MHC allele h indicating whether the MHC allele h will present the corresponding neoantigen based on at least the allele interacting features $\boldsymbol{x_h^k}$, and in particular, based on

2026201462 26 Feb 2026

positions of amino acids of the peptide sequence of peptide $\boldsymbol{p^k}$. For example, the dependency score for the MHC allele *h* may have a high value if the MHC allele *h* is likely to present the peptide $\boldsymbol{p^k}$, and may have a low value if presentation is not likely. The transformation function $f(\cdot)$ transforms the input, and more specifically, transforms the dependency score generated by $g_h(\boldsymbol{x_h^k};\boldsymbol{\theta_h})$ in this case, to an appropriate value to indicate the likelihood that the peptide $\boldsymbol{p^k}$ will be presented by an MHC allele.

[00582] In one particular implementation referred throughout the remainder of the specification, $f(\cdot)$ is a function having the range within [0, 1] for an appropriate domain range. In one example, $f(\cdot)$ is the expit function given by:

$$f(z) = \frac{\exp(z)}{1 + \exp(z)}. \tag{4}$$

As another example, $f(\cdot)$ can also be the hyperbolic tangent function given by:

$$f(z) = \tanh(z) \tag{5}$$

when the values for the domain *z* is equal to or greater than 0. Alternatively, when predictions are made for the mass spectrometry ion current that have values outside the range [0, 1], $f(\cdot)$ can be any function such as the identity function, the exponential function, the log function, and the like.

[00583] Thus, the per-allele likelihood that a peptide sequence $\boldsymbol{p^k}$ will be presented by a MHC allele *h* can be generated by applying the dependency function $g_h(\cdot)$ for the MHC allele h to the encoded version of the peptide sequence $\boldsymbol{p^k}$ to generate the corresponding dependency score. The dependency score may be transformed by the transformation function $f(\cdot)$ to generate a per-allele like*l*ihood that the peptide sequence $\boldsymbol{p^k}$ will be presented by the MHC allele *h*.

X.B.1 Dependency Functions for Allele Interacting Variables

[00584] In one particular implementation referred throughout the specification, the dependency function $g_h(\cdot)$ is an affine function given by:

$$g_h(\boldsymbol{x_h^i};\boldsymbol{\theta_h}) = \boldsymbol{x_h^i} \cdot \boldsymbol{\theta_h}. \tag{6}$$

that linearly combines each allele-interacting variable in $\boldsymbol{x_h^k}$ with a corresponding parameter in the set of parameters $\boldsymbol{\theta_h}$ determined for the associated MHC allele *h*.

[00585] In another particular implementation referred throughout the specification, the dependency function $\boldsymbol{g_h(\cdot)}$ is a network function given by:

$$g_h(\boldsymbol{x_h^i};\boldsymbol{\theta_h}) = NN_h(\boldsymbol{x_h^i};\boldsymbol{\theta_h}). \tag{7}$$

2026201462 26 Feb 2026

represented by a network model $NN_h(\cdot)$ having a series of nodes arranged in one or more layers. A node may be connected to other nodes through connections each having an associated parameter in the set of parameters $\boldsymbol{\theta_h}$. A value at one particular node may be represented as a sum of the values of nodes connected to the particular node weighted by the associated parameter mapped by an activation function associated with the particular node. In contrast to the affine function, network models are advantageous because the presentation model can incorporate non-linearity and process data having different lengths of amino acid sequences. Specifically, through non-linear modeling, network models can capture interaction between amino acids at different positions in a peptide sequence and how this interaction affects peptide presentation.

[00586] In general, network models $NN_h(\cdot)$ may be structured as feed-forward networks, such as artificial neural networks (ANN), convolutional neural networks (CNN), deep neural networks (DNN), and/or recurrent networks, such as long short-term memory networks (LSTM), bi-directional recurrent networks, deep bi-directional recurrent networks, and the like.

[00587] In one instance referred throughout the remainder of the specification, each MHC allele in $h=1,2,\ldots, m$ is associated with a separate network model, and $NN_h(\cdot)$ denotes the output(s) from a network model associated with MHC allele h.

[00588] FIG. 5 illustrates an example network model $NN_3(\cdot)$ in association with an arbitrary MHC allele h=3. As shown in FIG. 5, the network model $NN_3(\cdot)$ for MHC allele $h=3$ includes three input nodes at layer $l=1$, four nodes at layer $l=2$, two nodes at layer $l=3$, and one output node at layer $l=4$. The network model $NN_3(\cdot)$ is associated with a set of ten parameters $\theta_3(1)$, $\theta_3(2)$, ..., $\theta_3(10)$. The network model $NN_3(\cdot)$ receives input values (individual data instances including encoded polypeptide sequence data and any other training data used) for three allele-interacting variables $x_3^k(1)$, $x_3^k(2)$, and $x_3^k(3)$ for MHC allele $h=3$ and outputs the value $NN_3(x_3^k)$. The network function may also include one or more network models each taking different allele interacting variables as input.

[00589] In another instance, the identified MHC alleles $h=1, 2, \ldots, m$ are associated with a single network model $NN_H(\cdot)$, and $NN_h(\cdot)$ denotes one or more outputs of the single network model associated with MHC allele h. In such an instance, the set of parameters $\boldsymbol{\theta_h}$ may correspond to a set of parameters for the single network model, and thus, the set of parameters $\boldsymbol{\theta_h}$ may be shared by all MHC alleles.

[00590] FIG. 6A illustrates an example network model $NN_H(\cdot)$ shared by MHC alleles $h=1,2, \ldots,m$. As shown in FIG. 6A, the network model $NN_H(\cdot)$includes m output nodes each

2026201462 26 Feb 2026

corresponding to an MHC allele. The network model $NN_3(\cdot)$ receives the allele-interacting variables $\boldsymbol{x_3^k}$ for MHC allele $h=3$ and outputs m values including the value $NN_3(x_3^k)$ corresponding to the MHC allele $h=3$.

[00591] In yet another instance, the single network model $NN_H(\cdot)$ may be a network model that outputs a dependency score given the allele interacting variables $\boldsymbol{x_h^k}$ and the encoded protein sequence $\boldsymbol{d_h}$ of an MHC allele h. In such an instance, the set of parameters $\boldsymbol{\theta_h}$ may again correspond to a set of parameters for the single network model, and thus, the set of parameters $\boldsymbol{\theta_h}$ may be shared by all MHC alleles. Thus, in such an instance, $NN_h(\cdot)$ may denote the output of the single network model $NN_H(\cdot)$ given inputs $[\boldsymbol{x_h^k}\ \boldsymbol{d_h}]$ to the single network model. Such a network model is advantageous because peptide presentation probabilities for MHC alleles that were unknown in the training data can be predicted just by identification of their protein sequence.

[00592] FIG. 6B illustrates an example network model $NN_H(\cdot)$ shared by MHC alleles. As shown in FIG. 6B, the network model $NN_H(\cdot)$ receives the allele interacting variables and protein sequence of MHC allele $h=3$ as input, and outputs a dependency score $NN_3(x_3^k)$ corresponding to the MHC allele $h=3$.

[00593] In yet another instance, the dependency function $\boldsymbol{g_h(\cdot)}$ can be expressed as:

$$g_h\left(\boldsymbol{x_h^k};\boldsymbol{\theta_h}\right) = g'_h\left(\boldsymbol{x_h^k};\boldsymbol{\theta'_h}\right) + \theta_h^0$$

where $g'_h(\boldsymbol{x_h^k};\boldsymbol{\theta'_h})$ is the affine function with a set of parameters $\boldsymbol{\theta'_h}$, the network function, or the like, with a bias parameter $\boldsymbol{\theta_h^0}$ in the set of parameters for allele interacting variables for the MHC allele that represents a baseline probability of presentation for the MHC allele h.

[00594] In another implementation, the bias parameter $\boldsymbol{\theta_h^0}$ may be shared according to the gene family of the MHC allele h. That is, the bias parameter $\boldsymbol{\theta_h^0}$ for MHC allele h may be equal to $\boldsymbol{\theta_{gene(h)}^0}$, where $gene(h)$ is the gene family of MHC allele h. For example, class I MHC alleles HLA-A*02:01, HLA-A*02:02, and HLA-A*02:03 may be assigned to the gene family of "HLA-A," and the bias parameter $\boldsymbol{\theta_h^0}$ for each of these MHC alleles may be shared. As another example, class II MHC alleles HLA-DRB1:10:01, HLA-DRB1:11:01, and HLA-DRB3:01:01 may be assigned to the gene family of "HLA-DRB," and the bias parameter $\boldsymbol{\theta_h^0}$ for each of these MHC alleles may be shared.

[00595] Returning to equation (2), as an example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by MHC allele $h=3$, among $m=4$ different identified MHC alleles using the affine dependency function $g_h(\cdot)$, can be generated by:

$$u_k^3 = f\left(\boldsymbol{x_3^k} \cdot \boldsymbol{\theta_3}\right),$$

26 Feb 2026
2026201462

where $\boldsymbol{x_3^k}$ are the identified allele-interacting variables for MHC allele $h=3$, and $\boldsymbol{\theta_3}$ are the set of parameters determined for MHC allele $h=3$ through loss function minimization.

[00596] As another example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by MHC allele $h=3$, among $m=4$ different identified MHC alleles using separate network transformation functions $g_h(\cdot)$, can be generated by:

$$u_k^3 = f\big(NN_3(\boldsymbol{x_3^k}; \boldsymbol{\theta_3})\big),$$

where $\boldsymbol{x_3^k}$ are the identified allele-interacting variables for MHC allele $h=3$, and $\boldsymbol{\theta_3}$ are the set of parameters determined for the network model $NN_3(\cdot)$ associated with MHC allele $h=3$.

[00597] FIG. 7 illustrates generating a presentation likelihood for peptide $\boldsymbol{p^k}$ in association with MHC allele h=3 using an example network model $NN_3(\cdot)$. As shown in FIG. 7, the network model $NN_3(\cdot)$ receives the allele-interacting variables $\boldsymbol{x_3^k}$ for MHC allele $h=3$ and generates the output $NN_3(\boldsymbol{x_3^k})$. The output is mapped by function $\boldsymbol{f(\cdot)}$ to generate the estimated presentation likelihood u_k.

X.B.2. Per-Allele with Allele-Noninteracting Variables

[00598] In one implementation, the training module 316 incorporates allele-noninteracting variables and models the estimated presentation likelihood u_k for peptide $\boldsymbol{p^k}$ by:

$$u_k^h = \Pr\big(\boldsymbol{p^k} \text{ presented}\big) = f\left(g_w\big(\boldsymbol{w^k}; \boldsymbol{\theta_w}\big) + g_h\big(\boldsymbol{x_h^i}; \boldsymbol{\theta_h}\big)\right), \tag{8}$$

where $\boldsymbol{w^k}$ denotes the encoded allele-noninteracting variables for peptide $\boldsymbol{p^k}$, $g_w(\cdot)$ is a function for the allele-noninteracting variables $\boldsymbol{w^k}$ based on a set of parameters $\boldsymbol{\theta_w}$ determined for the allele-noninteracting variables. Specifically, the values for the set of parameters $\boldsymbol{\theta_h}$ for each MHC allele h and the set of parameters $\boldsymbol{\theta_w}$ for allele-noninteracting variables can be determined by minimizing the loss function with respect to $\boldsymbol{\theta_h}$ and $\boldsymbol{\theta_w}$, where i is each instance in the subset S of training data 170 generated from cells expressing single MHC alleles.

[00599] The output of the dependency function $g_w(\boldsymbol{w^k};\boldsymbol{\theta_w})$ represents a dependency score for the allele noninteracting variables indicating whether the peptide $\boldsymbol{p^k}$ will be presented by one or more MHC alleles based on the impact of allele noninteracting variables. For example, the dependency score for the allele noninteracting variables may have a high value if the peptide $\boldsymbol{p^k}$ is associated with a C-terminal flanking sequence that is known to positively impact presentation of the peptide $\boldsymbol{p^k}$, and may have a low value if the peptide $\boldsymbol{p^k}$ is associated with a C-terminal flanking sequence that is known to negatively impact presentation of the peptide $\boldsymbol{p^k}$.

[00600] According to equation (8), the per-allele likelihood that a peptide sequence $\boldsymbol{p^k}$ will be presented by a MHC allele h can be generated by applying the function $g_h(\cdot)$ for the MHC

2026201462 26 Feb 2026

allele h to the encoded version of the peptide sequence $\boldsymbol{p^k}$ to generate the corresponding dependency score for allele interacting variables. The function $g_w(\cdot)$ for the allele noninteracting variables are also applied to the encoded version of the allele noninteracting variables to generate the dependency score for the allele noninteracting variables. Both scores are combined, and the combined score is transformed by the transformation function $f(\cdot)$ to generate a per-allele likelihood that the peptide sequence $\boldsymbol{p^k}$ will be presented by the MHC allele h.

[00601] Alternatively, the training module 316 may include allele-noninteracting variables $\boldsymbol{w^k}$ in the prediction by adding the allele-noninteracting variables $\boldsymbol{w^k}$ to the allele-interacting variables $\boldsymbol{x_h^k}$ in equation (2). Thus, the presentation likelihood can be given by:

$$u_k^h = \Pr\left(\boldsymbol{p^k} \text{ presented; allele } h\right) = f\left(g_h\left([\boldsymbol{x_h^k}\, \boldsymbol{w^k}]; \boldsymbol{\theta_h}\right)\right). \quad (9)$$

X.B.3 Dependency Functions for Allele-Noninteracting Variables

[00602] Similarly to the dependency function $g_h(\cdot)$ for allele-interacting variables, the dependency function $g_w(\cdot)$ for allele noninteracting variables may be an affine function or a network function in which a separate network model is associated with allele-noninteracting variables $\boldsymbol{w^k}$.

[00603] Specifically, the dependency function $g_w(\cdot)$is an affine function given by:

$$g_w\left(\boldsymbol{w^k}; \boldsymbol{\theta_w}\right) = \boldsymbol{w^k} \cdot \boldsymbol{\theta_w}.$$

that linearly combines the allele-noninteracting variables in $\boldsymbol{w^k}$ with a corresponding parameter in the set of parameters $\boldsymbol{\theta_w}$.

[00604] The dependency function $\boldsymbol{g_w(\cdot)}$ may also be a network function given by:

$$g_h\left(\boldsymbol{w^k}; \boldsymbol{\theta_w}\right) = NN_w(\boldsymbol{w^k}; \boldsymbol{\theta_w}).$$

represented by a network model $NN_w(\cdot)$ having an associated parameter in the set of parameters $\boldsymbol{\theta_w}$. The network function may also include one or more network models each taking different allele noninteracting variables as input.

[00605] In another instance, the dependency function $\boldsymbol{g_w(\cdot)}$ for the allele-noninteracting variables can be given by:

$$g_w\left(\boldsymbol{w^k}; \boldsymbol{\theta_w}\right) = g'_w\left(\boldsymbol{w^k}; \boldsymbol{\theta'_w}\right) + h(m^k; \theta_w^m), \quad (10)$$

where $g'_w(\boldsymbol{w^k};\boldsymbol{\theta'_w})$ is the affine function, the network function with the set of allele noninteracting parameters $\boldsymbol{\theta'_w}$, or the like, m^k is the mRNA quantification measurement for peptide $\boldsymbol{p^k}$, $h(\cdot)$ is a function transforming the quantification measurement, and θ_w^m is a parameter in the set of parameters for allele noninteracting variables that is combined with the

2026201462 26 Feb 2026

mRNA quantification measurement to generate a dependency score for the mRNA quantification measurement. In one particular embodiment referred throughout the remainder of the specification, $h(\cdot)$ is the log function, however in practice $h(\cdot)$ may be any one of a variety of different functions.

[00606] In yet another instance, the dependency function $\boldsymbol{g_w(\cdot)}$ for the allele-noninteracting variables can be given by:

$$g_w(\boldsymbol{w^k}; \boldsymbol{\theta_w}) = g'_w(\boldsymbol{w^k}; \boldsymbol{\theta'_w}) + \boldsymbol{\theta_w^o} \cdot \boldsymbol{o^k}, \tag{11}$$

where $g'_w(\boldsymbol{w^k};\boldsymbol{\theta'_w})$ is the affine function, the network function with the set of allele noninteracting parameters $\boldsymbol{\theta'_w}$, or the like, $\boldsymbol{o^k}$ is the indicator vector described above representing proteins and isoforms in the human proteome for peptide $\boldsymbol{p^k}$, and $\boldsymbol{\theta_w^o}$ is a set of parameters in the set of parameters for allele noninteracting variables that is combined with the indicator vector. In one variation, when the dimensionality of $\boldsymbol{o^k}$ and the set of parameters $\boldsymbol{\theta_w^o}$ are significantly high, a parameter regularization term, such as $\lambda \cdot ||\boldsymbol{\theta_w^o}||$, where $||\cdot||$ represents L1 norm, L2 norm, a combination, or the like, can be added to the loss function when determining the value of the parameters. The optimal value of the hyperparameter λ can be determined through appropriate methods.

[00607] In yet another instance, the dependency function $\boldsymbol{g_w(\cdot)}$ for the allele-noninteracting variables can be given by:

$$g_w(\boldsymbol{w^k}; \boldsymbol{\theta_w}) = g'_w(\boldsymbol{w^k}; \boldsymbol{\theta'_w}) + \sum_{\boldsymbol{l=1}}^{\boldsymbol{L}} \mathbb{1}\left(\text{gene}(\boldsymbol{p^k} = l)\right) \cdot \boldsymbol{\theta_w^l}, \tag{12}$$

where $g'_w(\boldsymbol{w^k};\boldsymbol{\theta'_w})$ is the affine function, the network function with the set of allele noninteracting parameters $\boldsymbol{\theta'_w}$, or the like, $\mathbb{1}(\text{gene}(\boldsymbol{p^k}=l))$ is the indicator function that equals to 1 if peptide $\boldsymbol{p^k}$ is from source gene l as described above in reference to allele noninteracting variables, and $\boldsymbol{\theta_w^l}$ is a parameter indicating "antigenicity" of source gene l. In one variation, when L is significantly high, and thus, the number of parameters $\boldsymbol{\theta_w^{l=1, 2, ..., L}}$ are significantly high, a parameter regularization term, such as $\lambda \cdot ||\boldsymbol{\theta_w^l}||$, where $||\cdot||$ represents L1 norm, L2 norm, a combination, or the like, can be added to the loss function when determining the value of the parameters. The optimal value of the hyperparameter λ can be determined through appropriate methods.

[00608] In practice, the additional terms of any of equations (10), (11), and (12) may be combined to generate the dependency function $g_w(\cdot)$ for allele noninteracting variables. For example, the term $h(\cdot)$ indicating mRNA quantification measurement in equation (10) and the

2026201462 26 Feb 2026

term indicating source gene antigenicity in equation (12) may be summed together along with any other affine or network function to generate the dependency function for allele noninteracting variables.

[00609] Returning to equation (8), as an example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by MHC allele $h=3$, among $m=4$ different identified MHC alleles using the affine transformation functions $g_h(\cdot)$, $g_w(\cdot)$, can be generated by:

$$u_k^3 = f\left(\boldsymbol{w^k} \cdot \boldsymbol{\theta_w} + \boldsymbol{x_3^k} \cdot \boldsymbol{\theta_3}\right),$$

where $\boldsymbol{w^k}$ are the identified allele-noninteracting variables for peptide $\boldsymbol{p^k}$, and $\boldsymbol{\theta_w}$ are the set of parameters determined for the allele-noninteracting variables.

[00610] As another example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by MHC allele $h=3$, among $m=4$ different identified MHC alleles using the network transformation functions $g_h(\cdot)$, $g_w(\cdot)$, can be generated by:

$$u_k^3 = f\left(NN_w\left(\boldsymbol{w^k}; \boldsymbol{\theta_w}\right) + NN_3(\boldsymbol{x_3^k}; \boldsymbol{\theta_3})\right)$$

where $\boldsymbol{w^k}$ are the identified allele-interacting variables for peptide $\boldsymbol{p^k}$, and $\boldsymbol{\theta_w}$ are the set of parameters determined for allele-noninteracting variables.

[00611] FIG. 8 illustrates generating a presentation likelihood for peptide $\boldsymbol{p^k}$ in association with MHC allele h=3 using example network models $NN_3(\cdot)$ and $NN_w(\cdot)$. As shown in FIG. 8, the network model $NN_3(\cdot)$ receives the allele-interacting variables $\boldsymbol{x_3^k}$ for MHC allele $h=3$ and generates the output $NN_3(\boldsymbol{x_3^k})$. The network model $NN_w(\cdot)$ receives the allele-noninteracting variables $\boldsymbol{w^k}$ for peptide $\boldsymbol{p^k}$ and generates the output $NN_w(\boldsymbol{w^k})$. The outputs are combined and mapped by function $f(\cdot)$ to generate the estimated presentation likelihood u_k.

X.C. Multiple-Allele Models

[00612] The training module 316 may also construct the presentation models to predict presentation likelihoods of peptides in a multiple-allele setting where two or more MHC alleles are present. In this case, the training module 316 may train the presentation models based on data instances S in the training data 170 generated from cells expressing single MHC alleles, cells expressing multiple MHC alleles, or a combination thereof.

X.C.1. Example 1: Maximum of Per-Allele Models

[00613] In one implementation, the training module 316 models the estimated presentation likelihood u_k for peptide $\boldsymbol{p^k}$ in association with a set of multiple MHC alleles H as a function of the presentation likelihoods $u_k^{h \in H}$ determined for each of the MHC alleles h in the set H determined based on cells expressing single-alleles, as described above in conjunction with

26 Feb 2026
2026201462

equations (2)-(11). Specifically, the presentation likelihood u_k can be any function of $u_k^{h \in H}$. In one implementation, as shown in equation (12), the function is the maximum function, and the presentation likelihood u_k can be determined as the maximum of the presentation likelihoods for each MHC allele h in the set H.

$$u_k = \Pr(\boldsymbol{p^k} \text{ presented; alleles } H) = \max(u_k^{h \in H}).$$

X.C.2. Example 2.1: Function-of-Sums Models

[00614] In one implementation, the training module 316 models the estimated presentation likelihood u_k for peptide $\boldsymbol{p^k}$ by:

$$u_k = \Pr(\boldsymbol{p^k} \text{ presented}) = f\left(\sum_{h=1}^{m} a_h^k \cdot g_h(\boldsymbol{x_h^k}; \boldsymbol{\theta_h})\right), \quad (13)$$

where elements a_h^k are 1 for the multiple MHC alleles H associated with peptide sequence $\boldsymbol{p^k}$ and $\boldsymbol{x_h^k}$ denotes the encoded allele-interacting variables for peptide $\boldsymbol{p^k}$ and the corresponding MHC alleles. The values for the set of parameters $\boldsymbol{\theta_h}$ for each MHC allele h can be determined by minimizing the loss function with respect to $\boldsymbol{\theta_h}$, where i is each instance in the subset S of training data 170 generated from cells expressing single MHC alleles and/or cells expressing multiple MHC alleles. The dependency function $\boldsymbol{g_h}$ may be in the form of any of the dependency functions $\boldsymbol{g_h}$ introduced above in sections X.B.1.

[00615] According to equation (13), the presentation likelihood that a peptide sequence $\boldsymbol{p^k}$ will be presented by one or more MHC alleles h can be generated by applying the dependency function $g_h(\cdot)$ to the encoded version of the peptide sequence $\boldsymbol{p^k}$ for each of the MHC alleles H to generate the corresponding score for the allele interacting variables. The scores for each MHC allele h are combined, and transformed by the transformation function $f(\cdot)$ to generate the presentation likelihood that peptide sequence $\boldsymbol{p^k}$ will be presented by the set of MHC alleles H.

[00616] The presentation model of equation (13) is different from the per-allele model of equation (2), in that the number of associated alleles for each peptide $\boldsymbol{p^k}$ can be greater than 1. In other words, more than one element in a_h^k can have values of 1 for the multiple MHC alleles H associated with peptide sequence $\boldsymbol{p^k}$.

[00617] As an example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by MHC alleles $h=2$, $h=3$, among $m=4$ different identified MHC alleles using the affine transformation functions $g_h(\cdot)$, can be generated by:

$$u_k = f(\boldsymbol{x_2^k} \cdot \boldsymbol{\theta_2} + \boldsymbol{x_3^k} \cdot \boldsymbol{\theta_3}),$$

2026201462 26 Feb 2026

where $\boldsymbol{x_2^k}$, $\boldsymbol{x_3^k}$ are the identified allele-interacting variables for MHC alleles $h=2$, $h=3$, and $\boldsymbol{\theta_2}$, $\boldsymbol{\theta_3}$ are the set of parameters determined for MHC alleles $h=2$, $h=3$.

[00618] As another example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by MHC alleles $h=2$, $h=3$, among $m=4$ different identified MHC alleles using the network transformation functions $g_h(\cdot)$, $g_w(\cdot)$, can be generated by:

$$\boldsymbol{u_k} = f\big(NN_2(\boldsymbol{x_2^k}; \boldsymbol{\theta_2}) + NN_3(\boldsymbol{x_3^k}; \boldsymbol{\theta_3})\big),$$

where $NN_2(\cdot)$, $NN_3(\cdot)$ are the identified network models for MHC alleles $h=2$, $h=3$, and $\boldsymbol{\theta_2}$, $\boldsymbol{\theta_3}$ are the set of parameters determined for MHC alleles $h=2$, $h=3$.

[00619] FIG. 9 illustrates generating a presentation likelihood for peptide $\boldsymbol{p^k}$ in association with MHC alleles $h=2$, $h=3$ using example network models $NN_2(\cdot)$ and $NN_3(\cdot)$. As shown in FIG. 9, the network model $NN_2(\cdot)$ receives the allele-interacting variables $\boldsymbol{x_2^k}$ for MHC allele $h=2$ and generates the output $NN_2(\boldsymbol{x_2^k})$ and the network model $NN_3(\cdot)$ receives the allele-interacting variables $\boldsymbol{x_3^k}$ for MHC allele $h=3$ and generates the output $NN_3(\boldsymbol{x_3^k})$. The outputs are combined and mapped by function $f(\cdot)$ to generate the estimated presentation likelihood u_k.

X.C.3. Example 2.2: Function-of-Sums Models with Allele-Noninteracting Variables

[00620] In one implementation, the training module 316 incorporates allele-noninteracting variables and models the estimated presentation likelihood u_k for peptide $\boldsymbol{p^k}$ by:

$$u_k = \Pr\big(\boldsymbol{p^k} \text{ presented}\big) = f\left(g_w\big(\boldsymbol{w^k}; \boldsymbol{\theta_w}\big) + \sum_{h=1}^{m} a_h^k \cdot g_h\big(\boldsymbol{x_h^k}; \boldsymbol{\theta_h}\big)\right), \tag{14}$$

where $\boldsymbol{w^k}$ denotes the encoded allele-noninteracting variables for peptide $\boldsymbol{p^k}$. Specifically, the values for the set of parameters $\boldsymbol{\theta_h}$ for each MHC allele h and the set of parameters $\boldsymbol{\theta_w}$ for allele-noninteracting variables can be determined by minimizing the loss function with respect to $\boldsymbol{\theta_h}$ and $\boldsymbol{\theta_w}$, where i is each instance in the subset S of training data 170 generated from cells expressing single MHC alleles and/or cells expressing multiple MHC alleles. The dependency function $\boldsymbol{g_w}$ may be in the form of any of the dependency functions $\boldsymbol{g_w}$ introduced above in sections X.B.3.

[00621] Thus, according to equation (14), the presentation likelihood that a peptide sequence $\boldsymbol{p^k}$ will be presented by one or more MHC alleles H can be generated by applying the function $g_h(\cdot)$ to the encoded version of the peptide sequence $\boldsymbol{p^k}$ for each of the MHC alleles H to generate the corresponding dependency score for allele interacting variables for each MHC allele h. The function $g_w(\cdot)$ for the allele noninteracting variables is also applied to the encoded version of the allele noninteracting variables to generate the dependency score for the allele

2026201462 26 Feb 2026

noninteracting variables. The scores are combined, and the combined score is transformed by the transformation function $f(\cdot)$ to generate the presentation likelihood that peptide sequence $\boldsymbol{p^k}$ will be presented by the MHC alleles H.

[00622] In the presentation model of equation (14), the number of associated alleles for each peptide $\boldsymbol{p^k}$ can be greater than 1. In other words, more than one element in a_h^k can have values of 1 for the multiple MHC alleles H associated with peptide sequence $\boldsymbol{p^k}$.

[00623] As an example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by MHC alleles $h=2$, $h=3$, among $m=4$ different identified MHC alleles using the affine transformation functions $g_h(\cdot)$, $g_w(\cdot)$, can be generated by:

$$u_k = f\left(\boldsymbol{w^k} \cdot \boldsymbol{\theta_w} + \boldsymbol{x_2^k} \cdot \boldsymbol{\theta_2} + \boldsymbol{x_3^k} \cdot \boldsymbol{\theta_3}\right),$$

where $\boldsymbol{w^k}$ are the identified allele-noninteracting variables for peptide $\boldsymbol{p^k}$, and $\boldsymbol{\theta_w}$ are the set of parameters determined for the allele-noninteracting variables.

[00624] As another example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by MHC alleles $h=2$, $h=3$, among $m=4$ different identified MHC alleles using the network transformation functions $g_h(\cdot)$, $g_w(\cdot)$, can be generated by:

$$u_k = f\left(NN_w\left(\boldsymbol{w^k}; \boldsymbol{\theta_w}\right) + NN_2(\boldsymbol{x_2^k}; \boldsymbol{\theta_2}) + NN_3(\boldsymbol{x_3^k}; \boldsymbol{\theta_3})\right)$$

where $\boldsymbol{w^k}$ are the identified allele-interacting variables for peptide $\boldsymbol{p^k}$, and $\boldsymbol{\theta_w}$ are the set of parameters determined for allele-noninteracting variables.

[00625] FIG. 10 illustrates generating a presentation likelihood for peptide $\boldsymbol{p^k}$ in association with MHC alleles $h=2$, $h=3$ using example network models $NN_2(\cdot)$, $NN_3(\cdot)$, and $NN_w(\cdot)$. As shown in FIG. 10, the network model $NN_2(\cdot)$ receives the allele-interacting variables $\boldsymbol{x_2^k}$ for MHC allele $h=2$ and generates the output $NN_2(\boldsymbol{x_2^k})$. The network model $NN_3(\cdot)$ receives the allele-interacting variables $\boldsymbol{x_3^k}$ for MHC allele $h=3$ and generates the output $NN_3(\boldsymbol{x_3^k})$. The network model $NN_w(\cdot)$ receives the allele-noninteracting variables $\boldsymbol{w^k}$ for peptide $\boldsymbol{p^k}$ and generates the output $NN_w(\boldsymbol{w^k})$. The outputs are combined and mapped by function $f(\cdot)$ to generate the estimated presentation likelihood u_k.

[00626] Alternatively, the training module 316 may include allele-noninteracting variables $\boldsymbol{w^k}$ in the prediction by adding the allele-noninteracting variables $\boldsymbol{w^k}$ to the allele-interacting variables $\boldsymbol{x_h^k}$ in equation (15). Thus, the presentation likelihood can be given by:

$$u_k = \Pr\left(\boldsymbol{p^k} \text{ presented}\right) = f\left(\sum_{h=1}^{m} a_h^k \cdot g_h\left([\boldsymbol{x_h^k}\, \boldsymbol{w^k}]; \boldsymbol{\theta_h}\right)\right). \quad (15)$$

X.C.4. Example 3.1: Models Using Implicit Per-Allele Likelihoods

2026201462 26 Feb 2026

[00627] In another implementation, the training module 316 models the estimated presentation likelihood u_k for peptide $\boldsymbol{p^k}$ by:

$$u_k = \Pr(\boldsymbol{p^k} \text{ presented}) = r\left(s\left(\boldsymbol{v} = \left[a_1^k \cdot u'^1_k(\boldsymbol{\theta}) \ldots a_m^k \cdot u'^m_k(\boldsymbol{\theta})\right]\right)\right), \quad (16)$$

where elements a_h^k are 1 for the multiple MHC alleles $h \in H$ associated with peptide sequence $\boldsymbol{p^k}$, u'^h_k is an implicit per-allele presentation likelihood for MHC allele h, vector $\boldsymbol{v}$ is a vector in which element v_h corresponds to $a_h^k \cdot u'^h_k$, $s(\cdot)$ is a function mapping the elements of $\boldsymbol{v}$, and $r(\cdot)$ is a clipping function that clips the value of the input into a given range. As described below in more detail, $s(\cdot)$ may be the summation function or the second-order function, but it is appreciated that in other embodiments, $s(\cdot)$ can be any function such as the maximum function. The values for the set of parameters $\boldsymbol{\theta}$ for the implicit per-allele likelihoods can be determined by minimizing the loss function with respect to $\boldsymbol{\theta}$, where i is each instance in the subset S of training data 170 generated from cells expressing single MHC alleles and/or cells expressing multiple MHC alleles.

[00628] The presentation likelihood in the presentation model of equation (17) is modeled as a function of implicit per-allele presentation likelihoods u'^h_k that each correspond to the likelihood peptide $\boldsymbol{p^k}$ will be presented by an individual MHC allele h. The implicit per-allele likelihood is distinct from the per-allele presentation likelihood of section X.B in that the parameters for implicit per-allele likelihoods can be learned from multiple allele settings, in which direct association between a presented peptide and the corresponding MHC allele is unknown, in addition to single-allele settings. Thus, in a multiple-allele setting, the presentation model can estimate not only whether peptide $\boldsymbol{p^k}$ will be presented by a set of MHC alleles H as a whole, but can also provide individual likelihoods $u'^{h\in H}_k$ that indicate which MHC allele h most likely presented peptide $\boldsymbol{p^k}$. An advantage of this is that the presentation model can generate the implicit likelihoods without training data for cells expressing single MHC alleles.

[00629] In one particular implementation referred throughout the remainder of the specification, $r(\cdot)$ is a function having the range [0, 1]. For example, $r(\cdot)$ may be the clip function:

$$r(z) = \min(\max(z, 0), 1),$$

where the minimum value between z and 1 is chosen as the presentation likelihood u_k. In another implementation, $r(\cdot)$ is the hyperbolic tangent function given by:

$$r(z) = \tanh(z)$$

2026201462 26 Feb 2026

when the values for the domain z is equal to or greater than 0.

2026201462 26 Feb 2026

X.C.5. Example 3.2: Sum-of-Functions Model

[00630] In one particular implementation, $s(\cdot)$ is a summation function, and the presentation likelihood is given by summing the implicit per-allele presentation likelihoods:

$$u_k = \Pr(\boldsymbol{p^k} \text{ presented}) = r\left(\sum_{h=1}^{m} a_h^k \cdot u'^h_k(\boldsymbol{\theta})\right). \quad (17)$$

[00631] In one implementation, the implicit per-allele presentation likelihood for MHC allele h is generated by:

$$u'^h_k = f\left(g_h(\boldsymbol{x_h^k}; \boldsymbol{\theta_h})\right), \quad (18)$$

such that the presentation likelihood is estimated by:

$$u_k = \Pr(\boldsymbol{p^k} \text{ presented}) = r\left(\sum_{h=1}^{m} a_h^k \cdot f\left(g_h(\boldsymbol{x_h^k}; \boldsymbol{\theta_h})\right)\right). \quad (19)$$

[00632] According to equation (19), the presentation likelihood that a peptide sequence $\boldsymbol{p^k}$ will be presented by one or more MHC alleles H can be generated by applying the function $g_h(\cdot)$ to the encoded version of the peptide sequence $\boldsymbol{p^k}$ for each of the MHC alleles H to generate the corresponding dependency score for allele interacting variables. Each dependency score is first transformed by the function $f(\cdot)$ to generate implicit per-allele presentation likelihoods u'^h_k. The per-allele likelihoods u'^h_k are combined, and the clipping function may be applied to the combined likelihoods to clip the values into a range [0, 1] to generate the presentation likelihood that peptide sequence $\boldsymbol{p^k}$ will be presented by the set of MHC alleles H. The dependency function $\boldsymbol{g_h}$ may be in the form of any of the dependency functions $\boldsymbol{g_h}$ introduced above in sections X.B.1.

[00633] As an example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by MHC alleles $h=2$, $h=3$, among $m=4$ different identified MHC alleles using the affine transformation functions $g_h(\cdot)$, can be generated by:

$$u_k = r\left(f\left(\boldsymbol{x_2^k} \cdot \boldsymbol{\theta_2}\right) + f\left(\boldsymbol{x_3^k} \cdot \boldsymbol{\theta_3}\right)\right),$$

where $\boldsymbol{x_2^k}, \boldsymbol{x_3^k}$ are the identified allele-interacting variables for MHC alleles $h=2$, $h=3$, and $\boldsymbol{\theta_2}$, $\boldsymbol{\theta_3}$ are the set of parameters determined for MHC alleles $h=2$, $h=3$.

[00634] As another example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by MHC alleles $h=2$, $h=3$, among $m=4$ different identified MHC alleles using the network transformation functions $g_h(\cdot)$, $g_w(\cdot)$, can be generated by:

$$u_k = r\left(f\left(NN_2(\boldsymbol{x_2^k}; \boldsymbol{\theta_2})\right) + f\left(NN_3(\boldsymbol{x_3^k}; \boldsymbol{\theta_3})\right)\right),$$

2026201462 26 Feb 2026

where $NN_2(\cdot)$, $NN_3(\cdot)$ are the identified network models for MHC alleles $h=2$, $h=3$, and $\boldsymbol{\theta_2}, \boldsymbol{\theta_3}$ are the set of parameters determined for MHC alleles $h=2$, $h=3$.

[00635] FIG. 11 illustrates generating a presentation likelihood for peptide $\boldsymbol{p^k}$ in association with MHC alleles h=2, h=3 using example network models $NN_2(\cdot)$ and $NN_3(\cdot)$. As shown in FIG. 9, the network model $NN_2(\cdot)$ receives the allele-interacting variables $\boldsymbol{x_2^k}$ for MHC allele $h=2$ and generates the output $NN_2(\boldsymbol{x_2^k})$ and the network model $NN_3(\cdot)$ receives the allele-interacting variables $\boldsymbol{x_3^k}$ for MHC allele $h=3$ and generates the output $NN_3(\boldsymbol{x_3^k})$. Each output is mapped by function $f(\cdot)$ and combined to generate the estimated presentation likelihood u_k.

[00636] In another implementation, when the predictions are made for the log of mass spectrometry ion currents, $r(\cdot)$ is the log function and $f(\cdot)$ is the exponential function.

X.C.6. Example 3.3: Sum-of-Functions Models with Allele-noninteracting Variables

[00637] In one implementation, the implicit per-allele presentation likelihood for MHC allele h is generated by:

$$u_k'^{\,h} = f\left(g_h\left(\boldsymbol{x_h^k}; \boldsymbol{\theta_h}\right) + g_w\left(\boldsymbol{w^k}; \boldsymbol{\theta_w}\right)\right), \tag{20}$$

such that the presentation likelihood is generated by:

$$u_k = \Pr\left(\boldsymbol{p^k} \text{ presented}\right) = r\left(\sum_{h=1}^{m} a_h^k \cdot f\left(g_w\left(\boldsymbol{w^k}; \boldsymbol{\theta_w}\right) + g_h\left(\boldsymbol{x_h^k}; \boldsymbol{\theta_h}\right)\right)\right), \tag{21}$$

to incorporate the impact of allele noninteracting variables on peptide presentation.

[00638] According to equation (21), the presentation likelihood that a peptide sequence $\boldsymbol{p^k}$ will be presented by one or more MHC alleles H can be generated by applying the function $g_h(\cdot)$ to the encoded version of the peptide sequence $\boldsymbol{p^k}$ for each of the MHC alleles H to generate the corresponding dependency score for allele interacting variables for each MHC allele h. The function $g_w(\cdot)$ for the allele noninteracting variables is also applied to the encoded version of the allele noninteracting variables to generate the dependency score for the allele noninteracting variables. The score for the allele noninteracting variables are combined to each of the dependency scores for the allele interacting variables. Each of the combined scores are transformed by the function $f(\cdot)$ to generate the implicit per-allele presentation likelihoods. The implicit likelihoods are combined, and the clipping function may be applied to the combined outputs to clip the values into a range [0,1] to generate the presentation likelihood that peptide sequence $\boldsymbol{p^k}$ will be presented by the MHC alleles H. The dependency function $\boldsymbol{g_w}$ may be in the form of any of the dependency functions $\boldsymbol{g_w}$ introduced above in sections X.B.3.

2026201462 26 Feb 2026

[00639] As an example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by MHC alleles $h=2$, $h=3$, among $m=4$ different identified MHC alleles using the affine transformation functions $g_h(\cdot)$, $g_w(\cdot)$, can be generated by:

$$u_k = r\left(f\left(\boldsymbol{w^k}\cdot\boldsymbol{\theta_w} + \boldsymbol{x_2^k}\cdot\boldsymbol{\theta_2}\right) + f\left(\boldsymbol{w^k}\cdot\boldsymbol{\theta_w} + \boldsymbol{x_3^k}\cdot\boldsymbol{\theta_3}\right)\right),$$

where $\boldsymbol{w^k}$ are the identified allele-noninteracting variables for peptide $\boldsymbol{p^k}$, and $\boldsymbol{\theta_w}$ are the set of parameters determined for the allele-noninteracting variables.

[00640] As another example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by MHC alleles $h=2$, $h=3$, among $m=4$ different identified MHC alleles using the network transformation functions $g_h(\cdot)$, $g_w(\cdot)$, can be generated by:

$$u_k = r\left(f\left(NN_w\left(\boldsymbol{w^k};\boldsymbol{\theta_w}\right) + NN_2(\boldsymbol{x_2^k};\boldsymbol{\theta_2})\right) + f\left(NN_w\left(\boldsymbol{w^k};\boldsymbol{\theta_w}\right) + NN_3(\boldsymbol{x_3^k};\boldsymbol{\theta_3})\right)\right)$$

where $\boldsymbol{w^k}$ are the identified allele-interacting variables for peptide $\boldsymbol{p^k}$, and $\boldsymbol{\theta_w}$ are the set of parameters determined for allele-noninteracting variables.

[00641] FIG. 12 illustrates generating a presentation likelihood for peptide $\boldsymbol{p^k}$ in association with MHC alleles $h=2$, $h=3$ using example network models $NN_2(\cdot)$, $NN_3(\cdot)$, and $NN_w(\cdot)$. As shown in FIG. 12, the network model $NN_2(\cdot)$ receives the allele-interacting variables $\boldsymbol{x_2^k}$ for MHC allele $h=2$ and generates the output $NN_2(\boldsymbol{x_2^k})$. The network model $NN_w(\cdot)$ receives the allele-noninteracting variables $\boldsymbol{w^k}$ for peptide $\boldsymbol{p^k}$ and generates the output $NN_w(\boldsymbol{w^k})$. The outputs are combined and mapped by function $f(\cdot)$. The network model $NN_3(\cdot)$ receives the allele-interacting variables $\boldsymbol{x_3^k}$ for MHC allele $h=3$ and generates the output $NN_3(\boldsymbol{x_3^k})$, which is again combined with the output $NN_w(\boldsymbol{w^k})$ of the same network model $NN_w(\cdot)$ and mapped by function $f(\cdot)$. Both outputs are combined to generate the estimated presentation likelihood u_k.

[00642] In another implementation, the implicit per-allele presentation likelihood for MHC allele h is generated by:

$$u_k'^{\,h} = f\left(g_h\left([\boldsymbol{x_h^k}\,\boldsymbol{w^k}];\boldsymbol{\theta_h}\right)\right). \tag{22}$$

such that the presentation likelihood is generated by:

$$u_k = \Pr\left(\boldsymbol{p^k}\text{ presented}\right) = r\left(\sum_{h=1}^{m} a_h^k \cdot f\left(g_h\left([\boldsymbol{x_h^k}\,\boldsymbol{w^k}];\boldsymbol{\theta_h}\right)\right)\right).$$

X.C.7. Example 4: Second Order Models

[00643] In one implementation, , $s(\cdot)$ is a second-order function, and the estimated presentation likelihood u_k for peptide $\boldsymbol{p^k}$ is given by:

2026201462 26 Feb 2026

$$u_k = \Pr(\boldsymbol{p^k} \text{ presented}) = \sum_{h=1}^{m} a_h^k \cdot u_k'^h(\boldsymbol{\theta}) - \sum_{h=1}^{m}\sum_{j<h} a_h^k \cdot a_j^k \cdot u_k'^h(\boldsymbol{\theta}) \cdot u_k'^j(\boldsymbol{\theta}) \quad (23)$$

where elements $u'_k{}^h$ are the implicit per-allele presentation likelihood for MHC allele h. The values for the set of parameters $\boldsymbol{\theta}$ for the implicit per-allele likelihoods can be determined by minimizing the loss function with respect to $\boldsymbol{\theta}$, where i is each instance in the subset S of training data 170 generated from cells expressing single MHC alleles and/or cells expressing multiple MHC alleles. The implicit per-allele presentation likelihoods may be in any form shown in equations (18), (20), and (22) described above.

[00644] In one aspect, the model of equation (23) may imply that there exists a possibility peptide $\boldsymbol{p^k}$ will be presented by two MHC alleles simultaneously, in which the presentation by two HLA alleles is statistically independent.

[00645] According to equation (23), the presentation likelihood that a peptide sequence $\boldsymbol{p^k}$ will be presented by one or more MHC alleles H can be generated by combining the implicit per-allele presentation likelihoods and subtracting the likelihood that each pair of MHC alleles will simultaneously present the peptide $\boldsymbol{p^k}$ from the summation to generate the presentation likelihood that peptide sequence $\boldsymbol{p^k}$ will be presented by the MHC alleles H.

[00646] As an example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by HLA alleles $h=2$, $h=3$, among $m=4$ different identified HLA alleles using the affine transformation functions $g_h(\cdot)$, can be generated by:

$$u_k = f(\boldsymbol{x_2^k} \cdot \boldsymbol{\theta_2}) + f(\boldsymbol{x_3^k} \cdot \boldsymbol{\theta_3}) - f(\boldsymbol{x_2^k} \cdot \boldsymbol{\theta_2}) \cdot f(\boldsymbol{x_3^k} \cdot \boldsymbol{\theta_3}),$$

where $\boldsymbol{x_2^k}, \boldsymbol{x_3^k}$ are the identified allele-interacting variables for HLA alleles $h=2$, $h=3$, and $\boldsymbol{\theta_2}, \boldsymbol{\theta_3}$ are the set of parameters determined for HLA alleles $h=2$, $h=3$.

[00647] As another example, the likelihood that peptide $\boldsymbol{p^k}$ will be presented by HLA alleles $h=2$, $h=3$, among $m=4$ different identified HLA alleles using the network transformation functions $g_h(\cdot)$, $g_w(\cdot)$, can be generated by:

$$u_k = f(NN_2(\boldsymbol{x_2^k}; \boldsymbol{\theta_2})) + f(NN_3(\boldsymbol{x_3^k}; \boldsymbol{\theta_3})) - f(NN_2(\boldsymbol{x_2^k}; \boldsymbol{\theta_2})) \cdot f(NN_3(\boldsymbol{x_3^k}; \boldsymbol{\theta_3})),$$

where $NN_2(\cdot)$, $NN_3(\cdot)$ are the identified network models for HLA alleles $h=2$, $h=3$, and $\boldsymbol{\theta_2}, \boldsymbol{\theta_3}$ are the set of parameters determined for HLA alleles $h=2$, $h=3$.

XI.A Example 5: Prediction Module

[00648] The prediction module 320 receives sequence data and selects candidate neoantigens in the sequence data using the presentation models. Specifically, the sequence data may be DNA sequences, RNA sequences, and/or protein sequences extracted from tumor

2026201462 26 Feb 2026

tissue cells of patients. The prediction module 320 processes the sequence data into a plurality of peptide sequences $\boldsymbol{p^k}$ having 8-15 amino acids for MHC-I or 6-30 amino acids for MHC-II. For example, the prediction module 320 may process the given sequence "IEFROEIFJEF into three peptide sequences having 9 amino acids "IEFROEIFJ," "EFROEIFJE," and "FROEIFJEF." In one embodiment, the prediction module 320 may identify candidate neoantigens that are mutated peptide sequences by comparing sequence data extracted from normal tissue cells of a patient with the sequence data extracted from tumor tissue cells of the patient to identify portions containing one or more mutations.

[00649] The presentation module 320 applies one or more of the presentation models to the processed peptide sequences to estimate presentation likelihoods of the peptide sequences. Specifically, the prediction module 320 may select one or more candidate neoantigen peptide sequences that are likely to be presented on tumor HLA molecules by applying the presentation models to the candidate neoantigens. In one implementation, the presentation module 320 selects candidate neoantigen sequences that have estimated presentation likelihoods above a predetermined threshold. In another implementation, the presentation model selects the *N* candidate neoantigen sequences that have the highest estimated presentation likelihoods (where *N* is generally the maximum number of epitopes that can be delivered in a vaccine). A vaccine including the selected candidate neoantigens for a given patient can be injected into the patient to induce immune responses.

XI.B. Example 6: Cassette Design Module

XI.B.1 Overview

[00650] The cassette design module 324 generates a vaccine cassette sequence based on the *v* selected candidate peptides for injection into a patient. Specifically, for a set of selected peptides $\boldsymbol{p^k}$, *k=1, 2, ..., v* for inclusion in a vaccine of capacity *v*, the cassette sequence is given by concatenation of a series of therapeutic epitope sequences $\boldsymbol{p'^k}$, *k=1, 2, ..., v* that each include the sequence of a corresponding peptide $\boldsymbol{p^k}$. In one embodiment, the cassette design module 324 may concatenate the epitopes directly adjacent to one another. For example, a vaccine cassette **C** may be represented as:

$$\mathbf{C} = [\boldsymbol{p'^{t_1}}\ \boldsymbol{p'^{t_2}}\ \cdots\ \boldsymbol{p'^{t_v}}] \tag{24}$$

where $\boldsymbol{p'^{ti}}$ denotes the *i*-th epitope of the cassette. Thus, t_i corresponds to an index *k=1, 2, ..., v* for the selected peptide at the *i*-th position of the cassette. In another embodiment, the cassette

2026201462 26 Feb 2026

design module 324 may concatenate the epitopes with one or more optional linker sequences in between adjacent epitopes. For example, a vaccine cassette **C** may be represented as:

$$\mathbf{C} = [\boldsymbol{p}'^{\mathbf{t}_1}\ \boldsymbol{l}_{(\mathbf{t}_1,\mathbf{t}_2)}\ \boldsymbol{p}'^{\mathbf{t}_2}\ \boldsymbol{l}_{(\mathbf{t}_2,\mathbf{t}_3)} \cdots\ \boldsymbol{l}_{(\mathbf{t}_{v-1},\mathbf{t}_v)}\ \boldsymbol{p}'^{\mathbf{t}_v}] \quad (25)$$

where $\boldsymbol{l}_{(ti,tj)}$ denotes a linker sequence placed between the *i*-th epitope $\boldsymbol{p}'^{ti}$ and the *j=i+1*-th epitope $\boldsymbol{p}'^{j=i+1}$ of the cassette. The cassette design module 324 determines which of the selected epitopes $\boldsymbol{p}'^{k}$, *k=1, 2, ..., v* are arranged at the different positions of the cassette, as well as any linker sequences placed between the epitopes. A cassette sequence **C** can be loaded as a vaccine based on any of the methods described in the present specification.

[00651] In one embodiment, the set of therapeutic epitopes may be generated based on the selected peptides determined by the prediction module 320 associated with presentation likelihoods above a predetermined threshold, where the presentation likelihoods are determined by the presentation models. However it is appreciated that in other embodiments, the set of therapeutic epitopes may be generated based on any one or more of a number of methods (alone or in combination), for example, based on binding affinity or predicted binding affinity to HLA class I or class II alleles of the patient, binding stability or predicted binding stability to HLA class I or class II alleles of the patient, random sampling, and the like.

[00652] In one embodiment, the therapeutic epitopes $\boldsymbol{p}'^{k}$ may correspond to the selected peptides $\boldsymbol{p}^{k}$ themselves. In another embodiment, the therapeutic epitopes $\boldsymbol{p}'^{k}$ may also include C- and / or N-terminal flanking sequences in addition to the selected peptides. For example, an epitope $\boldsymbol{p}'^{k}$ included in the cassette may be represented as a sequence $[\boldsymbol{n}^{k}\ \boldsymbol{p}^{k}\ \boldsymbol{c}^{k}]$ where $\boldsymbol{c}^{k}$ is a C-terminal flanking sequence attached the C-terminus of the selected peptide $\boldsymbol{p}^{k}$, and $\boldsymbol{n}^{k}$ is an N-terminal flanking sequence attached to the N-terminus of the selected peptide $\boldsymbol{p}^{k}$. In one instance referred throughout the remainder of the specification, the N- and C-terminal flanking sequences are the native N- and C-terminal flanking sequences of the therapeutic vaccine epitope in the context of its source protein. In one instance referred throughout the remainder of the specification, the therapeutic epitope $\boldsymbol{p}'^{k}$ represents a fixed-length epitope. In another instance, the therapeutic epitope $\boldsymbol{p}'^{k}$ can represent a variable-length epitope, in which the length of the epitope can be varied depending on, for example, the length of the C- or N-flanking sequence. For example, the C-terminal flanking sequence $\boldsymbol{c}^{k}$ and the N-terminal flanking sequence $\boldsymbol{n}^{k}$ can each have varying lengths of 2-5 residues, resulting in 16 possible choices for the epitope $\boldsymbol{p}'^{k}$.

2026201462 26 Feb 2026

[00653] In one embodiment, the cassette design module 324 generates cassette sequences by taking into account presentation of junction epitopes that span the junction between a pair of therapeutic epitopes in the cassette. Junction epitopes are novel non-self but irrelevant epitope sequences that arise in the cassette due to the process of concatenating therapeutic epitopes and linker sequences in the cassette. The novel sequences of junction epitopes are different from the therapeutic epitopes of the cassette themselves. A junction epitope spanning epitopes $\boldsymbol{p}^{\prime ti}$ and $\boldsymbol{p}^{\prime tj}$ may include any epitope sequence that overlaps with both $\boldsymbol{p}^{\prime ti}$ or $\boldsymbol{p}^{\prime tj}$ that is different from the sequences of therapeutic epitopes $\boldsymbol{p}^{\prime ti}$ and $\boldsymbol{p}^{\prime tj}$ themselves. Specifically, each junction between epitope $\boldsymbol{p}^{\prime ti}$ and an adjacent epitope $\boldsymbol{p}^{\prime tj}$ of the cassette with or without an optional linker sequence $\boldsymbol{l}^{(ti,tj)}$ may be associated with $n_{(ti,tj)}$ junction epitopes $\boldsymbol{e}_n^{(ti,tj)}$, $n=1, 2, \ldots, n_{(ti,tj)}$. The junction epitopes may be sequences that at least partially overlap with both epitopes $\boldsymbol{p}^{\prime ti}$ and $\boldsymbol{p}^{\prime tj}$, or may be sequences that at least partially overlap with linker sequences placed between the epitopes $\boldsymbol{p}^{\prime ti}$ and $\boldsymbol{p}^{\prime tj}$. Junction epitopes may be presented by MHC class I, MHC class II, or both.

[00654] FIG. 38 shows two example cassette sequences, cassette 1 ($\mathbf{C_1}$) and cassette 2 ($\mathbf{C_2}$). Each cassette has a vaccine capacity of $v=2$, and includes therapeutic epitopes $\boldsymbol{p}^{\prime t1} = \boldsymbol{p}^{1}$ = SINFEKL and $\boldsymbol{p}^{\prime t2} = \boldsymbol{p}^{2}$ = LLLLLVVVV, and a linker sequence $\boldsymbol{l}^{(t1,t2)}$ = AAY in between the two epitopes. Specifically, the sequence of cassette $\mathbf{C_1}$ is given by $[\boldsymbol{p}^{1}\ \boldsymbol{l}^{(t1,t2)}\ \boldsymbol{p}^{2}]$, while the sequence of cassette $\mathbf{C_2}$ is given by $[\boldsymbol{p}^{2}\ \boldsymbol{l}^{(t1,t2)}\ \boldsymbol{p}^{1}]$. Example junction epitopes $\boldsymbol{e}_n^{(1,2)}$ of cassette $\mathbf{C_1}$ may be sequences such as EKLAAYLLL, KLAAYLLLLL, and FEKLAAYL that span across both epitopes $\boldsymbol{p}^{\prime 1}$ and $\boldsymbol{p}^{\prime 2}$ in the cassette, and may be sequences such as AAYLLLLL and YLLLLLVVV that span across the linker sequence and a single selected epitope in the cassette. Similarly, example junction epitopes $\boldsymbol{e}_m^{(2,1)}$ of cassette $\mathbf{C_2}$ may be sequences such as VVVVAAYSIN, VVVVAAY, and AYSINFEK. Although both cassettes involve the same set of sequences $\boldsymbol{p}^{1}$, $\boldsymbol{l}^{(c1,c2)}$, and $\boldsymbol{p}^{2}$, the set of junction epitopes that are identified are different depending on the ordered sequence of the therapeutic epitopes within the cassette.

[00655] In one embodiment, the cassette design module 324 generates a cassette sequence that reduces the likelihood that junction epitopes are presented in the patient. Specifically, when the cassette is injected into the patient, junction epitopes have the potential to be presented by HLA class I or HLA class II alleles of the patient, and stimulate a CD8 or CD4 T-cell response, respectively. Such reactions are often times undesirable because T-cells reactive to the junction epitopes have no therapeutic benefit, and may diminish the immune response to the selected therapeutic epitopes in the cassette by antigenic competition.[76]

2026201462 26 Feb 2026

[00656] In one embodiment, the cassette design module 324 iterates through one or more candidate cassettes, and determines a cassette sequence for which a presentation score of junction epitopes associated with that cassette sequence is below a numerical threshold. The junction epitope presentation score is a quantity associated with presentation likelihoods of the junction epitopes in the cassette, and a higher value of the junction epitope presentation score indicates a higher likelihood that junction epitopes of the cassette will be presented by HLA class I or HLA class II or both.

[00657] In one embodiment, the cassette design module 324 may determine a cassette sequence associated with the lowest junction epitope presentation score among the candidate cassette sequences. In one instance, the presentation score for a given cassette sequence **C** is determined based on a set of distance metrics $d(\boldsymbol{e}_n^{(ti,tj)}, n=1, 2, \ldots, n_{(ti,tj)}) = d_{(ti,tj)}$ each associated with a junction in the cassette **C**. Specifically, a distance metric $d_{(ti,tj)}$ specifies a likelihood that one or more of the junction epitopes spanning between the pair of adjacent therapeutic epitopes $\boldsymbol{p}^{ti}$ and $\boldsymbol{p}^{tj}$ will be presented. The junction epitope presentation score for cassette **C** can then be determined by applying a function (e.g., summation, statistical function) to the set of distance metrics for the cassette C. Mathematically, the presentation score is given by:

$$score = h(d_{(t_1,t_2)}, d_{(t_2,t_3)}, \ldots, d_{(t_{v-1},t_v)}) \tag{26}$$

where $h(\cdot)$ is some function mapping the distance metrics of each junction to a score. In one particular instance referred throughout the remainder of the specification, the function $h(\cdot)$ is the summation across the distance metrics of the cassette.

[00658] The cassette design module 324 may iterate through one or more candidate cassette sequences, determine the junction epitope presentation score for the candidate cassettes, and identify an optimal cassette sequence associated with a junction epitope presentation score below the threshold. In one particular embodiment referred throughout the remainder of the specification, the distance metric $d(\cdot)$ for a given junction may be given by the sum of the presentation likelihoods or the expected number presented junction epitopes as determined by the presentation models described in sections VII and VIII of the specification. However, it is appreciated that in other embodiments, the distance metric may be derived from other factors alone or in combination with the models like the one exemplified above, where these other factors may include deriving the distance metric from any one or more of (alone or in combination): HLA binding affinity or stability measurements or predictions for HLA class I or HLA class II, and a presentation or immunogenicity model trained on HLA

2026201462 26 Feb 2026

mass spectrometry or T-cell epitope data, for HLA class I or HLA class II. In one embodiment, the distance metric may combine information about HLA class I and HLA class II presentation. For example, the distance metric could be the number of junction epitopes predicted to bind any of the patient's HLA class I or HLA class II alleles with binding affinity below a threshold. In another example, the distance metric could be the expected number of epitopes predicted to be presented by any of the patient's HLA class I or HLA class II alleles.

[00659] The cassette design module 324 may further check the one or more candidate cassette sequences to identify if any of the junction epitopes in the candidate cassette sequences are self-epitopes for a given patient for whom the vaccine is being designed. To accomplish this, the cassette design module 324 checks the junction epitopes against a known database such as BLAST. In one embodiment, the cassette design module may be configured to design cassettes that avoid junction self-epitopes by setting the distance metric $d_{(ti,tj)}$ to a very large value (e.g., 100) for pairs of epitopes t_i,t_j where contatenating epitope t_i to the N-terminus of epitope t_j results in the formation of a junction self-epitope.

[00660] Returning to the example in FIG. 38 the cassette design module 324 determines (for example) a distance metric $d_{(t1,t2)} = d_{(1,2)} = 0.39$ for the single junction (t_1,t_2) in cassette $\mathbf{C_1}$ given by the summation of presentation likelihoods of all possible junction epitopes $\boldsymbol{e}_n^{(t1,t2)} = \boldsymbol{e}_n^{(1,2)}$ having lengths, for example, from 8 to 15 amino acids for MHC class I, or 6-30 amino acids for MHC class II. Since no other junctions are present in cassette $\mathbf{C_1}$, the junction epitope presentation score, which is a summation across the distance metrics for cassette $\mathbf{C_1}$, is also given by 0.39. The cassette design module 324 also determines a distance metric $d_{(t1,t2)} = d_{(2,1)} = 0.068$ for the single junction in cassette $\mathbf{C_2}$ given by the summation of presentation likelihoods of all possible junction epitopes $\boldsymbol{e}_n^{(t1,t2)} = \boldsymbol{e}_n^{(2,1)}$ having lengths from 8 to 15 for MHC class I, or 9-30 amino acids for MHC class II. In this example, the junction epitope presentation score for cassette $\mathbf{C_2}$ is also given by the distance metric of the single junction 0.068. The cassette design module 324 outputs the cassette sequence of $\mathbf{C_2}$ as the optimal cassette since the junction epitope presentation score is lower than the cassette sequence of $\mathbf{C_1}$.

[00661] In some cases, the cassette design module 324 can perform a brute force approach and iterates through all or most possible candidate cassette sequences to select the sequence with the smallest junction epitope presentation score. However, the number of such candidate cassettes can be prohibitively large as the capacity of the vaccine v increases. For

2026201462 26 Feb 2026

example, for a vaccine capacity of *v=20* epitopes, the cassette design module 324 has to iterate through ~10^{18} possible candidate cassettes to determine the cassette with the lowest junction epitope presentation score. This determination may be computationally burdensome (in terms of computational processing resources required), and sometimes intractable, for the cassette design module 324 to complete within a reasonable amount of time to generate the vaccine for the patient. Moreover, accounting for the possible junction epitopes for each candidate cassette can be even more burdensome. Thus, the cassette design module 324 may select a cassette sequence based on ways of iterating through a number of candidate cassette sequences that are significantly smaller than the number of candidate cassette sequences for the brute force approach.

[00662] In one embodiment, the cassette design module 324 generates a subset of randomly or at least pseudo-randomly generated candidate cassettes, and selects the candidate cassette associated with a junction epitope presentation score below a predetermined threshold as the cassette sequence. Additionally, the cassette design module 324 may select the candidate cassette from the subset with the lowest junction epitope presentation score as the cassette sequence. For example, the cassette design module 324 may generate a subset of ~1 million candidate cassettes for a set of *v=20* selected epitopes, and select the candidate cassette with the smallest junction epitope presentation score. Although generating a subset of random cassette sequences and selecting a cassette sequence with a low junction epitope presentation score out of the subset may be sub-optimal relative to the brute force approach, it requires significantly less computational resources thereby making its implementation technically feasible. Further, performing the brute force method as opposed to this more efficient technique may only result in a minor or even negligible improvement in junction epitope presentation score, thus making it not worthwhile from a resource allocation perspective.

[00663] In another embodiment, the cassette design module 324 determines an improved cassette configuration by formulating the epitope sequence for the cassette as an asymmetric traveling salesman problem (TSP). Given a list of nodes and distances between each pair of nodes, the TSP determines a sequence of nodes associated with the shortest total distance to visit each node exactly once and return to the original node. For example, given cities A, B, and C with known distances between each other, the solution of the TSP generates a closed sequence of cities, for which the total distance traveled to visit each city exactly once is the smallest among possible routes. The asymmetric version of the TSP determines the optimal

2026201462 26 Feb 2026

sequence of nodes when the distance between a pair of nodes are asymmetric. For example, the "distance" for traveling from node A to node B may be different from the "distance" for traveling from node B to node A.

[00664] The cassette design module 324 determines an improved cassette sequence by solving an asymmetric TSP, in which each node corresponds to a therapeutic epitope $\boldsymbol{p'^{k}}$. The distance from a node corresponding to epitope $\boldsymbol{p'^{k}}$ to another node corresponding to epitope $\boldsymbol{p'^{m}}$ is given by the junction epitope distance metric $d_{(k,m)}$, while the distance from the node corresponding to the epitope $\boldsymbol{p'^{m}}$ to the node corresponding to epitope $\boldsymbol{p'^{k}}$ is given by the distance metric $d_{(m,k)}$ that may be different from the distance metric $d_{(k,m)}$. By solving for an improved optimal cassette using an asymmetric TSP, the cassette design module 324 can find a cassette sequence that results in a reduced presentation score across the junctions between epitopes of the cassette. The solution of the asymmetric TSP indicates a sequence of therapeutic epitopes that correspond to the order in which the epitopes should be concatenated in a cassette to minimize the junction epitope presentation score across the junctions of the cassette. Specifically, given the set of therapeutic epitopes $k=1, 2, ..., v$, the cassette design module 324 determines the distance metrics $d_{(k,m)}$, $k,m = 1, 2, ..., v$ for each possible ordered pair of therapeutic epitopes in the cassette. In other words, for a given pair k, m of epitopes, both the distance metric $d_{(k,m)}$ for concatenating therapeutic epitope $\boldsymbol{p'^{m}}$ after epitope $\boldsymbol{p'^{k}}$ and the distance metric $d_{(m,k)}$ for concatenating therapeutic epitope $\boldsymbol{p'^{k}}$ after epitope $\boldsymbol{p'^{m}}$ is determined, since these distance metrics may be different from each other.

[00665] In one embodiment, the cassette design module 324 solves the asymmetric TSP through an integer linear programming problem. Specifically, the cassette design module 324 generates a $(v+1) \times (v+1)$ path matrix **P** given by the following:

$$\mathbf{P} = \begin{bmatrix} 0 & \mathbf{0}^{1\times v} \\ \mathbf{0}^{v\times 1} & \mathbf{D} \end{bmatrix} \quad (26).$$

The v x v matrix **D** is an asymmetric distance matrix, where each element D(k, m), $k=1, 2, ..., v; m=1, 2, ..., v$ corresponds to the distance metric for a junction from epitope $\boldsymbol{p'^{k}}$ to epitope $\boldsymbol{p'^{m}}$. Rows $k = 2, ..., v$ of **P** correspond to nodes of the original epitopes, while row 1 and column 1 corresponds to a "ghost node" that is at zero distance from all other nodes. The addition of the "ghost node" to the matrix encodes the notion that the vaccine cassette is linear rather than circular, so there is no junction between the first and last epitopes. In other words, the sequence is not circular, and the first epitope is not assumed to be concatenated after the last epitope in the sequence. Let x_{km} denote a binary variable whose value is 1 if there is a

2026201462 26 Feb 2026

directed path (i.e., an epitope-epitope junction in the cassette) where epitope $\boldsymbol{p'^{k}}$ is concatenated to the N-terminus of epitope $\boldsymbol{p'^{m}}$ and 0 otherwise. In addition, let E denote the set of all v therapeutic vaccine epitopes, and let $S \subset E$ denote a subset of epitopes. For any such subset S, let out(S) denote the number of epitope-epitope junctions $x_{km} = 1$ where k is an epitope in S and m is an epitope in $E \backslash S$. Given a known path matrix **P**, the cassette design module 324 finds a path matrix **X** that solves the following integer linear programming problem:

$$\min_{x} \sum_{k=1}^{v+1} \sum_{k \neq m, m=1}^{v+1} \mathrm{P}_{km} \cdot x_{km} \tag{27}$$

in which P_{km} denotes element P(k,m) of the path matrix **P**, subject to the following constraints:

$$\sum_{k=1}^{v+1} x_{km} = 1\,, \quad m = 1, 2, \ldots, v+1$$

$$\sum_{m=1}^{v+1} x_{km} = 1\,, \quad k = 1, 2, \ldots, v+1$$

$$x_{kk} = 0, \quad k = 1, 2, \ldots, v+1$$

$$\mathrm{out(S)} \geq 1, \quad S \subset E, 2 \leq |S| \leq |V|/2$$

The first two constraints guarantee that each epitope appears exactly once in the cassette. The last constraint ensures that the cassette is connected. In other words, the cassette encoded by x is a connected linear protein sequence.

[00666] The solutions for x_{km}, $k,m = 1, 2, \ldots, v+1$ in the integer linear programming problem of equation (27) indicates the closed sequence of nodes and ghost nodes that can be used to infer one or more sequences of therapeutic epitopes for the cassette that lower the presentation score of junction epitopes. Specifically, a value of $x_{km} = 1$ indicates that a "path" exists from node k to node m, or in other words, that therapeutic epitope $\boldsymbol{p'^{m}}$ should be concatenated after therapeutic epitope $\boldsymbol{p'^{k}}$ in the improved cassette sequence. A solution of $x_{km} = 0$ indicates that no such path exists, or in other words, that therapeutic epitope $\boldsymbol{p'^{m}}$ should not be concatenated after therapeutic epitope $\boldsymbol{p'^{k}}$ in the improved cassette sequence. Collectively, the values of x_{km} in the integer programming problem of equation (27) represent a sequence of nodes and the ghost node, in which the path enters and exists each node exactly once . For example, the values of $x_{ghost,1}=1$, $x_{13}=1$, $x_{32}=1$, *and* $x_{2,ghost}=1$ (0 otherwise) may indicate a sequence *ghost→1→3→2→ghost* of nodes and ghost nodes.

2026201462 26 Feb 2026

[00667] Once the sequence has been solved for, the ghost nodes are deleted from the sequence to generate a refined sequence with only the original nodes corresponding to therapeutic epitopes in the cassette. The refined sequence indicates the order in which selected epitopes should be concatenated in the cassette to improve the presentation score. For example, continuing from the example in the previous paragraph, the ghost node may be deleted to generate a refined sequence $1 \rightarrow 3 \rightarrow 2$. The refined sequence indicates one possible way to concatenate epitopes in the cassette, namely $\boldsymbol{p}^1 \rightarrow \boldsymbol{p}^3 \rightarrow \boldsymbol{p}^2$.

[00668] In one embodiment, when the therapeutic epitopes $\boldsymbol{p}'^k$ are variable-length epitopes, the cassette design module 324 determines candidate distance metrics corresponding to different lengths of the therapeutic epitopes $\boldsymbol{p}'^k$ and $\boldsymbol{p}'^m$, and identifies the distance metric $d_{(k,m)}$ as the smallest candidate distance metric. For example, epitopes $\boldsymbol{p}'^k=[\boldsymbol{n}^k\ \boldsymbol{p}^k\ \boldsymbol{c}^k]$ and $\boldsymbol{p}'^m=[\boldsymbol{n}^m\ \boldsymbol{p}^m\ \boldsymbol{c}^m]$ may each include a corresponding N- and C-terminal flanking sequence that can vary from (in one embodiment) 2-5 amino acids. Thus, the junction between epitopes $\boldsymbol{p}'^k$ and $\boldsymbol{p}'^m$ is associated with 16 different sets of junction epitopes based on the 4 possible length values of $\boldsymbol{n}^k$ and the 4 possible length values of $\boldsymbol{c}^m$ that are placed in the junction. The cassette design module 324 may determine candidate distance metrics for each set of junction epitopes, and determine the distance metric $d_{(k,m)}$ as the smallest value. The cassette design module 324 can then construct the path matrix **P** and solve for the integer linear programming problem in equation (27) to determine the cassette sequence.

[00669] Compared to the random sampling approach, solving for the cassette sequence using the integer programming problem requires determination of v x (v-1) distance metrics each corresponding to a pair of therapeutic epitopes in the vaccine. A cassette sequence determined through this approach can result in a sequence with significantly less presentation of junction epitopes while potentially requiring significantly less computational resources than the random sampling approach, especially when the number of generated candidate cassette sequences is large.

XI.B.2. Comparison of Junction Epitope Presentation for Cassette Sequences Generated by Random Sampling vs. Asymmetric TSP

[00670] Two cassette sequences including v=20 therapeutic epitopes were generated by random sampling 1,000,000 permutations (cassette sequence $\mathbf{C}_1$), and by solving the integer linear programming problem in equation (27) (cassette sequence $\mathbf{C}_2$). The distance metrics, and thus, the presentation score was determined based on the presentation model described in equation (14), in which f is the sigmoid function, $\boldsymbol{x}_h^i$ is the sequence of peptide $\boldsymbol{p}^i$, $\mathbf{g}_h(\cdot)$ is the

2026201462 26 Feb 2026

neural network function, **w** includes the flanking sequence, the log transcripts per kilobase million (TPM) of peptide $\boldsymbol{p}^i$, the antigenicity of the protein of peptide $\boldsymbol{p}^i$, and the sample ID of origin of peptide $\boldsymbol{p}^i$, and $\mathbf{g}_\mathbf{w}(\cdot)$ of the flanking sequence and the log TPM are neural network functions, respectively. Each of the neural network functions for $\mathbf{g}_\mathbf{h}(\cdot)$ included one output node of a one-hidden-layer multilayer perceptron (MLP) with input dimensions 231 (11 residues x 21 characters per residue, including pad characters), width 256, rectified linear unit (ReLU) activations in the hidden layer, linear activations in the output layer, and one output node per HLA allele in the training data set. The neural network function for the flanking sequence was a one hidden-layer MLP with input dimension 210 (5 residues of N-terminal flanking sequence + 5 residues of C-terminal flanking sequence x 21 characters per residue, including the pad characters), width 32, ReLU activations in the hidden layer and linear activation in the output layer. The neural network function for the RNA log TPM was a one hidden layer MLP with input dimension 1, width 16, ReLU activations in the hidden layer and linear activation in the output layer. The presentation models were constructed for HLA alleles HLA-A*02:04, HLA-A*02:07, HLA-B*40:01, HLA-B*40:02, HLA-C*16:02, and HLA-C*16:04. The presentation score indicating the expected number of presented junction epitopes of the two cassette sequences were compared. Results showed that the presentation score for the cassette sequence generated by solving the equation of (27) was associated with a ~4 fold improvement over the presentation score for the cassette sequence generated by random sampling.

[00671] Specifically, the v=20 epitopes were given by:

$\boldsymbol{p}'^1$ = YNYSYWISIFAHTMWYNIWHVQWNK
$\boldsymbol{p}'^2$ = IEALPYVFLQDQFELRLLKGEQGNN
$\boldsymbol{p}'^3$ = DSEETNTNYLHYCHFHWTWAQQTTV
$\boldsymbol{p}'^4$ = GMLSQYELKDCSLGFSWNDPAKYLR
$\boldsymbol{p}'^5$ = VRIDKFLMYVWYSAPFSAYPLYQDA
$\boldsymbol{p}'^6$ = CVHIYNNYPRMLGIPFSVMVSGFAM
$\boldsymbol{p}'^7$ = FTFKGNIWIEMAGQFERTWNYPLSL
$\boldsymbol{p}'^8$ = ANDDTPDFRKCYIEDHSFRFSQTMN
$\boldsymbol{p}'^9$ = AAQYIACMVNRQMTIVYHLTRWGMK
$\boldsymbol{p}'^{10}$ = KYLKEFTQLLTFVDCYMWITFCGPD
$\boldsymbol{p}'^{11}$ = AMHYRTDIHGYWIEYRQVDNQMWNT
$\boldsymbol{p}'^{12}$ = THVNEHQLEAVYRFHQVHCRFPYEN
$\boldsymbol{p}'^{13}$ = QTFSECLFFHCLKVWNNVKYAKSLK
$\boldsymbol{p}'^{14}$ = SFSSWHYKESHIALLMSPKKNHNNT
$\boldsymbol{p}'^{15}$ = ILDGIMSRWEKVCTRQTRYSYCQCA
$\boldsymbol{p}'^{16}$ = YRAAQMSKWPNKYFDFPEFMAYMPI

2026201462 26 Feb 2026

p'^{17} = PRPGMPCQHHNTHGLNDRQAFDDFV
p'^{18} = HNIISDETEVWEQAPHITWVYMWCR
p'^{19} = AYSWPVVPMKWIPYRALCANHPPGT
p'^{20} = HVMPHVAMNICNWYEFLYRISHIGR.

In the first example, 1,000,000 different candidate cassette sequences were randomly generated with the 20 therapeutic epitopes. The presentation score was generated for each of the candidate cassette sequences. The candidate cassette sequence identified to have the lowest presentation score was:

$\mathbf{C_1}$ = THVNEHQLEAVYRFHQVHCRFPYENAMHYQMWNTYRAAQMSKWPNKYFDFPEFMAYMPICVH
IYNNYPRMLGIPFSVMVSGFAMAYSWPVVPMKWIPYRALCANHPPGTANDDTPDFRKCYIEDHSFRFSQTMNI
EALPYVFLQDQFELRLLKGEQGNNDSEETNTNYLHYCHFHWTWAQQTTVILDGIMSRWEKVCTRQTRYSYCQC
AFTFKGNIWIEMAGQFERTWNYPLSLSFSSWHYKESHIALLMSPKKNHNNTQTFSECLFFHCLKVWNNVKYAK
SLKHVMPHVAMNICNWYEFLYRISHIGRHNIISDETEVWEQAPHITWVYMWCRVRIDKFLMYVWYSAPFSAYP
LYQDAKYLKEFTQLLTFVDCYMWITFCGPDAAQYIACMVNRQMTIVYHLTRWGMKYNYSYWISIFAHTMWYNI
WHVQWNKGMLSQYELKDCSLGFSWNDPAKYLRPRPGMPCQHHNTHGLNDRQAFDDFV

with a presentation score of 6.1 expected number of presented junction epitopes. The median presentation score of the 1,000,000 random sequences was 18.3. The experiment shows that the expected number of presented junction epitopes can be significantly reduced by identifying a cassette sequence among randomly sampled cassettes.

[00672] In the second example, a cassette sequence $\mathbf{C_2}$ was identified by solving the integer linear programming problem in equation (27). Specifically, the distance metric of each potential junction between a pair of therapeutic epitopes was determined. The distance metrics were used to solve for the solution to the integer programming problem. The cassette sequence identified by this approach was:

$\mathbf{C_2}$ = IEALPYVFLQDQFELRLLKGEQGNNILDGIMSRWEKVCTRQTRYSYCQCAHVMPHVAMNICN
WYEFLYRISHIGRTHVNEHQLEAVYRFHQVHCRFPYENFTFKGNIWIEMAGQFERTWNYPLSLAMHYQMWNTS
FSSWHYKESHIALLMSPKKNHNNTVRIDKFLMYVWYSAPFSAYPLYQDAQTFSECLFFHCLKVWNNVKYAKSL
KYRAAQMSKWPNKYFDFPEFMAYMPIAYSWPVVPMKWIPYRALCANHPPGTCVHIYNNYPRMLGIPFSVMVSG
FAMHNIISDETEVWEQAPHITWVYMWCRAAQYIACMVNRQMTIVYHLTRWGMKYNYSYWISIFAHTMWYNIWH
VQWNKGMLSQYELKDCSLGFSWNDPAKYLRKYLKEFTQLLTFVDCYMWITFCGPDANDDTPDFRKCYIEDHSF
RFSQTMNDSEETNTNYLHYCHFHWTWAQQTTVPRPGMPCQHHNTHGLNDRQAFDDFV

with a presentation score of 1.7. The presentation score of cassette sequence $\mathbf{C_2}$ showed a ~4 fold improvement over the presentation score of cassette sequence $\mathbf{C_1}$, and a ~11 fold improvement over the median presentation score of the 1,000,000 randomly generated candidate cassettes. The run-time for generating cassette $\mathbf{C_1}$ was 20 seconds on a single thread of a 2.30 GHz Intel Xeon E5-2650 CPU. The run-time for generating cassette $\mathbf{C_2}$ was 1 second on a single thread of the same CPU. Thus in this example, the cassette sequence identified by

2026201462 26 Feb 2026

solving the integer programming problem of equation (27) produces a ~4-fold better solution at 20-fold reduced computational cost.

[00673] The results show that the integer programming problem can potentially provide a cassette sequence with a lower number of presented junction epitopes than one identified from random sampling, potentially with less computation resources.

XI.B.3. Comparison of Junction Epitope Presentation for Cassette Sequence Selection Generated by MHCflurry and the Presentation Model

[00674] In this example, cassette sequences including v=20 therapeutic epitopes were selecte d based off tumor/normal exome sequencing, tumor transcriptome sequencing and HLA typin g of a lung cancer sample were generated by random sampling 1,000,000 permutations, and b y solving the integer linear programming problem in equation (27). The distance metrics, and thus, the presentation score were determined based on the number of junction epitopes predict ed by MHCflurry, an HLA-peptide binding affinity predictor, to bind the patient's HLAs with affinity below a variety of thresholds (e.g., 50-1000nM, or higher, or lower). In this example, the 20 nonsynoymous somatic mutations chosen as therapeutic epitopes were selected from a mong the 98 somatic mutations identified in the tumor sample by ranking the mutations accor ding to the presentation model in Section XI.B above. However, it is appreciated that in other embodiments, the therapeutic epitopes may be selected based on other criteria; such as those based stability, or combinations of criteria such as presentation score, affinity, and so on. In a ddition, it is appreciated that the criteria used for prioritizing therapuetic epitopes for inclusio n in the vaccine need not be the same as the criteria used for determining the distance metric D(k, m) used in the cassette design module 324.

[00675] The patient's HLA class I alleles were HLA-A*01:01, HLA-A*03:01, HLA-B*07:0 2, HLA-B*35:03, HLA-C*07:02, HLA-C*14:02.

[00676] Specifically in this example, the v=20 therapuetic epitopes were

SSTPYLYYGTSSVSYQFPMVPGGDR
EMAGKIDLLRDSYIFQLFWREAAEP
ALKQRTWQALAHKYNSQPSVSLRDF
VSSHSSQATKDSAVGLKYSASTPVR
KEAIDAWAPYLPEYIDHVISPGVTS
SPVITAPPSSPVFDTSDIRKEPMNI
PAEVAEQYSEKLVYMPHTFFIGDHA
MADLDKLNIHSIIQRLLEVRGS
AAAYNEKSGRITLLSLLFQKVFAQI

2026201462 26 Feb 2026

KIEEVRDAMENEIRTQLRRQAAAHT
DRGHYVLCDFGSTTNKFQNPQTEGV
QVDNRKAEAEEAIKRLSYISQKVSD
CLSDAGVRKMTAAVRVMKRGLENLT
LPPRSLPSDPFSQVPASPQSQSSSQ
ELVLEDLQDGDVKMGGSFRGAFSNS
VTMDGVREEDLASFSLRKRWESEPH
IVGVMFFERAFDEGADAIYDHINEG
TVTPTPTPTGTQSPTPTPITTTTTV
QEEMPPRPCGGHTSSSLPKSHLEPS
PNIQAVLLPKKTDSHHKAKGK

[00677] Results from this example in the table below compare the number of junction epitopes predicted by MHCflurry to bind the patient's HLAs with affinity below the value in the threshold column (where nM stands for nanoMolar) as found via three example methods. For the first method, the optimal cassette found via the traveling salesman problem (ATSP) formulation described above with 1s run-time. For the second method, the optimal cassette as determined by taking the best cassette found after 1 million random samples. For the third method, the median number of junction epitopes was found in the 1 million random samples.

Threshold (nM)	ATSP # Binding Junction Epitopes	Random Sampling # Binding Junction Epitopes	Median # Binding Junction Epitopes
50	0	0	3
100	0	0	7
150	0	1	12
500	15	26	55
1000	68	91	131

[00678] The results of this example illustrate that any one of a number of criteria may be used to identify whether or not a given cassette design meets design requirements. Specifically, as demonstrated by prior examples, the selected cassette sequence out of many candidates may be specified by the cassette sequence having a lowest junction epitope presentation score, or at least such a score below an identified threshold. This example represents that another criteria, such as binding affinity, may be used to specify whether or not a given cassette design meets design requirements. For this criteria, a threshold binding affinity (e.g., 50-1000, or greater or lower) may be set specifying that the cassette design sequence should have fewer than some threshold number of junction epitopes above the threshold (e.g., 0), and any one of a number of methods may be used (e.g., methods one

2026201462 26 Feb 2026

through three illustrated in the table) can be used to identify if a given candidate cassette sequence meets those requirements. These example methods further illustrate that depending on the method used, the thresholds may need to be set differently. Other criteria may be envisioned, such as those based stability, or combinations of criteria such as presentation score, affinity, and so on.

[00679] In another example, the same cassettes were generated using the same HLA type and 20 therapeutic epitopes from earlier in this section (XI.C), but instead of using distance metrics based off binding affinity prediction, the distance metric for epitopes m, k was the number of peptides spanning the m to k junction predicted to be presented by the patient's HLA class I alleles with probability of presentation above a series of thresholds (between probability of 0.005 and 0.5, or higher, or lower), where the probabilities of presentation were determined by the presentation model in Section XI.B above. This example further illustrates the breadth of criteria that may be considered in identifying whether a given candidate cassette sequence meets design requirements for use in the vaccine.

Threshold (probability)	ATSP # Junction Epitopes	Random Sampling # Junction Epitopes	Median # Junction Epitopes
0.005	58	79	118
0.01	39	59	93
0.05	7	33	47
0.1	5	14	35
0.2	1	8	25
0.5	0	2	14

[00680] The examples above have identified that the criteria for determining whether a candidate cassette sequence may vary by implementation. Each of these examples has illustrated that the count of the number of junction epitopes falling above or below the criteria may be a count used in determining whether the candidate cassette sequence meets that criteria. For example, if the criteria is number of epitopes meeting or exceeding a threshold binding affinity for HLA, whether the candidate cassette sequence has greater or fewer than that number may determine whether the candidate cassette sequence meets the criteria for use as the selected cassette for the vaccine. Similarly if the criteria is the number of junction epitopes exceeding a threshold presentation likelihood.

2026201462 26 Feb 2026

[00681] However, in other embodiments, calculations other than counting can be performed to determine whether a candidate cassette sequence meets the design criteria. For example, rather than the count of epitopes exceeding / falling below some threshold, it may instead be determined what proportion of junction epitopes exceed or fall below the threshold, for example whether the top X% of junction epitopes have a presentation likelihood above some threshold Y, or whether X% percent of junction epitopes have an HLA binding affinity less than or greater than Z nM. These are merely examples, generally the criteria may be based on any attribute of either individual junction epitopes, or statistics derived from aggregations of some or all of the junction epitopes. Here, X can generally be any number between 0 and 100% (e.g., 75% or less) and Y can be any value between 0 and 1, and Z can be any number suitable to the criteria in question. These values may be determined empirically, and depend on the models and criteria used, as well as the quality of the training data used.

[00682] As such, in certain aspects, junction epitopes with high probabilities of presentation can be removed; junction epitopes with low probabilities of presentation can be retained; junction epitopes that bind tightly, i.e., junction epitopes with binding affinity below 1000nM or 500nM or some other threshold can be removed; and/or junction epitopes that bind weakly, i.e., junction epitopes with binding affinity above 1000nM or 500nM or some other threshold can be retained.

[00683] Although the examples above have identified candidate sequences using an implementation of the presentation model described above, these principles apply equally to an implementation where the epitopes for arrangement in the cassette sequences are identified based on other types of models as well, such as those based on affinity, stability, and so on.

XII. Example 7: Experimentation Results Showing Example Presentation Model Performance

[00684] The validity of the various presentation models described above were tested on test data *T* that were subsets of training data 170 that were not used to train the presentation models or a separate dataset from the training data 170 that have similar variables and data structures as the training data 170.

[00685] A relevant metric indicative of the performance of a presentation models is:

$$\text{Positive Predictive Value (PPV)} = P(y_{i\in T} = 1 \mid u_{i\in T} \geq t) = \frac{\sum_{i\in T} \mathbb{1}(y_i = 1,\ u_i \geq t)}{\sum_{i\in T} \mathbb{1}(u_i \geq t)}$$

2026201462 26 Feb 2026

that indicates the ratio of the number of peptide instances that were correctly predicted to be presented on associated HLA alleles to the number of peptide instances that were predicted to be presented on the HLA alleles. In one implementation, a peptide $\boldsymbol{p^i}$ in the test data T was predicted to be presented on one or more associated HLA alleles if the corresponding likelihood estimate u_i is greater or equal to a given threshold value t. Another relevant metric indicative of the performance of presentation models is:

$$\text{Recall} = P(u_{i\in T} \geq t | \, y_{i\in T} = 1) = \frac{\sum_{i\in T} \mathbb{1}(y_i = 1, \, u_i \geq t)}{\sum_{i\in T} \mathbb{1}(y_i = 1)}$$

that indicates the ratio of the number of peptide instances that were correctly predicted to be presented on associated HLA alleles to the number of peptide instances that were known to be presented on the HLA alleles. Another relevant metric indicative of the performance of presentation models is the area-under-curve (AUC) of the receiver operating characteristic (ROC). The ROC plots the recall against the false positive rate (FPR), which is given by:

$$\text{FPR} = P(u_{i\in T} \geq t | \, y_{i\in T} = 0) = \frac{\sum_{i\in T} \mathbb{1}(y_i = 0, \, u_i \geq t)}{\sum_{i\in T} \mathbb{1}(y_i = 0)}.$$

XII.A. Comparison of Presentation Model Performance on Mass Spectrometry Data Against State-of-the-Art Model

[00686] FIG. 13A compares performance results of an example presentation model, as presented herein, and state-of-the-art models for predicting peptide presentation on multiple-allele mass spectrometry data. Results showed that the example presentation model performed significantly better at predicting peptide presentation than state-of-the-art models based on affinity and stability predictions.

[00687] Specifically, the example presentation model shown in FIG. 13A as "MS" was the maximum of per-alleles presentation model shown in equation (12), using the affine dependency function $g_h(\cdot)$ and the expit function $f(\cdot)$. The example presentation model was trained based on a subset of the single-allele HLA-A*02:01 mass spectrometry data from the IEDB data set (data set "D1") (data can be found at http://www.iedb.org/doc/mhc_ligand_full.zip) and a subset of the single-allele HLA-B*07:02 mass spectrometry from the IEDB data set (data set "D2") (data can be found at http://www.iedb.org/doc/mhc_ligand_full.zip). All peptides from source protein that contain presented peptides in the test set were eliminated from the training data such that the example presentation model could not simply memorize the sequences of presented antigens.

2026201462 26 Feb 2026

[00688] The model shown in FIG. 13A as "Affinity" was a model similar to the current state-of-the-art model that predicts peptide presentation based on affinity predictions NETMHCpan. Implementation of NETMHCpan is provided in detail at http://www.cbs.dtu.dk/services/NetMHCpan/. The model shown in FIG. 13A as "Stability" was a model similar to the current state-of-the-art model that predicts peptide presentation based on stability predictions NETMHCstab. Implementation of NETMHCstab is provided in detail at http://www.cbs.dtu.dk/services/NetMHCstab-1.0/. The test data that is a subset of the multiple-allele JY cell line HLA-A*02:01 and HLA-B*07:02 mass spectrometry data from the Bassani-Sternberg data set (data set "D3") (data can be found at www.ebi.ac.uk/pride/archive/projects/PXD000394). The error bars (as indicated in solid lines) show 95% confidence intervals.

[00689] As shown in the results of FIG. 13A, the example presentation model trained on mass spectrometry data had a significantly higher PPV value at 10% recall rate relative to the state-of-the-art models that predict peptide presentation based on MHC binding affinity predictions or MHC binding stability predictions. Specifically, the example presentation model had approximately 14% higher PPV than the model based on affinity predictions, and had approximately 12% higher PPV than the model based on stability predictions.

[00690] These results demonstrate that the example presentation model had significantly better performance than the state-of-the-art models that predict peptide presentation based on MHC binding affinity or MHC binding stability predictions even though the example presentation model was not trained based on protein sequences that contained presented peptides.

XII.B. Comparison of Presentation Model Performance on T-cell Epitope Data Against State-of-the-Art Models

[00691] FIG. 13B compares performance results of another example presentation model, as presented herein, and state-of-the-art models for predicting peptide presentation on T-cell epitope data. T-cell epitope data contains peptide sequences that were presented by MHC alleles on the cell surface, and recognized by T-cells. Results showed that even though the example presentation model is trained based on mass spectrometry data, the example presentation model performed significantly better at predicting T-cell epitopes than state-of-the-art models based on affinity and stability predictions. In other words, the results of FIG. 13B indicated that not only did the example presentation model perform better than state-of-the-art models at predicting peptide presentation on mass spectrometry test data, but the

2026201462 26 Feb 2026

example presentation model also performed significantly better than state-of-the-art models at predicting epitopes that were actually recognized by T-cells. This is an indication that the variety of presentation models as presented herein can provide improved identification of antigens that are likely to induce immunogenic responses in the immune system.

[00692] Specifically, the example presentation model shown in FIG. 13B as "MS" was the per-allele presentation model shown in equation (2), using the affine transformation function $g_h(\cdot)$ and the expit function $f(\cdot)$ that was trained based on a subset of data set D1. All peptides from source protein that contain presented peptides in the test set were eliminated from the training data such that the presentation model could not simply memorize the sequences of presented antigens.

[00693] Each of the models were applied to the test data that is a subset of mass spectrometry data on HLA-A*02:01 T-cell epitope data (data set "D4") (data can be found at www.iedb.org/doc/tcell full v3.zip). The model shown in FIG. 13B as "Affiinity" was a model similar to the current state-of-the-art model that predicts peptide presentation based on affinity predictions NETMHCpan, and the model shown in FIG. 13B as "Stability" was a model similar to the current state-of-the-art model that predicts peptide presentation based on stability predictions NETMHCstab. The error bars (as indicated in solid lines) show 95% confidence intervals.

[00694] As shown in the results of FIG. 13A, the per-allele presentation model trained on mass spectrometry data had a significantly higher PPV value at 10% recall rate than the state-of-the-art models that predict peptide presentation based on MHC binding affinity or MHC binding stability predictions even though the presentation model was not trained based on protein sequences that contained presented peptides. Specifically, the per-allele presentation model had approximately 9% higher PPV than the model based on affinity predictions, and had approximately 8% higher PPV than the model based on stability predictions.

[00695] These results demonstrated that the example presentation model trained on mass spectrometry data performed significantly better than state-of-the-art models on predicting epitopes that were recognized by T-cells.

XII.C. Comparison of Different Presentation Model Performances on Mass Spectrometry Data

[00696] FIG. 13C compares performance results for an example function-of-sums model (equation (13)), an example sum-of-functions model (equation (19)), and an example second order model (equation (23)) for predicting peptide presentation on multiple-allele mass

2026201462 26 Feb 2026

spectrometry data. Results showed that the sum-of-functions model and second order model performed better than the function-of-sums model. This is because the function-of-sums model implies that alleles in a multiple-allele setting can interfere with each other for peptide presentation, when in reality, the presentation of peptides are effectively independent.

[00697] Specifically, the example presentation model labeled as "sigmoid-of-sums" in FIG. 13C was the function-of-sums model using a network dependency function $g_h(\cdot)$, the identity function $f(\cdot)$, and the expit function $r(\cdot)$. The example model labeled as "sum-of-sigmoids" was the sum-of-functions model in equation (19) with a network dependency function $g_h(\cdot)$, the expit function $f(\cdot)$, and the identity function $r(\cdot)$. The example model labeled as "hyperbolic tangent" was the sum-of-functions model in equation (19) with a network dependency function $g_h(\cdot)$, the expit function $f(\cdot)$, and the hyperbolic tangent function $r(\cdot)$. The example model labeled as "second order" was the second order model in equation (23) using an implicit per-allele presentation likelihood form shown in equation (18) with a network dependency function $g_h(\cdot)$ and the expit function $f(\cdot)$. Each model was trained based on a subset of data set D1, D2, and D3. The example presentation models were applied to a test data that is a random subset of data set D3 that did not overlap with the training data.

[00698] As shown in FIG. 13C, the first column refers to the AUC of the ROC when each presentation model was applied to the test set, the second column refers to the value of the negative log likelihood loss, and the third column refers to the PPV at 10% recall rate. As shown in FIG. 13C, the performance of presentation models "sum-of-sigmoids," "hyperbolic tangent," and "second order" were approximately tied at approximately 15-16% PPV at 10% recall, while the performance of the model "sigmoid-of-sums" was slightly lower at approximately 11%.

[00699] As discussed previously in section X.C.4., the results showed that the presentation models "sum-of-sigmoids," "hyperbolic tangent," and "second order" have high values of PPV compared to the "sigmoid-of-sums" model because the models correctly account for how peptides are presented independently by each MHC allele in a multiple-allele setting.

XII.D. Comparison of Presentation Model Performance With and Without Training on Single-Allele Mass Spectrometry Data

[00700] FIG. 13D compares performance results for two example presentation models that are trained with and without single-allele mass spectrometry data on predicting peptide presentation for multiple-allele mass spectrometry data. The results indicated that example

2026201462 26 Feb 2026

presentation models that are trained without single-allele data achieve comparable performance to that of example presentation models trained with single-allele data.

[00701] The example model "with A2/B7 single-allele data" was the "sum-of-sigmoids" presentation model in equation (19) with a network dependency function $g_h(\cdot)$, the expit function $f(\cdot)$, and the identity function $r(\cdot)$. The model was trained based on a subset of data set D3 and single-allele mass spectrometry data for a variety of MHC alleles from the IEDB database (data can be found at: http://www.iedb.org/doc/mhc_ligand_full.zip). The example model "without A2/B7 single-allele data" was the same model, but trained based on a subset of the multiple-allele D3 data set without single-allele mass spectrometry data for alleles HLA-A*02:01 and HLA-B*07:02, but with single-allele mass spectrometry data for other alleles. Within the multiple-allele training data, cell line HCC1937 expressed HLA-B*07:02 but not HLA-A*02:01, and cell line HCT116 expressed HLA-A*02:01 but not HLA-B*07:02. The example presentation models were applied to a test data that was a random subset of data set D3 and did not overlap with the training data.

[00702] As shown in FIG. 13D, the predictions based on the implicit per-allele presentation likelihoods for MHC allele HLA-A*02:01 performed significantly better on single-allele test data for MHC allele HLA-A*02:01 rather than for MHC allele HLA-B*07:02. Similar results are shown for MHC allele HLA-B*07:02.

[00703] These results indicate that the implicit per-allele presentation likelihoods of the presentation model can correctly predict and distinguish binding motifs to individual MHC alleles, even though direct association between the peptides and each individual MHC allele was not known in the training data.

XII.E. Comparison of Per-Allele Prediction Performance without Training on Single-Allele Mass Spectrometry Data

[00704] FIG. 13E shows performance for the "without A2/B7 single-allele data" and "with A2/B7 single-allele data" example models shown in FIG. 13D on single-allele mass spectrometry data for alleles HLA-A*02:01 and HLA-B*07:02 that were held out in the analysis shown in FIG. 13D. Results indicate that even through the example presentation model is trained without single-allele mass spectrometry data for these two alleles, the model is able to learn binding motifs for each MHC allele.

[00705] The column "Correlation" refers to the correlation between the actual labels that indicate whether the peptide was presented on the corresponding allele in the test data, and the label for prediction. As shown in FIG. 13E, "A2 model predicting B7" indicates the

2026201462 26 Feb 2026

performance of the model when peptide presentation is predicted for single-allele HLA-B*07:02 data based on the implicit per-allele presentation likelihood estimate for MHC allele HLA-A*02:01. Similarly, "A2 model predicting A2" indicates the performance of the model when peptide presentation is predicted for single-allele HLA-A*02:01 based on the implicit per-allele presentation likelihood estimate for MHC allele HLA-A*02:01. "B7 model predicting B7" indicates the performance of the model when peptide presentation is predicted for single-allele HLA-B*07:02 data based on the implicit per-allele presentation likelihood estimate for MHC allele HLA-B*07:02. "B7 model predicting A2" indicates the performance of the model when peptide presentation is predicted for single-allele HLA-A*02:01 based on the implicit per-allele presentation likelihood estimate for MHC allele HLA-B*07:02.

[00706] As shown in FIG. 13E, the predictive capacity of implicit per-allele likelihoods for an HLA allele is significantly higher for the intended allele, and significantly lower for the other HLA allele. Similarly to the results shown in FIG. 13D, the example presentation models correctly learned to differentiate peptide presentation of individual alleles HLA-A*02:01 and HLA-B*07:02, even though direct association between peptide presentation and these alleles were not present in the multiple-allele training data.

XII.F. Frequently Ocurring Anchor Residues in Per-Allele Predictions Match Known Canonical Anchor Motifs

[00707] FIG. 13F shows the common anchor residues at positions 2 and 9 among nonamers predicted by the "without A2/B7 single-allele data" example model shown in FIG. 13D. The peptides were predicted to be presented if the estimated likelihood was above 5%. Results show that most common anchor residues in the peptides identified for presentation on the MHC alleles HLA-A*02:01 and HLA-B*07:02 matched previously known anchor motifs for these MHC alleles. This indicates that the example presentation models correctly learned peptide binding based on particular positions of amino acids of the peptide sequences, as expected.

[00708] As shown in FIG. 13F, amino acids L/M at position 2 and amino acids V/L at position 9 were known to be canonical anchor residue motifs (as shown in Table 4 of https://link.springer.com/article/10.1186/1745-7580-4-2) for HLA-A*02:01, and amino acid P at position 2 and amino acids L/V at position 9 were known to be canonical anchor residue motifs for HLA-B*07:02. The most common anchor residue motifs at positions 2 and 9 for peptides identified the model matched the known canonical anchor residue motifs for both HLA alleles.

2026201462 26 Feb 2026

XII.G. Comparison of Presentation Model Performances With and Withtout Allele Noninteracting Variables

[00709] FIG. 13G compares performance results between an example presentation model that incorporated C- and N-terminal flanking sequences as allele-interacting variables, and an example presentation model that incorporated C- and N-terminal flanking sequences as allele-noninteracting variables. Results showed that incorporating C- and N-terminal flanking sequences as allele noninteracting variables significantly improved model performance. More specifically, it is valuable to identify appropriate features for peptide presentation that are common across different MHC alleles, and model them such that statistical strength for these allele-noninteracting variables are shared across MHC alleles to improve presentation model performance.

[00710] The example "allele-interacting" model was the sum-of-functions model using the form of implicit per-allele presentation likelihoods in equation (22) that incorporated C- and N-terminal flanking sequences as allele-interacting variables, with a network dependency function $g_h(\cdot)$ and the expit function $f(\cdot)$. The example "allele-noninteracting" model was the sum-of-functions model shown in equation (21) that incorporated C- and N-terminal flanking sequences as allele-noninteracting variables, with a network dependency function $g_h(\cdot)$ and the expit function $f(\cdot)$. The allele-noninteracting variables were modeled through a separate network dependency function $g_w(\cdot)$. Both models were trained on a subset of data set D3 and single-allele mass spectrometry data for a variety of MHC alleles from the IEDB database (data can be found at: http://www.iedb.org/doc/mhc_ligand_full.zip). Each of the presentation models was applied to a test data set that is a random subset of data set D3 that did not overlap with the training data.

[00711] As shown in FIG. 13G, incorporating C-and N-terminal flanking sequences in the example presentation model as allele-noninteracting variables achieved an approximately 3% improvement in PPV value relative to modeling them as allele-interacting variables. This is because, in general, the "allele-noninteracting" example presentation model was able to share statistical strength of allele-noninteracting variables across MHC alleles by modeling the effect with a separate network dependency function with very little addition in computing power.

2026201462 26 Feb 2026

XII.H. Dependency Between Presented Peptides and mRNA Quantification

[00712] FIG. 13H shows the dependency between mRNA abundance and the frequency of peptides presented on a tumor cell as determined by mass-spectrometry. Results show that there is a strong dependency between mRNA expression and peptide presentation.

[00713] Specifically, the horizontal axis in FIG.13H indicates mRNA expression in terms of transcripts per million (TPM) quartiles. The vertical axis in FIG. 13H indicates fraction of presented epitopes from genes in corresponding mRNA expression quartiles. Each solid line is a plot relating the two measurements from a tumor sample that is associated with corresponding mass spectrometry data and mRNA expression measurements. As shown in FIG. 13H, there is a strong positive correlation between mRNA expression, and the fraction of peptides in the corresponding gene. Specifically, peptides from genes in the top quartile of RNA expression are more than 20 times likely to be presented than the bottom quartile. Moreover, essentially 0 peptides are presented from genes that are not detected through RNA.

[00714] The results indicate that the performance of the presentation model can be greatly improved by incorporating mRNA quantification measurements, as these measurements are strongly predictive of peptide presentation.

XII.I. Comparison of Presentation Model Performance With Incorporation of RNA Quantification Data

[00715] FIG. 13I shows performance of two example presentation models, one of which is trained based on mass spectrometry tumor cell data, another of which incorporates mRNA quantification data and mass spectrometry tumor cell data. As expected from FIG. 13H, results indicated that there is a significant improvement in performance by incorporating mRNA quantification measurements in the example presentation model, since the mRNA expression is a strong indicator of peptide presentation.

[00716] "MHCflurry + RNA filter" was a model similar to the current state-of-the-art model that predicts peptide presentation based on affinity predictions. It was implemented using MHCflurry along with a standard gene expression filter that removed all peptides from proteins with mRNA quantification measurements that were less than 3.2 FPKM. Implementation of MHCflurry is provided in detail at https://github.com/hammerlab/mhcflurry/, and at http://biorxiv.org/content/early/2016/05/22/054775. The "Example Model, no RNA" model was the "sum-of-sigmoids" example presentation model shown in equation (21) with the network dependency function $g_h(\cdot)$, the network dependency function $g_w(\cdot)$, and the expit

2026201462 26 Feb 2026

function $f(\cdot)$. The "Example Model, no RNA" model incorporated C-terminal flanking sequences as allele-noninteracting variables through a network dependency function $g_w(\cdot)$.

[00717] The "Example Model, with RNA" model was the "sum-of-sigmoids" presentation model shown in equation (19) with network dependency function $g_h(\cdot)$, the network dependency function $g_w(\cdot)$ in equation (10) incorporating mRNA quantification data through a log function, and the expit function $f(\cdot)$. The "Example Model, with RNA" model incorporated C-terminal flanking sequences as allele-noninteracting variables through the network dependency functions $g_w(\cdot)$ and incorporated mRNA quantification measurements through the log function.

[00718] Each model was trained on a combination of the single-allele mass spectrometry data from the IEDB data set, 7 cell lines from the multiple-allele mass spectrometry data from the Bassani-Sternberg data set, and 20 mass spectrometry tumor samples. Each model was applied to a test set including 5,000 held-out proteins from 7 tumor samples that constituted 9,830 presented peptides from a total of 52,156,840 peptides.

[00719] As shown in the first two bar graphs of FIG. 13I, the "Example Model, no RNA" model has a PPV value at 20% Recall of 21%, while that of the state-of-the-art model is approximately 3%, This indicates an initial performance improvement of 18% in PPV value, even without the incorporation of mRNA quantification measurements. As shown in the third bar graph of FIG. 13I, the "Example Model, with RNA" model that incorporates mRNA quantification data into the presentation model shows a PPV value of approximately 30%, which is almost a 10% increase in performance compared to the example presentation model without mRNA quantification measurements.

[00720] Thus, results indicate that as expected from the findings in FIG. 13H, mRNA expression is indeed a strong predictor of peptide prediction, that allows significant improvement in the performance of a presentation model with very little addition of computational complexity.

XII.J. Example of Parameters Determined for MHC Allele HLA-C*16:04

[00721] FIG. 13J compares probability of peptide presentation for different peptide lengths between results generated by the "Example Model, with RNA" presentation model described in reference to FIG. 13I, and predicted results by state-of-the-art models that do not account for peptide length when predicting peptide presentation. Results indicated that the "Example

2026201462 26 Feb 2026

Model, with RNA" example presentation model from FIG. 13I captured variation in likelihoods across peptides of differing lengths.

[00722] The horizontal axis denoted samples of peptides with lengths 8, 9, 10, and 11. The vertical axis denoted the probability of peptide presentation conditioned on the lengths of the peptide. The plot "Truth (Blind Test Data)" showed the proportion of presented peptides according to the length of the peptide in a sample test data set. The presentation likelihood varied with the length of the peptide. For example, as shown in FIG. 13J, a 10mer peptide with canonical HLA-A2 L/V anchor motifs was approximately 3 times less likely to be presented than a 9mer with the same anchor residues. The plot "Models Ignoring Length" indicated predicted measurements if state-of-the-art models that ignore peptide length were to be applied to the same test data set for presentation prediction. These models may be NetMHC versions before version 4.0, NetMHCpan versions before version 3.0, and MHCflurry, that do not take into account variation in peptide presentation according to peptide length. As shown in FIG. 13J, the proportion of presented peptides would be constant across different values of peptide length, indicating that these models would fail to capture variation in peptide presentation according to length. The plot "Example Model, with RNA" indicated measurements generated from the "Example Model, with RNA" presentation model. As shown in FIG. 13J, the measurements generated by the "Example Model, with RNA" model closely followed those shown in "Truth (Blind Test Data)" and correctly accounted for different degrees of peptide presentation for lengths 8, 9, 10, and 11.

[00723] Thus, the results showed that the example presentation models as presented herein generated improved predictions not only for 9mer peptides, but also for peptides of other lengths between 8-15, which account for up to 40% of the presented peptides in HLA class I alleles.

XII.K. Example of Parameters Determined for MHC Allele HLA-C*16:04

[00724] The following shows a set of parameters determined for a variation of the per-allele presentation model (equation (2)) for MHC allele HLA-C*16:04 denoted by h:

$$u_k = \text{expit}\left(\text{relu}\left(\boldsymbol{x_h^k} \cdot \boldsymbol{W_h^1} + \boldsymbol{b_h^1}\right) \cdot \boldsymbol{W_h^2} + b_h^2\right),$$

where relu(·) is the rectified linear unit (RELU) function, and $\boldsymbol{W_h^1}$, $\boldsymbol{b_h^1}$, $\boldsymbol{W_h^2}$, and b_h^2 are the set of parameters $\boldsymbol{\theta}$ determined for the model. The allele interacting variables $\boldsymbol{x_h^k}$ consist of peptide sequences. The dimensions of $\boldsymbol{W_h^1}$ are (231 x 256), the dimensions of $\boldsymbol{b_h^1}$ (1 x 256), the dimensions of $\boldsymbol{W_h^2}$ are (256 x 1), and $\boldsymbol{b_h^2}$ is a scalar. For demonstration purposes, values for

2026201462 26 Feb 2026

b_h^1, b_h^2, W_h^1, and W_h^2 are described in detail in PCT publication WO2017106638, herein incorporated by reference for all that it teaches.

XII.L. MHC II Example 1

[00725] Methods for determining MHC class II neoantigens are described in more detail in international application PCT/US2018/028438, herein incorporated by reference for all that it teaches.

[00726] FIG. 13K is a histogram of lengths of peptides eluted from class II MHC alleles on human tumor cells and tumor infiltrating lymphocytes (TIL) using mass spectrometry. Specifically, mass spectrometry peptidomics was performed on HLA-DRB1*12:01 homozygote alleles ("Dataset 1") and HLA-DRB1*12:01, HLA-DRB1*10:01 multi-allele samples ("Dataset 2"). Results show that lengths of peptides eluted from class II MHC alleles range from 6-30 amino acids. The frequency distribution shown in FIG. 13K is similar to that of lengths of peptides eluted from class II MHC alleles using state-of-the-art mass spectrometry techniques, as shown in FIG. 1C of reference 91.

[00727] FIG. 13L illustrates the dependency between mRNA quantification and presented peptides per residue for Dataset 1 and Dataset 2. Results show that there is a strong dependency between mRNA expression and peptide presentation for class II MHC alleles.

[00728] Specifically, the horizontal axis in FIG.13B indicates mRNA expression in terms of $\log_{10}$ transcripts per million (TPM) bins. The vertical axis in FIG. 13L indicates peptide presentation per residue as a multiple of that of the lowest bin corresponding to mRNA expression between $10^{-2} < \log_{10}\text{TPM} < 10^{-1}$. One solid line is a plot relating mRNA quantification and peptide presentation for Dataset 1, and another is for Dataset 2. As shown in FIG. 13L, there is a strong positive correlation between mRNA expression, and peptide presentation per residue in the corresponding gene. Specifically, peptides from genes in the range of $10^1 < \log_{10}\text{TPM} < 10^2$ of RNA expression are more than 5 times likely to be presented than the bottom bin.

[00729] The results indicate that the performance of the presentation model can be greatly improved by incorporating mRNA quantification measurements, as these measurements are strongly predictive of peptide presentation.

[00730] FIG. 13M compares performance results for example presentation models trained and tested using Dataset 1 and Dataset 2. For each set of model features of the example presentation models, FIG. 13M depicts a PPV value at 10% recall when the features in the set

2026201462 26 Feb 2026

of model features are classified as allele interacting features, and alternatively when the features in the set of model features are classified as allele non-interacting features variables. As seen in FIG. 13M, for each set of model features of the example presentation models, a PPV value at 10% recall that was identified when the features in the set of model features were classified as allele interacting features is shown on the left side, and a PPV value at 10% recall that was identified when the features in the set of model features were classified as allele non-interacting features is shown on the right side. Note that the feature of peptide sequence was always classified as an allele interacting feature for the purposes of FIG. 13M. Results showed that the presentation models achieved a PPV value at 10% recall varying from 14% up to 29%, which are significantly (approximately 500-fold) higher than PPV for a random prediction.

[00731] Peptide sequences of lengths 9-20 were considered for this experiment. The data was split into training, validation, and testing sets. Blocks of peptides of 50 residue blocks from both Dataset 1 and Dataset 2 were assigned to training and testing sets. Peptides that were duplicated anywhere in the proteome were removed, ensuring that no peptide sequence appeared both in the training and testing set. The prevalence of peptide presentation in the training and testing set was increased by 50 times by removing non-presented peptides. This is because Dataset 1 and Dataset 2 are from human tumor samples in which only a fraction of the cells are class II HLA alleles, resulting in peptide yields that were roughly 10 times lower than in pure samples of class II HLA alleles, which is still an underestimate due to imperfect mass spectrometry sensitivity. The training set contained 1,064 presented and 3,810,070 non-presented peptides. The test set contained 314 presented and 807,400 non-presented peptides.

[00732] Example model 1 was the sum-of-functions model in equation (22) using a network dependency function $g_h(\cdot)$, the expit function $f(\cdot)$, and the identity function $r(\cdot)$. The network dependency function $g_h(\cdot)$ was structured as a multi-layer perceptron (MLP) with 256 hidden nodes and rectified linear unit (ReLU) activations. In addition to the peptide sequence, the allele interacting variables $\boldsymbol{w}$ contained the one-hot encoded C-terminal and N-terminal flanking sequence, a categorical variable indicating index of source gene G=gene($\boldsymbol{p}^i$) of peptide $\boldsymbol{p}^i$, and a variable indicating mRNA quantification measurement. Example model 2 was identical to example model 1, except that the C-terminal and N-terminal flanking sequence was omitted from the allele interacting variables. Example model 3 was identical to example model 1, except that the index of source gene was omitted from the allele interacting variables. Example model 4 was identical to example model 1, except that the mRNA quantification measurement was omitted from the allele interacting variables.

2026201462 26 Feb 2026

[00733] Example model 5 was the sum-of-functions model in equation (20) with a network dependency function $g_h(\cdot)$, the expit function f(·),the identity function r(·), and the dependency function $g_w(\cdot)$ of equation (12). The dependency function $g_w(\cdot)$ also included a network model taking mRNA quantification measurement as input, structured as a MLP with 16 hidden nodes and ReLU activations, and a network model taking C-flanking sequence as input, structured as a MLP with 32 hidden nodes and ReLU activations. The network dependency function $g_h(\cdot)$ was structured as a multi-layer perceptron with 256 hidden nodes and rectified linear unit (ReLU) activations. Example model 6 was identical to example model 5, except that the network model for C-terminal and N-terminal flanking sequence was omitted. Example model 7 was identical to example model 5, except that the index of source gene was omitted from the allele noninteracting variables. Example model 8 was identical to example model 5, except that the network model for mRNA quantification measurement was omitted.

[00734] The prevalence of presented peptides in the test set was approximately 1/2400, and therefore, the PPV of a random prediction would also be approximately 1/2400 = 0.00042. As shown in FIG. 13M, the best-performing presentation model achieved a PPV value of approximately 29%, which is roughly 500 times better than the PPV value of a random prediction.

XII.M. MHC II Example 2

[00735] FIG. 13N is a histogram that depicts the quantity of peptides sequenced using mass spectrometry for each sample of a total of 39 samples comprising HLA class II molecules. Furthermore, for each sample of the plurality of samples, the histogram shown in FIG. 13N depicts the quantity of peptides sequenced using mass spectrometry at different q-value thresholds. Specifically, for each sample of the plurality of samples, FIG. 13N depicts the quantity of peptides sequenced using mass spectrometry with a q-value of less than 0.01, with a q-value of less than 0.05, and with a q-value of less than 0.2.

[00736] As noted above, each sample of the 39 samples of FIG. 13N comprised HLA class II molecules. More specifically, each sample of the 39 samples of FIG. 13N comprised HLA-DR molecules. The HLA-DR molecule is one type of HLA class II molecule. Even more specifically, each sample of the 39 samples of FIG. 13N comprised HLA-DRB1 molecules, HLA-DRB3 molecules, HLA-DRB4 molecules, and/or HLA-DRB5 molecules. The HLA-DRB1 molecule, the HLA-DRB3 molecule, the HLA-DRB4 molecule, and the HLA-DRB5 molecule are types of the HLA-DR molecule.

2026201462 26 Feb 2026

[00737] While this particular experiment was performed using samples comprising HLA-DR molecules, and particularly HLA-DRB1 molecules, HLA-DRB3 molecules, HLA-DRB4 molecules, and HLA-DRB5 molecules, in alternative embodiments, this experiment can be performed using samples comprising one or more of any type(s) of HLA class II molecules. For example, in alterative embodiments, identical experiments can be performed using samples comprising HLA-DP and/or HLA-DQ molecules. This ability to model any type(s) of MHC class II molecules using the same techniques, and still achieve reliable results, is well known by those skilled in the art. For instance, Jensen, Kamilla Kjaergaard, et al.[76] is one example of a recent scientific paper that uses identical methods for modeling binding affinity for HLA-DR molecules as well as for HLA-DQ and HLA-DP molecules. Therefore, one skilled in the art would understand that the experiments and models described herein can be used to separately or simultaneously model not only HLA-DR molecules, but any other MHC class II molecule, while still producing reliable results.

[00738] To sequence the peptides of each sample of the 39 total samples, mass spectrometry was performed for each sample. The resulting mass spectrum for the sample was then searched with Comet and scored with Percolator to sequence the peptides. Then, the quantity of peptides sequenced in the sample was identified for a plurality of different Percolator q-value thresholds. Specifically, for the sample, the quantity of peptides sequenced with a Percolator q-value of less than 0.01, with a Percolator q-value of less than 0.05, and with a Percolator q-value of less than 0.2 were determined.

[00739] For each sample of the 39 samples, the quantity of peptides sequenced at each of the different Percolator q-value thresholds is depicted in FIG. 13N. For example, as seen in FIG. 13N, for the first sample, approximately 4000 peptides with a q-value of less than 0.2 were sequenced using mass spectrometry, approximately 2800 peptides with a q-value of less than 0.05 were sequenced using mass spectrometry, and approximately 2300 peptides with a q-value of less than 0.01 were sequenced using mass spectrometry.

[00740] Overall, FIG. 13N demonstrates the ability to use mass spectrometry to sequence a large quantity of peptides from samples containing MHC class II molecules, at low q-values. In other words, the data depicted in FIG. 13N demonstrate the ability to reliably sequence peptides that may be presented by MHC class II molecules, using mass spectrometry.

[00741] FIG. 13O is a histogram that depicts the quantity of samples in which a particular MHC class II molecule allele was identified. More specifically, for the 39 total samples

2026201462 26 Feb 2026

comprising HLA class II molecules, FIG. 13O depicts the quantity of samples in which certain MHC class II molecule alleles were identified.

[00742] As discussed above with regard to FIG. 13N, each sample of the 39 samples of FIG. 13N comprised HLA-DRB1 molecules, HLA-DRB3 molecules, HLA-DRB4 molecules, and/or HLA-DRB5 molecules. Therefore, FIG. 13O depicts the quantity of samples in which certain alleles for HLA-DRB1, HLA-DRB3, HLA-DRB4, and HLA-DRB5 molecules were identified. To identify the HLA alleles present in a sample, HLA class II DR typing is performed for the sample. Then, to identify the quantity of samples in which a particular HLA allele was identified, the number of samples in which the HLA allele was identified using HLA class II DR typing is simply summed. For example, as depicted in FIG. 13O, 19 samples of the 39 total samples contained the HLA class II molecule allele HLA-DRB4*01:03. In other words, 19 samples of the 39 total samples contained the allele HLA-DRB4*01:03 for the HLA-DRB4 molecule. Overall, FIG. 13O depicts the ability to identify a wide range of HLA class II molecule alleles from the 39 samples comprising HLA class II molecules.

[00743] FIG. 13P is a histogram that depicts the proportion of peptides presented by the MHC class II molecules in the 39 total samples, for each peptide length of a range of peptide lengths. To determine the length of each peptide in each sample of the 39 total samples, each peptide was sequenced using mass spectrometry as discussed above with regard to FIG. 13N, and then the number of residues in the sequenced peptide was simply quantified.

[00744] As noted above, MHC class II molecules typically present peptides with lengths of between 9-20 amino acids. Accordingly, FIG. 13P depicts the proportion of peptides presented by the MHC class II molecules in the 39 samples for each peptide length between 9-20 amino acids, inclusive. For example, as shown in FIG. 13P, approximately 22% of the peptides presented by the MHC class II molecules in the 39 samples comprise a length of 14 amino acids.

[00745] Based on the data depicted in FIG. 13P, modal lengths for the peptides presented by the MHC class II molecules in the 39 samples were identified to be 14 and 15 amino acids in length. These modal lengths identified for the peptides presented by the MHC class II molecules in the 39 samples are consistent with previous reports of modal lengths for peptides presented by MHC class II molecules. Additionally, as also consistent with previous reports, the data of FIG. 13P indicates that more than 60% of the peptides presented by the MHC class II molecules from the 39 samples comprise lengths other than 14 and 15 amino acids. In other words, FIG. 13P indicates that while peptides presented by MHC class II molecules are most

2026201462 26 Feb 2026

frequently 14 or 15 amino acids in length, a large proportion of peptides presented by MHC class II molecules are *not* 14 or 15 amino acids in length. Accordingly, it is a poor assumption to assume that peptides of all lengths have equal probabilities of being presented by MHC class II molecules, or that only peptides that comprise a length of 14 or 15 amino acids are presented by MHC class II molecules. As discussed in detail below with regard to FIG. 13T, these faulty assumptions are currently used in many state-of-the-art models for predicting peptide presentation by MHC class II molecules, and therefore, the presentation likelihoods predicted by these models are often unreliable.

[00746] FIG. 13Q is a line graph that depicts the relationship between gene expression and prevalence of presentation of the gene expression product by a MHC class II molecule, for genes present in the 39 samples. More specifically, FIG. 13Q depicts the relationship between gene expression and the proportion of residues resulting from the gene expression that form the N-terminus of a peptide presented by a MHC class II molecule. To quantify gene expression in each sample of the 39 total samples, RNA sequencing is perfomed on the RNA included in each sample. In FIG. 13Q, gene expression is measured by RNA sequencing in units of transcripts per million (TPM). To identify prevalence of presentation of gene expression products for each sample of the 39 samples, identification of HLA class II DR peptidomic data was performed for each sample.

[00747] As depicted in FIG. 13Q, for the 39 samples, there is a strong correlation between gene expression level and presentation of residues of the expressed gene product by a MHC class II molecule. Specifically, as shown in FIG. 13Q, peptides resulting from expression of the least-expressed genes are more than 100-fold less likely to be presented by a MHC class II molecule, than peptides resulting from expression of the most-expressed genes. In simpler terms, the products of more highly expressed genes are more frequently presented by MHC class II molecules.

[00748] FIGS. 13H-J are line graphs that compare the performance of various presentation models at predicting the likelihood that peptides in a testing dataset of peptides will be presented by at least one of the MHC class II molecules present in the testing dataset. As shown in FIGS. 13H-J, the performance of a model at predicting the likelihood that a peptide will be presented by at least one of the MHC class II molecules present in the testing dataset is determined by identifying a ratio of a true positive rate to a false positive rate for each prediction made by the model. These ratios identified for a given model can be visualized as a ROC (receiver operator characteristic) curve, in a line graph with an x-axis quantifying false

2026201462 26 Feb 2026

positive rate and a y-axis quantifying true positive rate. An area under the curve (AUC) is used to quantify the performance of the model. Specifically, a model with a greater AUC has a higher performance (i.e., greater accuracy) relative to a model with a lesser AUC. In FIGS. 13H-J, the blacked dashed line with a slope of 1 (i.e., a ratio of true positive rate to false positive rate of 1) depicts the expected curve for randomly guessing likelihoods of peptide presentation. The AUC for the dashed line is 0.5. ROC curves and the AUC metric are discussed in detail with regard to the top portion of Section XII. above.

[00749] FIG. 13R is a line graph that compares the performance of five example presentation models at predicting the likelihood that peptides in a testing dataset of peptides will be presented by a MHC class II molecule, given different sets of allele interacting and allele non-interacting variables. In other words, FIG. 13R quantifies the relative importance of various allele interacting and allele non-interacting variables for predicting the likelihood that a peptide will be presented by a MHC class II molecule.

[00750] The model architecture of each example presentation model of the five example presentations models used to generate the ROC curves of the line graph of FIG. 13R, comprised an ensemble of five sum-of-sigmoids models. Each sum-of-sigmoids model in the ensemble was configured to model peptide presentation for up to four unique HLA-DR alleles per sample. Furthermore, each sum-of-sigmoids model in the ensemble was configured to make predictions of peptide presentation likelihood based on the following allele interacting and allele non-interacting variables: peptide sequence, flanking sequence, RNA expression in units of TPM, gene identifier, and sample identifier. The allele interacting component of each sum-of-sigmoids model in the ensemble was a one-hidden-layer MLP with ReLu activations as 256 hidden units.

[00751] Prior to using the example models to predict the likelihood that the peptides in a testing dataset of peptides will be presented by a MHC class II molecule, the example models were trained and validated. To train, validate, and finally test the example models, the data described above for the 39 samples was split into training, validation, and testing datasets.

[00752] To ensure that no peptides appeared in more than one of the training, validation, and testing datasets, the following procedure was performed. First all peptides from the 39 total samples that appeared in more than one location in the proteome were removed. Then, the peptides from the 39 total samples were partitioned into blocks of 10 adjacent peptides. Each block of the peptides from the 39 total samples was assigned uniquely to the training dataset,

2026201462 26 Feb 2026

the validation dataset, or the testing dataset. In this way, no peptide appeared in more than one dataset of the training, validation, and testing datasets.

[00753] Out of the 28,081,944 peptides in the 39 total samples, the training dataset comprised 21,077 peptides presented by MHC class II molecules from 38 of the 39 total samples. The 21,077 peptides included in the training dataset were between lengths of 9 and 20 amino acids, inclusive. The example models used to generate the ROC curves in FIG. 13R were trained on the training dataset using the ADAM optimizer and early stopping.

[00754] The validation dataset consisted of 2,346 peptides presented by MHC class II molecules from the same 38 samples used in the training dataset. The validation set was used only for early stopping.

[00755] The testing dataset comprised peptides presented by MHC class II molecules that were identified from a tumor sample using mass spectrometry. Specifically, the testing dataset comprised 203 peptides presented by MHC class II molecules—specifically HLA-DRB1*07:01, HLA-DRB1*15:01, HLA-DRB4*01:03, and HLA-DRB5*01:01 molecules—that were identified from the tumor sample. The peptides included in the testing dataset were held out of the training dataset described above.

[00756] As noted above, FIG. 13R quantifies the relative importance of various allele interacting variables and allele non-interacting variables for predicting the likelihood that a peptide will be presented by a MHC class II molecule. As also noted above, the example models used to generate the ROC curves of the line graph of FIG. 13R were configured to make predictions of peptide presentation likelihood based on the following allele interacting and allele non-interacting variables: peptide sequence, flanking sequence, RNA expression in units of TPM, gene identifier, and sample identifier. To quantify the relative importance of four of these five variables (peptide sequence, flanking sequence, RNA expression, and gene identifier) for predicting the likelihood that a peptide will be presented by a MHC class II molecule, each example model of the five the example models described above was tested using data from the testing dataset, with a different combination of the four variables. Specifically, for each peptide of the testing dataset, an example model 1 generated predictions of peptide presentation likelihood based on a peptide sequence, a flanking sequence, a gene identifier, and a sample identifier, but not on RNA expression. Similarly, for each peptide of the testing dataset, an example model 2 generated predictions of peptide presentation likelihood based on a peptide sequence, RNA expression, a gene identifier, and a sample identifier, but not on a flanking sequence. Similarly, for each peptide of the testing dataset, an example model

2026201462 26 Feb 2026

3 generated predictions of peptide presentation likelihood based on a flanking sequence, RNA expression, a gene identifier, and a sample identifier, but not on a peptide sequence. Similarly, for each peptide of the testing dataset, an example model 4 generated predictions of peptide presentation likelihood based on a flanking sequence, RNA expression, a peptide sequence, and a sample identifier, but not on a gene identifier. Finally, for each peptide of the testing dataset, an example model 5 generated predictions of peptide presentation likelihood based on all five variables of flanking sequence, RNA expression, peptide sequence, sample identifier, and gene identifier.

[00757] The performance of each of these five example models is depicted in the line graph of FIG. 13R. Specifically, each of the five example models is associated with a ROC curve that depicts a ratio of a true positive rate to a false positive rate for each prediction made by the model. For instance, FIG. 13R depicts a curve for the example model 1 that generated predictions of peptide presentation likelihood based on a peptide sequence, a flanking sequence, a gene identifier, and a sample identifier, but not on RNA expression. FIG. 13R depicts a curve for the example model 2 that generated predictions of peptide presentation likelihood based on a peptide sequence, RNA expression, a gene identifier, and a sample identifier, but not on a flanking sequence. FIG. 13R also depicts a curve for the example model 3 that generated predictions of peptide presentation likelihood based on a flanking sequence, RNA expression, a gene identifier, and a sample identifier, but not on a peptide sequence. FIG. 13R also depicts a curve for the example model 4 that generated predictions of peptide presentation likelihood based on a flanking sequence, RNA expression, a peptide sequence, and a sample identifier, but not on a gene identifier. And finally FIG. 13R depicts a curve for the example model 5 that generated predictions of peptide presentation likelihood based on all five variables of flanking sequence, RNA expression, peptide sequence, sample identifier, and gene identifier.

[00758] As noted above, the performance of a model at predicting the likelihood that a peptide will be presented by a MHC class II molecule is quantified by identifying an AUC for a ROC curve that depicts a ratio of a true positive rate to a false positive rate for each prediction made by the model. A model with a greater AUC has a higher performance (i.e., greater accuracy) relative to a model with a lesser AUC. As shown in FIG. 13R, the curve for the example model 5 that generated predictions of peptide presentation likelihood based on all five variables of flanking sequence, RNA expression, peptide sequence, sample identifier, and gene identifier, achieved the highest AUC of 0.98. Therefore the example model 5 that used all five

2026201462 26 Feb 2026

variables to generate predictions of peptide presentation achieved the best performance. The curve for the example model 2 that generated predictions of peptide presentation likelihood based on a peptide sequence, RNA expression, a gene identifier, and a sample identifier, but not on a flanking sequence, achieved the second highest AUC of 0.97. Therefore, the flanking sequence can be identified as the least important variable for predicting the likelihood that a peptide will be presented by a MHC class II molecule. The curve for the example model 4 generated predictions of peptide presentation likelihood based on a flanking sequence, RNA expression, a peptide sequence, and a sample identifier, but not on a gene identifier, achieved the third highest AUC of 0.96. Therefore, the gene identifier can be identified as the second least important variable for predicting the likelihood that a peptide will be presented by a MHC class II molecule. The curve for the example model 3 that generated predictions of peptide presentation likelihood based on a flanking sequence, RNA expression, a gene identifier, and a sample identifier, but not on a peptide sequence, achieved the lowest AUC of 0.88. Therefore, the peptide sequence can be identified as the most important variable for predicting the likelihood that a peptide will be presented by a MHC class II molecule. The curve for the example model 1 that generated predictions of peptide presentation likelihood based on a peptide sequence, a flanking sequence, a gene identifier, and a sample identifier, but not on RNA expression, achieved the second lowest AUC of 0.95. Therefore, RNA expression can be identified as the second most important variable for predicting the likelihood that a peptide will be presented by a MHC class II molecule.

[00759] FIG. 13S is a line graph that compares the performance of four different presentation models at predicting the likelihood that peptides in a testing dataset of peptides will be presented by a MHC class II molecule.

[00760] The first model tested in FIG. 13S is referred to herein as a "full non-interacting model." The full non-interacting model is one embodiment of the presentation models described above in which allele-noninteracting variables $\boldsymbol{w}^k$ and allele-interacting variables $\boldsymbol{x}_h^k$ are input into separate dependency functions such as, for example, a neural network, and then the outputs of these separate dependency functions are added. Specifically, the full non-interacting model is one embodiment of the presentation models described above in which allele-noninteracting variables $\boldsymbol{w}^k$ are input into a dependency function $\boldsymbol{g}_w$, allele-interacting variables $\boldsymbol{x}_h^k$ are input into separate dependency function $\boldsymbol{g}_h$, and the outputs of the dependency function $\boldsymbol{g}_w$ and the dependency function $\boldsymbol{g}_h$ are added together. Therefore, in some embodiments, the full non-interacting model determines the likelihood of peptide presentation

2026201462 26 Feb 2026

using equation 8 as shown above. Furthermore, embodiments of the full non-interacting model in which allele-noninteracting variables $\boldsymbol{w}^k$ are input into a dependency function $\boldsymbol{g}_w$, allele-interacting variables $\boldsymbol{x}_h^k$ are input into separate dependency function $\boldsymbol{g}_h$, and the outputs of the dependency function $\boldsymbol{g}_w$ and the dependency function $\boldsymbol{g}_h$ are added, are discussed in detail above with regard to the top portion of Section X.B.2., the bottom portion of Section X.B.3., the top portion of Section X.C.3., and the top portion of Section X.C.6..

[00761] The second model tested in FIG. 13S is referred to herein as a "full interacting model." The full interacting model is one embodiment of the presentation models described above in which allele-noninteracting variables $\boldsymbol{w}^k$ are concatenated directly to allele-interacting variables $\boldsymbol{x}_h^k$ before being input into a dependency function such as, for example, a neural network. Therefore, in some embodiments, the full interacting model determines the likelihood of peptide presentation using equation 9 as shown above. Furthermore, embodiments of the full interacting model in which allele-noninteracting variables $\boldsymbol{w}^k$ are concatenated with allele-interacting variables $\boldsymbol{x}_h^k$ before the variables are input into a dependency function are discussed in detail above with regard to the bottom portion of Section X.B.2., the bottom portion of Section X.C.2., and the bottom portion of Section X.C.5..

[00762] The third model tested in FIG. 13S is referred to herein as a "CNN model." The CNN model comprises a convolutional neural network, and is similar to the full non-interacting model described above. However, the layers of the convolutional neural network of the CNN model differ from the layers of the neural network of the full non-interacting model. Specifically, the input layer of the convolutional neural network of the CNN model accepts a 20-mer peptide string and subsequently embeds the 20-mer peptide string as a (n, 20, 21) tensor. The next layers of the convolutional neural network of the CNN model comprise a 1-D convolutional kernel layer of size 5 with a stride of 1, a global max pooling layer, a dropout layer with p=0.2, and finally a dense 34-node layer with a ReLu activation.

[00763] The fourth and final model tested in FIG. 13S is referred to herein as a "LSTM model." The LSTM model comprises a long short-term memory neural network. The input layer of the long short-term memory neural network of the LSTM model accepts a 20-mer peptide string and subsequently embeds the 20-mer peptide string as a (n, 20, 21) tensor. The next layers of the long short-term memory neural network of the LSTM model comprise a long short-term memory layer with 128 nodes, a dropout layer with p =0.2, and finally a dense 34-node layer with a ReLu activation.

2026201462 26 Feb 2026

[00764] Prior to using each of the four models of FIG. 13S to predict the likelihood that the peptides in the testing dataset of peptides will be presented by a MHC class II molecule, the models were trained using the 38-sample training dataset described above and validated using the validation dataset described above. Following this training and validation of the models, each of the four models was tested using the held-out 39th sample testing dataset described above. Specifically, for each of the four models, each peptide of the testing dataset was input into the model, and the model subsequently output a presentation likelihood for the peptide.

[00765] The performance of each of the four models is depicted in the line graph in FIG. 13S. Specifically, each of the four models is associated with a ROC curve that depicts a ratio of a true positive rate to a false positive rate for each prediction made by the model. For instance, FIG. 13S depicts a ROC curve for the CNN model, a ROC curve for the full interacting model, a ROC curve for the LSTM model, and a ROC curve for the full non-interacting model.

[00766] As noted above, the performance of a model at predicting the likelihood that a peptide will be presented by a MHC class II molecule is quantified by identifying an AUC for a ROC curve that depicts a ratio of a true positive rate to a false positive rate for each prediction made by the model. A model with a greater AUC has a higher performance (i.e., greater accuracy) relative to a model with a lesser AUC. As shown in FIG. 13S, the curve for the full interacting model achieved the highest AUC of 0.982. Therefore the full interacting model achieved the best performance. The curve for the full non-interacting model achieved the second highest AUC of 0.977. Therefore, the full non-interacting model achieved the second best performance. The curve for the CNN model achieved the lowest AUC of 0.947. Therefore the CNN model achieved the worst performance. The curve for the LSTM model achieved the second lowest AUC of 0.952. Therefore, the LSTM model achieved the second worst performance. However, note that all models tested in FIG. 13S have an AUC that is greater than 0.9. Accordingly, despite the architectural variance between them, all models tested in FIG. 13S are capable of achieving relatively accurate predictions of peptide presentation.

[00767] FIG. 13T is a line graph that compares the performance of two example best-in-class prior art models given two different criteria, and two example presentation models given two different sets of allele interacting and allele non-interacting variables, at predicting the likelihood that peptides in a testing dataset of peptides will be presented by a MHC class II molecule. Specifically, FIG. 13T is a line graph that compares the performance of an example best-in-class prior art model that utilizes minimum NetMHCII 2.3 predicted binding affinity as a criterion to generate predictions (example model 1), an example best-in-class prior art model

2026201462 26 Feb 2026

that utilizes minimum NetMHCII 2.3 predicted binding rank as a criterion to generate predictions (example model 2), an example presentation model that generates predictions of peptide presentation likelihood based on MHC class II molecule type and peptide sequence (example model 4), and an example presentation model that generates predictions of peptide presentation likelihood based on MHC class II molecule type, peptide sequence, RNA expression, gene identifier, and flanking sequence (example model 3).

[00768] The best-in-class prior art model used as example model 1 and example model 2 in FIG. 13T is the NetMHCII 2.3 model. The NetMHCII 2.3 model generates predictions of peptide presentation likelihood based on MHC class II molecule type and peptide sequence. The NetMHCII 2.3 model was tested using the NetMHCII 2.3 website (www.cbs.dtu.dk/services/NetMHCII/, PMID 29315598)[76].

[00769] As noted above, the NetMHCII 2.3 model was tested according to two different criteria. Specifically, example model 1 model generated predictions of peptide presentation likelihood according to minimum NetMHCII 2.3 predicted binding affinity, and example model 2 generated predictions of peptide presentation likelihood according to minimum NetMHCII 2.3 predicted binding rank.

[00770] The presentation model used as example model 3 and example model 4 is an embodiment of the presentation model disclosed herein that is trained using data obtained via mass spectrometry. As noted above, the presentation model generated predictions of peptide presentation likelihood based on two different sets of allele interacting and allele non-interacting variables. Specifically, example model 4 generated predictions of peptide presentation likelihood based on MHC class II molecule type and peptide sequence (the same variable used by the NetMHCII 2.3 model), and example model 3 generated predictions of peptide presentation likelihood based on MHC class II molecule type, peptide sequence, RNA expression, gene identifier, and flanking sequence.

[00771] Prior using the example models of FIG. 13T to predict the likelihood that the peptides in the testing dataset of peptides will be presented by a MHC class II molecule, the models were trained and validated. The NetMHCII 2.3 model (example model 1 and example model 2) was trained and validated using its own training and validation datasets based on HLA-peptide binding affinity assays deposited in the immune epitope database (IEDB, www.iedb.org).. The training dataset used to train the NetMHCII 2.3 model is known to comprise almost exclusively 15-mer peptides. On the other hand, example models 3 and 4 were

2026201462 26 Feb 2026

trained using the training dataset described above with regard to FIG. 13R and validated and using the validation dataset described above with regard to FIG. 13R.

[00772] Following the training and validation of the models, each of the models was tested using a testing dataset. As noted above, the NetMHCII 2.3 model is trained on a dataset comprising almost exclusively 15-mer peptides, meaning that NetMHCII 3.2 does not have the ability to give different priority to peptides of different weights, thereby reducing the predictive performance for NetMHCII 3.2 on HLA class II presentation mass spectrometry data containing peptides of all lengths. Therefore, to provide a fair comparison between the models not affected by variable peptide length, the testing dataset included exclusively 15-mer peptides. Specifically, the testing dataset comprised 933 15-mer peptides. 40 of the 933 peptides in the testing dataset were presented by MHC class II molecules—specifically by HLA-DRB1*07:01, HLA-DRB1*15:01, HLA-DRB4*01:03, and HLA-DRB5*01:01 molecules. The peptides included in the testing dataset were held out of the training datasets described above.

[00773] To test the example models using the testing dataset, for each of the example models, for each peptide of the 933 peptides in the testing dataset, the model generated a prediction of presentation likelihood for the peptide. Specifically, for each peptide in the testing dataset, the example 1 model generated a presentation score for the peptide by the MHC class II molecules using MHC class II molecule types and peptide sequence, by ranking the peptide by the minimum NetMHCII 2.3 predicted binding affinity across the four HLA class II DR alleles in the testing dataset. Similarly, for each peptide in the testing dataset, the example 2 model generated a presentation score for the peptide by the MHC class II molecules using MHC class II molecule types and peptide sequence, by ranking the peptide by the minimum NetMHCII 2.3 predicted binding rank (i.e., quantile normalized binding affinity) across the four HLA class II DR alleles in the testing dataset. For each peptide in the testing dataset, the example 4 model generated a presentation likelihood for the peptide by the MHC class II molecules based on MHC class II molecule type and peptide sequence. Similarly, for each peptide in the testing dataset, the example model 3 generated a presentation likelihood for the peptide by the MHC class II molecules based on MHC class II molecule types, peptide sequence, RNA expression, gene identifier, and flanking sequence.

[00774] The performance of each of the four example models is depicted in the line graph in FIG. 13T. Specifically, each of the four example models is associated with a ROC curve that depicts a ratio of a true positive rate to a false positive rate for each prediction made by the

2026201462 26 Feb 2026

model. For instance, FIG. 13T depicts a ROC curve for the example 1 model that utilized minimum NetMHCII 2.3 predicted binding affinity to generate predictions, a ROC curve for the example 2 model that utilized minimum NetMHCII 2.3 predicted binding rank to generate predictions, a ROC curve for the example 4 model that generated peptide presentation likelihoods based on MHC class II molecule type and peptide sequence, and a ROC curve for the example 3 model that generated peptide presentation likelihoods based on MHC class II molecule type, peptide sequence, RNA expression, gene identifier, and flanking sequence.

[00775] As noted above, the performance of a model at predicting the likelihood that a peptide will be presented by a MHC class II molecule is quantified by identifying an AUC for a ROC curve that depicts a ratio of a true positive rate to a false positive rate for each prediction made by the model. A model with a greater AUC has a higher performance (i.e., greater accuracy) relative to a model with a lesser AUC. As shown in FIG. 13T, the curve for the example 3 model that generated peptide presentation likelihoods based on MHC class II molecule type, peptide sequence, RNA expression, gene identifier, and flanking sequence, achieved the highest AUC of 0.95. Therefore the example 3 model that generated peptide presentation likelihoods based on MHC class II molecule type, peptide sequence, RNA expression, gene identifier, and flanking sequence achieved the best performance. The curve for the example 4 model that generated peptide presentation likelihoods based on MHC class II molecule type and peptide sequence achieved the second highest AUC of 0.91. Therefore, the example 4 model that generated peptide presentation likelihoods based on MHC class II molecule type and peptide sequence achieved the second best performance. The curve for the example 1 model that utilized minimum NetMHCII 2.3 predicted binding affinity to generate predictions achieved the lowest AUC of 0.75. Therefore the example 1 model that utilized minimum NetMHCII 2.3 predicted binding affinity to generate predictions achieved the worst performance. The curve for the example 2 model that utilized minimum NetMHCII 2.3 predicted binding rank to generate predictions achieved the second lowest AUC of 0.76. Therefore, the example 2 model that utilized minimum NetMHCII 2.3 predicted binding rank to generate predictions achieved the second worst performance.

[00776] As shown in FIG. 13T, the discrepancy in performance between the example models 1 and 2 and the example models 3 and 4 is large. Specifically, the performance of the NetMHCII 2.3 model (that utilizes either criterion of minimum NetMHCII 2.3 predicted binding affinity or minimum NetMHCII 2.3 predicted binding rank) is almost 25% lower than the performance of the presentation model disclosed herein (that generates peptide presentation

2026201462 26 Feb 2026

likelihoods based on either MHC class II molecule type and peptide sequence, or on MHC class II molecule type, peptide sequence, RNA expression, gene identifier, and flanking sequence). Therefore, FIG. 13T demonstrates that the presentation models disclosed herein are capable of achieving significantly more accurate presentation predictions than the current best-in-class prior art model, the NetMHCII 2.3 model.

[00777] Even further, as discussed above, the NetMHCII 2.3 model is trained on a training dataset that comprises almost exclusively 15-mer peptides. As a result, the NetMHCII 2.3 model is not trained to learn which peptides lengths are more likely to be presented by MHC class II molecules. Therefore, the NetMHCII 2.3 model does not weight its predictions of likelihood of peptide presentation by MHC class II molecules according to the length of the peptide. In other words, the NetMHCII 2.3 model does not modify its predictions of likelihood of peptide presentation by MHC class II molecules for peptides that have lengths outside of the modal peptide length of 15 amino acids. As a result, the NetMHCII 2.3 model overpredicts the likelihood of presentation of peptides with lengths greater or less than 15 amino acids.

[00778] On the other hand, the presentation models disclosed herein are trained using peptide data obtained via mass spectrometry, and therefore can be trained on training dataset that comprise peptides of all different lengths. As a result, the presentation models disclosed herein are able to learn which peptides lengths are more likely to be presented by MHC class II molecules. Therefore, the presentation models disclosed herein can weight predictions of likelihood of peptide presentation by MHC class II molecules according to the length of the peptide. In other words, the presentation models disclosed herein are able to modify their predictions of likelihood of peptide presentation by MHC class II molecules for peptides that have lengths outside of the modal peptide length of 15 amino acids. As a result, the presentation models disclosed herein are capable of achieving significantly more accurate presentation predictions for peptides of lengths greater than or less than 15 amino acids, than the current best-in-class prior art model, the NetMHCII 2.3 model. This is one advantage of using the presentation models disclosed herein to predict likelihood of peptide presentation by MHC class II molecules.

2026201462 26 Feb 2026

XII.N. Example of Parameters Determined for MHC II Alleles

[00779] The following shows a set of parameters determined for a variation of the multi-allele presentation model (equation (16)) generating implicit per-allele presentation likelihoods for class II MHC alleles HLA-DRB1*12:01 and HLA-DRB1*10:01:

$$\boldsymbol{u} = \text{expit}(\text{relu}(\mathbf{X} \cdot \mathbf{W^1} + \mathbf{b^1}) \cdot \mathbf{W^2} + \mathbf{b^2}),$$

where relu(·) is the rectified linear unit (RELU) function, $\mathbf{W^1}$, $\mathbf{b^1}$, $\mathbf{W^2}$, and $\mathbf{b^2}$ are the set of parameters $\boldsymbol{\theta}$ determined for the model. The allele-interacting variables $\mathbf{X}$ are contained in a 1 x 399) matrix consisting of 1 row of one-hot encoded and middle-padded peptide sequences per input peptide. The dimensions of $\mathbf{W^1}$ are (399 x 256), the dimensions of $\mathbf{b^1}$ (1 x 256), the dimensions of $\mathbf{W^2}$ are (256 x 2), and $\mathbf{b^2}$ are (1 x 2). The first column of the output indicates the implicit per-allele probability of presentation for the peptide sequence by the allele HLA-DRB1*12:01, and the second column of the output indicates the implicit per-allele for the peptide sequence by the allele HLA-DRB1*10:01. For demonstration purposes, values for $\mathbf{W^1}$, $\mathbf{b^1}$, $\mathbf{W^2}$, and $\mathbf{b^2}$ are described in detail in international application PCT/US2018/028438, herein incorporated by reference for all that it teaches.

XIII. Example Computer

[00780] FIG. 14 illustrates an example computer 1400 for implementing the entities shown in FIGS. 1 and 3. The computer 1400 includes at least one processor 1402 coupled to a chipset 1404. The chipset 1404 includes a memory controller hub 1420 and an input/output (I/O) controller hub 1422. A memory 1406 and a graphics adapter 1412 are coupled to the memory controller hub 1420, and a display 1418 is coupled to the graphics adapter 1412. A storage device 1408, an input device 1414, and network adapter 1416 are coupled to the I/O controller hub 1422. Other embodiments of the computer 1400 have different architectures.

[00781] The storage device 1408 is a non-transitory computer-readable storage medium such as a hard drive, compact disk read-only memory (CD-ROM), DVD, or a solid-state memory device. The memory 1406 holds instructions and data used by the processor 1402. The input interface 1414 is a touch-screen interface, a mouse, track ball, or other type of pointing device, a keyboard, or some combination thereof, and is used to input data into the computer 1400. In some embodiments, the computer 1400 may be configured to receive input (e.g., commands) from the input interface 1414 via gestures from the user. The graphics adapter 1412 displays images and other information on the display 1418. The network adapter 1416 couples the computer 1400 to one or more computer networks.

2026201462 26 Feb 2026

[00782] The computer 1400 is adapted to execute computer program modules for providing functionality described herein. As used herein, the term "module" refers to computer program logic used to provide the specified functionality. Thus, a module can be implemented in hardware, firmware, and/or software. In one embodiment, program modules are stored on the storage device 1408, loaded into the memory 1406, and executed by the processor 1402.

[00783] The types of computers 1400 used by the entities of FIG. 1 can vary depending upon the embodiment and the processing power required by the entity. For example, the presentation identification system 160 can run in a single computer 1400 or multiple computers 1400 communicating with each other through a network such as in a server farm. The computers 1400 can lack some of the components described above, such as graphics adapters 1412, and displays 1418.

XIV. Neoantigen Delivery Vector Example

[00784] Below are examples of specific embodiments for carrying out the present invention. The examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way. Efforts have been made to ensure accuracy with respect to numbers used (e.g., amounts, temperatures, etc.), but some experimental error and deviation should, of course, be allowed for.

[00785] The practice of the present invention will employ, unless otherwise indicated, conventional methods of protein chemistry, biochemistry, recombinant DNA techniques and pharmacology, within the skill of the art. Such techniques are explained fully in the literature. See, e.g., T.E. Creighton, *Proteins: Structures and Molecular Properties* (W.H. Freeman and Company, 1993); A.L. Lehninger, *Biochemistry* (Worth Publishers, Inc., current addition); Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); *Methods In Enzymology* (S. Colowick and N. Kaplan eds., Academic Press, Inc.); *Remington's Pharmaceutical Sciences*, 18th Edition (Easton, Pennsylvania: Mack Publishing Company, 1990); Carey and Sundberg *Advanced Organic Chemistry 3rd Ed.* (Plenum Press) Vols A and B(1992).

XIV.A. Neoantigen Cassette Design

[00786] Through vaccination, multiple class I MHC restricted tumor-specific neoantigens (TSNAs) that stimulate the corresponding cellular immune response(s) can be delivered. In one example, a vaccine cassette was engineered to encode multiple epitopes as a single gene product where the epitopes were either embedded within their natural, surrounding peptide

2026201462 26 Feb 2026

sequence or spaced by non-natural linker sequences. Several design parameters were identified that could potentially impact antigen processing and presentation and therefore the magnitude and breadth of the TSNA specific CD8 T cell responses. In the present example, several model cassettes were designed and constructed to evaluate: (1) whether robust T cell responses could be generated to multiple epitopes incorporated in a single expression cassette; (2) what makes an optimal linker placed between the TSNAs within the expression cassette- that leads to optimal processing and presentation of all epitopes; (3) if the relative position of the epitopes within the cassette impact T cell responses; (4) whether the number of epitopes within a cassette influences the magnitude or quality of the T cell responses to individual epitopes; (5) if the addition of cellular targeting sequences improves T cell responses.

[00787] Two readouts were developed to evaluate antigen presentation and T cell responses specific for marker epitopes within the model cassettes: (1) an *in vitro* cell-based screen which allowed assessment of antigen presentation as gauged by the activation of specially engineered reporter T cells (Aarnoudse et al., 2002; Nagai et al., 2012); and (2) an *in vivo* assay that used HLA-A2 transgenic mice (Vitiello et al., 1991) to assess post-vaccination immunogenicity of cassette-derived epitopes of human origin by their corresponding epitope-specific T cell responses (Cornet et al., 2006; Depla et al., 2008; Ishioka et al., 1999).

2026201462 26 Feb 2026

XIV.B. Neoantigen Cassette Design Evaluation

XIV.B.1. Methods and Materials

TCR and cassette design and cloning

[00788] The selected TCRs recognize peptides NLVPMVATV (PDB# 5D2N), CLGGLLTMV (PDB#3REV), GILGFVFTL (PDB#1OGA) LLFGYPVYV (PDB#1AO7) when presented by A*0201. Transfer vectors were constructed that contain 2A peptide-linked TCR subunits (beta followed by alpha), the EMCV IRES, and 2A-linked CD8 subunits (beta followed by alpha and by the puromycin resistance gene). Open reading frame sequences were codon-optimized and synthesized by GeneArt.

Cell line generation for in vitro epitope processing and presentation studies

[00789] Peptides were purchased from ProImmune or Genscript diluted to 10mg/mL with 10mM tris(2-carboxyethyl)phosphine (TCEP) in water/DMSO (2:8, v/v). Cell culture medium and supplements, unless otherwise noted, were from Gibco. Heat inactivated fetal bovine serum (FBShi) was from Seradigm. QUANTI-Luc Substrate, Zeocin, and Puromycin were from InvivoGen. Jurkat-Lucia NFAT Cells (InvivoGen) were maintained in RPMI 1640 supplemented with 10% FBShi, Sodium Pyruvate, and 100µg/mL Zeocin. Once transduced, these cells additionally received 0.3 µg/mL Puromycin. T2 cells (ATCC CRL-1992) were cultured in Iscove's Medium (IMDM) plus 20% FBShi. U-87 MG (ATCC HTB-14) cells were maintained in MEM Eagles Medium supplemented with 10% FBShi.

[00790] Jurkat-Lucia NFAT cells contain an NFAT-inducible Lucia reporter construct. The Lucia gene, when activated by the engagement of the T cell receptor (TCR), causes secretion of a coelenterazine-utilizing luciferase into the culture medium. This luciferase can be measured using the QUANTI-Luc luciferase detection reagent. Jurkat-Lucia cells were transduced with lentivirus to express antigen-specific TCRs. The HIV-derived lentivirus transfer vector was obtained from GeneCopoeia, and lentivirus support plasmids expressing VSV-G (pCMV-VsvG), Rev (pRSV-Rev) and Gag-pol (pCgpV) were obtained from Cell Design Labs.

[00791] Lentivirus was prepared by transfection of 50-80% confluent T75 flasks of HEK293 cells with Lipofectamine 2000 (Thermo Fisher), using 40 µl of lipofectamine and 20 µg of the DNA mixture (4:2:1:1 by weight of the transfer plasmid:pCgpV:pRSV-Rev:pCMV-VsvG). 8-10 mL of the virus-containing media were concentrated using the Lenti-X system (Clontech), and the virus resuspended in 100-200 µl of fresh medium. This volume was used to overlay an equal volume of Jurkat-Lucia cells (5x10E4-1x10E6 cells were used in different experiments).

2026201462 26 Feb 2026

Following culture in 0.3 µg/ml puromycin-containing medium, cells were sorted to obtain clonality. These Jurkat-Lucia TCR clones were tested for activity and selectivity using peptide loaded T2 cells.

In vitro epitope processing and presentation assay

[00792] T2 cells are routinely used to examine antigen recognition by TCRs. T2 cells lack a peptide transporter for antigen processing (TAP deficient) and cannot load endogenous peptides in the endoplasmic reticulum for presentation on the MHC. However, the T2 cells can easily be loaded with exogenous peptides. The five marker peptides (NLVPMVATV, CLGGLLTMV, GLCTLVAML, LLFGYPVYV, GILGFVFTL) and two irrelevant peptides (WLSLLVPFV, FLLTRICT) were loaded onto T2 cells. Briefly, T2 cells were counted and diluted to 1x106 cells/mL with IMDM plus 1% FBShi. Peptides were added to result in 10 µg peptide/1x106 cells. Cells were then incubated at 37oC for 90 minutes. Cells were washed twice with IMDM plus 20% FBShi, diluted to 5x10E5 cells/mL and 100 µL plated into a 96-well Costar tissue culture plate. Jurkat-Lucia TCR clones were counted and diluted to 5x10E5 cells/mL in RPMI 1640 plus 10% FBShi and 100 µL added to the T2 cells. Plates were incubated overnight at 37ºC, 5% CO2. Plates were then centrifuged at 400g for 3 minutes and 20 µL supernatant removed to a white flat bottom Greiner plate. QUANTI-Luc substrate was prepared according to instructions and 50 µL/well added. Luciferase expression was read on a Molecular Devices SpectraMax iE3x.

[00793] To test marker epitope presentation by the adenoviral cassettes, U-87 MG cells were used as surrogate antigen presenting cells (APCs) and were transduced with the adenoviral vectors. U-87 MG cells were harvested and plated in culture media as 5x10E5 cells/100 µl in a 96-well Costar tissue culture plate. Plates were incubated for approximately 2 hours at 37ºC. Adenoviral cassettes were diluted with MEM plus 10% FBShi to an MOI of 100, 50, 10, 5, 1 and 0 and added to the U-87 MG cells as 5µl/well. Plates were again incubated for approximately 2 hours at 37ºC. Jurkat-Lucia TCR clones were counted and diluted to 5x10E5 cells/mL in RPMI plus 10% FBShi and added to the U-87 MG cells as 100 µL/well. Plates were then incubated for approximately 24 hours at 37ºC, 5% CO2. Plates were centrifuged at 400g for 3 minutes and 20 µL supernatant removed to a white flat bottom Greiner plate. QUANTI-Luc substrate was prepared according to instructions and 50 µL/well added. Luciferase expression was read on a Molecular Devices SpectraMax iE3x.

Mouse strains for immunogenicity studies

2026201462 26 Feb 2026

[00794] Transgenic HLA-A2.1 (HLA-A2 Tg) mice were obtained from Taconic Labs, Inc. These mice carry a transgene consisting of a chimeric class I molecule comprised of the human HLA-A2.1 leader, α1, and α2 domains and the murine H2-Kb α3, transmembrane, and cytoplasmic domains (Vitiello et al., 1991). Mice used for these studies were the first generation offspring (F1) of wild type BALB/cAnNTac females and homozygous HLA-A2.1 Tg males on the C57Bl/6 background.

Adenovirus vector (Ad5v) immunizations

[00795] HLA-A2 Tg mice were immunized with $1x10^{10}$ to $1x10^{6}$ viral particles of adenoviral vectors via bilateral intramuscular injection into the tibialis anterior. Immune responses were measured at 12 days post-immunization.

Lymphocyte isolation

[00796] Lymphocytes were isolated from freshly harvested spleens and lymph nodes of immunized mice. Tissues were dissociated in RPMI containing 10% fetal bovine serum with penicillin and streptomycin (complete RPMI) using the GentleMACS tissue dissociator according to the manufacturer's instructions.

Ex vivo enzyme-linked immunospot (ELISPOT) analysis

[00797] ELISPOT analysis was performed according to ELISPOT harmonization guidelines (Janetzki et al., 2015) with the mouse IFNg ELISpotPLUS kit (MABTECH). $1x10^{5}$ splenocytes were incubated with 10uM of the indicated peptides for 16 hours in 96-well IFNg antibody coated plates. Spots were developed using alkaline phosphatase. The reaction was timed for 10 minutes and was quenched by running the plate under tap water. Spots were counted using an AID vSpot Reader Spectrum. For ELISPOT analysis, wells with saturation >50% were recorded as "too numerous to count". Samples with deviation of replicate wells > 10% were excluded from analysis. Spot counts were then corrected for well confluency using the formula: spot count + 2 x (spot count x %confluence /[100% - %confluence]). Negative background was corrected by subtraction of spot counts in the negative peptide stimulation wells from the antigen stimulated wells. Finally, wells labeled too numerous to count were set to the highest observed corrected value, rounded up to the nearest hundred.

Ex vivo intracellular cytokine staining (ICS) and flow cytometry analysis

[00798] Freshly isolated lymphocytes at a density of $2\text{-}5x10^{6}$ cells/mL were incubated with 10uM of the indicated peptides for 2 hours. After two hours, brefeldin A was added to a concentration of 5ug/ml and cells were incubated with stimulant for an additional 4 hours. Following stimulation, viable cells were labeled with fixable viability dye eFluor780 according to manufacturer's protocol and stained with anti-CD8 APC (clone 53-6.7, BioLegend) at 1:400

2026201462 26 Feb 2026

dilution. Anti-IFNg PE (clone XMG1.2, BioLegend) was used at 1:100 for intracellular staining. Samples were collected on an Attune NxT Flow Cytometer (Thermo Scientific). Flow cytometry data was plotted and analyzed using FlowJo. To assess degree of antigen-specific response, both the percent IFNg+ of CD8+ cells and the total IFNg+ cell number/1x10^6 live cells were calculated in response to each peptide stimulant.

XIV.B.2. *In Vitro* Evaluation of Neoantigen Cassette Designs

[00799] As an example of neoantigen cassette design evaluation, an in vitro cell-based assay was developed to assess whether selected human epitopes within model vaccine cassettes were being expressed, processed, and presented by antigen-presenting cells (Fig. 15). Upon recognition, Jurkat-Lucia reporter T cells that were engineered to express one of five TCRs specific for well-characterized peptide-HLA combinations become activated and translocate the nuclear factor of activated T cells (NFAT) into the nucleus which leads to transcriptional activation of a luciferase reporter gene. Antigenic stimulation of the individual reporter CD8 T cell lines was quantified by bioluminescence.

[00800] Individual Jurkat-Lucia reporter lines were modified by lentiviral transduction with an expression construct that includes an antigen-specific TCR beta and TCR alpha chain separated by a P2A ribosomal skip sequence to ensure equimolar amounts of translated product (Banu et al., 2014). The addition of a second CD8 beta-P2A-CD8 alpha element to the lentiviral construct provided expression of the CD8 co-receptor, which the parent reporter cell line lacks, as CD8 on the cell surface is crucial for the binding affinity to target pMHC molecules and enhances signaling through engagement of its cytoplasmic tail (Lyons et al., 2006; Yachi et al., 2006).

[00801] After lentiviral transduction, the Jurkat-Lucia reporters were expanded under puromycin selection, subjected to single cell fluorescence assisted cell sorting (FACS), and the monoclonal populations tested for luciferase expression. This yielded stably transduced reporter cell lines for specific peptide antigens 1, 2, 4, and 5 with functional cell responses. (Table 2).

2026201462 26 Feb 2026

Table 2: Development of an *in vitro* T cell activation assay. Peptide-specific T cell recognition as measured by induction of luciferase indicates effective processing and presentation of the vaccine cassette antigens.

	Short Cassette Design
Epitope	**AAY**
1	24.5 ± 0.5
2	11.3 ± 0.4
3*	n/a
4	26.1 ± 3.1
5	46.3 ± 1.9

* Reporter T cell for epitope 3 not yet generated

[00802] In another example, a series of short cassettes, all marker epitopes were incorporated in the same position (Fig. 16A) and only the linkers separating the HLA-A*0201 restricted epitopes (Fig. 16B) were varied. Reporter T cells were individually mixed with U-87 antigen-presenting cells (APCs) that were infected with adenoviral constructs expressing these short cassettes, and luciferase expression was measured relative to uninfected controls. All four antigens in the model cassettes were recognized by matching reporter T cells, demonstrating efficient processing and presentation of multiple antigens. The magnitude of T cell responses follow largely similar trends for the natural and AAY-linkers. The antigens released from the RR-linker based cassette show lower luciferase inductions (Table 3). The DPP-linker, designed to disrupt antigen processing, produced a vaccine cassette that led to low epitope presentation (Table 3).

2026201462 26 Feb 2026

Table 3: Evaluation of linker sequences in short cassettes. Luciferase induction in the *in vitro* T cell activation assay indicated that, apart from the DPP-based cassette, all linkers facilitated efficient release of the cassette antigens. T cell epitope only (no linker) = 9AA, natural linker one side = 17AA, natural linker both sides = 25AA, non-natural linkers = AAY, RR, DPP

	Short Cassette Designs					
Epitope	**9AA**	**17AA**	**25AA**	**AAY**	**RR**	**DPP**
1	33.6 ± 0.9	42.8 ± 2.1	42.3 ± 2.3	24.5 ± 0.5	21.7 ± 0.9	0.9 ± 0.1
2	12.0 ± 0.9	10.3 ± 0.6	14.6 ± 04	11.3 ± 0.4	8.5 ± 0.3	1.1 ± 0.2
3*	n/a	n/a	n/a	n/a	n/a	n/a
4	26.6 ± 2.5	16.1 ± 0.6	16.6 ± 0.8	26.1 ± 3.1	12.5 ± 0.8	1.3 ± 0.2
5	29.7 ± 0.6	21.2 ± 0.7	24.3 ± 1.4	46.3 ± 1.9	19.7 ± 0.4	1.3 ± 0.1

* Reporter T cell for epitope 3 not yet generated

[00803] In another example, an additional series of short cassettes were constructed that, besides human and mouse epitopes, contained targeting sequences such as ubiquitin (Ub), MHC and Ig-kappa signal peptides (SP), and/or MHC transmembrane (TM) motifs positioned on either the N- or C-terminus of the cassette. (Fig. 17). When delivered to U-87 APCs by adenoviral vector, the reporter T cells again demonstrated efficient processing and presentation of multiple cassette-derived antigens. However, the magnitude of T cell responses were not substantially impacted by the various targeting features (Table 4).

Table 4: Evaluation of cellular targeting sequences added to model vaccine cassettes. Employing the *in vitro* T cell activation assay demonstrated that the four HLA-A*0201 restricted marker epitopes are liberated efficiently from the model cassettes and targeting sequences did not substantially improve T cell recognition and activation.

	Short Cassette Designs									
Epitope	**A**	**B**	**C**	**D**	**E**	**F**	**G**	**H**	**I**	**J**
1	32.5 ± 1.5	31.8 ± 0.8	29.1 ± 1.2	29.1 ± 1.1	28.4 ± 0.7	20.4 ± 0.5	35.0 ± 1.3	30.3 ± 2.0	22.5 ± 0.9	38.1 ± 1.6
2	6.1 ± 0.2	6.3 ± 0.2	7.6 ± 0.4	7.0 ± 0.5	5.9 ± 0.2	3.7 ± 0.2	7.6 ± 0.4	5.4 ± 0.3	6.2 ± 0.4	6.4 ± 0.3
3*	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
4	12.3 ± 1.1	14.1 ± 0.7	12.2 ± 0.8	13.7 ± 1.0	11.7 ± 0.8	10.6 ± 0.4	11.0 ± 0.6	7.6 ± 0.6	16.1 ± 0.5	8.7 ± 0.5
5	44.4 ± 2.8	53.6 ± 1.6	49.9 ± 3.3	50.5 ± 2.8	41.7 ± 2.8	36.1 ± 1.1	46.5 ± 2.1	31.4 ± 0.6	75.4 ± 1.6	35.7 ± 2.2

* Reporter T cell for epitope 3 not yet generated

XIV.B.3. *In Vivo* Evaluation of Neoantigen Cassette Designs

2026201462 26 Feb 2026

[00804] As another example of neoantigen cassette design evaluation, vaccine cassettes were designed to contain 5 well-characterized human class I MHC epitopes known to stimulate CD8 T cells in an HLA-A*02:01 restricted fashion (Fig. 16A, 17, 19A). For the evaluation of their in vivo immunogenicity, vaccine cassettes containing these marker epitopes were incorporated in adenoviral vectors and used to infect HLA-A2 transgenic mice (Fig. 18). This mouse model carries a transgene consisting partly of human HLA-A*0201 and mouse H2-Kb thus encoding a chimeric class I MHC molecule consisting of the human HLA-A2.1 leader, α1 and α2 domains ligated to the murine α3, transmembrane and cytoplasmic H2-Kb domain (Vitiello et al., 1991). The chimeric molecule allows HLA-A*02:01-restricted antigen presentation whilst maintaining the species-matched interaction of the CD8 co-receptor with the α3 domain on the MHC.

[00805] For the short cassettes, all marker epitopes generated a T cell response, as determined by IFN-gamma ELISPOT, that was approximately 10-50x stronger of what has been commonly reported (Cornet et al., 2006; Depla et al., 2008; Ishioka et al., 1999). Of all the linkers evaluated, the concatamer of 25mer sequences, each containing a minimal epitope flanked by their natural amino acids sequences, generated the largest and broadest T cell response (Table 5). Intracellular cytokine staining (ICS) and flow cytometry analysis revealed that the antigen-specific T cell responses are derived from CD8 T cells.

Table 5: In vivo evaluation of linker sequences in short cassettes. ELISPOT data indicated that HLA-A2 transgenic mice, 17 days post-infection with 1e11 adenovirus viral particles, generated a T cell response to all class I MHC restricted epitopes in the cassette.

	Short Cassette Designs					
Epitope	**9AA**	**17AA**	**25AA**	**AAY**	**RR**	**DPP**
1	2020+/-583	2505+/-1281	6844+/-956	1489+/-762	1675+/-690	1781+/-774
2	4472+/-755	3792+/-1319	7629+/-996	3851+/-1748	4726+/-1715	5868+/-1427
3	5830+/-315	3629+/-862	7253+/-491	4813+/-1761	6779+/-1033	7328+/-1700
4	5536+/-375	2446+/-955	2961+/-1487	4230+/-1759	6518+/-909	7222+/-1824
5	8800+/-0	7943+/-821	8423+/-442	8312+/-696	8800+/-0	1836+/-328

[00806] In another example, a series of long vaccine cassettes was constructed and incorporated in adenoviral vectors that, next to the original 5 marker epitopes, contained an additional 16 HLA-A*02:01, A*03:01 and B*44:05 epitopes with known CD8 T cell reactivity (Fig. 19A, B). The size of these long cassettes closely mimicked the final clinical cassette design, and only the position of the epitopes relative to each other was varied. The CD8 T cell responses were comparable in magnitude and breadth for both long and short vaccine cassettes,

2026201462 26 Feb 2026

demonstrating that (a) the addition of more epitopes did not substantially impact the magnitude of immune response to the original set of epitopes, and (b) the position of an epitope in a cassette did not substantially influence the ensuing T cell response to it (Table 6).

Table 6: In vivo evaluation of the impact of epitope position in long cassettes. ELISPOT data indicated that HLA-A2 transgenic mice, 17 days post-infection with 5e10 adenovirus viral particles, generated a T cell response comparable in magnitude for both long and short vaccine cassettes.

	Long Cassette Designs		
Epitope	**Standard**	**Scrambled**	**Short**
1	863+/-1080	804+/-1113	1871+/-2859
2	6425+/-1594	28+/-62	5390+/-1357
3*	23+/-30	36+/-18	0+/-48
4	2224+/-1074	2727+/-644	2637+/-1673
5	7952+/-297	8100+/-0	8100+/-0

* Suspected technical error caused an absence of a T cell response.

XIV.B.4. Neoantigen Cassette Design for Immunogenicity and Toxicology Studies

[00807] In summary, the findings of the model cassette evaluations (Fig. 16-19, Tables 2-6) demonstrated that, for model vaccine cassettes, robustimmunogenicity was achieved when a "string of beads" approach was employed that encodes around 20 epitopes in the context of an adenovirus-based vector. The epitopes were assembled by concatenating 25mer sequences, each embedding a minimal CD8 T cell epitope (e.g. 9 amino acid residues) that were flanked on both sides by its natural, surrounding peptide sequence (e.g. 8 amino acid residues on each side). As used herein, a "natural" or "native" flanking sequence refers to the N- and/or C-terminal flanking sequence of a given epitope in the naturally occurring context of that epitope within its source protein. For example, the HCMV pp65 MHC I epitope NLVPMVATV is flanked on its 5' end by the native 5' sequence WQAGILAR and on its 3' end by the native 3' sequence QGQNLKYQ, thus generating the WQAGILARNLVPMVATVQGQNLKYQ 25mer peptide found within the HCMV pp65 source protein. The natural or native sequence can also refer to a nucleotide sequence that encodes an epitope flanked by native flanking sequence(s). Each 25mer sequence is directly connected to the following 25mer sequence. In instances where the minimal CD8 T cell epitope is greater than or less than 9 amino acids, the flanking peptide length can be adjusted such that the total length is still a 25mer peptide sequence. For example, a 10 amino acid CD8 T cell epitope can be flanked by an 8 amino acid sequence and a 7 amino acid. The concatamer was followed by two universal class II MHC epitopes that were included to stimulate CD4 T helper cells and improve overall *in vivo* immunogenicity of

2026201462 26 Feb 2026

the vaccine cassette antigens. (Alexander et al., 1994; Panina-Bordignon et al., 1989) The class II epitopes were linked to the final class I epitope by a GPGPG amino acid linker (SEQ ID NO:56). The two class II epitopes were also linked to each other by a GPGPG amino acid linker, as a well as flanked on the C-terminus by a GPGPG amino acid linker. Neither the position nor the number of epitopes appeared to substantially impact T cell recognition or response. Targeting sequences also did not appear to substantially impact the immunogenicity of cassette-derived antigens.

[00808] As a further example, based on the in vitro and in vivo data obtained with model cassettes (Fig. 16-19, Tables 2-6), a cassette design was generated that alternates well-characterized T cell epitopes known to be immunogenic in nonhuman primates (NHPs), mice and humans. The 20 epitopes, all embedded in their natural 25mer sequences, are followed by the two universal class II MHC epitopes that were present in all model cassettes evaluated (Fig. 20). This cassette design was used to study immunogenicity as well as pharmacology and toxicology studies in multiple species.

XV. ChAd Neoantigen Cassette Delivery Vector

XV.A. ChAd Neoantigen Cassette Delivery Vector Construction

[00809] In one example, Chimpanzee adenovirus (ChAd) was engineered to be a delivery vector for neoantigen cassettes. In a further example, a full-length ChAdV68 vector was synthesized based on AC_000011.1 (sequence 2 from Patent US 6083716) with E1 (nt 457 to 3014) and E3 (nt 27,816- 31,332) sequences deleted. Reporter genes under the control of the CMV promoter/enhancer were inserted in place of the deleted E1 sequences. Transfection of this clone into HEK293 cells did not yield infectious virus. To confirm the sequence of the wild-type C68 virus, isolate VR-594 was obtained from the ATCC, passaged, and then independently sequenced (SEQ ID NO:10). When comparing the AC_000011.1 sequence to the ATCC VR-594 sequence (SEQ ID NO:10) of wild-type ChAdV68 virus , 6 nucleotide differences were identified. In one example, a modified ChAdV68 vector was generated based on AC_000011.1, with the corresponding ATCC VR-594 nucleotides substituted at five positions (ChAdV68.5WTnt SEQ ID NO:1).

[00810] In another example, a modified ChAdV68 vector was generated based on AC_000011.1 with E1 (nt 577 to 3403) and E3 (nt 27,816- 31,332) sequences deleted and the corresponding ATCC VR-594 nucleotides substituted at four positions. A GFP reporter (ChAdV68.4WTnt.GFP; SEQ ID NO:11) or model neoantigen cassette

2026201462 26 Feb 2026

(ChAdV68.4WTnt.MAG25mer; SEQ ID NO:12) under the control of the CMV promoter/enhancer was inserted in place of deleted E1 sequences.

[00811] In another example, a modified ChAdV68 vector was generated based on AC_000011.1 with E1 (nt 577 to 3403) and E3 (nt 27,125- 31,825) sequences deleted and the corresponding ATCC VR-594 nucleotides substituted at five positions. A GFP reporter (ChAdV68.5WTnt.GFP; SEQ ID NO:13) or model neoantigen cassette (ChAdV68.5WTnt.MAG25mer; SEQ ID NO:2) under the control of the CMV promoter/enhancer was inserted in place of deleted E1 sequences.

Full-Length ChAdVC68 sequence "ChAdV68.5WTnt" (SEQ ID NO:1); AC_000011.1 sequence with corresponding ATCC VR-594 nucleotides substituted at five positions.

CCATCTTCAATAATATACCTCAAACTTTTTGTGCGCGTTAATATGCAAATGAGGCGTTTGAATTTGGGGAGGAA
GGGCGGTGATTGGTCGAGGGATGAGCGACCGTTAGGGGCGGGGCGAGTGACGTTTTGATGACGTGGTTGCGAGG
AGGAGCCAGTTTGCAAGTTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTTGAACACGGAAATACTCAAT
TTTCCCGCGCTCTCTGACAGGAAATGAGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGCCATTTTCGCGCGAA
AACTGAATGAGGAAGTGAAAATCTGAGTAATTTCGCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGCCGAGTA
GACTTTGACCGATTACGTGGGGGTTTCGATTACCGTGTTTTTCACCTAAATTTCCGCGTACGGTGTCAAAGTCC
GGTGTTTTTACGTAGGTGTCAGCTGATCGCCAGGGTATTTAAACCTGCGCTCTCCAGTCAAGAGGCCACTCTTG
AGTGCCAGCGAGAAGAGTTTTCTCCTCCGCGCCGCGAGTCAGATCTACACTTTGAAAGATGAGGCACCTGAGAG
ACCTGCCCGATGAGAAAATCATCATCGCTTCCGGGAACGAGATTCTGGAACTGGTGGTAAATGCCATGATGGGC
GACGACCCTCCGGAGCCCCCCACCCCATTTGAGACACCTTCGCTGCACGATTTGTATGATCTGGAGGTGGATGT
GCCCGAGGACGATCCCAATGAGGAGGCGGTAAATGATTTTTTTAGCGATGCCGCGCTGCTAGCTGCCGAGGAGG
CTTCGAGCTCTAGCTCAGACAGCGACTCTTCACTGCATACCCCTAGACCCGGCAGAGGTGAGAAAAAGATCCCC
GAGCTTAAAGGGGAAGAGATGGACTTGCGCTGCTATGAGGAATGCTTGCCCCCGAGCGATGATGAGGACGAGCA
GGCGATCCAGAACGCAGCGAGCCAGGGAGTGCAAGCCGCCAGCGAGAGCTTTGCGCTGGACTGCCCGCCTCTGC
CCGGACACGGCTGTAAGTCTTGTGAATTTCATCGCATGAATACTGGAGATAAAGCTGTGTTGTGTGCACTTTGC
TATATGAGAGCTTACAACCATTGTGTTTACAGTAAGTGTGATTAAGTTGAACTTTAGAGGGAGGCAGAGAGCAG
GGTGACTGGGCGATGACTGGTTTATTTATGTATATATGTTCTTTATATAGGTCCCGTCTCTGACGCAGATGATG
AGACCCCCACTACAAAGTCCACTTCGTCACCCCCAGAAATTGGCACATCTCCACCTGAGAATATTGTTAGACCA
GTTCCTGTTAGAGCCACTGGGAGGAGAGCAGCTGTGGAATGTTTGGATGACTTGCTACAGGGTGGGGTTGAACC
TTTGGACTTGTGTACCCGGAAACGCCCCAGGCACTAAGTGCCACACATGTGTGTTTACTTGAGGTGATGTCAGT
ATTTATAGGGTGTGGAGTGCAATAAAAAATGTGTTGACTTTAAGTGCGTGGTTTATGACTCAGGGGTGGGGACT
GTGAGTATATAAGCAGGTGCAGACCTGTGTGGTTAGCTCAGAGCGGCATGGAGATTTGGACGGTCTTGGAAGAC
TTTCACAAGACTAGACAGCTGCTAGAGAACGCCTCGAACGGAGTCTCTTACCTGTGGAGATTCTGCTTCGGTGG
CGACCTAGCTAGGCTAGTCTACAGGGCCAAACAGGATTATAGTGAACAATTTGAGGTTATTTTGAGAGAGTGTT
CTGGTCTTTTTGACGCTCTTAACTTGGGCCATCAGTCTCACTTTAACCAGAGGATTTCGAGAGCCCTTGATTTT
ACTACTCCTGGCAGAACCACTGCAGCAGTAGCCTTTTTTGCTTTTATTCTTGACAAATGGAGTCAAGAAACCCA
TTTCAGCAGGGATTACCAGCTGGATTTCTTAGCAGTAGCTTTGTGGAGAACATGGAAGTGCCAGCGCCTGAATG
CAATCTCCGGCTACTTGCCGGTACAGCCGCTAGACACTCTGAGGATCCTGAATCTCCAGGAGAGTCCCAGGGCA
CGCCAACGTCGCCAGCAGCAGCAGCAGGAGGAGGATCAAGAAGAGAACCCGAGAGCCGGCCTGGACCCTCCGGC
GGAGGAGGAGGAGTAGCTGACCTGTTTCCTGAACTGCGCCGGGTGCTGACTAGGTCTTCGAGTGGTCGGGAGAG
GGGGATTAAGCGGGAGAGGCATGATGAGACTAATCACAGAACTGAACTGACTGTGGGTCTGATGAGTCGCAAGC
GCCCAGAAACAGTGTGGTGGCATGAGGTGCAGTCGACTGGCACAGATGAGGTGTCGGTGATGCATGAGAGGTTT
TCTCTAGAACAAGTCAAGACTTGTTGGTTAGAGCCTGAGGATGATTGGGAGGTAGCCATCAGGAATTATGCCAA
GCTGGCTCTGAGGCCAGACAAGAAGTACAAGATTACTAAGCTGATAAATATCAGAAATGCCTGCTACATCTCAG
GGAATGGGGCTGAAGTGGAGATCTGTCTCCAGGAAAGGGTGGCTTTCAGATGCTGCATGATGAATATGTACCCG
GGAGTGGTGGGCATGGATGGGGTTACCTTTATGAACATGAGGTTCAGGGGAGATGGGTATAATGGCACGGTCTT
TATGGCCAATACCAAGCTGACAGTCCATGGCTGCTCCTTCTTTGGGTTTAATAACACCTGCATCGAGGCCTGGG
GTCAGGTCGGTGTGAGGGGCTGCAGTTTTTCAGCCAACTGGATGGGGGTCGTGGGCAGGACCAAGAGTATGCTG
TCCGTGAAGAAATGCTTGTTTGAGAGGTGCCACCTGGGGGTGATGAGCGAGGGCGAAGCCAGAATCCGCCACTG
CGCCTCTACCGAGACGGGCTGCTTTGTGCTGTGCAAGGGCAATGCTAAGATCAAGCATAATATGATCTGTGGAG

2026201462 26 Feb 2026

CCTCGGACGAGCGCGGCTACCAGATGCTGACCTGCGCCGGCGGGAACAGCCATATGCTGGCCACCGTACATGTG
GCTTCCCATGCTCGCAAGCCCTGGCCCGAGTTCGAGCACAATGTCATGACCAGGTGCAATATGCATCTGGGGTC
CCGCCGAGGCATGTTCATGCCCTACCAGTGCAACCTGAATTATGTGAAGGTGCTGCTGGAGCCCGATGCCATGT
CCAGAGTGAGCCTGACGGGGGTGTTTGACATGAATGTGGAGGTGTGGAAGATTCTGAGATATGATGAATCCAAG
ACCAGGTGCCGAGCCTGCGAGTGCGGAGGGAAGCATGCCAGGTTCCAGCCCGTGTGTGTGGATGTGACGGAGGA
CCTGCGACCCGATCATTTGGTGTTGCCCTGCACCGGGACGGAGTTCGGTTCCAGCGGGGAAGAATCTGACTAGA
GTGAGTAGTGTTCTGGGGCGGGGGAGGACCTGCATGAGGGCCAGAATAACTGAAATCTGTGCTTTTCTGTGTGT
TGCAGCAGCATGAGCGGAAGCGGCTCCTTTGAGGGAGGGGTATTCAGCCCTTATCTGACGGGGCGTCTCCCCTC
CTGGGCGGGAGTGCGTCAGAATGTGATGGGATCCACGGTGGACGGCCGGCCCGTGCAGCCCGCGAACTCTTCAA
CCCTGACCTATGCAACCCTGAGCTCTTCGTCGTTGGACGCAGCTGCCGCCGCAGCTGCTGCATCTGCCGCCAGC
GCCGTGCGCGGAATGGCCATGGGCGCCGGCTACTACGGCACTCTGGTGGCCAACTCGAGTTCCACCAATAATCC
CGCCAGCCTGAACGAGGAGAAGCTGTTGCTGCTGATGGCCCAGCTCGAGGCCTTGACCCAGCGCCTGGGCGAGC
TGACCCAGCAGGTGGCTCAGCTGCAGGAGCAGACGCGGGCCGCGGTTGCCACGGTGAAATCCAAATAAAAAATG
AATCAATAAATAAACGGAGACGGTTGTTGATTTTAACACAGAGTCTGAATCTTTATTTGATTTTTCGCGCGCGG
TAGGCCCTGGACCACCGGTCTCGATCATTGAGCACCCGGTGGATCTTTTCCAGGACCCGGTAGAGGTGGGCTTG
GATGTTGAGGTACATGGGCATGAGCCCGTCCCGGGGGTGGAGGTAGCTCCATTGCAGGGCCTCGTGCTCGGGGG
TGGTGTTGTAAATCACCCAGTCATAGCAGGGGCGCAGGGCATGGTGTTGCACAATATCTTTGAGGAGGAGACTG
ATGGCCACGGGCAGCCCTTTGGTGTAGGTGTTTACAAATCTGTTGAGCTGGGAGGGATGCATGCGGGGGGAGAT
GAGGTGCATCTTGGCCTGGATCTTGAGATTGGCGATGTTACCGCCCAGATCCCGCCTGGGGTTCATGTTGTGCA
GGACCACCAGCACGGTGTATCCGGTGCACTTGGGGAATTTATCATGCAACTTGGAAGGGAAGGCGTGAAAGAAT
TTGGCGACGCCTTTGTGCCCGCCCAGGTTTTCCATGCACTCATCCATGATGATGGCGATGGGCCCGTGGGCGGC
GGCCTGGGCAAAGACGTTTCGGGGGTCGGACACATCATAGTTGTGGTCCTGGGTGAGGTCATCATAGGCCATTT
TAATGAATTTGGGGCGGAGGGTGCCGGACTGGGGGACAAAGGTACCCTCGATCCCGGGGGCGTAGTTCCCCTCA
CAGATCTGCATCTCCCAGGCTTTGAGCTCGGAGGGGGGGATCATGTCCACCTGCGGGGCGATAAAGAACACGGT
TTCCGGGGCGGGGGAGATGAGCTGGGCCGAAAGCAAGTTCCGGAGCAGCTGGGACTTGCCGCAGCCGGTGGGGC
CGTAGATGACCCCGATGACCGGCTGCAGGTGGTAGTTGAGGGAGAGACAGCTGCCGTCCTCCCGGAGGAGGGGG
GCCACCTCGTTCATCATCTCGCGCACGTGCATGTTCTCGCGCACCAGTTCCGCCAGGAGGCGCTCTCCCCCCAG
GGATAGGAGCTCCTGGAGCGAGGCGAAGTTTTTCAGCGGCTTGAGTCCGTCGGCCATGGGCATTTTGGAGAGGG
TTTGTTGCAAGAGTTCCAGGCGGTCCCAGAGCTCGGTGATGTGCTCTACGGCATCTCGATCCAGCAGACCTCCT
CGTTTCGCGGGTTGGGACGGCTGCGGGAGTAGGGCACCAGACGATGGGCGTCCAGCGCAGCCAGGGTCCGGTCC
TTCCAGGGTCGCAGCGTCCGCGTCAGGGTGGTCTCCGTCACGGTGAAGGGGTGCGCGCCGGGCTGGGCGCTTGC
GAGGGTGCGCTTCAGGCTCATCCGGCTGGTCGAAAACCGCTCCCGATCGGCGCCCTGCGCGTCGGCCAGGTAGC
AATTGACCATGAGTTCGTAGTTGAGCGCCTCGGCCGCGTGGCCTTTGGCGCGGAGCTTACCTTTGGAAGTCTGC
CCGCAGGCGGGACAGAGGAGGGACTTGAGGGCGTAGAGCTTGGGGGCGAGGAAGACGGACTCGGGGGCGTAGGC
GTCCGCGCCGCAGTGGGCGCAGACGGTCTCGCACTCCACGAGCCAGGTGAGGTCGGGCTGGTCGGGGTCAAAAA
CCAGTTTCCCGCCGTTCTTTTTGATGCGTTTCTTACCTTTGGTCTCCATGAGCTCGTGTCCCCGCTGGGTGACA
AAGAGGCTGTCCGTGTCCCCGTAGACCGACTTTATGGGCCGGTCCTCGAGCGGTGTGCCGCGGTCCTCCTCGTA
GAGGAACCCCGCCCACTCCGAGACGAAAGCCCGGGTCCAGGCCAGCACGAAGGAGGCCACGTGGGACGGGTAGC
GGTCGTTGTCCACCAGCGGGTCCACCTTTTCCAGGGTATGCAAACACATGTCCCCCTCGTCCACATCCAGGAAG
GTGATTGGCTTGTAAGTGTAGGCCACGTGACCGGGGGTCCCGGCCGGGGGGGTATAAAAGGGTGCGGGTCCCTG
CTCGTCCTCACTGTCTTCCGGATCGCTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATTCCCTCTCGAAGGCGG
GCATGACCTCGGCACTCAGGTTGTCAGTTTCTAGAAACGAGGAGGATTTGATATTGACGGTGCCGGCGGAGATG
CCTTTCAAGAGCCCCTCGTCCATCTGGTCAGAAAAGACGATCTTTTTGTTGTCGAGCTTGGTGGCGAAGGAGCC
GTAGAGGGCGTTGGAGAGGAGCTTGGCGATGGAGCGCATGGTCTGGTTTTTTTCCTTGTCGGCGCGCTCCTTGG
CGGCGATGTTGAGCTGCACGTACTCGCGCGCCACGCACTTCCATTCGGGGAAGACGGTGGTCAGCTCGTCGGGC
ACGATTCTGACCTGCCAGCCCCGATTATGCAGGGTGATGAGGTCCACACTGGTGGCCACCTCGCCGCGCAGGGG
CTCATTAGTCCAGCAGAGGCGTCCGCCCTTGCGCGAGCAGAAGGGGGGCAGGGGGTCCAGCATGACCTCGTCGG
GGGGGTCGGCATCGATGGTGAAGATGCCGGGCAGGAGGTCGGGGTCAAAGTAGCTGATGGAAGTGGCCAGATCG
TCCAGGGCAGCTTGCCATTCGCGCACGGCCAGCGCGCGCTCGTAGGGACTGAGGGGCGTGCCCCAGGGCATGGG
ATGGGTAAGCGCGGAGGCGTACATGCCGCAGATGTCGTAGACGTAGAGGGGCTCCTCGAGGATGCCGATGTAGG
TGGGGTAGCAGCGCCCCCCGCGGATGCTGGCGCGCACGTAGTCATACAGCTCGTGCGAGGGGGCGAGGAGCCCC
GGGCCCAGGTTGGTGCGACTGGGCTTTTCGGCGCGGTAGACGATCTGGCGGAAAATGGCATGCGAGTTGGAGGA
GATGGTGGGCCTTTGGAAGATGTTGAAGTGGGCGTGGGGCAGTCCGACCGAGTCGCGGATGAAGTGGGCGTAGG
AGTCTTGCAGCTTGGCGACGAGCTCGGCGGTGACTAGGACGTCCAGAGCGCAGTAGTCGAGGGTCTCCTGGATG
ATGTCATACTTGAGCTGTCCCTTTTGTTTCCACAGCTCGCGGTTGAGAAGGAACTCTTCGCGGTCCTTCCAGTA
CTCTTCGAGGGGGAACCCGTCCTGATCTGCACGGTAAGAGCCTAGCATGTAGAACTGGTTGACGGCCTTGTAGG
CGCAGCAGCCCTTCTCCACGGGGAGGGCGTAGGCCTGGGCGGCCTTGCGCAGGGAGGTGTGCGTGAGGGCGAAA
GTGTCCCTGACCATGACCTTGAGGAACTGGTGCTTGAAGTCGATATCGTCGCAGCCCCCCTGCTCCCAGAGCTG
GAAGTCCGTGCGCTTCTTGTAGGCGGGGTTGGGCAAAGCGAAAGTAACATCGTTGAAGAGGATCTTGCCCGCGC
GGGGCATAAAGTTGCGAGTGATGCGGAAAGGTTGGGGCACCTCGGCCCGGTTGTTGATGACCTGGGCGGCGAGC

2026201462 26 Feb 2026

ACGATCTCGTCGAAGCCGTTGATGTTGTGGCCCACGATGTAGAGTTCCACGAATCGCGGACGGCCCTTGACGTG
GGGCAGTTTCTTGAGCTCCTCGTAGGTGAGCTCGTCGGGGTCGCTGAGCCCGTGCTGCTCGAGCGCCCAGTCGG
CGAGATGGGGGTTGGCGCGGAGGAAGGAAGTCCAGAGATCCACGGCCAGGGCGGTTTGCAGACGGTCCCGGTAC
TGACGGAACTGCTGCCCGACGGCCATTTTTTCGGGGGTGACGCAGTAGAAGGTGCGGGGGTCCCCGTGCCAGCG
ATCCCATTTGAGCTGGAGGGCGAGATCGAGGGCGAGCTCGACGAGCCGGTCGTCCCCGGAGAGTTTCATGACCA
GCATGAAGGGGACGAGCTGCTTGCCGAAGGACCCCATCCAGGTGTAGGTTTCCACATCGTAGGTGAGGAAGAGC
CTTTCGGTGCGAGGATGCGAGCCGATGGGGAAGAACTGGATCTCCTGCCACCAATTGGAGGAATGGCTGTTGAT
GTGATGGAAGTAGAAATGCCGACGGCGCGCCGAACACTCGTGCTTGTGTTTATACAAGCGGCCACAGTGCTCGC
AACGCTGCACGGGATGCACGTGCTGCACGAGCTGTACCTGAGTTCCTTTGACGAGGAATTTCAGTGGGAAGTGG
AGTCGTGGCGCCTGCATCTCGTGCTGTACTACGTCGTGGTGGTCGGCCTGGCCCTCTTCTGCCTCGATGGTGGT
CATGCTGACGAGCCCGCGCGGGAGGCAGGTCCAGACCTCGGCGCGAGCGGGTCGGAGAGCGAGGACGAGGGCGC
GCAGGCCGGAGCTGTCCAGGGTCCTGAGACGCTGCGGAGTCAGGTCAGTGGGCAGCGGCGGCGCGCGGTTGACT
TGCAGGAGTTTTTCCAGGGCGCGCGGGAGGTCCAGATGGTACTTGATCTCCACCGCGCCATTGGTGGCGACGTC
GATGGCTTGCAGGGTCCCGTGCCCCTGGGGTGTGACCACCGTCCCCCGTTTCTTCTTGGGCGGCTGGGGCGACG
GGGGCGGTGCCTCTTCCATGGTTAGAAGCGGCGGCGAGGACGCGCGCCGGGCGGCAGGGGCGGCTCGGGGCCCG
GAGGCAGGGGCGGCAGGGGCACGTCGGCGCCGCGCGCGGGTAGGTTCTGGTACTGCGCCCGGAGAAGACTGGCG
TGAGCGACGACGCGACGGTTGACGTCCTGGATCTGACGCCTCTGGGTGAAGGCCACGGGACCCGTGAGTTTGAA
CCTGAAAGAGAGTTCGACAGAATCAATCTCGGTATCGTTGACGGCGGCCTGCCGCAGGATCTCTTGCACGTCGC
CCGAGTTGTCCTGGTAGGCGATCTCGGTCATGAACTGCTCGATCTCCTCCTCTTGAAGGTCTCCGCGGCCGGCG
CGCTCCACGGTGGCCGCGAGGTCGTTGGAGATGCGGCCCATGAGCTGCGAGAAGGCGTTCATGCCCGCCTCGTT
CCAGACGCGGCTGTAGACCACGACGCCCTCGGGATCGCgGGCGCGCATGACCACCTGGGCGAGGTTGAGCTCCA
CGTGGCGCGTGAAGACCGCGTAGTTGCAGAGGCGCTGGTAGAGGTAGTTGAGCGTGGTGGCGATGTGCTCGGTG
ACGAAGAAATACATGATCCAGCGGCGGAGCGGCATCTCGCTGACGTCGCCCAGCGCCTCCAAACGTTCCATGGC
CTCGTAAAAGTCCACGGCGAAGTTGAAAAACTGGGAGTTGCGCGCCGAGACGGTCAACTCCTCCTCCAGAAGAC
GGATGAGCTCGGCGATGGTGGCGCGCACCTCGCGCTCGAAGGCCCCCGGGAGTTCCTCCACTTCCTCTTCTTCC
TCCTCCACTAACATCTCTTCTACTTCCTCCTCAGGCGGCAGTGGTGGCGGGGGAGGGGGCCTGCGTCGCCGGCG
GCGCACGGGCAGACGGTCGATGAAGCGCTCGATGGTCTCGCCGCGCCGGCGTCGCATGGTCTCGGTGACGGCGC
GCCCGTCCTCGCGGGGCCGCAGCGTGAAGACGCCGCCGCGCATCTCCAGGTGGCCGGGGGGGTCCCCGTTGGGC
AGGGAGAGGGCGCTGACGATGCATCTTATCAATTGCCCCGTAGGGACTCCGCGCAAGGACCTGAGCGTCTCGAG
ATCCACGGGATCTGAAAACCGCTGAACGAAGGCTTCGAGCCAGTCGCAGTCGCAAGGTAGGCTGAGCACGGTTT
CTTCTGGCGGGTCATGTTGGTTGGGAGCGGGGCGGGCGATGCTGCTGGTGATGAAGTTGAAATAGGCGGTTCTG
AGACGGCGGATGGTGGCGAGGAGCACCAGGTCTTTGGGCCCGGCTTGCTGGATGCGCAGACGGTCGGCCATGCC
CCAGGCGTGGTCCTGACACCTGGCCAGGTCCTTGTAGTAGTCCTGCATGAGCCGCTCCACGGGCACCTCCTCCT
CGCCCGCGCGGCCGTGCATGCGCGTGAGCCCGAAGCCGCGCTGGGGCTGGACGAGCGCCAGGTCGGCGACGACG
CGCTCGGCGAGGATGGCTTGCTGGATCTGGGTGAGGGTGGTCTGGAAGTCATCAAAGTCGACGAAGCGGTGGTA
GGCTCCGGTGTTGATGGTGTAGGAGCAGTTGGCCATGACGGACCAGTTGACGGTCTGGTGGCCCGGACGCACGA
GCTCGTGGTACTTGAGGCGCGAGTAGGCGCGCGTGTCGAAGATGTAGTCGTTGCAGGTGCGCACCAGGTACTGG
TAGCCGATGAGGAAGTGCGGCGGCGGCTGGCGGTAGAGCGGCCATCGCTCGGTGGCGGGGGCGCCGGGCGCGAG
GTCCTCGAGCATGGTGCGGTGGTAGCCGTAGATGTACCTGGACATCCAGGTGATGCCGGCGGCGGTGGTGGAGG
CGCGCGGGAACTCGCGGACGCGGTTCCAGATGTTGCGCAGCGGCAGGAAGTAGTTCATGGTGGGCACGGTCTGG
CCCGTGAGGCGCGCGCAGTCGTGGATGCTCTATACGGGCAAAAACGAAAGCGGTCAGCGGCTCGACTCCGTGGC
CTGGAGGCTAAGCGAACGGGTTGGGCTGCGCGTGTACCCCGGTTCGAATCTCGAATCAGGCTGGAGCCGCAGCT
AACGTGGTATTGGCACTCCCGTCTCGACCCAAGCCTGCACCAACCCTCCAGGATACGGAGGCGGGTCGTTTTGC
AACTTTTTTTTGGAGGCCGGATGAGACTAGTAAGCGCGGAAAGCGGCCGACCGCGATGGCTCGCTGCCGTAGTC
TGGAGAAGAATCGCCAGGGTTGCGTTGCGGTGTGCCCCGGTTCGAGGCCGGCCGGATTCCGCGGCTAACGAGGG
CGTGGCTGCCCCGTCGTTTCCAAGACCCCATAGCCAGCCGACTTCTCCAGTTACGGAGCGAGCCCCTCTTTTGT
TTTGTTTGTTTTTGCCAGATGCATCCCGTACTGCGGCAGATGCGCCCCCACCACCCTCCACCGCAACAACAGCC
CCCTCCACAGCCGGCGCTTCTGCCCCCGCCCCAGCAGCAACTTCCAGCCACGACCGCCGCGGCCGCCGTGAGCG
GGGCTGGACAGAGTTATGATCACCAGCTGGCCTTGGAAGAGGGCGAGGGGCTGGCGCGCCTGGGGGCGTCGTCG
CCGGAGCGGCACCCGCGCGTGCAGATGAAAAGGGACGCTCGCGAGGCCTACGTGCCCAAGCAGAACCTGTTCAG
AGACAGGAGCGGCGAGGAGCCCGAGGAGATGCGCGCGGCCCGGTTCCACGCGGGGCGGGAGCTGCGGCGCGGCC
TGGACCGAAAGAGGGTGCTGAGGGACGAGGATTTCGAGGCGGACGAGCTGACGGGGATCAGCCCCGCGCGCGCG
CACGTGGCCGCGGCCAACCTGGTCACGGCGTACGAGCAGACCGTGAAGGAGGAGAGCAACTTCCAAAAATCCTT
CAACAACCACGTGCGCACCCTGATCGCGCGCGAGGAGGTGACCCTGGGCCTGATGCACCTGTGGGACCTGCTGG
AGGCCATCGTGCAGAACCCCACCAGCAAGCCGCTGACGGCGCAGCTGTTCCTGGTGGTGCAGCATAGTCGGGAC
AACGAAGCGTTCAGGGAGGCGCTGCTGAATATCACCGAGCCCGAGGGCCGCTGGCTCCTGGACCTGGTGAACAT
TCTGCAGAGCATCGTGGTGCAGGAGCGCGGGCTGCCGCTGTCCGAGAAGCTGGCGGCCATCAACTTCTCGGTGC
TGAGTTTGGGCAAGTACTACGCTAGGAAGATCTACAAGACCCCGTACGTGCCCATAGACAAGGAGGTGAAGATC
GACGGGTTTTACATGCGCATGACCCTGAAAGTGCTGACCCTGAGCGACGATCTGGGGGTGTACCGCAACGACAG
GATGCACCGTGCGGTGAGCGCCAGCAGGCGGCGCGAGCTGAGCGACCAGGAGCTGATGCATAGTCTGCAGCGGG

2026201462 26 Feb 2026

CCCTGACCGGGGCCGGGACCGAGGGGGAGAGCTACTTTGACATGGGCGCGGACCTGCACTGGCAGCCCAGCCGC
CGGGCCTTGGAGGCGGCGGCAGGACCCTACGTAGAAGAGGTGGACGATGAGGTGGACGAGGAGGGCGAGTACCT
GGAAGACTGATGGCGCGACCGTATTTTTGCTAGATGCAACAACAACAGCCACCTCCTGATCCCGCGATGCGGGC
GGCGCTGCAGAGCCAGCCGTCCGGCATTAACTCCTCGGACGATTGGACCCAGGCCATGCAACGCATCATGGCGC
TGACGACCCGCAACCCCGAAGCCTTTAGACAGCAGCCCCAGGCCAACCGGCTCTCGGCCATCCTGGAGGCCGTG
GTGCCCTCGCGCTCCAACCCCACGCACGAGAAGGTCCTGGCCATCGTGAACGCGCTGGTGGAGAACAAGGCCAT
CCGCGGCGACGAGGCCGGCCTGGTGTACAACGCGCTGCTGGAGCGCGTGGCCCGCTACAACAGCACCAACGTGC
AGACCAACCTGGACCGCATGGTGACCGACGTGCGCGAGGCCGTGGCCCAGCGCGAGCGGTTCCACCGCGAGTCC
AACCTGGGATCCATGGTGGCGCTGAACGCCTTCCTCAGCACCCAGCCCGCCAACGTGCCCCGGGGCCAGGAGGA
CTACACCAACTTCATCAGCGCCCTGCGCCTGATGGTGACCGAGGTGCCCCAGAGCGAGGTGTACCAGTCCGGGC
CGGACTACTTCTTCCAGACCAGTCGCCAGGGCTTGCAGACCGTGAACCTGAGCCAGGCTTTCAAGAACTTGCAG
GGCCTGTGGGGCGTGCAGGCCCCGGTCGGGGACCGCGCGACGGTGTCGAGCCTGCTGACGCCGAACTCGCGCCT
GCTGCTGCTGCTGGTGGCCCCCTTCACGGACAGCGGCAGCATCAACCGCAACTCGTACCTGGGCTACCTGATTA
ACCTGTACCGCGAGGCCATCGGCCAGGCGCACGTGGACGAGCAGACCTACCAGGAGATCACCCACGTGAGCCGC
GCCCTGGGCCAGGACGACCCGGGCAACCTGGAAGCCACCCTGAACTTTTTGCTGACCAACCGGTCGCAGAAGAT
CCCGCCCCAGTACGCGCTCAGCACCGAGGAGGAGCGCATCCTGCGTTACGTGCAGCAGAGCGTGGGCCTGTTCC
TGATGCAGGAGGGGGCCACCCCCAGCGCCGCGCTCGACATGACCGCGCGCAACATGGAGCCCAGCATGTACGCC
AGCAACCGCCCGTTCATCAATAAACTGATGGACTACTTGCATCGGGCGGCCGCCATGAACTCTGACTATTTCAC
CAACGCCATCCTGAATCCCCACTGGCTCCCGCCGCCGGGGTTCTACACGGGCGAGTACGACATGCCCGACCCCA
ATGACGGGTTCCTGTGGGACGATGTGGACAGCAGCGTGTTCTCCCCCCGACCGGGTGCTAACGAGCGCCCCTTG
TGGAAGAAGGAAGGCAGCGACCGACGCCCGTCCTCGGCGCTGTCCGGCCGCGAGGGTGCTGCCGCGGCGGTGCC
CGAGGCCGCCAGTCCTTTCCCGAGCTTGCCCTTCTCGCTGAACAGTATCCGCAGCAGCGAGCTGGGCAGGATCA
CGCGCCCGCGCTTGCTGGGCGAAGAGGAGTACTTGAATGACTCGCTGTTGAGACCCGAGCGGGAGAAGAACTTC
CCCAATAACGGGATAGAAAGCCTGGTGGACAAGATGAGCCGCTGGAAGACGTATGCGCAGGAGCACAGGGACGA
TCCCCGGGCGTCGCAGGGGGCCACGAGCCGGGGCAGCGCCGCCCGTAAACGCCGGTGGCACGACAGGCAGCGGG
GACAGATGTGGGACGATGAGGACTCCGCCGACGACAGCAGCGTGTTGGACTTGGGTGGGAGTGGTAACCCGTTC
GCTCACCTGCGCCCCCGTATCGGGCGCATGATGTAAGAGAAACCGAAAATAAATGATACTCACCAAGGCCATGG
CGACCAGCGTGCGTTCGTTTCTTCTCTGTTGTTGTTGTATCTAGTATGATGAGGCGTGCGTACCCGGAGGGTCC
TCCTCCCTCGTACGAGAGCGTGATGCAGCAGGCGATGGCGGCGGCGGCGATGCAGCCCCCGCTGGAGGCTCCTT
ACGTGCCCCCGCGGTACCTGGCGCCTACGGAGGGGCGGAACAGCATTCGTTACTCGGAGCTGGCACCCTTGTAC
GATACCACCCGGTTGTACCTGGTGGACAACAAGTCGGCGGACATCGCCTCGCTGAACTACCAGAACGACCACAG
CAACTTCCTGACCACCGTGGTGCAGAACAATGACTTCACCCCCACGGAGGCCAGCACCCAGACCATCAACTTTG
ACGAGCGCTCGCGGTGGGGCGGCCAGCTGAAAACCATCATGCACACCAACATGCCCAACGTGAACGAGTTCATG
TACAGCAACAAGTTCAAGGCGCGGGTGATGGTCTCCCGCAAGACCCCCAATGGGGTGACAGTGACAGAGGATTA
TGATGGTAGTCAGGATGAGCTGAAGTATGAATGGGTGGAATTTGAGCTGCCCGAAGGCAACTTCTCGGTGACCA
TGACCATCGACCTGATGAACAACGCCATCATCGACAATTACTTGGCGGTGGGGCGGCAGAACGGGGTGCTGGAG
AGCGACATCGGCGTGAAGTTCGACACTAGGAACTTCAGGCTGGGCTGGGACCCCGTGACCGAGCTGGTCATGCC
CGGGGTGTACACCAACGAGGCTTTCCATCCCGATATTGTCTTGCTGCCCGGCTGCGGGGTGGACTTCACCGAGA
GCCGCCTCAGCAACCTGCTGGGCATTCGCAAGAGGCAGCCCTTCCAGGAAGGCTTCCAGATCATGTACGAGGAT
CTGGAGGGGGGCAACATCCCCGCGCTCCTGGATGTCGACGCCTATGAGAAAAGCAAGGAGGATGCAGCAGCTGA
AGCAACTGCAGCCGTAGCTACCGCCTCTACCGAGGTCAGGGGCGATAATTTTGCAAGCGCCGCAGCAGTGGCAG
CGGCCGAGGCGGCTGAAACCGAAAGTAAGATAGTCATTCAGCCGGTGGAGAAGGATAGCAAGAACAGGAGCTAC
AACGTACTACCGGACAAGATAAACACCGCCTACCGCAGCTGGTACCTAGCCTACAACTATGGCGACCCCGAGAA
GGGCGTGCGCTCCTGGACGCTGCTCACCACCTCGGACGTCACCTGCGGCGTGGAGCAAGTCTACTGGTCGCTGC
CCGACATGATGCAAGACCCGGTCACCTTCCGCTCCACGCGTCAAGTTAGCAACTACCCGGTGGTGGGCGCCGAG
CTCCTGCCCGTCTACTCCAAGAGCTTCTTCAACGAGCAGGCCGTCTACTCGCAGCAGCTGCGCGCCTTCACCTC
GCTTACGCACGTCTTCAACCGCTTCCCCGAGAACCAGATCCTCGTCCGCCCGCCCGCGCCCACCATTACCACCG
TCAGTGAAAACGTTCCTGCTCTCACAGATCACGGGACCCTGCCGCTGCGCAGCAGTATCCGGGGAGTCCAGCGC
GTGACCGTTACTGACGCCAGACGCCGCACCTGCCCCTACGTCTACAAGGCCCTGGGCATAGTCGCGCCGCGCGT
CCTCTCGAGCCGCACCTTCTAAATGTCCATTCTCATCTCGCCCAGTAATAACACCGGTTGGGGCCTGCGCGCGC
CCAGCAAGATGTACGGAGGCGCTCGCCAACGCTCCACGCAACACCCCGTGCGCGTGCGCGGGCACTTCCGCGCT
CCCTGGGGCGCCCTCAAGGGCCGCGTGCGGTCGCGCACCACCGTCGACGACGTGATCGACCAGGTGGTGGCCGA
CGCGCGCAACTACACCCCCGCCGCCGCGCCCGTCTCCACCGTGGACGCCGTCATCGACAGCGTGGTGGCcGACG
CGCGCCGGTACGCCCGCGCCAAGAGCCGGCGGCGGCGCATCGCCCGGCGGCACCGGAGCACCCCCGCCATGCGC
GCGGCGCGAGCCTTGCTGCGCAGGGCCAGGCGCACGGGACGCAGGGCCATGCTCAGGGCGGCCAGACGCGCGGC
TTCAGGCGCCAGCGCCGGCAGGACCCGGAGACGCGCGGCCACGGCGGCGGCAGCGGCCATCGCCAGCATGTCCC
GCCCGCGGCGAGGGAACGTGTACTGGGTGCGCGACGCCGCCACCGGTGTGCGCGTGCCCGTGCGCACCCGCCCC
CCTCGCACTTGAAGATGTTCACTTCGCGATGTTGATGTGTCCCAGCGGCGAGGAGGATGTCCAAGCGCAAATTC
AAGGAAGAGATGCTCCAGGTCATCGCGCCTGAGATCTACGGCCCTGCGGTGGTGAAGGAGGAAAGAAAGCCCCG
CAAAATCAAGCGGGTCAAAAAGGACAAAAAGGAAGAAGAAAGTGATGTGGACGGATTGGTGGAGTTTGTGCGCG

2026201462 26 Feb 2026

AGTTCGCCCCCCGGCGGCGCGTGCAGTGGCGCGGGCGGAAGGTGCAACCGGTGCTGAGACCCGGCACCACCGTG
GTCTTCACGCCCGGCGAGCGCTCCGGCACCGCTTCCAAGCGCTCCTACGACGAGGTGTACGGGGATGATGATAT
TCTGGAGCAGGCGGCCGAGCGCCTGGGCGAGTTTGCTTACGGCAAGCGCAGCCGTTCCGCACCGAAGGAAGAGG
CGGTGTCCATCCCGCTGGACCACGGCAACCCCACGCCGAGCCTCAAGCCCGTGACCTTGCAGCAGGTGCTGCCG
ACCGCGGCGCCGCGCCGGGGGTTCAAGCGCGAGGGCGAGGATCTGTACCCCACCATGCAGCTGATGGTGCCCAA
GCGCCAGAAGCTGGAAGACGTGCTGGAGACCATGAAGGTGGACCCGGACGTGCAGCCCGAGGTCAAGGTGCGGC
CCATCAAGCAGGTGGCCCCGGGCCTGGGCGTGCAGACCGTGGACATCAAGATTCCCACGGAGCCCATGGAAACG
CAGACCGAGCCCATGATCAAGCCCAGCACCAGCACCATGGAGGTGCAGACGGATCCCTGGATGCCATCGGCTCC
TAGTCGAAGACCCCGGCGCAAGTACGGCGCGGCCAGCCTGCTGATGCCCAACTACGCGCTGCATCCTTCCATCA
TCCCCACGCCGGGCTACCGCGGCACGCGCTTCTACCGCGGTCATACCAGCAGCCGCCGCCGCAAGACCACCACT
CGCCGCCGCCGTCGCCGCACCGCCGCTGCAACCACCCCTGCCGCCCTGGTGCGGAGAGTGTACCGCCGCGGCCG
CGCACCTCTGACCCTGCCGCGCGCGCGCTACCACCCGAGCATCGCCATTTAAACTTTCGCCtGCTTTGCAGATC
AATGGCCCTCACATGCCGCCTTCGCGTTCCCATTACGGGCTACCGAGGAAGAAAACCGCGCCGTAGAAGGCTGG
CGGGGAACGGGATGCGTCGCCACCACCACCGGCGGCGGCGCGCCATCAGCAAGCGGTTGGGGGGAGGCTTCCTG
CCCGCGCTGATCCCCATCATCGCCGCGGCGATCGGGGCGATCCCCGGCATTGCTTCCGTGGCGGTGCAGGCCTC
TCAGCGCCACTGAGACACACTTGGAAACATCTTGTAATAAACCaATGGACTCTGACGCTCCTGGTCCTGTGATG
TGTTTTCGTAGACAGATGGAAGACATCAATTTTTCGTCCCTGGCTCCGCGACACGGCACGCGGCCGTTCATGGG
CACCTGGAGCGACATCGGCACCAGCCAACTGAACGGGGGCGCCTTCAATTGGAGCAGTCTCTGGAGCGGGCTTA
AGAATTTCGGGTCCACGCTTAAAACCTATGGCAGCAAGGCGTGGAACAGCACCACAGGGCAGGCGCTGAGGGAT
AAGCTGAAAGAGCAGAACTTCCAGCAGAAGGTGGTCGATGGGCTCGCCTCGGGCATCAACGGGGTGGTGGACCT
GGCCAACCAGGCCGTGCAGCGGCAGATCAACAGCCGCCTGGACCCGGTGCCGCCCGCCGGCTCCGTGGAGATGC
CGCAGGTGGAGGAGGAGCTGCCTCCCCTGGACAAGCGGGGCGAGAAGCGACCCCGCCCCGATGCGGAGGAGACG
CTGCTGACGCACACGGACGAGCCGCCCCCGTACGAGGAGGCGGTGAAACTGGGTCTGCCCACCACGCGGCCCAT
CGCGCCCCTGGCCACCGGGGTGCTGAAACCCGAAAAGCCCGCGACCCTGGACTTGCCTCCTCCCCAGCCTTCCC
GCCCCTCTACAGTGGCTAAGCCCCTGCCGCCGGTGGCCGTGGCCCGCGCGCGACCCGGGGGCACCGCCCGCCCT
CATGCGAACTGGCAGAGCACTCTGAACAGCATCGTGGGTCTGGGAGTGCAGAGTGTGAAGCGCCGCCGCTGCTA
TTAAACCTACCGTAGCGCTTAACTTGCTTGTCTGTGTGTGTATGTATTATGTCGCCGCCGCCGCTGTCCACCAG
AAGGAGGAGTGAAGAGGCGCGTCGCCGAGTTGCAAGATGGCCACCCCATCGATGCTGCCCCAGTGGGCGTACAT
GCACATCGCCGGACAGGACGCTTCGGAGTACCTGAGTCCGGGTCTGGTGCAGTTTGCCCGCGCCACAGACACCT
ACTTCAGTCTGGGGAACAAGTTTAGGAACCCCACGGTGGCGCCCACGCACGATGTGACCACCGACCGCAGCCAG
CGGCTGACGCTGCGCTTCGTGCCCGTGGACCGCGAGGACAACACCTACTCGTACAAAGTGCGCTACACGCTGGC
CGTGGGCGACAACCGCGTGCTGGACATGGCCAGCACCTACTTTGACATCCGCGGCGTGCTGGATCGGGGCCCTA
GCTTCAAACCCTACTCCGGCACCGCCTACAACAGTCTGGCCCCCAAGGGAGCACCCAACACTTGTCAGTGGACA
TATAAAGCCGATGGTGAAACTGCCACAGAAAAAACCTATACATATGGAAATGCACCCGTGCAGGGCATTAACAT
CACAAAAGATGGTATTCAACTTGGAACTGACACCGATGATCAGCCAATCTACGCAGATAAAACCTATCAGCCTG
AACCTCAAGTGGGTGATGCTGAATGGCATGACATCACTGGTACTGATGAAAAGTATGGAGGCAGAGCTCTTAAG
CCTGATACCAAAATGAAGCCTTGTTATGGTTCTTTTGCCAAGCCTACTAATAAAGAAGGAGGTCAGGCAAATGT
GAAAACAGGAACAGGCACTACTAAAGAATATGACATAGACATGGCTTTCTTTGACAACAGAAGTGCGGCTGCTG
CTGGCCTAGCTCCAGAAATTGTTTTGTATACTGAAAATGTGGATTTGGAAACTCCAGATACCCATATTGTATAC
AAAGCAGGCACAGATGACAGCAGCTCTTCTATTAATTTGGGTCAGCAAGCCATGCCCAACAGACCTAACTACAT
TGGTTTCAGAGACAACTTTATCGGGCTCATGTACTACAACAGCACTGGCAATATGGGGGTGCTGGCCGGTCAGG
CTTCTCAGCTGAATGCTGTGGTTGACTTGCAAGACAGAAACACCGAGCTGTCCTACCAGCTCTTGCTTGACTCT
CTGGGTGACAGAACCCGGTATTTCAGTATGTGGAATCAGGCGGTGGACAGCTATGATCCTGATGTGCGCATTAT
TGAAAATCATGGTGTGGAGGATGAACTTCCCAACTATTGTTTCCCTCTGGATGCTGTTGGCAGAACAGATACTT
ATCAGGGAATTAAGGCTAATGGAACTGATCAAACCACATGGACCAAAGATGACAGTGTCAATGATGCTAATGAG
ATAGGCAAGGGTAATCCATTCGCCATGGAAATCAACATCCAAGCCAACCTGTGGAGGAACTTCCTCTACGCCAA
CGTGGCCCTGTACCTGCCCGACTCTTACAAGTACACGCCGGCCAATGTTACCCTGCCCACCAACACCAACACCT
ACGATTACATGAACGGCCGGGTGGTGGCGCCCTCGCTGGTGGACTCCTACATCAACATCGGGGCGCGCTGGTCG
CTGGATCCCATGGACAACGTGAACCCCTTCAACCACCACCGCAATGCGGGGCTGCGCTACCGCTCCATGCTCCT
GGGCAACGGGCGCTACGTGCCCTTCCACATCCAGGTGCCCCAGAAATTTTTCGCCATCAAGAGCCTCCTGCTCC
TGCCCGGGTCCTACACCTACGAGTGGAACTTCCGCAAGGACGTCAACATGATCCTGCAGAGCTCCCTCGGCAAC
GACCTGCGCACGGACGGGGCCTCCATCTCCTTCACCAGCATCAACCTCTACGCCACCTTCTTCCCCATGGCGCA
CAACACGGCCTCCACGCTCGAGGCCATGCTGCGCAACGACACCAACGACCAGTCCTTCAACGACTACCTCTCGG
CGGCCAACATGCTCTACCCCATCCCGGCCAACGCCACCAACGTGCCCATCTCCATCCCCTCGCGCAACTGGGCC
GCCTTCCGCGGCTGGTCCTTCACGCGTCTCAAGACCAAGGAGACGCCCTCGCTGGGCTCCGGGTTCGACCCCTA
CTTCGTCTACTCGGGCTCCATCCCCTACCTCGACGGCACCTTCTACCTCAACCACACCTTCAAGAAGGTCTCCA
TCACCTTCGACTCCTCCGTCAGCTGGCCCGGCAACGACCGGCTCCTGACGCCCAACGAGTTCGAAATCAAGCGC
ACCGTCGACGGCGAGGGCTACAACGTGGCCCAGTGCAACATGACCAAGGACTGGTTCCTGGTCCAGATGCTGGC
CCACTACAACATCGGCTACCAGGGCTTCTACGTGCCCGAGGGCTACAAGGACCGCATGTACTCCTTCTTCCGCA
ACTTCCAGCCCATGAGCCGCCAGGTGGTGGACGAGGTCAACTACAAGGACTACCAGGCCGTCACCCTGGCCTAC

2026201462 26 Feb 2026

CAGCACAACAACTCGGGCTTCGTCGGCTACCTCGCGCCCACCATGCGCCAGGGCCAGCCCTACCCCGCCAACTA
CCCCTACCCGCTCATCGGCAAGAGCGCCGTCACCAGCGTCACCCAGAAAAAGTTCCTCTGCGACAGGGTCATGT
GGCGCATCCCCTTCTCCAGCAACTTCATGTCCATGGGCGCGCTCACCGACCTCGGCCAGAACATGCTCTATGCC
AACTCCGCCCACGCGCTAGACATGAATTTCGAAGTCGACCCCATGGATGAGTCCACCCTTCTCTATGTTGTCTT
CGAAGTCTTCGACGTCGTCCGAGTGCACCAGCCCCACCGCGGCGTCATCGAGGCCGTCTACCTGCGCACCCCCT
TCTCGGCCGGTAACGCCACCACCTAAGCTCTTGCTTCTTGCAAGCCATGGCCGCGGGCTCCGGCGAGCAGGAGC
TCAGGGCCATCATCCGCGACCTGGGCTGCGGGCCCTACTTCCTGGGCACCTTCGATAAGCGCTTCCCGGGATTC
ATGGCCCCGCACAAGCTGGCCTGCGCCATCGTCAACACGGCCGGCCGCGAGACCGGGGGCGAGCACTGGCTGGC
CTTCGCCTGGAACCCGCGCTCGAACACCTGCTACCTCTTCGACCCCTTCGGGTTCTCGGACGAGCGCCTCAAGC
AGATCTACCAGTTCGAGTACGAGGGCCTGCTGCGCCGCAGCGCCCTGGCCACCGAGGACCGCTGCGTCACCCTG
GAAAAGTCCACCCAGACCGTGCAGGGTCCGCGCTCGGCCGCCTGCGGGCTCTTCTGCTGCATGTTCCTGCACGC
CTTCGTGCACTGGCCCGACCGCCCCATGGACAAGAACCCCACCATGAACTTGCTGACGGGGGTGCCCAACGGCA
TGCTCCAGTCGCCCCAGGTGGAACCCACCCTGCGCCGCAACCAGGAGGCGCTCTACCGCTTCCTCAACTCCCAC
TCCGCCTACTTTCGCTCCCACCGCGCGCGCATCGAGAAGGCCACCGCCTTCGACCGCATGAATCAAGACATGTA
AACCGTGTGTGTATGTTAAATGTCTTTAATAAACAGCACTTTCATGTTACACATGCATCTGAGATGATTTATTT
AGAAATCGAAAGGGTTCTGCCGGGTCTCGGCATGGCCCGCGGGCAGGGACACGTTGCGGAACTGGTACTTGGCC
AGCCACTTGAACTCGGGGATCAGCAGTTTGGGCAGCGGGGTGTCGGGGAAGGAGTCGGTCCACAGCTTCCGCGT
CAGTTGCAGGGCGCCCAGCAGGTCGGGCGCGGAGATCTTGAAATCGCAGTTGGGACCCGCGTTCTGCGCGCGGG
AGTTGCGGTACACGGGGTTGCAGCACTGGAACACCATCAGGGCCGGGTGCTTCACGCTCGCCAGCACCGTCGCG
TCGGTGATGCTCTCCACGTCGAGGTCCTCGGCGTTGGCCATCCCGAAGGGGGTCATCTTGCAGGTCTGCCTTCC
CATGGTGGGCACGCACCCGGGCTTGTGGTTGCAATCGCAGTGCAGGGGGATCAGCATCATCTGGGCCTGGTCGG
CGTTCATCCCCGGGTACATGGCCTTCATGAAAGCCTCCAATTGCCTGAACGCCTGCTGGGCCTTGGCTCCCTCG
GTGAAGAAGACCCCGCAGGACTTGCTAGAGAACTGGTTGGTGGCGCACCCGGCGTCGTGCACGCAGCAGCGCGC
GTCGTTGTTGGCCAGCTGCACCACGCTGCGCCCCCAGCGGTTCTGGGTGATCTTGGCCCGGTCGGGGTTCTCCT
TCAGCGCGCGCTGCCCGTTCTCGCTCGCCACATCCATCTCGATCATGTGCTCCTTCTGGATCATGGTGGTCCCG
TGCAGGCACCGCAGCTTGCCCTCGGCCTCGGTGCACCCGTGCAGCCACAGCGCGCACCCGGTGCACTCCCAGTT
CTTGTGGGCGATCTGGGAATGCGCGTGCACGAAGCCCTGCAGGAAGCGGCCCATCATGGTGGTCAGGGTCTTGT
TGCTAGTGAAGGTCAGCGGAATGCCGCGGTGCTCCTCGTTGATGTACAGGTGGCAGATGCGGCGGTACACCTCG
CCCTGCTCGGGCATCAGCTGGAAGTTGGCTTTCAGGTCGGTCTCCACGCGGTAGCGGTCCATCAGCATAGTCAT
GATTTCCATACCCTTCTCCCAGGCCGAGACGATGGGCAGGCTCATAGGGTTCTTCACCATCATCTTAGCGCTAG
CAGCCGCGGCCAGGGGGTCGCTCTCGTCCAGGGTCTCAAAGCTCCGCTTGCCGTCCTTCTCGGTGATCCGCACC
GGGGGGTAGCTGAAGCCCACGGCCGCCAGCTCCTCCTCGGCCTGTCTTTCGTCCTCGCTGTCCTGGCTGACGTC
CTGCAGGACCACATGCTTGGTCTTGCGGGGTTTCTTCTTGGGCGGCAGCGGCGGCGGAGATGTTGGAGATGGCG
AGGGGGAGCGCGAGTTCTCGCTCACCACTACTATCTCTTCCTCTTCTTGGTCCGAGGCCACGCGGCGGTAGGTA
TGTCTCTTCGGGGGCAGAGGCGGAGGCGACGGGCTCTCGCCGCCGCGACTTGGCGGATGGCTGGCAGAGCCCCT
TCCGCGTTCGGGGGTGCGCTCCCGGCGGCGCTCTGACTGACTTCCTCCGCGGCCGGCCATTGTGTTCTCCTAGG
GAGGAACAACAAGCATGGAGACTCAGCCATCGCCAACCTCGCCATCTGCCCCCACCGCCGACGAGAAGCAGCAG
CAGCAGAATGAAAGCTTAACCGCCCCGCCGCCCAGCCCCGCCACCTCCGACGCGGCCGTCCCAGACATGCAAGA
GATGGAGGAATCCATCGAGATTGACCTGGGCTATGTGACGCCCGCGGAGCACGAGGAGGAGCTGGCAGTGCGCT
TTTCACAAGAAGAGATACACCAAGAACAGCCAGAGCAGGAAGCAGAGAATGAGCAGAGTCAGGCTGGGCTCGAG
CATGACGGCGACTACCTCCACCTGAGCGGGGGGGAGGACGCGCTCATCAAGCATCTGGCCCGGCAGGCCACCAT
CGTCAAGGATGCGCTGCTCGACCGCACCGAGGTGCCCCTCAGCGTGGAGGAGCTCAGCCGCGCCTACGAGTTGA
ACCTCTTCTCGCCGCGCGTGCCCCCCAAGCGCCAGCCCAATGGCACCTGCGAGCCCAACCCGCGCCTCAACTTC
TACCCGGTCTTCGCGGTGCCCGAGGCCCTGGCCACCTACCACATCTTTTTCAAGAACCAAAAGATCCCCGTCTC
CTGCCGCGCCAACCGCACCCGCGCCGACGCCCTTTTCAACCTGGGTCCCGGCGCCCGCCTACCTGATATCGCCT
CCTTGGAAGAGGTTCCCAAGATCTTCGAGGGTCTGGGCAGCGACGAGACTCGGGCCGCGAACGCTCTGCAAGGA
GAAGGAGGAGAGCATGAGCACCACAGCGCCCTGGTCGAGTTGGAAGGCGACAACGCGCGGCTGGCGGTGCTCAA
ACGCACGGTCGAGCTGACCCATTTCGCCTACCCGGCTCTGAACCTGCCCCCCAAAGTCATGAGCGCGGTCATGG
ACCAGGTGCTCATCAAGCGCGCGTCGCCCATCTCCGAGGACGAGGGCATGCAAGACTCCGAGGAGGGCAAGCCC
GTGGTCAGCGACGAGCAGCTGGCCCGGTGGCTGGGTCCTAATGCTAGTCCCCAGAGTTTGGAAGAGCGGCGCAA
ACTCATGATGGCCGTGGTCCTGGTGACCGTGGAGCTGGAGTGCCTGCGCCGCTTCTTCGCCGACGCGGAGACCC
TGCGCAAGGTCGAGGAGAACCTGCACTACCTCTTCAGGCACGGGTTCGTGCGCCAGGCCTGCAAGATCTCCAAC
GTGGAGCTGACCAACCTGGTCTCCTACATGGGCATCTTGCACGAGAACCGCCTGGGGCAGAACGTGCTGCACAC
CACCCTGCGCGGGGAGGCCCGGCGCGACTACATCCGCGACTGCGTCTACCTCTACCTCTGCCACACCTGGCAGA
CGGGCATGGGCGTGTGGCAGCAGTGTCTGGAGGAGCAGAACCTGAAAGAGCTCTGCAAGCTCCTGCAGAAGAAC
CTCAAGGGTCTGTGGACCGGGTTCGACGAGCGCACCACCGCCTCGGACCTGGCCGACCTCATTTTCCCCGAGCG
CCTCAGGCTGACGCTGCGCAACGGCCTGCCCGACTTTATGAGCCAAAGCATGTTGCAAAACTTTCGCTCTTTCA
TCCTCGAACGCTCCGGAATCCTGCCCGCCACCTGCTCCGCGCTGCCCTCGGACTTCGTGCCGCTGACCTTCCGC
GAGTGCCCCCCGCCGCTGTGGAGCCACTGCTACCTGCTGCGCCTGGCCAACTACCTGGCCTACCACTCGGACGT
GATCGAGGACGTCAGCGGCGAGGGCCTGCTCGAGTGCCACTGCCGCTGCAACCTCTGCACGCCGCACCGCTCCC

2026201462 26 Feb 2026

TGGCCTGCAACCCCCAGCTGCTGAGCGAGACCCAGATCATCGGCACCTTCGAGTTGCAAGGGCCCAGCGAAGGC
GAGGGTTCAGCCGCCAAGGGGGGTCTGAAACTCACCCCGGGGCTGTGGACCTCGGCCTACTTGCGCAAGTTCGT
GCCCGAGGACTACCATCCCTTCGAGATCAGGTTCTACGAGGACCAATCCCATCCGCCCAAGGCCGAGCTGTCGG
CCTGCGTCATCACCCAGGGGGCGATCCTGGCCCAATTGCAAGCCATCCAGAAATCCCGCCAAGAATTCTTGCTG
AAAAAGGGCCGCGGGGTCTACCTCGACCCCCAGACCGGTGAGGAGCTCAACCCCGGCTTCCCCCAGGATGCCCC
GAGGAAACAAGAAGCTGAAAGTGGAGCTGCCGCCCGTGGAGGATTTGGAGGAAGACTGGGAGAACAGCAGTCAG
GCAGAGGAGGAGGAGATGGAGGAAGACTGGGACAGCACTCAGGCAGAGGAGGACAGCCTGCAAGACAGTCTGGA
GGAAGACGAGGAGGAGGCAGAGGAGGAGGTGGAAGAAGCAGCCGCCGCCAGACCGTCGTCCTCGGCGGGGGAGA
AAGCAAGCAGCACGGATACCATCTCCGCTCCGGGTCGGGGTCCCGCTCGACCACACAGTAGATGGGACGAGACC
GGACGATTCCCGAACCCCACCACCCAGACCGGTAAGAAGGAGCGGCAGGGATACAAGTCCTGGCGGGGGCACAA
AAACGCCATCGTCTCCTGCTTGCAGGCCTGCGGGGGCAACATCTCCTTCACCCGGCGCTACCTGCTCTTCCACC
GCGGGGTGAACTTTCCCCGCAACATCTTGCATTACTACCGTCACCTCCACAGCCCCTACTACTTCCAAGAAGAG
GCAGCAGCAGCAGAAAAAGACCAGCAGAAAACCAGCAGCTAGAAAATCCACAGCGGCGGCAGCAGGTGGACTGA
GGATCGCGGCGAACGAGCCGGCGCAAACCCGGGAGCTGAGGAACCGGATCTTTCCCACCCTCTATGCCATCTTC
CAGCAGAGTCGGGGGCAGGAGCAGGAACTGAAAGTCAAGAACCGTTCTCTGCGCTCGCTCACCCGCAGTTGTCT
GTATCACAAGAGCGAAGACCAACTTCAGCGCACTCTCGAGGACGCCGAGGCTCTCTTCAACAAGTACTGCGCGC
TCACTCTTAAAGAGTAGCCCGCGCCCGCCCAGTCGCAGAAAAAGGCGGGAATTACGTCACCTGTGCCCTTCGCC
CTAGCCGCCTCCACCCATCATCATGAGCAAAGAGATTCCCACGCCTTACATGTGGAGCTACCAGCCCCAGATGG
GCCTGGCCGCCGGTGCCGCCCAGGACTACTCCACCCGCATGAATTGGCTCAGCGCCGGGCCCGCGATGATCTCA
CGGGTGAATGACATCCGCGCCCACCGAAACCAGATACTCCTAGAACAGTCAGCGCTCACCGCCACGCCCCGCAA
TCACCTCAATCCGCGTAATTGGCCCGCCGCCCTGGTGTACCAGGAAATTCCCCAGCCCACGACCGTACTACTTC
CGCGAGACGCCCAGGCCGAAGTCCAGCTGACTAACTCAGGTGTCCAGCTGGCGGGCGGCGCCACCCTGTGTCGT
CACCGCCCCGCTCAGGGTATAAAGCGGCTGGTGATCCGGGGCAGAGGCACACAGCTCAACGACGAGGTGGTGAG
CTCTTCGCTGGGTCTGCGACCTGACGGAGTCTTCCAACTCGCCGGATCGGGGAGATCTTCCTTCACGCCTCGTC
AGGCCGTCCTGACTTTGGAGAGTTCGTCCTCGCAGCCCCGCTCGGGTGGCATCGGCACTCTCCAGTTCGTGGAG
GAGTTCACTCCCTCGGTCTACTTCAACCCCTTCTCCGGCTCCCCCGGCCACTACCCGGACGAGTTCATCCCGAA
CTTCGACGCCATCAGCGAGTCGGTGGACGGCTACGATTGAATGTCCCATGGTGGCGCAGCTGACCTAGCTCGGC
TTCGACACCTGGACCACTGCCGCCGCTTCCGCTGCTTCGCTCGGGATCTCGCCGAGTTTGCCTACTTTGAGCTG
CCCGAGGAGCACCCTCAGGGCCCGGCCCACGGAGTGCGGATCGTCGTCGAAGGGGGCCTCGACTCCCACCTGCT
TCGGATCTTCAGCCAGCGTCCGATCCTGGTCGAGCGCGAGCAAGGACAGACCCTTCTGACTCTGTACTGCATCT
GCAACCACCCCGGCCTGCATGAAAGTCTTTGTTGTCTGCTGTGTACTGAGTATAATAAAAGCTGAGATCAGCGA
CTACTCCGGACTTCCGTGTGTTCCTGAATCCATCAACCAGTCTTTGTTCTTCACCGGGAACGAGACCGAGCTCC
AGCTCCAGTGTAAGCCCCACAAGAAGTACCTCACCTGGCTGTTCCAGGGCTCCCCGATCGCCGTTGTCAACCAC
TGCGACAACGACGGAGTCCTGCTGAGCGGCCCTGCCAACCTTACTTTTTCCACCCGCAGAAGCAAGCTCCAGCT
CTTCCAACCCTTCCTCCCCGGGACCTATCAGTGCGTCTCGGGACCCTGCCATCACACCTTCCACCTGATCCCGA
ATACCACAGCGTCGCTCCCCGCTACTAACAACCAAACTAACCTCCACCAACGCCACCGTCGCGACCTTTCTGAA
TCTAATACTACCACCCACACCGGAGGTGAGCTCCGAGGTCAACCAACCTCTGGGATTTACTACGGCCCCTGGGA
GGTGGTTGGGTTAATAGCGCTAGGCCTAGTTGCGGGTGGGCTTTTGGTTCTCTGCTACCTATACCTCCCTTGCT
GTTCGTACTTAGTGGTGCTGTGTTGCTGGTTTAAGAAATGGGGAAGATCACCCTAGTGAGCTGCGGTGCGCTGG
TGGCGGTGTTGCTTTCGATTGTGGGACTGGGCGGTGCGGCTGTAGTGAAGGAGAAGGCCGATCCCTGCTTGCAT
TTCAATCCCAACAAATGCCAGCTGAGTTTTCAGCCCGATGGCAATCGGTGCGCGGTACTGATCAAGTGCGGATG
GGAATGCGAGAACGTGAGAATCGAGTACAATAACAAGACTCGGAACAATACTCTCGCGTCCGTGTGGCAGCCCG
GGGACCCCGAGTGGTACACCGTCTCTGTCCCCGGTGCTGACGGCTCCCCGCGCACCGTGAATAATACTTTCATT
TTTGCGCACATGTGCGACACGGTCATGTGGATGAGCAAGCAGTACGATATGTGGCCCCCCACGAAGGAGAACAT
CGTGGTCTTCTCCATCGCTTACAGCCTGTGCACGGCGCTAATCACCGCTATCGTGTGCCTGAGCATTCACATGC
TCATCGCTATTCGCCCCAGAAATAATGCCGAAAAAGAAAAACAGCCATAACGTTTTTTTTCACACCTTTTTCAG
ACCATGGCCTCTGTTAAATTTTTGCTTTTATTTGCCAGTCTCATTGCCGTCATTCATGGAATGAGTAATGAGAA
AATTACTATTTACACTGGCACTAATCACACATTGAAAGGTCCAGAAAAAGCCACAGAAGTTTCATGGTATTGTT
ATTTTAATGAATCAGATGTATCTACTGAACTCTGTGGAAACAATAACAAAAAAAAATGAGAGCATTACTCTCATC
AAGTTTCAATGTGGATCTGACTTAACCCTAATTAACATCACTAGAGACTATGTAGGTATGTATTATGGAACTAC
AGCAGGCATTTCGGACATGGAATTTTATCAAGTTTCTGTGTCTGAACCCACCACGCCTAGAATGACCACAACCA
CAAAAACTACACCTGTTACCACTATGCAGCTCACTACCAATAACATTTTTGCCATGCGTCAAATGGTCAACAAT
AGCACTCAACCCACCCCACCCAGTGAGGAAATTCCCAAATCCATGATTGGCATTATTGTTGCTGTAGTGGTGTG
CATGTTGATCATCGCCTTGTGCATGGTGTACTATGCCTTCTGCTACAGAAAGCACAGACTGAACGACAAGCTGG
AACACTTACTAAGTGTTGAATTTTAATTTTTTAGAACCATGAAGATCCTAGGCCTTTTAATTTTTTCTATCATT
ACCTCTGCTCTATGCAATTCTGACAATGAGGACGTTACTGTCGTTGTCGGATCAAATTATACACTGAAAGGTCC
AGCGAAGGGTATGCTTTCGTGGTATTGCTATTTTGGATCTGACACTACAGAAACTGAATTATGCAATCTTAAGA
ATGGCAAAATTCAAAATTCTAAAATTAACAATTATATATGCAATGGTACTGATCTGATACTCCTCAATATCACG
AAATCATATGCTGGCAGTTACACCTGCCCTGGAGATGATGCTGACAGTATGATTTTTTACAAAGTAACTGTTGT
TGATCCCACTACTCCACCTCCACCCACCACAACTACTCACACCACACACACAGATCAAACCGCAGCAGAGGAGG

CAGCAAAGTTAGCCTTGCAGGTCCAAGACAGTTCATTTGTTGGCATTACCCCTACACCTGATCAGCGGTGTCCG
GGGCTGCTAGTCAGCGGCATTGTCGGTGTGCTTTCGGGATTAGCAGTCATAATCATCTGCATGTTCATTTTTGC
TTGCTGCTATAGAAGGCTTTACCGACAAAAATCAGACCCACTGCTGAACCTCTATGTTTAATTTTTTCCAGAGT
CATGAAGGCAGTTAGCGCTCTAGTTTTTTGTTCTTTGATTGGCATTGTTTTTTGCAATCCTATTCCTAAAGTTA
GCTTTATTAAAGATGTGAATGTTACTGAGGGGGGCAATGTGACACTGGTAGGTGTAGAGGGTGCTGAAAACACC
ACCTGGACAAAATACCACCTCAATGGGTGGAAAGATATTTGCAATTGGAGTGTATTAGTTTATACATGTGAGGG
AGTTAATCTTACCATTGTCAATGCCACCTCAGCTCAAAATGGTAGAATTCAAGGACAAAGTGTCAGTGTATCTA
ATGGGTATTTTACCCAACATACTTTTATCTATGACGTTAAAGTCATACCACTGCCTACGCCTAGCCCACCTAGC
ACTACCACACAGACAACCCACACTACACAGACAACCACATACAGTACATTAAATCAGCCTACCACCACTACAGC
AGCAGAGGTTGCCAGCTCGTCTGGGGTCCGAGTGGCATTTTTGATGTGGGCCCCATCTAGCAGTCCCACTGCTA
GTACCAATGAGCAGACTACTGAATTTTTGTCCACTGTCGAGAGCCACACCACAGCTACCTCCAGTGCCTTCTCT
AGCACCGCCAATCTCTCCTCGCTTTCCTCTACACCAATCAGTCCCGCTACTACTCCTAGCCCCGCTCCTCTTCC
CACTCCCCTGAAGCAAACAGACGGCGGCATGCAATGGCAGATCACCCTGCTCATTGTGATCGGGTTGGTCATCC
TGGCCGTGTTGCTCTACTACATCTTCTGCCGCCGCATTCCCAACGCGCACCGCAAGCCGGTCTACAAGCCCATC
ATTGTCGGGCAGCCGGAGCCGCTTCAGGTGGAAGGGGGTCTAAGGAATCTTCTCTTCTCTTTTACAGTATGGTG
ATTGAACTATGATTCCTAGACAATTCTTGATCACTATTCTTATCTGCCTCCTCCAAGTCTGTGCCACCCTCGCT
CTGGTGGCCAACGCCAGTCCAGACTGTATTGGGCCCTTCGCCTCCTACGTGCTCTTTGCCTTCACCACCTGCAT
CTGCTGCTGTAGCATAGTCTGCCTGCTTATCACCTTCTTCCAGTTCATTGACTGGATCTTTGTGCGCATCGCCT
ACCTGCGCCACCACCCCCAGTACCGCGACCAGCGAGTGGCGCGGCTGCTCAGGCTCCTCTGATAAGCATGCGGG
CTCTGCTACTTCTCGCGCTTCTGCTGTTAGTGCTCCCCCGTCCCGTCGACCCCCGGTCCCCCACCCAGTCCCCC
GAGGAGGTCCGCAAATGCAAATTCCAAGAACCCTGGAAATTCCTCAAATGCTACCGCCAAAAATCAGACATGCA
TCCCAGCTGGATCATGATCATTGGGATCGTGAACATTCTGGCCTGCACCCTCATCTCCTTTGTGATTTACCCCT
GCTTTGACTTTGGTTGGAACTCGCCAGAGGCGCTCTATCTCCCGCCTGAACCTGACACACCACCACAGCAACCT
CAGGCACACGCACTACCACCACTACAGCCTAGGCCACAATACATGCCCATATTAGACTATGAGGCCGAGCCACA
GCGACCCATGCTCCCCGCTATTAGTTACTTCAATCTAACCGGCGGAGATGACTGACCCACTGGCCAACAACAAC
GTCAACGACCTTCTCCTGGACATGGACGGCCGCGCCTCGGAGCAGCGACTCGCCCAACTTCGCATTCGCCAGCA
GCAGGAGAGAGCCGTCAAGGAGCTGCAGGATGCGGTGGCCATCCACCAGTGCAAGAGAGGCATCTTCTGCCTGG
TGAAACAGGCCAAGATCTCCTACGAGGTCACTCCAAACGACCATCGCCTCTCCTACGAGCTCCTGCAGCAGCGC
CAGAAGTTCACCTGCCTGGTCGGAGTCAACCCCATCGTCATCACCCAGCAGTCTGGCGATACCAAGGGGTGCAT
CCACTGCTCCTGCGACTCCCCCGACTGCGTCCACACTCTGATCAAGACCCTCTGCGGCCTCCGCGACCTCCTCC
CCATGAACTAATCACCCCCTTATCCAGTGAAATAAAGATCATATTGATGATGATTTTACAGAAATAAAAAATAA
TCATTTGATTTGAAATAAAGATACAATCATATTGATGATTTGAGTTTAACAAAAAAATAAAGAATCACTTACTT
GAAATCTGATACCAGGTCTCTGTCCATGTTTTCTGCCAACACCACTTCACTCCCCTCTTCCCAGCTCTGGTACT
GCAGGCCCCGGCGGGCTGCAAACTTCCTCCACACGCTGAAGGGGATGTCAAATTCCTCCTGTCCCTCAATCTTC
ATTTTATCTTCTATCAGATGTCCAAAAAGCGCGTCCGGGTGGATGATGACTTCGACCCCGTCTACCCCTACGAT
GCAGACAACGCACCGACCGTGCCCTTCATCAACCCCCCCTTCGTCTCTTCAGATGGATTCCAAGAGAAGCCCCT
GGGGGTGTTGTCCCTGCGACTGGCCGACCCCGTCACCACCAAGAACGGGGAAATCACCCTCAAGCTGGGAGAGG
GGGTGGACCTCGATTCCTCGGGAAAACTCATCTCCAACACGGCCACCAAGGCCGCCGCCCCTCTCAGTTTTTCC
AACAACACCATTTCCCTTAACATGGATCACCCCTTTTACACTAAAGATGGAAAATTATCCTTACAAGTTTCTCC
ACCATTAAATATACTGAGAACAAGCATTCTAAACACACTAGCTTTAGGTTTTGGATCAGGTTTAGGACTCCGTG
GCTCTGCCTTGGCAGTACAGTTAGTCTCTCCACTTACATTTGATACTGATGGAAACATAAAGCTTACCTTAGAC
AGAGGTTTGCATGTTACAACAGGAGATGCAATTGAAAGCAACATAAGCTGGGCTAAAGGTTTAAAATTTGAAGA
TGGAGCCATAGCAACCAACATTGGAAATGGGTTAGAGTTTGGAAGCAGTAGTACAGAAACAGGTGTTGATGATG
CTTACCCAATCCAAGTTAAACTTGGATCTGGCCTTAGCTTTGACAGTACAGGAGCCATAATGGCTGGTAACAAA
GAAGACGATAAACTCACTTTGTGGACAACACCTGATCCATCACCAAACTGTCAAATACTCGCAGAAAATGATGC
AAAACTAACACTTTGCTTGACTAAATGTGGTAGTCAAATACTGGCCACTGTGTCAGTCTTAGTTGTAGGAAGTG
GAAACCTAAACCCCATTACTGGCACCGTAAGCAGTGCTCAGGTGTTTCTACGTTTTGATGCAAACGGTGTTCTT
TTAACAGAACATTCTACACTAAAAAAATACTGGGGGTATAGGCAGGGAGATAGCATAGATGGCACTCCATATAC
CAATGCTGTAGGATTCATGCCCAATTTAAAAGCTTATCCAAAGTCACAAAGTTCTACTACTAAAAATAATATAG
TAGGGCAAGTATACATGAATGGAGATGTTTCAAAACCTATGCTTCTCACTATAACCCTCAATGGTACTGATGAC
AGCAACAGTACATATTCAATGTCATTTTCATACACCTGGACTAATGGAAGCTATGTTGGAGCAACATTTGGGGC
TAACTCTTATACCTTCTCATACATCGCCCAAGAATGAACACTGTATCCCACCCTGCATGCCAACCCTTCCCACC
CCACTCTGTGGAACAAACTCTGAAACACAAAATAAAATAAAGTTCAAGTGTTTTATTGATTCAACAGTTTTACA
GGATTCGAGCAGTTATTTTTCCTCCACCCTCCCAGGACATGGAATACACCACCCTCTCCCCCCGCACAGCCTTG
AACATCTGAATGCCATTGGTGATGGACATGCTTTTGGTCTCCACGTTCCACACAGTTTCAGAGCGAGCCAGTCT
CGGGTCGGTCAGGGAGATGAAACCCTCCGGGCACTCCCGCATCTGCACCTCACAGCTCAACAGCTGAGGATTGT
CCTCGGTGGTCGGGATCACGGTTATCTGGAAGAAGCAGAAGAGCGGCGGTGGGAATCATAGTCCGCGAACGGGA
TCGGCCGGTGGTGTCGCATCAGGCCCCGCAGCAGTCGCTGCCGCCGCCGCTCCGTCAAGCTGCTGCTCAGGGGG
TCCGGGTCCAGGGACTCCCTCAGCATGATGCCCACGGCCCTCAGCATCAGTCGTCTGGTGCGGCGGGCGCAGCA
GCGCATGCGGATCTCGCTCAGGTCGCTGCAGTACGTGCAACACAGAACCACCAGGTTGTTCAACAGTCCATAGT

2026201462 26 Feb 2026

TCAACACGCTCCAGCCGAAACTCATCGCGGGAAGGATGCTACCCACGTGGCCGTCGTACCAGATCCTCAGGTAA
ATCAAGTGGTGCCCCCTCCAGAACACGCTGCCCACGTACATGATCTCCTTGGGCATGTGGCGGTTCACCACCTC
CCGGTACCACATCACCCTCTGGTTGAACATGCAGCCCCGGATGATCCTGCGGAACCACAGGGCCAGCACCGCCC
CGCCCGCCATGCAGCGAAGAGACCCCGGGTCCCGGCAATGGCAATGGAGGACCCACCGCTCGTACCCGTGGATC
ATCTGGGAGCTGAACAAGTCTATGTTGGCACAGCACAGGCATATGCTCATGCATCTCTTCAGCACTCTCAACTC
CTCGGGGGTCAAAACCATATCCCAGGGCACGGGGAACTCTTGCAGGACAGCGAACCCCGCAGAACAGGGCAATC
CTCGCACAGAACTTACATTGTGCATGGACAGGGTATCGCAATCAGGCAGCACCGGGTGATCCTCCACCAGAGAA
GCGCGGGTCTCGGTCTCCTCACAGCGTGGTAAGGGGGCCGGCCGATACGGGTGATGGCGGGACGCGGCTGATCG
TGTTCGCGACCGTGTCATGATGCAGTTGCTTTCGGACATTTTCGTACTTGCTGTAGCAGAACCTGGTCCGGGCG
CTGCACACCGATCGCCGGCGGCGGTCTCGGCGCTTGGAACGCTCGGTGTTGAAATTGTAAAACAGCCACTCTCT
CAGACCGTGCAGCAGATCTAGGGCCTCAGGAGTGATGAAGATCCCATCATGCCTGATGGCTCTGATCACATCGA
CCACCGTGGAATGGGCCAGACCCAGCCAGATGATGCAATTTTGTTGGGTTTCGGTGACGGCGGGGGAGGGAAGA
ACAGGAAGAACCATGATTAACTTTTAATCCAAACGGTCTCGGAGTACTTCAAAATGAAGATCGCGGAGATGGCA
CCTCTCGCCCCCGCTGTGTTGGTGGAAAATAACAGCCAGGTCAAAGGTGATACGGTTCTCGAGATGTTCCACGG
TGGCTTCCAGCAAAGCCTCCACGCGCACATCCAGAAACAAGACAATAGCGAAAGCGGGAGGGTTCTCTAATTCC
TCAATCATCATGTTACACTCCTGCACCATCCCCAGATAATTTTCATTTTTCCAGCCTTGAATGATTCGAACTAG
TTCcTGAGGTAAATCCAAGCCAGCCATGATAAAGAGCTCGCGCAGAGCGCCCTCCACCGGCATTCTTAAGCACA
CCCTCATAATTCCAAGATATTCTGCTCCTGGTTCACCTGCAGCAGATTGACAAGCGGAATATCAAAATCTCTGC
CGCGATCCCTGAGCTCCTCCCTCAGCAATAACTGTAAGTACTCTTTCATATCCTCTCCGAAATTTTTAGCCATA
GGACCACCAGGAATAAGATTAGGGCAAGCCACAGTACAGATAAACCGAAGTCCTCCCCAGTGAGCATTGCCAAA
TGCAAGACTGCTATAAGCATGCTGGCTAGACCCGGTGATATCTTCCAGATAACTGGACAGAAAATCGCCCAGGC
AATTTTTAAGAAAATCAACAAAAGAAAAATCCTCCAGGTGGACGTTTAGAGCCTCGGGAACAACGATGAAGTAA
ATGCAAGCGGTGCGTTCCAGCATGGTTAGTTAGCTGATCTGTAGAAAAAACAAAAATGAACATTAAACCATGCT
AGCCTGGCGAACAGGTGGGTAAATCGTTCTCTCCAGCACCAGGCAGGCCACGGGGTCTCCGGCGCGACCCTCGT
AAAAATTGTCGCTATGATTGAAAACCATCACAGAGAGACGTTCCCGGTGGCCGGCGTGAATGATTCGACAAGAT
GAATACACCCCCGGAACATTGGCGTCCGCGAGTGAAAAAAAGCGCCCGAGGAAGCAATAAGGCACTACAATGCT
CAGTCTCAAGTCCAGCAAAGCGATGCCATGCGGATGAAGCACAAAATTCTCAGGTGCGTACAAAATGTAATTAC
TCCCCTCCTGCACAGGCAGCAAAGCCCCCGATCCCTCCAGGTACACATACAAAGCCTCAGCGTCCATAGCTTAC
CGAGCAGCAGCACACAACAGGCGCAAGAGTCAGAGAAAGGCTGAGCTCTAACCTGTCCACCCGCTCTCTGCTCA
ATATATAGCCCAGATCTACACTGACGTAAAGGCCAAAGTCTAAAAATACCCGCCAAATAATCACACACGCCCAG
CACACGCCCAGAAACCGGTGACACACTCAAAAAAATACGCGCACTTCCTCAAACGCCCAAAACTGCCGTCATTT
CCGGGTTCCCACGCTACGTCATCAAAACACGACTTTCAAATTCCGTCGACCGTTAAAAACGTCACCCGCCCCGC
CCCTAACGGTCGCCCGTCTCTCAGCCAATCAGCGCCCCGCATCCCCAAATTCAAACACCTCATTTGCATATTAA
CGCGCACAAAAAGTTTGAGGTATATTATTGATGATGG

ATCC VR-594 C68 (SEQ ID NO:10); Indepentdently sequenced; Full-Length C68

CCATCTTCAATAATATACCTCAAACTTTTTGTGCGCGTTAATATGCAAATGAGGCGTTTGAATTTGGGGAGGAA
GGGCGGTGATTGGTCGAGGGATGAGCGACCGTTAGGGGCGGGGCGAGTGACGTTTTGATGACGTGGTTGCGAGG
AGGAGCCAGTTTGCAAGTTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTTGAACACGGAAATACTCAAT
TTTCCCGCGCTCTCTGACAGGAAATGAGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGCCATTTTCGCGCGAA
AACTGAATGAGGAAGTGAAAATCTGAGTAATTTCGCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGCCGAGTA
GACTTTGACCGATTACGTGGGGGTTTCGATTACCGTGTTTTTCACCTAAATTTCCGCGTACGGTGTCAAAGTCC
GGTGTTTTTACGTAGGTGTCAGCTGATCGCCAGGGTATTTAAACCTGCGCTCTCCAGTCAAGAGGCCACTCTTG
AGTGCCAGCGAGAAGAGTTTTCTCCTCCGCGCCGCGAGTCAGATCTACACTTTGAAAGATGAGGCACCTGAGAG
ACCTGCCCGATGAGAAAATCATCATCGCTTCCGGGAACGAGATTCTGGAACTGGTGGTAAATGCCATGATGGGC
GACGACCCTCCGGAGCCCCCCACCCCATTTGAGACACCTTCGCTGCACGATTTGTATGATCTGGAGGTGGATGT
GCCCGAGGACGATCCCAATGAGGAGGCGGTAAATGATTTTTTTAGCGATGCCGCGCTGCTAGCTGCCGAGGAGG
CTTCGAGCTCTAGCTCAGACAGCGACTCTTCACTGCATACCCCTAGACCCGGCAGAGGTGAGAAAAAGATCCCC
GAGCTTAAAGGGGAAGAGATGGACTTGCGCTGCTATGAGGAATGCTTGCCCCCGAGCGATGATGAGGACGAGCA
GGCGATCCAGAACGCAGCGAGCCAGGGAGTGCAAGCCGCCAGCGAGAGCTTTGCGCTGGACTGCCCGCCTCTGC
CCGGACACGGCTGTAAGTCTTGTGAATTTCATCGCATGAATACTGGAGATAAAGCTGTGTTGTGTGCACTTTGC
TATATGAGAGCTTACAACCATTGTGTTTACAGTAAGTGTGATTAAGTTGAACTTTAGAGGGAGGCAGAGAGCAG
GGTGACTGGGCGATGACTGGTTTATTTATGTATATATGTTCTTTATATAGGTCCCGTCTCTGACGCAGATGATG
AGACCCCCACTACAAAGTCCACTTCGTCACCCCCAGAAATTGGCACATCTCCACCTGAGAATATTGTTAGACCA
GTTCCTGTTAGAGCCACTGGGAGGAGAGCAGCTGTGGAATGTTTGGATGACTTGCTACAGGGTGGGGTTGAACC
TTTGGACTTGTGTACCCGGAAACGCCCCAGGCACTAAGTGCCACACATGTGTGTTTACTTGAGGTGATGTCAGT
ATTTATAGGGTGTGGAGTGCAATAAAAAATGTGTTGACTTTAAGTGCGTGGTTTATGACTCAGGGGTGGGGACT
GTGAGTATATAAGCAGGTGCAGACCTGTGTGGTTAGCTCAGAGCGGCATGGAGATTTGGACGGTCTTGGAAGAC
TTTCACAAGACTAGACAGCTGCTAGAGAACGCCTCGAACGGAGTCTCTTACCTGTGGAGATTCTGCTTCGGTGG
CGACCTAGCTAGGCTAGTCTACAGGGCCAAACAGGATTATAGTGAACAATTTGAGGTTATTTTGAGAGAGTGTT
CTGGTCTTTTTGACGCTCTTAACTTGGGCCATCAGTCTCACTTTAACCAGAGGATTTCGAGAGCCCTTGATTTT

2026201462 26 Feb 2026

ACTACTCCTGGCAGAACCACTGCAGCAGTAGCCTTTTTTGCTTTTATTCTTGACAAATGGAGTCAAGAAACCCA
TTTCAGCAGGGATTACCAGCTGGATTTCTTAGCAGTAGCTTTGTGGAGAACATGGAAGTGCCAGCGCCTGAATG
CAATCTCCGGCTACTTGCCGGTACAGCCGCTAGACACTCTGAGGATCCTGAATCTCCAGGAGAGTCCCAGGGCA
CGCCAACGTCGCCAGCAGCAGCAGCAGGAGGAGGATCAAGAAGAGAACCCGAGAGCCGGCCTGGACCCTCCGGC
GGAGGAGGAGGAGTAGCTGACCTGTTTCCTGAACTGCGCCGGGTGCTGACTAGGTCTTCGAGTGGTCGGGAGAG
GGGGATTAAGCGGGAGAGGCATGATGAGACTAATCACAGAACTGAACTGACTGTGGGTCTGATGAGTCGCAAGC
GCCCAGAAACAGTGTGGTGGCATGAGGTGCAGTCGACTGGCACAGATGAGGTGTCGGTGATGCATGAGAGGTTT
TCTCTAGAACAAGTCAAGACTTGTTGGTTAGAGCCTGAGGATGATTGGGAGGTAGCCATCAGGAATTATGCCAA
GCTGGCTCTGAGGCCAGACAAGAAGTACAAGATTACTAAGCTGATAAATATCAGAAATGCCTGCTACATCTCAG
GGAATGGGGCTGAAGTGGAGATCTGTCTCCAGGAAAGGGTGGCTTTCAGATGCTGCATGATGAATATGTACCCG
GGAGTGGTGGGCATGGATGGGGTTACCTTTATGAACATGAGGTTCAGGGGAGATGGGTATAATGGCACGGTCTT
TATGGCCAATACCAAGCTGACAGTCCATGGCTGCTCCTTCTTTGGGTTTAATAACACCTGCATCGAGGCCTGGG
GTCAGGTCGGTGTGAGGGGCTGCAGTTTTTCAGCCAACTGGATGGGGGTCGTGGGCAGGACCAAGAGTATGCTG
TCCGTGAAGAAATGCTTGTTTGAGAGGTGCCACCTGGGGGTGATGAGCGAGGGCGAAGCCAGAATCCGCCACTG
CGCCTCTACCGAGACGGGCTGCTTTGTGCTGTGCAAGGGCAATGCTAAGATCAAGCATAATATGATCTGTGGAG
CCTCGGACGAGCGCGGCTACCAGATGCTGACCTGCGCCGGCGGGAACAGCCATATGCTGGCCACCGTACATGTG
GCTTCCCATGCTCGCAAGCCCTGGCCCGAGTTCGAGCACAATGTCATGACCAGGTGCAATATGCATCTGGGGTC
CCGCCGAGGCATGTTCATGCCCTACCAGTGCAACCTGAATTATGTGAAGGTGCTGCTGGAGCCCGATGCCATGT
CCAGAGTGAGCCTGACGGGGGTGTTTGACATGAATGTGGAGGTGTGGAAGATTCTGAGATATGATGAATCCAAG
ACCAGGTGCCGAGCCTGCGAGTGCGGAGGGAAGCATGCCAGGTTCCAGCCCGTGTGTGTGGATGTGACGGAGGA
CCTGCGACCCGATCATTTGGTGTTGCCCTGCACCGGGACGGAGTTCGGTTCCAGCGGGGAAGAATCTGACTAGA
GTGAGTAGTGTTCTGGGGCGGGGGAGGACCTGCATGAGGGCCAGAATAACTGAAATCTGTGCTTTTCTGTGTGT
TGCAGCAGCATGAGCGGAAGCGGCTCCTTTGAGGGAGGGGTATTCAGCCCTTATCTGACGGGGCGTCTCCCCTC
CTGGGCGGGAGTGCGTCAGAATGTGATGGGATCCACGGTGGACGGCCGGCCCGTGCAGCCCGCGAACTCTTCAA
CCCTGACCTATGCAACCCTGAGCTCTTCGTCGTTGGACGCAGCTGCCGCCGCAGCTGCTGCATCTGCCGCCAGC
GCCGTGCGCGGAATGGCCATGGGCGCCGGCTACTACGGCACTCTGGTGGCCAACTCGAGTTCCACCAATAATCC
CGCCAGCCTGAACGAGGAGAAGCTGTTGCTGCTGATGGCCCAGCTCGAGGCCTTGACCCAGCGCCTGGGCGAGC
TGACCCAGCAGGTGGCTCAGCTGCAGGAGCAGACGCGGGCCGCGGTTGCCACGGTGAAATCCAAATAAAAAATG
AATCAATAAATAAACGGAGACGGTTGTTGATTTTAACACAGAGTCTGAATCTTTATTTGATTTTTCGCGCGCGG
TAGGCCCTGGACCACCGGTCTCGATCATTGAGCACCCGGTGGATCTTTTCCAGGACCCGGTAGAGGTGGGCTTG
GATGTTGAGGTACATGGGCATGAGCCCGTCCCGGGGGTGGAGGTAGCTCCATTGCAGGGCCTCGTGCTCGGGGG
TGGTGTTGTAAATCACCCAGTCATAGCAGGGGCGCAGGGCATGGTGTTGCACAATATCTTTGAGGAGGAGACTG
ATGGCCACGGGCAGCCCTTTGGTGTAGGTGTTTACAAATCTGTTGAGCTGGGAGGGATGCATGCGGGGGGAGAT
GAGGTGCATCTTGGCCTGGATCTTGAGATTGGCGATGTTACCGCCCAGATCCCGCCTGGGGTTCATGTTGTGCA
GGACCACCAGCACGGTGTATCCGGTGCACTTGGGGAATTTATCATGCAACTTGGAAGGGAAGGCGTGAAAGAAT
TTGGCGACGCCTTTGTGCCCGCCCAGGTTTTCCATGCACTCATCCATGATGATGGCGATGGGCCCGTGGGCGGC
GGCCTGGGCAAAGACGTTTCGGGGGTCGGACACATCATAGTTGTGGTCCTGGGTGAGGTCATCATAGGCCATTT
TAATGAATTTGGGGCGGAGGGTGCCGGACTGGGGGACAAAGGTACCCTCGATCCCGGGGGCGTAGTTCCCCTCA
CAGATCTGCATCTCCCAGGCTTTGAGCTCGGAGGGGGGGATCATGTCCACCTGCGGGGCGATAAAGAACACGGT
TTCCGGGGCGGGGGAGATGAGCTGGGCCGAAAGCAAGTTCCGGAGCAGCTGGGACTTGCCGCAGCCGGTGGGGC
CGTAGATGACCCCGATGACCGGCTGCAGGTGGTAGTTGAGGGAGAGACAGCTGCCGTCCTCCCGGAGGAGGGGG
GCCACCTCGTTCATCATCTCGCGCACGTGCATGTTCTCGCGCACCAGTTCCGCCAGGAGGCGCTCTCCCCCCAG
GGATAGGAGCTCCTGGAGCGAGGCGAAGTTTTTCAGCGGCTTGAGTCCGTCGGCCATGGGCATTTTGGAGAGGG
TTTGTTGCAAGAGTTCCAGGCGGTCCCAGAGCTCGGTGATGTGCTCTACGGCATCTCGATCCAGCAGACCTCCT
CGTTTCGCGGGTTGGGACGGCTGCGGGAGTAGGGCACCAGACGATGGGCGTCCAGCGCAGCCAGGGTCCGGTCC
TTCCAGGGTCGCAGCGTCCGCGTCAGGGTGGTCTCCGTCACGGTGAAGGGGTGCGCGCCGGGCTGGGCGCTTGC
GAGGGTGCGCTTCAGGCTCATCCGGCTGGTCGAAAACCGCTCCCGATCGGCGCCCTGCGCGTCGGCCAGGTAGC
AATTGACCATGAGTTCGTAGTTGAGCGCCTCGGCCGCGTGGCCTTTGGCGCGGAGCTTACCTTTGGAAGTCTGC
CCGCAGGCGGGACAGAGGAGGGACTTGAGGGCGTAGAGCTTGGGGGCGAGGAAGACGGACTCGGGGGCGTAGGC
GTCCGCGCCGCAGTGGGCGCAGACGGTCTCGCACTCCACGAGCCAGGTGAGGTCGGGCTGGTCGGGGTCAAAAA
CCAGTTTCCCGCCGTTCTTTTTGATGCGTTTCTTACCTTTGGTCTCCATGAGCTCGTGTCCCCGCTGGGTGACA
AAGAGGCTGTCCGTGTCCCCGTAGACCGACTTTATGGGCCGGTCCTCGAGCGGTGTGCCGCGGTCCTCCTCGTA
GAGGAACCCCGCCCACTCCGAGACGAAAGCCCGGGTCCAGGCCAGCACGAAGGAGGCCACGTGGGACGGGTAGC
GGTCGTTGTCCACCAGCGGGTCCACCTTTTCCAGGGTATGCAAACACATGTCCCCCTCGTCCACATCCAGGAAG
GTGATTGGCTTGTAAGTGTAGGCCACGTGACCGGGGGTCCCGGCCGGGGGGGTATAAAAGGGTGCGGGTCCCTG
CTCGTCCTCACTGTCTTCCGGATCGCTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATTCCCTCTCGAAGGCGG
GCATGACCTCGGCACTCAGGTTGTCAGTTTCTAGAAACGAGGAGGATTTGATATTGACGGTGCCGGCGGAGATG
CCTTTCAAGAGCCCCTCGTCCATCTGGTCAGAAAAGACGATCTTTTTGTTGTCGAGCTTGGTGGCGAAGGAGCC
GTAGAGGGCGTTGGAGAGGAGCTTGGCGATGGAGCGCATGGTCTGGTTTTTTTCCTTGTCGGCGCGCTCCTTGG
CGGCGATGTTGAGCTGCACGTACTCGCGCGCCACGCACTTCCATTCGGGGAAGACGGTGGTCAGCTCGTCGGGC

2026201462 26 Feb 2026

ACGATTCTGACCTGCCAGCCCCGATTATGCAGGGTGATGAGGTCCACACTGGTGGCCACCTCGCCGCGCAGGGG
CTCATTAGTCCAGCAGAGGCGTCCGCCCTTGCGCGAGCAGAAGGGGGGCAGGGGGTCCAGCATGACCTCGTCGG
GGGGGTCGGCATCGATGGTGAAGATGCCGGGCAGGAGGTCGGGGTCAAAGTAGCTGATGGAAGTGGCCAGATCG
TCCAGGGCAGCTTGCCATTCGCGCACGGCCAGCGCGCGCTCGTAGGGACTGAGGGGCGTGCCCCAGGGCATGGG
ATGGGTAAGCGCGGAGGCGTACATGCCGCAGATGTCGTAGACGTAGAGGGGCTCCTCGAGGATGCCGATGTAGG
TGGGGTAGCAGCGCCCCCCGCGGATGCTGGCGCGCACGTAGTCATACAGCTCGTGCGAGGGGGCGAGGAGCCCC
GGGCCCAGGTTGGTGCGACTGGGCTTTTCGGCGCGGTAGACGATCTGGCGGAAAATGGCATGCGAGTTGGAGGA
GATGGTGGGCCTTTGGAAGATGTTGAAGTGGGCGTGGGGCAGTCCGACCGAGTCGCGGATGAAGTGGGCGTAGG
AGTCTTGCAGCTTGGCGACGAGCTCGGCGGTGACTAGGACGTCCAGAGCGCAGTAGTCGAGGGTCTCCTGGATG
ATGTCATACTTGAGCTGTCCCTTTTGTTTCCACAGCTCGCGGTTGAGAAGGAACTCTTCGCGGTCCTTCCAGTA
CTCTTCGAGGGGGAACCCGTCCTGATCTGCACGGTAAGAGCCTAGCATGTAGAACTGGTTGACGGCCTTGTAGG
CGCAGCAGCCCTTCTCCACGGGGAGGGCGTAGGCCTGGGCGGCCTTGCGCAGGGAGGTGTGCGTGAGGGCGAAA
GTGTCCCTGACCATGACCTTGAGGAACTGGTGCTTGAAGTCGATATCGTCGCAGCCCCCCTGCTCCCAGAGCTG
GAAGTCCGTGCGCTTCTTGTAGGCGGGGTTGGGCAAAGCGAAAGTAACATCGTTGAAGAGGATCTTGCCCGCGC
GGGGCATAAAGTTGCGAGTGATGCGGAAAGGTTGGGGCACCTCGGCCCGGTTGTTGATGACCTGGGCGGCGAGC
ACGATCTCGTCGAAGCCGTTGATGTTGTGGCCCACGATGTAGAGTTCCACGAATCGCGGACGGCCCTTGACGTG
GGGCAGTTTCTTGAGCTCCTCGTAGGTGAGCTCGTCGGGGTCGCTGAGCCCGTGCTGCTCGAGCGCCCAGTCGG
CGAGATGGGGGTTGGCGCGGAGGAAGGAAGTCCAGAGATCCACGGCCAGGGCGGTTTGCAGACGGTCCCGGTAC
TGACGGAACTGCTGCCCGACGGCCATTTTTTCGGGGGTGACGCAGTAGAAGGTGCGGGGGTCCCCGTGCCAGCG
ATCCCATTTGAGCTGGAGGGCGAGATCGAGGGCGAGCTCGACGAGCCGGTCGTCCCCGGAGAGTTTCATGACCA
GCATGAAGGGGACGAGCTGCTTGCCGAAGGACCCCATCCAGGTGTAGGTTTCCACATCGTAGGTGAGGAAGAGC
CTTTCGGTGCGAGGATGCGAGCCGATGGGGAAGAACTGGATCTCCTGCCACCAATTGGAGGAATGGCTGTTGAT
GTGATGGAAGTAGAAATGCCGACGGCGCGCCGAACACTCGTGCTTGTGTTTATACAAGCGGCCACAGTGCTCGC
AACGCTGCACGGGATGCACGTGCTGCACGAGCTGTACCTGAGTTCCTTTGACGAGGAATTTCAGTGGGAAGTGG
AGTCGTGGCGCCTGCATCTCGTGCTGTACTACGTCGTGGTGGTCGGCCTGGCCCTCTTCTGCCTCGATGGTGGT
CATGCTGACGAGCCCGCGCGGGAGGCAGGTCCAGACCTCGGCGCGAGCGGGTCGGAGAGCGAGGACGAGGGCGC
GCAGGCCGGAGCTGTCCAGGGTCCTGAGACGCTGCGGAGTCAGGTCAGTGGGCAGCGGCGGCGCGCGGTTGACT
TGCAGGAGTTTTTCCAGGGCGCGCGGGAGGTCCAGATGGTACTTGATCTCCACCGCGCCATTGGTGGCGACGTC
GATGGCTTGCAGGGTCCCGTGCCCCTGGGGTGTGACCACCGTCCCCCGTTTCTTCTTGGGCGGCTGGGGCGACG
GGGGCGGTGCCTCTTCCATGGTTAGAAGCGGCGGCGAGGACGCGCGCCGGGCGGCAGGGGCGGCTCGGGGCCCG
GAGGCAGGGGCGGCAGGGGCACGTCGGCGCCGCGCGCGGGTAGGTTCTGGTACTGCGCCCGGAGAAGACTGGCG
TGAGCGACGACGCGACGGTTGACGTCCTGGATCTGACGCCTCTGGGTGAAGGCCACGGGACCCGTGAGTTTGAA
CCTGAAAGAGAGTTCGACAGAATCAATCTCGGTATCGTTGACGGCGGCCTGCCGCAGGATCTCTTGCACGTCGC
CCGAGTTGTCCTGGTAGGCGATCTCGGTCATGAACTGCTCGATCTCCTCCTCTTGAAGGTCTCCGCGGCCGGCG
CGCTCCACGGTGGCCGCGAGGTCGTTGGAGATGCGGCCCATGAGCTGCGAGAAGGCGTTCATGCCCGCCTCGTT
CCAGACGCGGCTGTAGACCACGACGCCCTCGGGATCGCgGGCGCGCATGACCACCTGGGCGAGGTTGAGCTCCA
CGTGGCGCGTGAAGACCGCGTAGTTGCAGAGGCGCTGGTAGAGGTAGTTGAGCGTGGTGGCGATGTGCTCGGTG
ACGAAGAAATACATGATCCAGCGGCGGAGCGGCATCTCGCTGACGTCGCCCAGCGCCTCCAAACGTTCCATGGC
CTCGTAAAAGTCCACGGCGAAGTTGAAAAACTGGGAGTTGCGCGCCGAGACGGTCAACTCCTCCTCCAGAAGAC
GGATGAGCTCGGCGATGGTGGCGCGCACCTCGCGCTCGAAGGCCCCCGGGAGTTCCTCCACTTCCTCTTCTTCC
TCCTCCACTAACATCTCTTCTACTTCCTCCTCAGGCGGCAGTGGTGGCGGGGGAGGGGGCCTGCGTCGCCGGCG
GCGCACGGGCAGACGGTCGATGAAGCGCTCGATGGTCTCGCCGCGCCGGCGTCGCATGGTCTCGGTGACGGCGC
GCCCGTCCTCGCGGGGCCGCAGCGTGAAGACGCCGCCGCGCATCTCCAGGTGGCCGGGGGGGTCCCCGTTGGGC
AGGGAGAGGGCGCTGACGATGCATCTTATCAATTGCCCCGTAGGGACTCCGCGCAAGGACCTGAGCGTCTCGAG
ATCCACGGGATCTGAAAACCGCTGAACGAAGGCTTCGAGCCAGTCGCAGTCGCAAGGTAGGCTGAGCACGGTTT
CTTCTGGCGGGTCATGTTGGTTGGGAGCGGGGCGGGCGATGCTGCTGGTGATGAAGTTGAAATAGGCGGTTCTG
AGACGGCGGATGGTGGCGAGGAGCACCAGGTCTTTGGGCCCGGCTTGCTGGATGCGCAGACGGTCGGCCATGCC
CCAGGCGTGGTCCTGACACCTGGCCAGGTCCTTGTAGTAGTCCTGCATGAGCCGCTCCACGGGCACCTCCTCCT
CGCCCGCGCGGCCGTGCATGCGCGTGAGCCCGAAGCCGCGCTGGGGCTGGACGAGCGCCAGGTCGGCGACGACG
CGCTCGGCGAGGATGGCTTGCTGGATCTGGGTGAGGGTGGTCTGGAAGTCATCAAAGTCGACGAAGCGGTGGTA
GGCTCCGGTGTTGATGGTGTAGGAGCAGTTGGCCATGACGGACCAGTTGACGGTCTGGTGGCCCGGACGCACGA
GCTCGTGGTACTTGAGGCGCGAGTAGGCGCGCGTGTCGAAGATGTAGTCGTTGCAGGTGCGCACCAGGTACTGG
TAGCCGATGAGGAAGTGCGGCGGCGGCTGGCGGTAGAGCGGCCATCGCTCGGTGGCGGGGGCGCCGGGCGCGAG
GTCCTCGAGCATGGTGCGGTGGTAGCCGTAGATGTACCTGGACATCCAGGTGATGCCGGCGGCGGTGGTGGAGG
CGCGCGGGAACTCGCGGACGCGGTTCCAGATGTTGCGCAGCGGCAGGAAGTAGTTCATGGTGGGCACGGTCTGG
CCCGTGAGGCGCGCGCAGTCGTGGATGCTCTATACGGGCAAAAACGAAAGCGGTCAGCGGCTCGACTCCGTGGC
CTGGAGGCTAAGCGAACGGGTTGGGCTGCGCGTGTACCCCGGTTCGAATCTCGAATCAGGCTGGAGCCGCAGCT
AACGTGGTATTGGCACTCCCGTCTCGACCCAAGCCTGCACCAACCCTCCAGGATACGGAGGCGGGTCGTTTTGC
AACTTTTTTTTGGAGGCCGGATGAGACTAGTAAGCGCGGAAAGCGGCCGACCGCGATGGCTCGCTGCCGTAGTC
TGGAGAAGAATCGCCAGGGTTGCGTTGCGGTGTGCCCCGGTTCGAGGCCGGCCGGATTCCGCGGCTAACGAGGG

2026201462 26 Feb 2026

CGTGGCTGCCCCGTCGTTTCCAAGACCCCATAGCCAGCCGACTTCTCCAGTTACGGAGCGAGCCCCTCTTTTGT
TTTGTTTGTTTTTGCCAGATGCATCCCGTACTGCGGCAGATGCGCCCCCACCACCCTCCACCGCAACAACAGCC
CCCTCCACAGCCGGCGCTTCTGCCCCCGCCCCAGCAGCAACTTCCAGCCACGACCGCCGCGGCCGCCGTGAGCG
GGGCTGGACAGAGTTATGATCACCAGCTGGCCTTGGAAGAGGGCGAGGGGCTGGCGCGCCTGGGGGCGTCGTCG
CCGGAGCGGCACCCGCGCGTGCAGATGAAAAGGGACGCTCGCGAGGCCTACGTGCCCAAGCAGAACCTGTTCAG
AGACAGGAGCGGCGAGGAGCCCGAGGAGATGCGCGCGGCCCGGTTCCACGCGGGGCGGGAGCTGCGGCGCGGCC
TGGACCGAAAGAGGGTGCTGAGGGACGAGGATTTCGAGGCGGACGAGCTGACGGGGATCAGCCCCGCGCGCGCG
CACGTGGCCGCGGCCAACCTGGTCACGGCGTACGAGCAGACCGTGAAGGAGGAGAGCAACTTCCAAAAATCCTT
CAACAACCACGTGCGCACCCTGATCGCGCGCGAGGAGGTGACCCTGGGCCTGATGCACCTGTGGGACCTGCTGG
AGGCCATCGTGCAGAACCCCACCAGCAAGCCGCTGACGGCGCAGCTGTTCCTGGTGGTGCAGCATAGTCGGGAC
AACGAAGCGTTCAGGGAGGCGCTGCTGAATATCACCGAGCCCGAGGGCCGCTGGCTCCTGGACCTGGTGAACAT
TCTGCAGAGCATCGTGGTGCAGGAGCGCGGGCTGCCGCTGTCCGAGAAGCTGGCGGCCATCAACTTCTCGGTGC
TGAGTTTGGGCAAGTACTACGCTAGGAAGATCTACAAGACCCCGTACGTGCCCATAGACAAGGAGGTGAAGATC
GACGGGTTTTACATGCGCATGACCCTGAAAGTGCTGACCCTGAGCGACGATCTGGGGGTGTACCGCAACGACAG
GATGCACCGTGCGGTGAGCGCCAGCAGGCGGCGCGAGCTGAGCGACCAGGAGCTGATGCATAGTCTGCAGCGGG
CCCTGACCGGGGCCGGGACCGAGGGGGAGAGCTACTTTGACATGGGCGCGGACCTGCACTGGCAGCCCAGCCGC
CGGGCCTTGGAGGCGGCGGCAGGACCCTACGTAGAAGAGGTGGACGATGAGGTGGACGAGGAGGGCGAGTACCT
GGAAGACTGATGGCGCGACCGTATTTTTGCTAGATGCAACAACAACAGCCACCTCCTGATCCCGCGATGCGGGC
GGCGCTGCAGAGCCAGCCGTCCGGCATTAACTCCTCGGACGATTGGACCCAGGCCATGCAACGCATCATGGCGC
TGACGACCCGCAACCCCGAAGCCTTTAGACAGCAGCCCCAGGCCAACCGGCTCTCGGCCATCCTGGAGGCCGTG
GTGCCCTCGCGCTCCAACCCCACGCACGAGAAGGTCCTGGCCATCGTGAACGCGCTGGTGGAGAACAAGGCCAT
CCGCGGCGACGAGGCCGGCCTGGTGTACAACGCGCTGCTGGAGCGCGTGGCCCGCTACAACAGCACCAACGTGC
AGACCAACCTGGACCGCATGGTGACCGACGTGCGCGAGGCCGTGGCCCAGCGCGAGCGGTTCCACCGCGAGTCC
AACCTGGGATCCATGGTGGCGCTGAACGCCTTCCTCAGCACCCAGCCCGCCAACGTGCCCCGGGGCCAGGAGGA
CTACACCAACTTCATCAGCGCCCTGCGCCTGATGGTGACCGAGGTGCCCCAGAGCGAGGTGTACCAGTCCGGGC
CGGACTACTTCTTCCAGACCAGTCGCCAGGGCTTGCAGACCGTGAACCTGAGCCAGGCTTTCAAGAACTTGCAG
GGCCTGTGGGGCGTGCAGGCCCCGGTCGGGGACCGCGCGACGGTGTCGAGCCTGCTGACGCCGAACTCGCGCCT
GCTGCTGCTGCTGGTGGCCCCCTTCACGGACAGCGGCAGCATCAACCGCAACTCGTACCTGGGCTACCTGATTA
ACCTGTACCGCGAGGCCATCGGCCAGGCGCACGTGGACGAGCAGACCTACCAGGAGATCACCCACGTGAGCCGC
GCCCTGGGCCAGGACGACCCGGGCAACCTGGAAGCCACCCTGAACTTTTTGCTGACCAACCGGTCGCAGAAGAT
CCCGCCCCAGTACGCGCTCAGCACCGAGGAGGAGCGCATCCTGCGTTACGTGCAGCAGAGCGTGGGCCTGTTCC
TGATGCAGGAGGGGGCCACCCCCAGCGCCGCGCTCGACATGACCGCGCGCAACATGGAGCCCAGCATGTACGCC
AGCAACCGCCCGTTCATCAATAAACTGATGGACTACTTGCATCGGGCGGCCGCCATGAACTCTGACTATTTCAC
CAACGCCATCCTGAATCCCCACTGGCTCCCGCCGCCGGGGTTCTACACGGGCGAGTACGACATGCCCGACCCCA
ATGACGGGTTCCTGTGGGACGATGTGGACAGCAGCGTGTTCTCCCCCCGACCGGGTGCTAACGAGCGCCCCTTG
TGGAAGAAGGAAGGCAGCGACCGACGCCCGTCCTCGGCGCTGTCCGGCCGCGAGGGTGCTGCCGCGGCGGTGCC
CGAGGCCGCCAGTCCTTTCCCGAGCTTGCCCTTCTCGCTGAACAGTATCCGCAGCAGCGAGCTGGGCAGGATCA
CGCGCCCGCGCTTGCTGGGCGAAGAGGAGTACTTGAATGACTCGCTGTTGAGACCCGAGCGGGAGAAGAACTTC
CCCAATAACGGGATAGAAAGCCTGGTGGACAAGATGAGCCGCTGGAAGACGTATGCGCAGGAGCACAGGGACGA
TCCCCGGGCGTCGCAGGGGGCCACGAGCCGGGGCAGCGCCGCCCGTAAACGCCGGTGGCACGACAGGCAGCGGG
GACAGATGTGGGACGATGAGGACTCCGCCGACGACAGCAGCGTGTTGGACTTGGGTGGGAGTGGTAACCCGTTC
GCTCACCTGCGCCCCCGTATCGGGCGCATGATGTAAGAGAAACCGAAAATAAATGATACTCACCAAGGCCATGG
CGACCAGCGTGCGTTCGTTTCTTCTCTGTTGTTGTTGTATCTAGTATGATGAGGCGTGCGTACCCGGAGGGTCC
TCCTCCCTCGTACGAGAGCGTGATGCAGCAGGCGATGGCGGCGGCGGCGATGCAGCCCCCGCTGGAGGCTCCTT
ACGTGCCCCCGCGGTACCTGGCGCCTACGGAGGGGCGGAACAGCATTCGTTACTCGGAGCTGGCACCCTTGTAC
GATACCACCCGGTTGTACCTGGTGGACAACAAGTCGGCGGACATCGCCTCGCTGAACTACCAGAACGACCACAG
CAACTTCCTGACCACCGTGGTGCAGAACAATGACTTCACCCCCACGGAGGCCAGCACCCAGACCATCAACTTTG
ACGAGCGCTCGCGGTGGGGCGGCCAGCTGAAAACCATCATGCACACCAACATGCCCAACGTGAACGAGTTCATG
TACAGCAACAAGTTCAAGGCGCGGGTGATGGTCTCCCGCAAGACCCCCAATGGGGTGACAGTGACAGAGGATTA
TGATGGTAGTCAGGATGAGCTGAAGTATGAATGGGTGGAATTTGAGCTGCCCGAAGGCAACTTCTCGGTGACCA
TGACCATCGACCTGATGAACAACGCCATCATCGACAATTACTTGGCGGTGGGGCGGCAGAACGGGGTGCTGGAG
AGCGACATCGGCGTGAAGTTCGACACTAGGAACTTCAGGCTGGGCTGGGACCCCGTGACCGAGCTGGTCATGCC
CGGGGTGTACACCAACGAGGCTTTCCATCCCGATATTGTCTTGCTGCCCGGCTGCGGGGTGGACTTCACCGAGA
GCCGCCTCAGCAACCTGCTGGGCATTCGCAAGAGGCAGCCCTTCCAGGAAGGCTTCCAGATCATGTACGAGGAT
CTGGAGGGGGGCAACATCCCCGCGCTCCTGGATGTCGACGCCTATGAGAAAAGCAAGGAGGATGCAGCAGCTGA
AGCAACTGCAGCCGTAGCTACCGCCTCTACCGAGGTCAGGGGCGATAATTTTGCAAGCGCCGCAGCAGTGGCAG
CGGCCGAGGCGGCTGAAACCGAAAGTAAGATAGTCATTCAGCCGGTGGAGAAGGATAGCAAGAACAGGAGCTAC
AACGTACTACCGGACAAGATAAACACCGCCTACCGCAGCTGGTACCTAGCCTACAACTATGGCGACCCCGAGAA
GGGCGTGCGCTCCTGGACGCTGCTCACCACCTCGGACGTCACCTGCGGCGTGGAGCAAGTCTACTGGTCGCTGC
CCGACATGATGCAAGACCCGGTCACCTTCCGCTCCACGCGTCAAGTTAGCAACTACCCGGTGGTGGGCGCCGAG

2026201462 26 Feb 2026

CTCCTGCCCGTCTACTCCAAGAGCTTCTTCAACGAGCAGGCCGTCTACTCGCAGCAGCTGCGCGCCTTCACCTC
GCTTACGCACGTCTTCAACCGCTTCCCCGAGAACCAGATCCTCGTCCGCCCGCCCGCGCCCACCATTACCACCG
TCAGTGAAAACGTTCCTGCTCTCACAGATCACGGGACCCTGCCGCTGCGCAGCAGTATCCGGGGAGTCCAGCGC
GTGACCGTTACTGACGCCAGACGCCGCACCTGCCCCTACGTCTACAAGGCCCTGGGCATAGTCGCGCCGCGCGT
CCTCTCGAGCCGCACCTTCTAAATGTCCATTCTCATCTCGCCCAGTAATAACACCGGTTGGGGCCTGCGCGCGC
CCAGCAAGATGTACGGAGGCGCTCGCCAACGCTCCACGCAACACCCCGTGCGCGTGCGCGGGCACTTCCGCGCT
CCCTGGGGCGCCCTCAAGGGCCGCGTGCGGTCGCGCACCACCGTCGACGACGTGATCGACCAGGTGGTGGCCGA
CGCGCGCAACTACACCCCCGCCGCCGCGCCCGTCTCCACCGTGGACGCCGTCATCGACAGCGTGGTGGCcGACG
CGCGCCGGTACGCCCGCGCCAAGAGCCGGCGGCGGCGCATCGCCCGGCGGCACCGGAGCACCCCCGCCATGCGC
GCGGCGCGAGCCTTGCTGCGCAGGGCCAGGCGCACGGGACGCAGGGCCATGCTCAGGGCGGCCAGACGCGCGGC
TTCAGGCGCCAGCGCCGGCAGGACCCGGAGACGCGCGGCCACGGCGGCGGCAGCGGCCATCGCCAGCATGTCCC
GCCCGCGGCGAGGGAACGTGTACTGGGTGCGCGACGCCGCCACCGGTGTGCGCGTGCCCGTGCGCACCCGCCCC
CCTCGCACTTGAAGATGTTCACTTCGCGATGTTGATGTGTCCCAGCGGCGAGGAGGATGTCCAAGCGCAAATTC
AAGGAAGAGATGCTCCAGGTCATCGCGCCTGAGATCTACGGCCCTGCGGTGGTGAAGGAGGAAAGAAAGCCCCG
CAAAATCAAGCGGGTCAAAAAGGACAAAAAGGAAGAAGAAAGTGATGTGGACGGATTGGTGGAGTTTGTGCGCG
AGTTCGCCCCCCGGCGGCGCGTGCAGTGGCGCGGGCGGAAGGTGCAACCGGTGCTGAGACCCGGCACCACCGTG
GTCTTCACGCCCGGCGAGCGCTCCGGCACCGCTTCCAAGCGCTCCTACGACGAGGTGTACGGGGATGATGATAT
TCTGGAGCAGGCGGCCGAGCGCCTGGGCGAGTTTGCTTACGGCAAGCGCAGCCGTTCCGCACCGAAGGAAGAGG
CGGTGTCCATCCCGCTGGACCACGGCAACCCCACGCCGAGCCTCAAGCCCGTGACCTTGCAGCAGGTGCTGCCG
ACCGCGGCGCCGCGCCGGGGGTTCAAGCGCGAGGGCGAGGATCTGTACCCCACCATGCAGCTGATGGTGCCCAA
GCGCCAGAAGCTGGAAGACGTGCTGGAGACCATGAAGGTGGACCCGGACGTGCAGCCCGAGGTCAAGGTGCGGC
CCATCAAGCAGGTGGCCCCGGGCCTGGGCGTGCAGACCGTGGACATCAAGATTCCCACGGAGCCCATGGAAACG
CAGACCGAGCCCATGATCAAGCCCAGCACCAGCACCATGGAGGTGCAGACGGATCCCTGGATGCCATCGGCTCC
TAGTCGAAGACCCCGGCGCAAGTACGGCGCGGCCAGCCTGCTGATGCCCAACTACGCGCTGCATCCTTCCATCA
TCCCCACGCCGGGCTACCGCGGCACGCGCTTCTACCGCGGTCATACCAGCAGCCGCCGCCGCAAGACCACCACT
CGCCGCCGCCGTCGCCGCACCGCCGCTGCAACCACCCCTGCCGCCCTGGTGCGGAGAGTGTACCGCCGCGGCCG
CGCACCTCTGACCCTGCCGCGCGCGCGCTACCACCCGAGCATCGCCATTTAAACTTTCGCCtGCTTTGCAGATC
AATGGCCCTCACATGCCGCCTTCGCGTTCCCATTACGGGCTACCGAGGAAGAAAACCGCGCCGTAGAAGGCTGG
CGGGGAACGGGATGCGTCGCCACCACCACCGGCGGCGGCGCGCCATCAGCAAGCGGTTGGGGGGAGGCTTCCTG
CCCGCGCTGATCCCCATCATCGCCGCGGCGATCGGGGCGATCCCCGGCATTGCTTCCGTGGCGGTGCAGGCCTC
TCAGCGCCACTGAGACACACTTGGAAACATCTTGTAATAAACCaATGGACTCTGACGCTCCTGGTCCTGTGATG
TGTTTTCGTAGACAGATGGAAGACATCAATTTTTCGTCCCTGGCTCCGCGACACGGCACGCGGCCGTTCATGGG
CACCTGGAGCGACATCGGCACCAGCCAACTGAACGGGGGCGCCTTCAATTGGAGCAGTCTCTGGAGCGGGCTTA
AGAATTTCGGGTCCACGCTTAAAACCTATGGCAGCAAGGCGTGGAACAGCACCACAGGGCAGGCGCTGAGGGAT
AAGCTGAAAGAGCAGAACTTCCAGCAGAAGGTGGTCGATGGGCTCGCCTCGGGCATCAACGGGGTGGTGGACCT
GGCCAACCAGGCCGTGCAGCGGCAGATCAACAGCCGCCTGGACCCGGTGCCGCCCGCCGGCTCCGTGGAGATGC
CGCAGGTGGAGGAGGAGCTGCCTCCCCTGGACAAGCGGGGCGAGAAGCGACCCCGCCCCGATGCGGAGGAGACG
CTGCTGACGCACACGGACGAGCCGCCCCCGTACGAGGAGGCGGTGAAACTGGGTCTGCCCACCACGCGGCCCAT
CGCGCCCCTGGCCACCGGGGTGCTGAAACCCGAAAAGCCCGCGACCCTGGACTTGCCTCCTCCCCAGCCTTCCC
GCCCCTCTACAGTGGCTAAGCCCCTGCCGCCGGTGGCCGTGGCCCGCGCGCGACCCGGGGGCACCGCCCGCCCT
CATGCGAACTGGCAGAGCACTCTGAACAGCATCGTGGGTCTGGGAGTGCAGAGTGTGAAGCGCCGCCGCTGCTA
TTAAACCTACCGTAGCGCTTAACTTGCTTGTCTGTGTGTGTATGTATTATGTCGCCGCCGCCGCTGTCCACCAG
AAGGAGGAGTGAAGAGGCGCGTCGCCGAGTTGCAAGATGGCCACCCCATCGATGCTGCCCCAGTGGGCGTACAT
GCACATCGCCGGACAGGACGCTTCGGAGTACCTGAGTCCGGGTCTGGTGCAGTTTGCCCGCGCCACAGACACCT
ACTTCAGTCTGGGGAACAAGTTTAGGAACCCCACGGTGGCGCCCACGCACGATGTGACCACCGACCGCAGCCAG
CGGCTGACGCTGCGCTTCGTGCCCGTGGACCGCGAGGACAACACCTACTCGTACAAAGTGCGCTACACGCTGGC
CGTGGGCGACAACCGCGTGCTGGACATGGCCAGCACCTACTTTGACATCCGCGGCGTGCTGGATCGGGGCCCTA
GCTTCAAACCCTACTCCGGCACCGCCTACAACAGTCTGGCCCCCAAGGGAGCACCCAACACTTGTCAGTGGACA
TATAAAGCCGATGGTGAAACTGCCACAGAAAAAACCTATACATATGGAAATGCACCCGTGCAGGGCATTAACAT
CACAAAAGATGGTATTCAACTTGGAACTGACACCGATGATCAGCCAATCTACGCAGATAAAACCTATCAGCCTG
AACCTCAAGTGGGTGATGCTGAATGGCATGACATCACTGGTACTGATGAAAAGTATGGAGGCAGAGCTCTTAAG
CCTGATACCAAAATGAAGCCTTGTTATGGTTCTTTTGCCAAGCCTACTAATAAAGAAGGAGGTCAGGCAAATGT
GAAAACAGGAACAGGCACTACTAAAGAATATGACATAGACATGGCTTTCTTTGACAACAGAAGTGCGGCTGCTG
CTGGCCTAGCTCCAGAAATTGTTTTGTATACTGAAAATGTGGATTTGGAAACTCCAGATACCCATATTGTATAC
AAAGCAGGCACAGATGACAGCAGCTCTTCTATTAATTTGGGTCAGCAAGCCATGCCCAACAGACCTAACTACAT
TGGTTTCAGAGACAACTTTATCGGGCTCATGTACTACAACAGCACTGGCAATATGGGGGTGCTGGCCGGTCAGG
CTTCTCAGCTGAATGCTGTGGTTGACTTGCAAGACAGAAACACCGAGCTGTCCTACCAGCTCTTGCTTGACTCT
CTGGGTGACAGAACCCGGTATTTCAGTATGTGGAATCAGGCGGTGGACAGCTATGATCCTGATGTGCGCATTAT
TGAAAATCATGGTGTGGAGGATGAACTTCCCAACTATTGTTTCCCTCTGGATGCTGTTGGCAGAACAGATACTT
ATCAGGGAATTAAGGCTAATGGAACTGATCAAACCACATGGACCAAAGATGACAGTGTCAATGATGCTAATGAG

2026201462 26 Feb 2026

ATAGGCAAGGGTAATCCATTCGCCATGGAAATCAACATCCAAGCCAACCTGTGGAGGAACTTCCTCTACGCCAA
CGTGGCCCTGTACCTGCCCGACTCTTACAAGTACACGCCGGCCAATGTTACCCTGCCCACCAACACCAACACCT
ACGATTACATGAACGGCCGGGTGGTGGCGCCCTCGCTGGTGGACTCCTACATCAACATCGGGGCGCGCTGGTCG
CTGGATCCCATGGACAACGTGAACCCCTTCAACCACCACCGCAATGCGGGGCTGCGCTACCGCTCCATGCTCCT
GGGCAACGGGCGCTACGTGCCCTTCCACATCCAGGTGCCCCAGAAATTTTTCGCCATCAAGAGCCTCCTGCTCC
TGCCCGGGTCCTACACCTACGAGTGGAACTTCCGCAAGGACGTCAACATGATCCTGCAGAGCTCCCTCGGCAAC
GACCTGCGCACGGACGGGGCCTCCATCTCCTTCACCAGCATCAACCTCTACGCCACCTTCTTCCCCATGGCGCA
CAACACGGCCTCCACGCTCGAGGCCATGCTGCGCAACGACACCAACGACCAGTCCTTCAACGACTACCTCTCGG
CGGCCAACATGCTCTACCCCATCCCGGCCAACGCCACCAACGTGCCCATCTCCATCCCCTCGCGCAACTGGGCC
GCCTTCCGCGGCTGGTCCTTCACGCGTCTCAAGACCAAGGAGACGCCCTCGCTGGGCTCCGGGTTCGACCCCTA
CTTCGTCTACTCGGGCTCCATCCCCTACCTCGACGGCACCTTCTACCTCAACCACACCTTCAAGAAGGTCTCCA
TCACCTTCGACTCCTCCGTCAGCTGGCCCGGCAACGACCGGCTCCTGACGCCCAACGAGTTCGAAATCAAGCGC
ACCGTCGACGGCGAGGGCTACAACGTGGCCCAGTGCAACATGACCAAGGACTGGTTCCTGGTCCAGATGCTGGC
CCACTACAACATCGGCTACCAGGGCTTCTACGTGCCCGAGGGCTACAAGGACCGCATGTACTCCTTCTTCCGCA
ACTTCCAGCCCATGAGCCGCCAGGTGGTGGACGAGGTCAACTACAAGGACTACCAGGCCGTCACCCTGGCCTAC
CAGCACAACAACTCGGGCTTCGTCGGCTACCTCGCGCCCACCATGCGCCAGGGCCAGCCCTACCCCGCCAACTA
CCCCTACCCGCTCATCGGCAAGAGCGCCGTCACCAGCGTCACCCAGAAAAAGTTCCTCTGCGACAGGGTCATGT
GGCGCATCCCCTTCTCCAGCAACTTCATGTCCATGGGCGCGCTCACCGACCTCGGCCAGAACATGCTCTATGCC
AACTCCGCCCACGCGCTAGACATGAATTTCGAAGTCGACCCCATGGATGAGTCCACCCTTCTCTATGTTGTCTT
CGAAGTCTTCGACGTCGTCCGAGTGCACCAGCCCCACCGCGGCGTCATCGAGGCCGTCTACCTGCGCACCCCCT
TCTCGGCCGGTAACGCCACCACCTAAGCTCTTGCTTCTTGCAAGCCATGGCCGCGGGCTCCGGCGAGCAGGAGC
TCAGGGCCATCATCCGCGACCTGGGCTGCGGGCCCTACTTCCTGGGCACCTTCGATAAGCGCTTCCCGGGATTC
ATGGCCCCGCACAAGCTGGCCTGCGCCATCGTCAACACGGCCGGCCGCGAGACCGGGGGCGAGCACTGGCTGGC
CTTCGCCTGGAACCCGCGCTCGAACACCTGCTACCTCTTCGACCCCTTCGGGTTCTCGGACGAGCGCCTCAAGC
AGATCTACCAGTTCGAGTACGAGGGCCTGCTGCGCCGCAGCGCCCTGGCCACCGAGGACCGCTGCGTCACCCTG
GAAAAGTCCACCCAGACCGTGCAGGGTCCGCGCTCGGCCGCCTGCGGGCTCTTCTGCTGCATGTTCCTGCACGC
CTTCGTGCACTGGCCCGACCGCCCCATGGACAAGAACCCCACCATGAACTTGCTGACGGGGGTGCCCAACGGCA
TGCTCCAGTCGCCCCAGGTGGAACCCACCCTGCGCCGCAACCAGGAGGCGCTCTACCGCTTCCTCAACTCCCAC
TCCGCCTACTTTCGCTCCCACCGCGCGCGCATCGAGAAGGCCACCGCCTTCGACCGCATGAATCAAGACATGTA
AACCGTGTGTGTATGTTAAATGTCTTTAATAAACAGCACTTTCATGTTACACATGCATCTGAGATGATTTATTT
AGAAATCGAAAGGGTTCTGCCGGGTCTCGGCATGGCCCGCGGGCAGGGACACGTTGCGGAACTGGTACTTGGCC
AGCCACTTGAACTCGGGGATCAGCAGTTTGGGCAGCGGGGTGTCGGGGAAGGAGTCGGTCCACAGCTTCCGCGT
CAGTTGCAGGGCGCCCAGCAGGTCGGGCGCGGAGATCTTGAAATCGCAGTTGGGACCCGCGTTCTGCGCGCGGG
AGTTGCGGTACACGGGGTTGCAGCACTGGAACACCATCAGGGCCGGGTGCTTCACGCTCGCCAGCACCGTCGCG
TCGGTGATGCTCTCCACGTCGAGGTCCTCGGCGTTGGCCATCCCGAAGGGGGTCATCTTGCAGGTCTGCCTTCC
CATGGTGGGCACGCACCCGGGCTTGTGGTTGCAATCGCAGTGCAGGGGGATCAGCATCATCTGGGCCTGGTCGG
CGTTCATCCCCGGGTACATGGCCTTCATGAAAGCCTCCAATTGCCTGAACGCCTGCTGGGCCTTGGCTCCCTCG
GTGAAGAAGACCCCGCAGGACTTGCTAGAGAACTGGTTGGTGGCGCACCCGGCGTCGTGCACGCAGCAGCGCGC
GTCGTTGTTGGCCAGCTGCACCACGCTGCGCCCCCAGCGGTTCTGGGTGATCTTGGCCCGGTCGGGGTTCTCCT
TCAGCGCGCGCTGCCCGTTCTCGCTCGCCACATCCATCTCGATCATGTGCTCCTTCTGGATCATGGTGGTCCCG
TGCAGGCACCGCAGCTTGCCCTCGGCCTCGGTGCACCCGTGCAGCCACAGCGCGCACCCGGTGCACTCCCAGTT
CTTGTGGGCGATCTGGGAATGCGCGTGCACGAAGCCCTGCAGGAAGCGGCCCATCATGGTGGTCAGGGTCTTGT
TGCTAGTGAAGGTCAGCGGAATGCCGCGGTGCTCCTCGTTGATGTACAGGTGGCAGATGCGGCGGTACACCTCG
CCCTGCTCGGGCATCAGCTGGAAGTTGGCTTTCAGGTCGGTCTCCACGCGGTAGCGGTCCATCAGCATAGTCAT
GATTTCCATACCCTTCTCCCAGGCCGAGACGATGGGCAGGCTCATAGGGTTCTTCACCATCATCTTAGCGCTAG
CAGCCGCGGCCAGGGGGTCGCTCTCGTCCAGGGTCTCAAAGCTCCGCTTGCCGTCCTTCTCGGTGATCCGCACC
GGGGGGTAGCTGAAGCCCACGGCCGCCAGCTCCTCCTCGGCCTGTCTTTCGTCCTCGCTGTCCTGGCTGACGTC
CTGCAGGACCACATGCTTGGTCTTGCGGGGTTTCTTCTTGGGCGGCAGCGGCGGCGGAGATGTTGGAGATGGCG
AGGGGGAGCGCGAGTTCTCGCTCACCACTACTATCTCTTCCTCTTCTTGGTCCGAGGCCACGCGGCGGTAGGTA
TGTCTCTTCGGGGGCAGAGGCGGAGGCGACGGGCTCTCGCCGCCGCGACTTGGCGGATGGCTGGCAGAGCCCCT
TCCGCGTTCGGGGGTGCGCTCCCGGCGGCGCTCTGACTGACTTCCTCCGCGGCCGGCCATTGTGTTCTCCTAGG
GAGGAACAACAAGCATGGAGACTCAGCCATCGCCAACCTCGCCATCTGCCCCCACCGCCGACGAGAAGCAGCAG
CAGCAGAATGAAAGCTTAACCGCCCCGCCGCCCAGCCCCGCCACCTCCGACGCGGCCGTCCCAGACATGCAAGA
GATGGAGGAATCCATCGAGATTGACCTGGGCTATGTGACGCCCGCGGAGCACGAGGAGGAGCTGGCAGTGCGCT
TTTCACAAGAAGAGATACACCAAGAACAGCCAGAGCAGGAAGCAGAGAATGAGCAGAGTCAGGCTGGGCTCGAG
CATGACGGCGACTACCTCCACCTGAGCGGGGGGGAGGACGCGCTCATCAAGCATCTGGCCCGGCAGGCCACCAT
CGTCAAGGATGCGCTGCTCGACCGCACCGAGGTGCCCCTCAGCGTGGAGGAGCTCAGCCGCGCCTACGAGTTGA
ACCTCTTCTCGCCGCGCGTGCCCCCCAAGCGCCAGCCCAATGGCACCTGCGAGCCCAACCCGCGCCTCAACTTC
TACCCGGTCTTCGCGGTGCCCGAGGCCCTGGCCACCTACCACATCTTTTTCAAGAACCAAAAGATCCCCGTCTC
CTGCCGCGCCAACCGCACCCGCGCCGACGCCCTTTTCAACCTGGGTCCCGGCGCCCGCCTACCTGATATCGCCT

2026201462 26 Feb 2026

CCTTGGAAGAGGTTCCCAAGATCTTCGAGGGTCTGGGCAGCGACGAGACTCGGGCCGCGAACGCTCTGCAAGGA
GAAGGAGGAGAGCATGAGCACCACAGCGCCCTGGTCGAGTTGGAAGGCGACAACGCGCGGCTGGCGGTGCTCAA
ACGCACGGTCGAGCTGACCCATTTCGCCTACCCGGCTCTGAACCTGCCCCCCAAAGTCATGAGCGCGGTCATGG
ACCAGGTGCTCATCAAGCGCGCGTCGCCCATCTCCGAGGACGAGGGCATGCAAGACTCCGAGGAGGGCAAGCCC
GTGGTCAGCGACGAGCAGCTGGCCCGGTGGCTGGGTCCTAATGCTAGTCCCCAGAGTTTGGAAGAGCGGCGCAA
ACTCATGATGGCCGTGGTCCTGGTGACCGTGGAGCTGGAGTGCCTGCGCCGCTTCTTCGCCGACGCGGAGACCC
TGCGCAAGGTCGAGGAGAACCTGCACTACCTCTTCAGGCACGGGTTCGTGCGCCAGGCCTGCAAGATCTCCAAC
GTGGAGCTGACCAACCTGGTCTCCTACATGGGCATCTTGCACGAGAACCGCCTGGGGCAGAACGTGCTGCACAC
CACCCTGCGCGGGGAGGCCCGGCGCGACTACATCCGCGACTGCGTCTACCTCTACCTCTGCCACACCTGGCAGA
CGGGCATGGGCGTGTGGCAGCAGTGTCTGGAGGAGCAGAACCTGAAAGAGCTCTGCAAGCTCCTGCAGAAGAAC
CTCAAGGGTCTGTGGACCGGGTTCGACGAGCGCACCACCGCCTCGGACCTGGCCGACCTCATTTTCCCCGAGCG
CCTCAGGCTGACGCTGCGCAACGGCCTGCCCGACTTTATGAGCCAAAGCATGTTGCAAAACTTTCGCTCTTTCA
TCCTCGAACGCTCCGGAATCCTGCCCGCCACCTGCTCCGCGCTGCCCTCGGACTTCGTGCCGCTGACCTTCCGC
GAGTGCCCCCCGCCGCTGTGGAGCCACTGCTACCTGCTGCGCCTGGCCAACTACCTGGCCTACCACTCGGACGT
GATCGAGGACGTCAGCGGCGAGGGCCTGCTCGAGTGCCACTGCCGCTGCAACCTCTGCACGCCGCACCGCTCCC
TGGCCTGCAACCCCCAGCTGCTGAGCGAGACCCAGATCATCGGCACCTTCGAGTTGCAAGGGCCCAGCGAAGGC
GAGGGTTCAGCCGCCAAGGGGGGTCTGAAACTCACCCCGGGGCTGTGGACCTCGGCCTACTTGCGCAAGTTCGT
GCCCGAGGACTACCATCCCTTCGAGATCAGGTTCTACGAGGACCAATCCCATCCGCCCAAGGCCGAGCTGTCGG
CCTGCGTCATCACCCAGGGGGCGATCCTGGCCCAATTGCAAGCCATCCAGAAATCCCGCCAAGAATTCTTGCTG
AAAAAGGGCCGCGGGGTCTACCTCGACCCCCAGACCGGTGAGGAGCTCAACCCCGGCTTCCCCCAGGATGCCCC
GAGGAAACAAGAAGCTGAAAGTGGAGCTGCCGCCCGTGGAGGATTTGGAGGAAGACTGGGAGAACAGCAGTCAG
GCAGAGGAGGAGGAGATGGAGGAAGACTGGGACAGCACTCAGGCAGAGGAGGACAGCCTGCAAGACAGTCTGGA
GGAAGACGAGGAGGAGGCAGAGGAGGAGGTGGAAGAAGCAGCCGCCGCCAGACCGTCGTCCTCGGCGGGGGAGA
AAGCAAGCAGCACGGATACCATCTCCGCTCCGGGTCGGGGTCCCGCTCGACCACACAGTAGATGGGACGAGACC
GGACGATTCCCGAACCCCACCACCCAGACCGGTAAGAAGGAGCGGCAGGGATACAAGTCCTGGCGGGGGCACAA
AAACGCCATCGTCTCCTGCTTGCAGGCCTGCGGGGGCAACATCTCCTTCACCCGGCGCTACCTGCTCTTCCACC
GCGGGGTGAACTTTCCCCGCAACATCTTGCATTACTACCGTCACCTCCACAGCCCCTACTACTTCCAAGAAGAG
GCAGCAGCAGCAGAAAAAGACCAGCAGAAAACCAGCAGCTAGAAAATCCACAGCGGCGGCAGCAGGTGGACTGA
GGATCGCGGCGAACGAGCCGGCGCAAACCCGGGAGCTGAGGAACCGGATCTTTCCCACCCTCTATGCCATCTTC
CAGCAGAGTCGGGGGCAGGAGCAGGAACTGAAAGTCAAGAACCGTTCTCTGCGCTCGCTCACCCGCAGTTGTCT
GTATCACAAGAGCGAAGACCAACTTCAGCGCACTCTCGAGGACGCCGAGGCTCTCTTCAACAAGTACTGCGCGC
TCACTCTTAAAGAGTAGCCCGCGCCCGCCCAGTCGCAGAAAAAGGCGGGAATTACGTCACCTGTGCCCTTCGCC
CTAGCCGCCTCCACCCATCATCATGAGCAAAGAGATTCCCACGCCTTACATGTGGAGCTACCAGCCCCAGATGG
GCCTGGCCGCCGGTGCCGCCCAGGACTACTCCACCCGCATGAATTGGCTCAGCGCCGGGCCCGCGATGATCTCA
CGGGTGAATGACATCCGCGCCCACCGAAACCAGATACTCCTAGAACAGTCAGCGCTCACCGCCACGCCCCGCAA
TCACCTCAATCCGCGTAATTGGCCCGCCGCCCTGGTGTACCAGGAAATTCCCCAGCCCACGACCGTACTACTTC
CGCGAGACGCCCAGGCCGAAGTCCAGCTGACTAACTCAGGTGTCCAGCTGGCGGGCGGCGCCACCCTGTGTCGT
CACCGCCCCGCTCAGGGTATAAAGCGGCTGGTGATCCGGGGCAGAGGCACACAGCTCAACGACGAGGTGGTGAG
CTCTTCGCTGGGTCTGCGACCTGACGGAGTCTTCCAACTCGCCGGATCGGGGAGATCTTCCTTCACGCCTCGTC
AGGCCGTCCTGACTTTGGAGAGTTCGTCCTCGCAGCCCCGCTCGGGTGGCATCGGCACTCTCCAGTTCGTGGAG
GAGTTCACTCCCTCGGTCTACTTCAACCCCTTCTCCGGCTCCCCCGGCCACTACCCGGACGAGTTCATCCCGAA
CTTCGACGCCATCAGCGAGTCGGTGGACGGCTACGATTGAATGTCCCATGGTGGCGCAGCTGACCTAGCTCGGC
TTCGACACCTGGACCACTGCCGCCGCTTCCGCTGCTTCGCTCGGGATCTCGCCGAGTTTGCCTACTTTGAGCTG
CCCGAGGAGCACCCTCAGGGCCCGGCCCACGGAGTGCGGATCGTCGTCGAAGGGGGCCTCGACTCCCACCTGCT
TCGGATCTTCAGCCAGCGTCCGATCCTGGTCGAGCGCGAGCAAGGACAGACCCTTCTGACTCTGTACTGCATCT
GCAACCACCCCGGCCTGCATGAAAGTCTTTGTTGTCTGCTGTGTACTGAGTATAATAAAAGCTGAGATCAGCGA
CTACTCCGGACTTCCGTGTGTTCCTGAATCCATCAACCAGTCTTTGTTCTTCACCGGGAACGAGACCGAGCTCC
AGCTCCAGTGTAAGCCCCACAAGAAGTACCTCACCTGGCTGTTCCAGGGCTCCCCGATCGCCGTTGTCAACCAC
TGCGACAACGACGGAGTCCTGCTGAGCGGCCCTGCCAACCTTACTTTTTCCACCCGCAGAAGCAAGCTCCAGCT
CTTCCAACCCTTCCTCCCCGGGACCTATCAGTGCGTCTCGGGACCCTGCCATCACACCTTCCACCTGATCCCGA
ATACCACAGCGTCGCTCCCCGCTACTAACAACCAAACTAACCTCCACCAACGCCACCGTCGCGACCTTTCTGAA
TCTAATACTACCACCCACACCGGAGGTGAGCTCCGAGGTCAACCAACCTCTGGGATTTACTACGGCCCCTGGGA
GGTGGTTGGGTTAATAGCGCTAGGCCTAGTTGCGGGTGGGCTTTTGGTTCTCTGCTACCTATACCTCCCTTGCT
GTTCGTACTTAGTGGTGCTGTGTTGCTGGTTTAAGAAATGGGGAAGATCACCCTAGTGAGCTGCGGTGCGCTGG
TGGCGGTGTTGCTTTCGATTGTGGGACTGGGCGGTGCGGCTGTAGTGAAGGAGAAGGCCGATCCCTGCTTGCAT
TTCAATCCCAACAAATGCCAGCTGAGTTTTCAGCCCGATGGCAATCGGTGCGCGGTACTGATCAAGTGCGGATG
GGAATGCGAGAACGTGAGAATCGAGTACAATAACAAGACTCGGAACAATACTCTCGCGTCCGTGTGGCAGCCCG
GGGACCCCGAGTGGTACACCGTCTCTGTCCCCGGTGCTGACGGCTCCCCGCGCACCGTGAATAATACTTTCATT
TTTGCGCACATGTGCGACACGGTCATGTGGATGAGCAAGCAGTACGATATGTGGCCCCCCACGAAGGAGAACAT
CGTGGTCTTCTCCATCGCTTACAGCCTGTGCACGGCGCTAATCACCGCTATCGTGTGCCTGAGCATTCACATGC

2026201462 26 Feb 2026

TCATCGCTATTCGCCCCAGAAATAATGCCGAAAAAGAAAAACAGCCATAACGTTTTTTTTCACACCTTTTTCAG
ACCATGGCCTCTGTTAAATTTTTGCTTTTATTTGCCAGTCTCATTGCCGTCATTCATGGAATGAGTAATGAGAA
AATTACTATTTACACTGGCACTAATCACACATTGAAAGGTCCAGAAAAAGCCACAGAAGTTTCATGGTATTGTT
ATTTTAATGAATCAGATGTATCTACTGAACTCTGTGGAAACAATAACAAAAAAAATGAGAGCATTACTCTCATC
AAGTTTCAATGTGGATCTGACTTAACCCTAATTAACATCACTAGAGACTATGTAGGTATGTATTATGGAACTAC
AGCAGGCATTTCGGACATGGAATTTTATCAAGTTTCTGTGTCTGAACCCACCACGCCTAGAATGACCACAACCA
CAAAAACTACACCTGTTACCACTATGCAGCTCACTACCAATAACATTTTTGCCATGCGTCAAATGGTCAACAAT
AGCACTCAACCCACCCCACCCAGTGAGGAAATTCCCAAATCCATGATTGGCATTATTGTTGCTGTAGTGGTGTG
CATGTTGATCATCGCCTTGTGCATGGTGTACTATGCCTTCTGCTACAGAAAGCACAGACTGAACGACAAGCTGG
AACACTTACTAAGTGTTGAATTTTAATTTTTTAGAACCATGAAGATCCTAGGCCTTTTAATTTTTTCTATCATT
ACCTCTGCTCTATGCAATTCTGACAATGAGGACGTTACTGTCGTTGTCGGATCAAATTATACACTGAAAGGTCC
AGCGAAGGGTATGCTTTCGTGGTATTGCTATTTTGGATCTGACACTACAGAAACTGAATTATGCAATCTTAAGA
ATGGCAAAATTCAAAATTCTAAAATTAACAATTATATATGCAATGGTACTGATCTGATACTCCTCAATATCACG
AAATCATATGCTGGCAGTTACACCTGCCCTGGAGATGATGCTGACAGTATGATTTTTTACAAAGTAACTGTTGT
TGATCCCACTACTCCACCTCCACCCACCACAACTACTCACACCACACACACAGATCAAACCGCAGCAGAGGAGG
CAGCAAAGTTAGCCTTGCAGGTCCAAGACAGTTCATTTGTTGGCATTACCCCTACACCTGATCAGCGGTGTCCG
GGGCTGCTAGTCAGCGGCATTGTCGGTGTGCTTTCGGGATTAGCAGTCATAATCATCTGCATGTTCATTTTTGC
TTGCTGCTATAGAAGGCTTTACCGACAAAAATCAGACCCACTGCTGAACCTCTATGTTTAATTTTTTCCAGAGT
CATGAAGGCAGTTAGCGCTCTAGTTTTTTGTTCTTTGATTGGCATTGTTTTTTGCAATCCTATTCCTAAAGTTA
GCTTTATTAAAGATGTGAATGTTACTGAGGGGGGCAATGTGACACTGGTAGGTGTAGAGGGTGCTGAAAACACC
ACCTGGACAAAATACCACCTCAATGGGTGGAAAGATATTTGCAATTGGAGTGTATTAGTTTATACATGTGAGGG
AGTTAATCTTACCATTGTCAATGCCACCTCAGCTCAAAATGGTAGAATTCAAGGACAAAGTGTCAGTGTATCTA
ATGGGTATTTTACCCAACATACTTTTATCTATGACGTTAAAGTCATACCACTGCCTACGCCTAGCCCACCTAGC
ACTACCACACAGACAACCCACACTACACAGACAACCACATACAGTACATTAAATCAGCCTACCACCACTACAGC
AGCAGAGGTTGCCAGCTCGTCTGGGGTCCGAGTGGCATTTTTGATGTtGGCCCCATCTAGCAGTCCCACTGCTA
GTACCAATGAGCAGACTACTGAATTTTTGTCCACTGTCGAGAGCCACACCACAGCTACCTCCAGTGCCTTCTCT
AGCACCGCCAATCTCTCCTCGCTTTCCTCTACACCAATCAGTCCCGCTACTACTCCTAGCCCCGCTCCTCTTCC
CACTCCCCTGAAGCAAACAGACGGCGGCATGCAATGGCAGATCACCCTGCTCATTGTGATCGGGTTGGTCATCC
TGGCCGTGTTGCTCTACTACATCTTCTGCCGCCGCATTCCCAACGCGCACCGCAAGCCGGTCTACAAGCCCATC
ATTGTCGGGCAGCCGGAGCCGCTTCAGGTGGAAGGGGGTCTAAGGAATCTTCTCTTCTCTTTTACAGTATGGTG
ATTGAACTATGATTCCTAGACAATTCTTGATCACTATTCTTATCTGCCTCCTCCAAGTCTGTGCCACCCTCGCT
CTGGTGGCCAACGCCAGTCCAGACTGTATTGGGCCCTTCGCCTCCTACGTGCTCTTTGCCTTCACCACCTGCAT
CTGCTGCTGTAGCATAGTCTGCCTGCTTATCACCTTCTTCCAGTTCATTGACTGGATCTTTGTGCGCATCGCCT
ACCTGCGCCACCACCCCCAGTACCGCGACCAGCGAGTGGCGCGGCTGCTCAGGCTCCTCTGATAAGCATGCGGG
CTCTGCTACTTCTCGCGCTTCTGCTGTTAGTGCTCCCCCGTCCCGTCGACCCCCGGTCCCCCACCCAGTCCCCC
GAGGAGGTCCGCAAATGCAAATTCCAAGAACCCTGGAAATTCCTCAAATGCTACCGCCAAAAATCAGACATGCA
TCCCAGCTGGATCATGATCATTGGGATCGTGAACATTCTGGCCTGCACCCTCATCTCCTTTGTGATTTACCCCT
GCTTTGACTTTGGTTGGAACTCGCCAGAGGCGCTCTATCTCCCGCCTGAACCTGACACACCACCACAGCAACCT
CAGGCACACGCACTACCACCACTACAGCCTAGGCCACAATACATGCCCATATTAGACTATGAGGCCGAGCCACA
GCGACCCATGCTCCCCGCTATTAGTTACTTCAATCTAACCGGCGGAGATGACTGACCCACTGGCCAACAACAAC
GTCAACGACCTTCTCCTGGACATGGACGGCCGCGCCTCGGAGCAGCGACTCGCCCAACTTCGCATTCGCCAGCA
GCAGGAGAGAGCCGTCAAGGAGCTGCAGGATGCGGTGGCCATCCACCAGTGCAAGAGAGGCATCTTCTGCCTGG
TGAAACAGGCCAAGATCTCCTACGAGGTCACTCCAAACGACCATCGCCTCTCCTACGAGCTCCTGCAGCAGCGC
CAGAAGTTCACCTGCCTGGTCGGAGTCAACCCCATCGTCATCACCCAGCAGTCTGGCGATACCAAGGGGTGCAT
CCACTGCTCCTGCGACTCCCCCGACTGCGTCCACACTCTGATCAAGACCCTCTGCGGCCTCCGCGACCTCCTCC
CCATGAACTAATCACCCCCTTATCCAGTGAAATAAAGATCATATTGATGATGATTTTACAGAAATAAAAAATAA
TCATTTGATTTGAAATAAAGATACAATCATATTGATGATTTGAGTTTAACAAAAAAATAAAGAATCACTTACTT
GAAATCTGATACCAGGTCTCTGTCCATGTTTTCTGCCAACACCACTTCACTCCCCTCTTCCCAGCTCTGGTACT
GCAGGCCCCGGCGGGCTGCAAACTTCCTCCACACGCTGAAGGGGATGTCAAATTCCTCCTGTCCCTCAATCTTC
ATTTTATCTTCTATCAGATGTCCAAAAAGCGCGTCCGGGTGGATGATGACTTCGACCCCGTCTACCCCTACGAT
GCAGACAACGCACCGACCGTGCCCTTCATCAACCCCCCCTTCGTCTCTTCAGATGGATTCCAAGAGAAGCCCCT
GGGGGTGTTGTCCCTGCGACTGGCCGACCCCGTCACCACCAAGAACGGGGAAATCACCCTCAAGCTGGGAGAGG
GGGTGGACCTCGATTCCTCGGGAAAACTCATCTCCAACACGGCCACCAAGGCCGCCGCCCCTCTCAGTTTTTCC
AACAACACCATTTCCCTTAACATGGATCACCCCTTTTACACTAAAGATGGAAAATTATCCTTACAAGTTTCTCC
ACCATTAAATATACTGAGAACAAGCATTCTAAACACACTAGCTTTAGGTTTTGGATCAGGTTTAGGACTCCGTG
GCTCTGCCTTGGCAGTACAGTTAGTCTCTCCACTTACATTTGATACTGATGGAAACATAAAGCTTACCTTAGAC
AGAGGTTTGCATGTTACAACAGGAGATGCAATTGAAAGCAACATAAGCTGGGCTAAAGGTTTAAAATTTGAAGA
TGGAGCCATAGCAACCAACATTGGAAATGGGTTAGAGTTTGGAAGCAGTAGTACAGAAACAGGTGTTGATGATG
CTTACCCAATCCAAGTTAAACTTGGATCTGGCCTTAGCTTTGACAGTACAGGAGCCATAATGGCTGGTAACAAA
GAAGACGATAAACTCACTTTGTGGACAACACCTGATCCATCACCAAACTGTCAAATACTCGCAGAAAATGATGC

2026201462 26 Feb 2026

AAAACTAACACTTTGCTTGACTAAATGTGGTAGTCAAATACTGGCCACTGTGTCAGTCTTAGTTGTAGGAAGTG
GAAACCTAAACCCCATTACTGGCACCGTAAGCAGTGCTCAGGTGTTTCTACGTTTTGATGCAAACGGTGTTCTT
TTAACAGAACATTCTACACTAAAAAAATACTGGGGGTATAGGCAGGGAGATAGCATAGATGGCACTCCATATAC
CAATGCTGTAGGATTCATGCCCAATTTAAAAGCTTATCCAAAGTCACAAAGTTCTACTACTAAAAATAATATAG
TAGGGCAAGTATACATGAATGGAGATGTTTCAAAACCTATGCTTCTCACTATAACCCTCAATGGTACTGATGAC
AGCAACAGTACATATTCAATGTCATTTTCATACACCTGGACTAATGGAAGCTATGTTGGAGCAACATTTGGGGC
TAACTCTTATACCTTCTCATACATCGCCCAAGAATGAACACTGTATCCCACCCTGCATGCCAACCCTTCCCACC
CCACTCTGTGGAACAAACTCTGAAACACAAAATAAAATAAAGTTCAAGTGTTTTATTGATTCAACAGTTTTACA
GGATTCGAGCAGTTATTTTTCCTCCACCCTCCCAGGACATGGAATACACCACCCTCTCCCCCCGCACAGCCTTG
AACATCTGAATGCCATTGGTGATGGACATGCTTTTGGTCTCCACGTTCCACACAGTTTCAGAGCGAGCCAGTCT
CGGGTCGGTCAGGGAGATGAAACCCTCCGGGCACTCCCGCATCTGCACCTCACAGCTCAACAGCTGAGGATTGT
CCTCGGTGGTCGGGATCACGGTTATCTGGAAGAAGCAGAAGAGCGGCGGTGGGAATCATAGTCCGCGAACGGGA
TCGGCCGGTGGTGTCGCATCAGGCCCCGCAGCAGTCGCTGCCGCCGCCGCTCCGTCAAGCTGCTGCTCAGGGGG
TCCGGGTCCAGGGACTCCCTCAGCATGATGCCCACGGCCCTCAGCATCAGTCGTCTGGTGCGGCGGGCGCAGCA
GCGCATGCGGATCTCGCTCAGGTCGCTGCAGTACGTGCAACACAGAACCACCAGGTTGTTCAACAGTCCATAGT
TCAACACGCTCCAGCCGAAACTCATCGCGGGAAGGATGCTACCCACGTGGCCGTCGTACCAGATCCTCAGGTAA
ATCAAGTGGTGCCCCCTCCAGAACACGCTGCCCACGTACATGATCTCCTTGGGCATGTGGCGGTTCACCACCTC
CCGGTACCACATCACCCTCTGGTTGAACATGCAGCCCCGGATGATCCTGCGGAACCACAGGGCCAGCACCGCCC
CGCCCGCCATGCAGCGAAGAGACCCCGGGTCCCGGCAATGGCAATGGAGGACCCACCGCTCGTACCCGTGGATC
ATCTGGGAGCTGAACAAGTCTATGTTGGCACAGCACAGGCATATGCTCATGCATCTCTTCAGCACTCTCAACTC
CTCGGGGGTCAAAACCATATCCCAGGGCACGGGGAACTCTTGCAGGACAGCGAACCCCGCAGAACAGGGCAATC
CTCGCACAGAACTTACATTGTGCATGGACAGGGTATCGCAATCAGGCAGCACCGGGTGATCCTCCACCAGAGAA
GCGCGGGTCTCGGTCTCCTCACAGCGTGGTAAGGGGGCCGGCCGATACGGGTGATGGCGGGACGCGGCTGATCG
TGTTCGCGACCGTGTCATGATGCAGTTGCTTTCGGACATTTTCGTACTTGCTGTAGCAGAACCTGGTCCGGGCG
CTGCACACCGATCGCCGGCGGCGGTCTCGGCGCTTGGAACGCTCGGTGTTGAAATTGTAAAACAGCCACTCTCT
CAGACCGTGCAGCAGATCTAGGGCCTCAGGAGTGATGAAGATCCCATCATGCCTGATGGCTCTGATCACATCGA
CCACCGTGGAATGGGCCAGACCCAGCCAGATGATGCAATTTTGTTGGGTTTCGGTGACGGCGGGGGAGGGAAGA
ACAGGAAGAACCATGATTAACTTTTAATCCAAACGGTCTCGGAGTACTTCAAAATGAAGATCGCGGAGATGGCA
CCTCTCGCCCCCGCTGTGTTGGTGGAAAATAACAGCCAGGTCAAAGGTGATACGGTTCTCGAGATGTTCCACGG
TGGCTTCCAGCAAAGCCTCCACGCGCACATCCAGAAACAAGACAATAGCGAAAGCGGGAGGGTTCTCTAATTCC
TCAATCATCATGTTACACTCCTGCACCATCCCCAGATAATTTTCATTTTTCCAGCCTTGAATGATTCGAACTAG
TTCcTGAGGTAAATCCAAGCCAGCCATGATAAAGAGCTCGCGCAGAGCGCCCTCCACCGGCATTCTTAAGCACA
CCCTCATAATTCCAAGATATTCTGCTCCTGGTTCACCTGCAGCAGATTGACAAGCGGAATATCAAAATCTCTGC
CGCGATCCCTGAGCTCCTCCCTCAGCAATAACTGTAAGTACTCTTTCATATCCTCTCCGAAATTTTTAGCCATA
GGACCACCAGGAATAAGATTAGGGCAAGCCACAGTACAGATAAACCGAAGTCCTCCCCAGTGAGCATTGCCAAA
TGCAAGACTGCTATAAGCATGCTGGCTAGACCCGGTGATATCTTCCAGATAACTGGACAGAAAATCGCCCAGGC
AATTTTTAAGAAAATCAACAAAAGAAAAATCCTCCAGGTGGACGTTTAGAGCCTCGGGAACAACGATGAAGTAA
ATGCAAGCGGTGCGTTCCAGCATGGTTAGTTAGCTGATCTGTAGAAAAAACAAAAATGAACATTAAACCATGCT
AGCCTGGCGAACAGGTGGGTAAATCGTTCTCTCCAGCACCAGGCAGGCCACGGGGTCTCCGGCGCGACCCTCGT
AAAAATTGTCGCTATGATTGAAAACCATCACAGAGAGACGTTCCCGGTGGCCGGCGTGAATGATTCGACAAGAT
GAATACACCCCCGGAACATTGGCGTCCGCGAGTGAAAAAAAGCGCCCGAGGAAGCAATAAGGCACTACAATGCT
CAGTCTCAAGTCCAGCAAAGCGATGCCATGCGGATGAAGCACAAAATTCTCAGGTGCGTACAAAATGTAATTAC
TCCCCTCCTGCACAGGCAGCAAAGCCCCCGATCCCTCCAGGTACACATACAAAGCCTCAGCGTCCATAGCTTAC
CGAGCAGCAGCACACAACAGGCGCAAGAGTCAGAGAAAGGCTGAGCTCTAACCTGTCCACCCGCTCTCTGCTCA
ATATATAGCCCAGATCTACACTGACGTAAAGGCCAAAGTCTAAAAATACCCGCCAAATAATCACACACGCCCAG
CACACGCCCAGAAACCGGTGACACACTCAAAAAAATACGCGCACTTCCTCAAACGCCCAAAACTGCCGTCATTT
CCGGGTTCCCACGCTACGTCATCAAAACACGACTTTCAAATTCCGTCGACCGTTAAAAACGTCACCCGCCCCGC
CCCTAACGGTCGCCCGTCTCTCAGCCAATCAGCGCCCCGCATCCCCAAATTCAAACACCTCATTTGCATATTAA
CGCGCACAAAAAGTTTGAGGTATATTATTGATGATGG

ChAdV68.4WTnt.GFP (SEQ ID NO:11); AC_000011.1 with E1 (nt 577 to 3403) and E3 (nt 27,816- 31,332) sequences deleted; corresponding ATCC VR-594 nucleotides substituted at four positions; GFP reporter under the control of the CMV promoter/enhancer inserted in place of deleted E1

CCATCTTCAATAATATACCTCAAACTTTTTGTGCGCGTTAATATGCAAATGAGGCGTTTGAATTTGGGGAGGAA
GGGCGGTGATTGGTCGAGGGATGAGCGACCGTTAGGGGCGGGGCGAGTGACGTTTTGATGACGTGGTTGCGAGG
AGGAGCCAGTTTGCAAGTTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTTGAACACGGAAATACTCAAT
TTTCCCGCGCTCTCTGACAGGAAATGAGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGCCATTTTCGCGCGAA
AACTGAATGAGGAAGTGAAAATCTGAGTAATTTCGCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGCCGAGTA
GACTTTGACCGATTACGTGGGGGTTTCGATTACCGTGTTTTTCACCTAAATTTCCGCGTACGGTGTCAAAGTCC
GGTGTTTTTACGTAGGTGTCAGCTGATCGCCAGGGTATTTAAACCTGCGCTCTCCAGTCAAGAGGCCACTCTTG

2026201462 26 Feb 2026

AGTGCCAGCGAGAAGAGTTTTCTCCTCCGCGCCGCGAGTCAGATCTACACTTTGAAAGTAGGGATAACAGGGTA
ATgacattgattattgactagttGttaaTAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGT
TCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATA
ATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAAC
TGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCCTATTGACGTCAATGACGGTAAATGGC
CCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATC
GCTATTACCATGgTGATGCGGTTTTGGCAGTACACCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCC
AAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ATAACCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAgcTCGTTTA
GTGAACCGTCAGATCGCCTGGAACGCCATCCACGCTGTTTTGACCTCCATAGAAGACAGCGATCGCGccaccAT
GGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCC
ACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC
ACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTA
CCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCT
TCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATC
GAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCA
CAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGG
ACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC
AACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGA
GTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTtTACAAGTAGtgaGTTTAAACTCCCATTTAAA
TGTGAGGGTTAATGCTTCGAGCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAG
TGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACA
AGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGATGTGGGAGGTTTTTTAAAGCAAGT
AAAACCTCTACAAATGTGGTAAAATAACTATAACGGTCCTAAGGTAGCGAGTGAGTAGTGTTCTGGGGCGGGGG
AGGACCTGCATGAGGGCCAGAATAACTGAAATCTGTGCTTTTCTGTGTGTTGCAGCAGCATGAGCGGAAGCGGC
TCCTTTGAGGGAGGGGTATTCAGCCCTTATCTGACGGGGCGTCTCCCCTCCTGGGCGGGAGTGCGTCAGAATGT
GATGGGATCCACGGTGGACGGCCGGCCCGTGCAGCCCGCGAACTCTTCAACCCTGACCTATGCAACCCTGAGCT
CTTCGTCGTTGGACGCAGCTGCCGCCGCAGCTGCTGCATCTGCCGCCAGCGCCGTGCGCGGAATGGCCATGGGC
GCCGGCTACTACGGCACTCTGGTGGCCAACTCGAGTTCCACCAATAATCCCGCCAGCCTGAACGAGGAGAAGCT
GTTGCTGCTGATGGCCCAGCTCGAGGCCTTGACCCAGCGCCTGGGCGAGCTGACCCAGCAGGTGGCTCAGCTGC
AGGAGCAGACGCGGGCCGCGGTTGCCACGGTGAAATCCAAATAAAAAATGAATCAATAAATAAACGGAGACGGT
TGTTGATTTTAACACAGAGTCTGAATCTTTATTTGATTTTTCGCGCGCGGTAGGCCCTGGACCACCGGTCTCGA
TCATTGAGCACCCGGTGGATCTTTTCCAGGACCCGGTAGAGGTGGGCTTGGATGTTGAGGTACATGGGCATGAG
CCCGTCCCGGGGGTGGAGGTAGCTCCATTGCAGGGCCTCGTGCTCGGGGGTGGTGTTGTAAATCACCCAGTCAT
AGCAGGGGCGCAGGGCATGGTGTTGCACAATATCTTTGAGGAGGAGACTGATGGCCACGGGCAGCCCTTTGGTG
TAGGTGTTTACAAATCTGTTGAGCTGGGAGGGATGCATGCGGGGGGAGATGAGGTGCATCTTGGCCTGGATCTT
GAGATTGGCGATGTTACCGCCCAGATCCCGCCTGGGGTTCATGTTGTGCAGGACCACCAGCACGGTGTATCCGG
TGCACTTGGGGAATTTATCATGCAACTTGGAAGGGAAGGCGTGAAAGAATTTGGCGACGCCTTTGTGCCCGCCC
AGGTTTTCCATGCACTCATCCATGATGATGGCGATGGGCCCGTGGGCGGCGGCCTGGGCAAAGACGTTTCGGGG
GTCGGACACATCATAGTTGTGGTCCTGGGTGAGGTCATCATAGGCCATTTTAATGAATTTGGGGCGGAGGGTGC
CGGACTGGGGGACAAAGGTACCCTCGATCCCGGGGGCGTAGTTCCCCTCACAGATCTGCATCTCCCAGGCTTTG
AGCTCGGAGGGGGGGATCATGTCCACCTGCGGGGCGATAAAGAACACGGTTTCCGGGGCGGGGGAGATGAGCTG
GGCCGAAAGCAAGTTCCGGAGCAGCTGGGACTTGCCGCAGCCGGTGGGGCCGTAGATGACCCCGATGACCGGCT
GCAGGTGGTAGTTGAGGGAGAGACAGCTGCCGTCCTCCCGGAGGAGGGGGGCCACCTCGTTCATCATCTCGCGC
ACGTGCATGTTCTCGCGCACCAGTTCCGCCAGGAGGCGCTCTCCCCCCAGGGATAGGAGCTCCTGGAGCGAGGC
GAAGTTTTTCAGCGGCTTGAGTCCGTCGGCCATGGGCATTTTGGAGAGGGTTTGTTGCAAGAGTTCCAGGCGGT
CCCAGAGCTCGGTGATGTGCTCTACGGCATCTCGATCCAGCAGACCTCCTCGTTTCGCGGGTTGGGACGGCTGC
GGGAGTAGGGCACCAGACGATGGGCGTCCAGCGCAGCCAGGGTCCGGTCCTTCCAGGGTCGCAGCGTCCGCGTC
AGGGTGGTCTCCGTCACGGTGAAGGGGTGCGCGCCGGGCTGGGCGCTTGCGAGGGTGCGCTTCAGGCTCATCCG
GCTGGTCGAAAACCGCTCCCGATCGGCGCCCTGCGCGTCGGCCAGGTAGCAATTGACCATGAGTTCGTAGTTGA
GCGCCTCGGCCGCGTGGCCTTTGGCGCGGAGCTTACCTTTGGAAGTCTGCCCGCAGGCGGGACAGAGGAGGGAC
TTGAGGGCGTAGAGCTTGGGGGCGAGGAAGACGGACTCGGGGGCGTAGGCGTCCGCGCCGCAGTGGGCGCAGAC
GGTCTCGCACTCCACGAGCCAGGTGAGGTCGGGCTGGTCGGGGTCAAAAACCAGTTTCCCGCCGTTCTTTTTGA
TGCGTTTCTTACCTTTGGTCTCCATGAGCTCGTGTCCCCGCTGGGTGACAAAGAGGCTGTCCGTGTCCCCGTAG
ACCGACTTTATGGGCCGGTCCTCGAGCGGTGTGCCGCGGTCCTCCTCGTAGAGGAACCCCGCCCACTCCGAGAC
GAAAGCCCGGGTCCAGGCCAGCACGAAGGAGGCCACGTGGGACGGGTAGCGGTCGTTGTCCACCAGCGGGTCCA
CCTTTTCCAGGGTATGCAAACACATGTCCCCCTCGTCCACATCCAGGAAGGTGATTGGCTTGTAAGTGTAGGCC
ACGTGACCGGGGGTCCCGGCCGGGGGGGTATAAAAGGGTGCGGGTCCCTGCTCGTCCTCACTGTCTTCCGGATC
GCTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATTCCCTCTCGAAGGCGGGCATGACCTCGGCACTCAGGTTGT
CAGTTTCTAGAAACGAGGAGGATTTGATATTGACGGTGCCGGCGGAGATGCCTTTCAAGAGCCCCTCGTCCATC

2026201462 26 Feb 2026

TGGTCAGAAAAGACGATCTTTTTGTTGTCGAGCTTGGTGGCGAAGGAGCCGTAGAGGGCGTTGGAGAGGAGCTT
GGCGATGGAGCGCATGGTCTGGTTTTTTTCCTTGTCGGCGCGCTCCTTGGCGGCGATGTTGAGCTGCACGTACT
CGCGCGCCACGCACTTCCATTCGGGGAAGACGGTGGTCAGCTCGTCGGGCACGATTCTGACCTGCCAGCCCCGA
TTATGCAGGGTGATGAGGTCCACACTGGTGGCCACCTCGCCGCGCAGGGGCTCATTAGTCCAGCAGAGGCGTCC
GCCCTTGCGCGAGCAGAAGGGGGGCAGGGGGTCCAGCATGACCTCGTCGGGGGGGTCGGCATCGATGGTGAAGA
TGCCGGGCAGGAGGTCGGGGTCAAAGTAGCTGATGGAAGTGGCCAGATCGTCCAGGGCAGCTTGCCATTCGCGC
ACGGCCAGCGCGCtCTCGTAGGGACTGAGGGGCGTGCCCCAGGGCATGGGATGGGTAAGCGCGGAGGCGTACAT
GCCGCAGATGTCGTAGACGTAGAGGGGCTCCTCGAGGATGCCGATGTAGGTGGGGTAGCAGCGCCCCCCGCGGA
TGCTGGCGCGCACGTAGTCATACAGCTCGTGCGAGGGGGCGAGGAGCCCCGGGCCCAGGTTGGTGCGACTGGGC
TTTTCGGCGCGGTAGACGATCTGGCGGAAAATGGCATGCGAGTTGGAGGAGATGGTGGGCCTTTGGAAGATGTT
GAAGTGGGCGTGGGGCAGTCCGACCGAGTCGCGGATGAAGTGGGCGTAGGAGTCTTGCAGCTTGGCGACGAGCT
CGGCGGTGACTAGGACGTCCAGAGCGCAGTAGTCGAGGGTCTCCTGGATGATGTCATACTTGAGCTGTCCCTTT
TGTTTCCACAGCTCGCGGTTGAGAAGGAACTCTTCGCGGTCCTTCCAGTACTCTTCGAGGGGGAACCCGTCCTG
ATCTGCACGGTAAGAGCCTAGCATGTAGAACTGGTTGACGGCCTTGTAGGCGCAGCAGCCCTTCTCCACGGGGA
GGGCGTAGGCCTGGGCGGCCTTGCGCAGGGAGGTGTGCGTGAGGGCGAAAGTGTCCCTGACCATGACCTTGAGG
AACTGGTGCTTGAAGTCGATATCGTCGCAGCCCCCCTGCTCCCAGAGCTGGAAGTCCGTGCGCTTCTTGTAGGC
GGGGTTGGGCAAAGCGAAAGTAACATCGTTGAAGAGGATCTTGCCCGCGCGGGGCATAAAGTTGCGAGTGATGC
GGAAAGGTTGGGGCACCTCGGCCCGGTTGTTGATGACCTGGGCGGCGAGCACGATCTCGTCGAAGCCGTTGATG
TTGTGGCCCACGATGTAGAGTTCCACGAATCGCGGACGGCCCTTGACGTGGGGCAGTTTCTTGAGCTCCTCGTA
GGTGAGCTCGTCGGGGTCGCTGAGCCCGTGCTGCTCGAGCGCCCAGTCGGCGAGATGGGGGTTGGCGCGGAGGA
AGGAAGTCCAGAGATCCACGGCCAGGGCGGTTTGCAGACGGTCCCGGTACTGACGGAACTGCTGCCCGACGGCC
ATTTTTTCGGGGGTGACGCAGTAGAAGGTGCGGGGGTCCCCGTGCCAGCGATCCCATTTGAGCTGGAGGGCGAG
ATCGAGGGCGAGCTCGACGAGCCGGTCGTCCCCGGAGAGTTTCATGACCAGCATGAAGGGGACGAGCTGCTTGC
CGAAGGACCCCATCCAGGTGTAGGTTTCCACATCGTAGGTGAGGAAGAGCCTTTCGGTGCGAGGATGCGAGCCG
ATGGGGAAGAACTGGATCTCCTGCCACCAATTGGAGGAATGGCTGTTGATGTGATGGAAGTAGAAATGCCGACG
GCGCGCCGAACACTCGTGCTTGTGTTTATACAAGCGGCCACAGTGCTCGCAACGCTGCACGGGATGCACGTGCT
GCACGAGCTGTACCTGAGTTCCTTTGACGAGGAATTTCAGTGGGAAGTGGAGTCGTGGCGCCTGCATCTCGTGC
TGTACTACGTCGTGGTGGTCGGCCTGGCCCTCTTCTGCCTCGATGGTGGTCATGCTGACGAGCCCGCGCGGGAG
GCAGGTCCAGACCTCGGCGCGAGCGGGTCGGAGAGCGAGGACGAGGGCGCGCAGGCCGGAGCTGTCCAGGGTCC
TGAGACGCTGCGGAGTCAGGTCAGTGGGCAGCGGCGGCGCGCGGTTGACTTGCAGGAGTTTTTCCAGGGCGCGC
GGGAGGTCCAGATGGTACTTGATCTCCACCGCGCCATTGGTGGCGACGTCGATGGCTTGCAGGGTCCCGTGCCC
CTGGGGTGTGACCACCGTCCCCCGTTTCTTCTTGGGCGGCTGGGGCGACGGGGGCGGTGCCTCTTCCATGGTTA
GAAGCGGCGGCGAGGACGCGCGCCGGGCGGCAGGGGCGGCTCGGGGCCCGGAGGCAGGGGCGGCAGGGGCACGT
CGGCGCCGCGCGCGGGTAGGTTCTGGTACTGCGCCCGGAGAAGACTGGCGTGAGCGACGACGCGACGGTTGACG
TCCTGGATCTGACGCCTCTGGGTGAAGGCCACGGGACCCGTGAGTTTGAACCTGAAAGAGAGTTCGACAGAATC
AATCTCGGTATCGTTGACGGCGGCCTGCCGCAGGATCTCTTGCACGTCGCCCGAGTTGTCCTGGTAGGCGATCT
CGGTCATGAACTGCTCGATCTCCTCCTCTTGAAGGTCTCCGCGGCCGGCGCGCTCCACGGTGGCCGCGAGGTCG
TTGGAGATGCGGCCCATGAGCTGCGAGAAGGCGTTCATGCCCGCCTCGTTCCAGACGCGGCTGTAGACCACGAC
GCCCTCGGGATCGCgGGCGCGCATGACCACCTGGGCGAGGTTGAGCTCCACGTGGCGCGTGAAGACCGCGTAGT
TGCAGAGGCGCTGGTAGAGGTAGTTGAGCGTGGTGGCGATGTGCTCGGTGACGAAGAAATACATGATCCAGCGG
CGGAGCGGCATCTCGCTGACGTCGCCCAGCGCCTCCAAACGTTCCATGGCCTCGTAAAAGTCCACGGCGAAGTT
GAAAAACTGGGAGTTGCGCGCCGAGACGGTCAACTCCTCCTCCAGAAGACGGATGAGCTCGGCGATGGTGGCGC
GCACCTCGCGCTCGAAGGCCCCCGGGAGTTCCTCCACTTCCTCTTCTTCCTCCTCCACTAACATCTCTTCTACT
TCCTCCTCAGGCGGCAGTGGTGGCGGGGGAGGGGGCCTGCGTCGCCGGCGGCGCACGGGCAGACGGTCGATGAA
GCGCTCGATGGTCTCGCCGCGCCGGCGTCGCATGGTCTCGGTGACGGCGCGCCCGTCCTCGCGGGGCCGCAGCG
TGAAGACGCCGCCGCGCATCTCCAGGTGGCCGGGGGGGTCCCCGTTGGGCAGGGAGAGGGCGCTGACGATGCAT
CTTATCAATTGCCCCGTAGGGACTCCGCGCAAGGACCTGAGCGTCTCGAGATCCACGGGATCTGAAAACCGCTG
AACGAAGGCTTCGAGCCAGTCGCAGTCGCAAGGTAGGCTGAGCACGGTTTCTTCTGGCGGGTCATGTTGGTTGG
GAGCGGGGCGGGCGATGCTGCTGGTGATGAAGTTGAAATAGGCGGTTCTGAGACGGCGGATGGTGGCGAGGAGC
ACCAGGTCTTTGGGCCCGGCTTGCTGGATGCGCAGACGGTCGGCCATGCCCCAGGCGTGGTCCTGACACCTGGC
CAGGTCCTTGTAGTAGTCCTGCATGAGCCGCTCCACGGGCACCTCCTCCTCGCCCGCGCGGCCGTGCATGCGCG
TGAGCCCGAAGCCGCGCTGGGGCTGGACGAGCGCCAGGTCGGCGACGACGCGCTCGGCGAGGATGGCTTGCTGG
ATCTGGGTGAGGGTGGTCTGGAAGTCATCAAAGTCGACGAAGCGGTGGTAGGCTCCGGTGTTGATGGTGTAGGA
GCAGTTGGCCATGACGGACCAGTTGACGGTCTGGTGGCCCGGACGCACGAGCTCGTGGTACTTGAGGCGCGAGT
AGGCGCGCGTGTCGAAGATGTAGTCGTTGCAGGTGCGCACCAGGTACTGGTAGCCGATGAGGAAGTGCGGCGGC
GGCTGGCGGTAGAGCGGCCATCGCTCGGTGGCGGGGGCGCCGGGCGCGAGGTCCTCGAGCATGGTGCGGTGGTA
GCCGTAGATGTACCTGGACATCCAGGTGATGCCGGCGGCGGTGGTGGAGGCGCGCGGGAACTCGCGGACGCGGT
TCCAGATGTTGCGCAGCGGCAGGAAGTAGTTCATGGTGGGCACGGTCTGGCCCGTGAGGCGCGCGCAGTCGTGG
ATGCTCTATACGGGCAAAAACGAAAGCGGTCAGCGGCTCGACTCCGTGGCCTGGAGGCTAAGCGAACGGGTTGG
GCTGCGCGTGTACCCCGGTTCGAATCTCGAATCAGGCTGGAGCCGCAGCTAACGTGGTATTGGCACTCCCGTCT

2026201462 26 Feb 2026

CGACCCAAGCCTGCACCAACCCTCCAGGATACGGAGGCGGGTCGTTTTGCAACTTTTTTTTGGAGGCCGGATGA
GACTAGTAAGCGCGGAAAGCGGCCGACCGCGATGGCTCGCTGCCGTAGTCTGGAGAAGAATCGCCAGGGTTGCG
TTGCGGTGTGCCCCGGTTCGAGGCCGGCCGGATTCCGCGGCTAACGAGGGCGTGGCTGCCCCGTCGTTTCCAAG
ACCCCATAGCCAGCCGACTTCTCCAGTTACGGAGCGAGCCCCTCTTTTGTTTTGTTTGTTTTTGCCAGATGCAT
CCCGTACTGCGGCAGATGCGCCCCCACCACCCTCCACCGCAACAACAGCCCCCTCCACAGCCGGCGCTTCTGCC
CCCGCCCCAGCAGCAACTTCCAGCCACGACCGCCGCGGCCGCCGTGAGCGGGGCTGGACAGAGTTATGATCACC
AGCTGGCCTTGGAAGAGGGCGAGGGGCTGGCGCGCCTGGGGGCGTCGTCGCCGGAGCGGCACCCGCGCGTGCAG
ATGAAAAGGGACGCTCGCGAGGCCTACGTGCCCAAGCAGAACCTGTTCAGAGACAGGAGCGGCGAGGAGCCCGA
GGAGATGCGCGCGGCCCGGTTCCACGCGGGGCGGGAGCTGCGGCGCGGCCTGGACCGAAAGAGGGTGCTGAGGG
ACGAGGATTTCGAGGCGGACGAGCTGACGGGGATCAGCCCCGCGCGCGCGCACGTGGCCGCGGCCAACCTGGTC
ACGGCGTACGAGCAGACCGTGAAGGAGGAGAGCAACTTCCAAAAATCCTTCAACAACCACGTGCGCACCCTGAT
CGCGCGCGAGGAGGTGACCCTGGGCCTGATGCACCTGTGGGACCTGCTGGAGGCCATCGTGCAGAACCCCACCA
GCAAGCCGCTGACGGCGCAGCTGTTCCTGGTGGTGCAGCATAGTCGGGACAACGAAGCGTTCAGGGAGGCGCTG
CTGAATATCACCGAGCCCGAGGGCCGCTGGCTCCTGGACCTGGTGAACATTCTGCAGAGCATCGTGGTGCAGGA
GCGCGGGCTGCCGCTGTCCGAGAAGCTGGCGGCCATCAACTTCTCGGTGCTGAGTTTGGGCAAGTACTACGCTA
GGAAGATCTACAAGACCCCGTACGTGCCCATAGACAAGGAGGTGAAGATCGACGGGTTTTACATGCGCATGACC
CTGAAAGTGCTGACCCTGAGCGACGATCTGGGGGTGTACCGCAACGACAGGATGCACCGTGCGGTGAGCGCCAG
CAGGCGGCGCGAGCTGAGCGACCAGGAGCTGATGCATAGTCTGCAGCGGGCCCTGACCGGGGCCGGGACCGAGG
GGGAGAGCTACTTTGACATGGGCGCGGACCTGCACTGGCAGCCCAGCCGCCGGGCCTTGGAGGCGGCGGCAGGA
CCCTACGTAGAAGAGGTGGACGATGAGGTGGACGAGGAGGGCGAGTACCTGGAAGACTGATGGCGCGACCGTAT
TTTTGCTAGATGCAACAACAACAGCCACCTCCTGATCCCGCGATGCGGGCGGCGCTGCAGAGCCAGCCGTCCGG
CATTAACTCCTCGGACGATTGGACCCAGGCCATGCAACGCATCATGGCGCTGACGACCCGCAACCCCGAAGCCT
TTAGACAGCAGCCCCAGGCCAACCGGCTCTCGGCCATCCTGGAGGCCGTGGTGCCCTCGCGCTCCAACCCCACG
CACGAGAAGGTCCTGGCCATCGTGAACGCGCTGGTGGAGAACAAGGCCATCCGCGGCGACGAGGCCGGCCTGGT
GTACAACGCGCTGCTGGAGCGCGTGGCCCGCTACAACAGCACCAACGTGCAGACCAACCTGGACCGCATGGTGA
CCGACGTGCGCGAGGCCGTGGCCCAGCGCGAGCGGTTCCACCGCGAGTCCAACCTGGGATCCATGGTGGCGCTG
AACGCCTTCCTCAGCACCCAGCCCGCCAACGTGCCCCGGGGCCAGGAGGACTACACCAACTTCATCAGCGCCCT
GCGCCTGATGGTGACCGAGGTGCCCCAGAGCGAGGTGTACCAGTCCGGGCCGGACTACTTCTTCCAGACCAGTC
GCCAGGGCTTGCAGACCGTGAACCTGAGCCAGGCTTTCAAGAACTTGCAGGGCCTGTGGGGCGTGCAGGCCCCG
GTCGGGGACCGCGCGACGGTGTCGAGCCTGCTGACGCCGAACTCGCGCCTGCTGCTGCTGCTGGTGGCCCCCTT
CACGGACAGCGGCAGCATCAACCGCAACTCGTACCTGGGCTACCTGATTAACCTGTACCGCGAGGCCATCGGCC
AGGCGCACGTGGACGAGCAGACCTACCAGGAGATCACCCACGTGAGCCGCGCCCTGGGCCAGGACGACCCGGGC
AACCTGGAAGCCACCCTGAACTTTTTGCTGACCAACCGGTCGCAGAAGATCCCGCCCCAGTACGCGCTCAGCAC
CGAGGAGGAGCGCATCCTGCGTTACGTGCAGCAGAGCGTGGGCCTGTTCCTGATGCAGGAGGGGGCCACCCCCA
GCGCCGCGCTCGACATGACCGCGCGCAACATGGAGCCCAGCATGTACGCCAGCAACCGCCCGTTCATCAATAAA
CTGATGGACTACTTGCATCGGGCGGCCGCCATGAACTCTGACTATTTCACCAACGCCATCCTGAATCCCCACTG
GCTCCCGCCGCCGGGGTTCTACACGGGCGAGTACGACATGCCCGACCCCAATGACGGGTTCCTGTGGGACGATG
TGGACAGCAGCGTGTTCTCCCCCCGACCGGGTGCTAACGAGCGCCCCTTGTGGAAGAAGGAAGGCAGCGACCGA
CGCCCGTCCTCGGCGCTGTCCGGCCGCGAGGGTGCTGCCGCGGCGGTGCCCGAGGCCGCCAGTCCTTTCCCGAG
CTTGCCCTTCTCGCTGAACAGTATCCGCAGCAGCGAGCTGGGCAGGATCACGCGCCCGCGCTTGCTGGGCGAAG
AGGAGTACTTGAATGACTCGCTGTTGAGACCCGAGCGGGAGAAGAACTTCCCCAATAACGGGATAGAAAGCCTG
GTGGACAAGATGAGCCGCTGGAAGACGTATGCGCAGGAGCACAGGGACGATCCCCGGGCGTCGCAGGGGGCCAC
GAGCCGGGGCAGCGCCGCCCGTAAACGCCGGTGGCACGACAGGCAGCGGGGACAGATGTGGGACGATGAGGACT
CCGCCGACGACAGCAGCGTGTTGGACTTGGGTGGGAGTGGTAACCCGTTCGCTCACCTGCGCCCCCGTATCGGG
CGCATGATGTAAGAGAAACCGAAAATAAATGATACTCACCAAGGCCATGGCGACCAGCGTGCGTTCGTTTCTTC
TCTGTTGTTGTTGTATCTAGTATGATGAGGCGTGCGTACCCGGAGGGTCCTCCTCCCTCGTACGAGAGCGTGAT
GCAGCAGGCGATGGCGGCGGCGGCGATGCAGCCCCCGCTGGAGGCTCCTTACGTGCCCCCGCGGTACCTGGCGC
CTACGGAGGGGCGGAACAGCATTCGTTACTCGGAGCTGGCACCCTTGTACGATACCACCCGGTTGTACCTGGTG
GACAACAAGTCGGCGGACATCGCCTCGCTGAACTACCAGAACGACCACAGCAACTTCCTGACCACCGTGGTGCA
GAACAATGACTTCACCCCCACGGAGGCCAGCACCCAGACCATCAACTTTGACGAGCGCTCGCGGTGGGGCGGCC
AGCTGAAAACCATCATGCACACCAACATGCCCAACGTGAACGAGTTCATGTACAGCAACAAGTTCAAGGCGCGG
GTGATGGTCTCCCGCAAGACCCCCAATGGGGTGACAGTGACAGAGGATTATGATGGTAGTCAGGATGAGCTGAA
GTATGAATGGGTGGAATTTGAGCTGCCCGAAGGCAACTTCTCGGTGACCATGACCATCGACCTGATGAACAACG
CCATCATCGACAATTACTTGGCGGTGGGGCGGCAGAACGGGGTGCTGGAGAGCGACATCGGCGTGAAGTTCGAC
ACTAGGAACTTCAGGCTGGGCTGGGACCCCGTGACCGAGCTGGTCATGCCCGGGGGTGTACACCAACGAGGCTTT
CCATCCCGATATTGTCTTGCTGCCCGGCTGCGGGGTGGACTTCACCGAGAGCCGCCTCAGCAACCTGCTGGGCA
TTCGCAAGAGGCAGCCCTTCCAGGAAGGCTTCCAGATCATGTACGAGGATCTGGAGGGGGGCAACATCCCCGCG
CTCCTGGATGTCGACGCCTATGAGAAAAGCAAGGAGGATGCAGCAGCTGAAGCAACTGCAGCCGTAGCTACCGC
CTCTACCGAGGTCAGGGGCGATAATTTTGCAAGCGCCGCAGCAGTGGCAGCGGCCGAGGCGGCTGAAACCGAAA
GTAAGATAGTCATTCAGCCGGTGGAGAAGGATAGCAAGAACAGGAGCTACAACGTACTACCGGACAAGATAAAC

2026201462 26 Feb 2026

ACCGCCTACCGCAGCTGGTACCTAGCCTACAACTATGGCGACCCCGAGAAGGGCGTGCGCTCCTGGACGCTGCT
CACCACCTCGGACGTCACCTGCGGCGTGGAGCAAGTCTACTGGTCGCTGCCCGACATGATGCAAGACCCGGTCA
CCTTCCGCTCCACGCGTCAAGTTAGCAACTACCCGGTGGTGGGCGCCGAGCTCCTGCCCGTCTACTCCAAGAGC
TTCTTCAACGAGCAGGCCGTCTACTCGCAGCAGCTGCGCGCCTTCACCTCGCTTACGCACGTCTTCAACCGCTT
CCCCGAGAACCAGATCCTCGTCCGCCCGCCCGCGCCCACCATTACCACCGTCAGTGAAAACGTTCCTGCTCTCA
CAGATCACGGGACCCTGCCGCTGCGCAGCAGTATCCGGGGAGTCCAGCGCGTGACCGTTACTGACGCCAGACGC
CGCACCTGCCCCTACGTCTACAAGGCCCTGGGCATAGTCGCGCCGCGCGTCCTCTCGAGCCGCACCTTCTAAAT
GTCCATTCTCATCTCGCCCAGTAATAACACCGGTTGGGGCCTGCGCGCGCCCAGCAAGATGTACGGAGGCGCTC
GCCAACGCTCCACGCAACACCCCGTGCGCGTGCGCGGGCACTTCCGCGCTCCCTGGGGCGCCCTCAAGGGCCGC
GTGCGGTCGCGCACCACCGTCGACGACGTGATCGACCAGGTGGTGGCCGACGCGCGCAACTACACCCCCGCCGC
CGCGCCCGTCTCCACCGTGGACGCCGTCATCGACAGCGTGGTGGCcGACGCGCGCCGGTACGCCCGCGCCAAGA
GCCGGCGGCGGCGCATCGCCCGGCGGCACCGGAGCACCCCCGCCATGCGCGCGGCGCGAGCCTTGCTGCGCAGG
GCCAGGCGCACGGGACGCAGGGCCATGCTCAGGGCGGCCAGACGCGCGGCTTCAGGCGCCAGCGCCGGCAGGAC
CCGGAGACGCGCGGCCACGGCGGCGGCAGCGGCCATCGCCAGCATGTCCCGCCCGCGGCGAGGGAACGTGTACT
GGGTGCGCGACGCCGCCACCGGTGTGCGCGTGCCCGTGCGCACCCGCCCCCCTCGCACTTGAAGATGTTCACTT
CGCGATGTTGATGTGTCCCAGCGGCGAGGAGGATGTCCAAGCGCAAATTCAAGGAAGAGATGCTCCAGGTCATC
GCGCCTGAGATCTACGGCCCTGCGGTGGTGAAGGAGGAAAGAAAGCCCCGCAAAATCAAGCGGGTCAAAAAGGA
CAAAAAGGAAGAAGAAAGTGATGTGGACGGATTGGTGGAGTTTGTGCGCGAGTTCGCCCCCCGGCGGCGCGTGC
AGTGGCGCGGGCGGAAGGTGCAACCGGTGCTGAGACCCGGCACCACCGTGGTCTTCACGCCCGGCGAGCGCTCC
GGCACCGCTTCCAAGCGCTCCTACGACGAGGTGTACGGGGATGATGATATTCTGGAGCAGGCGGCCGAGCGCCT
GGGCGAGTTTGCTTACGGCAAGCGCAGCCGTTCCGCACCGAAGGAAGAGGCGGTGTCCATCCCGCTGGACCACG
GCAACCCCACGCCGAGCCTCAAGCCCGTGACCTTGCAGCAGGTGCTGCCGACCGCGGCGCCGCGCCGGGGGTTC
AAGCGCGAGGGCGAGGATCTGTACCCCACCATGCAGCTGATGGTGCCCAAGCGCCAGAAGCTGGAAGACGTGCT
GGAGACCATGAAGGTGGACCCGGACGTGCAGCCCGAGGTCAAGGTGCGGCCCATCAAGCAGGTGGCCCCGGGCC
TGGGCGTGCAGACCGTGGACATCAAGATTCCCACGGAGCCCATGGAAACGCAGACCGAGCCCATGATCAAGCCC
AGCACCAGCACCATGGAGGTGCAGACGGATCCCTGGATGCCATCGGCTCCTAGTCGAAGACCCCGGCGCAAGTA
CGGCGCGGCCAGCCTGCTGATGCCCAACTACGCGCTGCATCCTTCCATCATCCCCACGCCGGGCTACCGCGGCA
CGCGCTTCTACCGCGGTCATACCAGCAGCCGCCGCCGCAAGACCACCACTCGCCGCCGCCGTCGCCGCACCGCC
GCTGCAACCACCCCTGCCGCCCTGGTGCGGAGAGTGTACCGCCGCGGCCGCGCACCTCTGACCCTGCCGCGCGC
GCGCTACCACCCGAGCATCGCCATTTAAACTTTCGCCtGCTTTGCAGATCAATGGCCCTCACATGCCGCCTTCG
CGTTCCCATTACGGGCTACCGAGGAAGAAAACCGCGCCGTAGAAGGCTGGCGGGGAACGGGATGCGTCGCCACC
ACCACCGGCGGCGGCGCGCCATCAGCAAGCGGTTGGGGGGAGGCTTCCTGCCCGCGCTGATCCCCATCATCGCC
GCGGCGATCGGGGCGATCCCCGGCATTGCTTCCGTGGCGGTGCAGGCCTCTCAGCGCCACTGAGACACACTTGG
AAACATCTTGTAATAAACCaATGGACTCTGACGCTCCTGGTCCTGTGATGTGTTTTCGTAGACAGATGGAAGAC
ATCAATTTTTCGTCCCTGGCTCCGCGACACGGCACGCGGCCGTTCATGGGCACCTGGAGCGACATCGGCACCAG
CCAACTGAACGGGGGCGCCTTCAATTGGAGCAGTCTCTGGAGCGGGCTTAAGAATTTCGGGTCCACGCTTAAAA
CCTATGGCAGCAAGGCGTGGAACAGCACCACAGGGCAGGCGCTGAGGGATAAGCTGAAAGAGCAGAACTTCCAG
CAGAAGGTGGTCGATGGGCTCGCCTCGGGCATCAACGGGGTGGTGGACCTGGCCAACCAGGCCGTGCAGCGGCA
GATCAACAGCCGCCTGGACCCGGTGCCGCCCGCCGGCTCCGTGGAGATGCCGCAGGTGGAGGAGGAGCTGCCTC
CCCTGGACAAGCGGGGCGAGAAGCGACCCCGCCCCGATGCGGAGGAGACGCTGCTGACGCACACGGACGAGCCG
CCCCCGTACGAGGAGGCGGTGAAACTGGGTCTGCCCACCACGCGGCCCATCGCGCCCCTGGCCACCGGGGTGCT
GAAACCCGAAAAGCCCGCGACCCTGGACTTGCCTCCTCCCCAGCCTTCCCGCCCCTCTACAGTGGCTAAGCCCC
TGCCGCCGGTGGCCGTGGCCCGCGCGCGACCCGGGGGCACCGCCCGCCCTCATGCGAACTGGCAGAGCACTCTG
AACAGCATCGTGGGTCTGGGAGTGCAGAGTGTGAAGCGCCGCCGCTGCTATTAAACCTACCGTAGCGCTTAACT
TGCTTGTCTGTGTGTGTATGTATTATGTCGCCGCCGCCGCTGTCCACCAGAAGGAGGAGTGAAGAGGCGCGTCG
CCGAGTTGCAAGATGGCCACCCCATCGATGCTGCCCCAGTGGGCGTACATGCACATCGCCGGACAGGACGCTTC
GGAGTACCTGAGTCCGGGTCTGGTGCAGTTTGCCCGCGCCACAGACACCTACTTCAGTCTGGGGAACAAGTTTA
GGAACCCCACGGTGGCGCCCACGCACGATGTGACCACCGACCGCAGCCAGCGGCTGACGCTGCGCTTCGTGCCC
GTGGACCGCGAGGACAACACCTACTCGTACAAAGTGCGCTACACGCTGGCCGTGGGCGACAACCGCGTGCTGGA
CATGGCCAGCACCTACTTTGACATCCGCGGCGTGCTGGATCGGGGCCCTAGCTTCAAACCCTACTCCGGCACCG
CCTACAACAGTCTGGCCCCCAAGGGAGCACCCAACACTTGTCAGTGGACATATAAAGCCGATGGTGAAACTGCC
ACAGAAAAAACCTATACATATGGAAATGCACCCGTGCAGGGCATTAACATCACAAAAGATGGTATTCAACTTGG
AACTGACACCGATGATCAGCCAATCTACGCAGATAAAACCTATCAGCCTGAACCTCAAGTGGGTGATGCTGAAT
GGCATGACATCACTGGTACTGATGAAAAGTATGGAGGCAGAGCTCTTAAGCCTGATACCAAAATGAAGCCTTGT
TATGGTTCTTTTGCCAAGCCTACTAATAAAGAAGGAGGTCAGGCAAATGTGAAAACAGGAACAGGCACTACTAA
AGAATATGACATAGACATGGCTTTCTTTGACAACAGAAGTGCGGCTGCTGCTGGCCTAGCTCCAGAAATTGTTT
TGTATACTGAAAATGTGGATTTGGAAACTCCAGATACCCATATTGTATACAAAGCAGGCACAGATGACAGCAGC
TCTTCTATTAATTTGGGTCAGCAAGCCATGCCCAACAGACCTAACTACATTGGTTTCAGAGACAACTTTATCGG
GCTCATGTACTACAACAGCACTGGCAATATGGGGGTGCTGGCCGGTCAGGCTTCTCAGCTGAATGCTGTGGTTG
ACTTGCAAGACAGAAACACCGAGCTGTCCTACCAGCTCTTGCTTGACTCTCTGGGTGACAGAACCCGGTATTTC

2026201462 26 Feb 2026

AGTATGTGGAATCAGGCGGTGGACAGCTATGATCCTGATGTGCGCATTATTGAAAATCATGGTGTGGAGGATGA
ACTTCCCAACTATTGTTTCCCTCTGGATGCTGTTGGCAGAACAGATACTTATCAGGGAATTAAGGCTAATGGAA
CTGATCAAACCACATGGACCAAAGATGACAGTGTCAATGATGCTAATGAGATAGGCAAGGGTAATCCATTCGCC
ATGGAAATCAACATCCAAGCCAACCTGTGGAGGAACTTCCTCTACGCCAACGTGGCCCTGTACCTGCCCGACTC
TTACAAGTACACGCCGGCCAATGTTACCCTGCCCACCAACACCAACACCTACGATTACATGAACGGCCGGGTGG
TGGCGCCCTCGCTGGTGGACTCCTACATCAACATCGGGGCGCGCTGGTCGCTGGATCCCATGGACAACGTGAAC
CCCTTCAACCACCACCGCAATGCGGGGCTGCGCTACCGCTCCATGCTCCTGGGCAACGGGCGCTACGTGCCCTT
CCACATCCAGGTGCCCCAGAAATTTTTCGCCATCAAGAGCCTCCTGCTCCTGCCCGGGTCCTACACCTACGAGT
GGAACTTCCGCAAGGACGTCAACATGATCCTGCAGAGCTCCCTCGGCAACGACCTGCGCACGGACGGGGCCTCC
ATCTCCTTCACCAGCATCAACCTCTACGCCACCTTCTTCCCCATGGCGCACAACACGGCCTCCACGCTCGAGGC
CATGCTGCGCAACGACACCAACGACCAGTCCTTCAACGACTACCTCTCGGCGGCCAACATGCTCTACCCCATCC
CGGCCAACGCCACCAACGTGCCCATCTCCATCCCCTCGCGCAACTGGGCCGCCTTCCGCGGCTGGTCCTTCACG
CGTCTCAAGACCAAGGAGACGCCCTCGCTGGGCTCCGGGTTCGACCCCTACTTCGTCTACTCGGGCTCCATCCC
CTACCTCGACGGCACCTTCTACCTCAACCACACCTTCAAGAAGGTCTCCATCACCTTCGACTCCTCCGTCAGCT
GGCCCGGCAACGACCGGCTCCTGACGCCCAACGAGTTCGAAATCAAGCGCACCGTCGACGGCGAGGGCTACAAC
GTGGCCCAGTGCAACATGACCAAGGACTGGTTCCTGGTCCAGATGCTGGCCCACTACAACATCGGCTACCAGGG
CTTCTACGTGCCCGAGGGCTACAAGGACCGCATGTACTCCTTCTTCCGCAACTTCCAGCCCATGAGCCGCCAGG
TGGTGGACGAGGTCAACTACAAGGACTACCAGGCCGTCACCCTGGCCTACCAGCACAACAACTCGGGCTTCGTC
GGCTACCTCGCGCCCACCATGCGCCAGGGCCAGCCCTACCCCGCCAACTACCCCTACCCGCTCATCGGCAAGAG
CGCCGTCACCAGCGTCACCCAGAAAAAGTTCCTCTGCGACAGGGTCATGTGGCGCATCCCCTTCTCCAGCAACT
TCATGTCCATGGGCGCGCTCACCGACCTCGGCCAGAACATGCTCTATGCCAACTCCGCCCACGCGCTAGACATG
AATTTCGAAGTCGACCCCATGGATGAGTCCACCCTTCTCTATGTTGTCTTCGAAGTCTTCGACGTCGTCCGAGT
GCACCAGCCCCACCGCGGCGTCATCGAGGCCGTCTACCTGCGCACCCCCTTCTCGGCCGGTAACGCCACCACCT
AAGCTCTTGCTTCTTGCAAGCCATGGCCGCGGGCTCCGGCGAGCAGGAGCTCAGGGCCATCATCCGCGACCTGG
GCTGCGGGCCCTACTTCCTGGGCACCTTCGATAAGCGCTTCCCGGGATTCATGGCCCCGCACAAGCTGGCCTGC
GCCATCGTCAACACGGCCGGCCGCGAGACCGGGGGCGAGCACTGGCTGGCCTTCGCCTGGAACCCGCGCTCGAA
CACCTGCTACCTCTTCGACCCCTTCGGGTTCTCGGACGAGCGCCTCAAGCAGATCTACCAGTTCGAGTACGAGG
GCCTGCTGCGCCGCAGCGCCCTGGCCACCGAGGACCGCTGCGTCACCCTGGAAAAGTCCACCCAGACCGTGCAG
GGTCCGCGCTCGGCCGCCTGCGGGCTCTTCTGCTGCATGTTCCTGCACGCCTTCGTGCACTGGCCCGACCGCCC
CATGGACAAGAACCCCACCATGAACTTGCTGACGGGGGTGCCCAACGGCATGCTCCAGTCGCCCCAGGTGGAAC
CCACCCTGCGCCGCAACCAGGAGGCGCTCTACCGCTTCCTCAACTCCCACTCCGCCTACTTTCGCTCCCACCGC
GCGCGCATCGAGAAGGCCACCGCCTTCGACCGCATGAATCAAGACATGTAAACCGTGTGTGTATGTTAAATGTC
TTTAATAAACAGCACTTTCATGTTACACATGCATCTGAGATGATTTATTTAGAAATCGAAAGGGTTCTGCCGGG
TCTCGGCATGGCCCGCGGGCAGGGACACGTTGCGGAACTGGTACTTGGCCAGCCACTTGAACTCGGGGATCAGC
AGTTTGGGCAGCGGGGTGTCGGGGAAGGAGTCGGTCCACAGCTTCCGCGTCAGTTGCAGGGCGCCCAGCAGGTC
GGGCGCGGAGATCTTGAAATCGCAGTTGGGACCCGCGTTCTGCGCGCGGGAGTTGCGGTACACGGGGTTGCAGC
ACTGGAACACCATCAGGGCCGGGTGCTTCACGCTCGCCAGCACCGTCGCGTCGGTGATGCTCTCCACGTCGAGG
TCCTCGGCGTTGGCCATCCCGAAGGGGGTCATCTTGCAGGTCTGCCTTCCCATGGTGGGCACGCACCCGGGCTT
GTGGTTGCAATCGCAGTGCAGGGGGATCAGCATCATCTGGGCCTGGTCGGCGTTCATCCCCGGGTACATGGCCT
TCATGAAAGCCTCCAATTGCCTGAACGCCTGCTGGGCCTTGGCTCCCTCGGTGAAGAAGACCCCGCAGGACTTG
CTAGAGAACTGGTTGGTGGCGCACCCGGCGTCGTGCACGCAGCAGCGCGCGTCGTTGTTGGCCAGCTGCACCAC
GCTGCGCCCCCAGCGGTTCTGGGTGATCTTGGCCCGGTCGGGGTTCTCCTTCAGCGCGCGCTGCCCGTTCTCGC
TCGCCACATCCATCTCGATCATGTGCTCCTTCTGGATCATGGTGGTCCCGTGCAGGCACCGCAGCTTGCCCTCG
GCCTCGGTGCACCCGTGCAGCCACAGCGCGCACCCGGTGCACTCCCAGTTCTTGTGGGCGATCTGGGAATGCGC
GTGCACGAAGCCCTGCAGGAAGCGGCCCATCATGGTGGTCAGGGTCTTGTTGCTAGTGAAGGTCAGCGGAATGC
CGCGGTGCTCCTCGTTGATGTACAGGTGGCAGATGCGGCGGTACACCTCGCCCTGCTCGGGCATCAGCTGGAAG
TTGGCTTTCAGGTCGGTCTCCACGCGGTAGCGGTCCATCAGCATAGTCATGATTTCCATACCCTTCTCCCAGGC
CGAGACGATGGGCAGGCTCATAGGGTTCTTCACCATCATCTTAGCGCTAGCAGCCGCGGCCAGGGGGTCGCTCT
CGTCCAGGGTCTCAAAGCTCCGCTTGCCGTCCTTCTCGGTGATCCGCACCGGGGGGTAGCTGAAGCCCACGGCC
GCCAGCTCCTCCTCGGCCTGTCTTTCGTCCTCGCTGTCCTGGCTGACGTCCTGCAGGACCACATGCTTGGTCTT
GCGGGGTTTCTTCTTGGGCGGCAGCGGCGGCGGAGATGTTGGAGATGGCGAGGGGGAGCGCGAGTTCTCGCTCA
CCACTACTATCTCTTCCTCTTCTTGGTCCGAGGCCACGCGGCGGTAGGTATGTCTCTTCGGGGGCAGAGGCGGA
GGCGACGGGCTCTCGCCGCCGCGACTTGGCGGATGGCTGGCAGAGCCCCTTCCGCGTTCGGGGGTGCGCTCCCG
GCGGCGCTCTGACTGACTTCCTCCGCGGCCGGCCATTGTGTTCTCCTAGGGAGGAACAACAAGCATGGAGACTC
AGCCATCGCCAACCTCGCCATCTGCCCCCACCGCCGACGAGAAGCAGCAGCAGCAGAATGAAAGCTTAACCGCC
CCGCCGCCCAGCCCCGCCACCTCCGACGCGGCCGTCCCAGACATGCAAGAGATGGAGGAATCCATCGAGATTGA
CCTGGGCTATGTGACGCCCGCGGAGCACGAGGAGGAGCTGGCAGTGCGCTTTTCACAAGAAGAGATACACCAAG
AACAGCCAGAGCAGGAAGCAGAGAATGAGCAGAGTCAGGCTGGGCTCGAGCATGACGGCGACTACCTCCACCTG
AGCGGGGGGGAGGACGCGCTCATCAAGCATCTGGCCCGGCAGGCCACCATCGTCAAGGATGCGCTGCTCGACCG
CACCGAGGTGCCCCTCAGCGTGGAGGAGCTCAGCCGCGCCTACGAGTTGAACCTCTTCTCGCCGCGCGTGCCCC

2026201462 26 Feb 2026

CCAAGCGCCAGCCCAATGGCACCTGCGAGCCCAACCCGCGCCTCAACTTCTACCCGGTCTTCGCGGTGCCCGAG
GCCCTGGCCACCTACCACATCTTTTTCAAGAACCAAAAGATCCCCGTCTCCTGCCGCGCCAACCGCACCCGCGC
CGACGCCCTTTTCAACCTGGGTCCCGGCGCCCGCCTACCTGATATCGCCTCCTTGGAAGAGGTTCCCAAGATCT
TCGAGGGTCTGGGCAGCGACGAGACTCGGGCCGCGAACGCTCTGCAAGGAGAAGGAGGAGAGCATGAGCACCAC
AGCGCCCTGGTCGAGTTGGAAGGCGACAACGCGCGGCTGGCGGTGCTCAAACGCACGGTCGAGCTGACCCATTT
CGCCTACCCGGCTCTGAACCTGCCCCCCAAAGTCATGAGCGCGGTCATGGACCAGGTGCTCATCAAGCGCGCGT
CGCCCATCTCCGAGGACGAGGGCATGCAAGACTCCGAGGAGGGCAAGCCCGTGGTCAGCGACGAGCAGCTGGCC
CGGTGGCTGGGTCCTAATGCTAGTCCCCAGAGTTTGGAAGAGCGGCGCAAACTCATGATGGCCGTGGTCCTGGT
GACCGTGGAGCTGGAGTGCCTGCGCCGCTTCTTCGCCGACGCGGAGACCCTGCGCAAGGTCGAGGAGAACCTGC
ACTACCTCTTCAGGCACGGGTTCGTGCGCCAGGCCTGCAAGATCTCCAACGTGGAGCTGACCAACCTGGTCTCC
TACATGGGCATCTTGCACGAGAACCGCCTGGGGCAGAACGTGCTGCACACCACCCTGCGCGGGGAGGCCCGGCG
CGACTACATCCGCGACTGCGTCTACCTCTACCTCTGCCACACCTGGCAGACGGGCATGGGCGTGTGGCAGCAGT
GTCTGGAGGAGCAGAACCTGAAAGAGCTCTGCAAGCTCCTGCAGAAGAACCTCAAGGGTCTGTGGACCGGGTTC
GACGAGCGCACCACCGCCTCGGACCTGGCCGACCTCATTTTCCCCGAGCGCCTCAGGCTGACGCTGCGCAACGG
CCTGCCCGACTTTATGAGCCAAAGCATGTTGCAAAACTTTCGCTCTTTCATCCTCGAACGCTCCGGAATCCTGC
CCGCCACCTGCTCCGCGCTGCCCTCGGACTTCGTGCCGCTGACCTTCCGCGAGTGCCCCCCGCCGCTGTGGAGC
CACTGCTACCTGCTGCGCCTGGCCAACTACCTGGCCTACCACTCGGACGTGATCGAGGACGTCAGCGGCGAGGG
CCTGCTCGAGTGCCACTGCCGCTGCAACCTCTGCACGCCGCACCGCTCCCTGGCCTGCAACCCCCAGCTGCTGA
GCGAGACCCAGATCATCGGCACCTTCGAGTTGCAAGGGCCCAGCGAAGGCGAGGGTTCAGCCGCCAAGGGGGGT
CTGAAACTCACCCCGGGGCTGTGGACCTCGGCCTACTTGCGCAAGTTCGTGCCCGAGGACTACCATCCCTTCGA
GATCAGGTTCTACGAGGACCAATCCCATCCGCCCAAGGCCGAGCTGTCGGCCTGCGTCATCACCCAGGGGGCGA
TCCTGGCCCAATTGCAAGCCATCCAGAAATCCCGCCAAGAATTCTTGCTGAAAAAGGGCCGCGGGGTCTACCTC
GACCCCCAGACCGGTGAGGAGCTCAACCCCGGCTTCCCCCAGGATGCCCCGAGGAAACAAGAAGCTGAAAGTGG
AGCTGCCGCCCGTGGAGGATTTGGAGGAAGACTGGGAGAACAGCAGTCAGGCAGAGGAGGAGGAGATGGAGGAA
GACTGGGACAGCACTCAGGCAGAGGAGGACAGCCTGCAAGACAGTCTGGAGGAAGACGAGGAGGAGGCAGAGGA
GGAGGTGGAAGAAGCAGCCGCCGCCAGACCGTCGTCCTCGGCGGGGGAGAAAGCAAGCAGCACGGATACCATCT
CCGCTCCGGGTCGGGGTCCCGCTCGACCACACAGTAGATGGGACGAGACCGGACGATTCCCGAACCCCACCACC
CAGACCGGTAAGAAGGAGCGGCAGGGATACAAGTCCTGGCGGGGGCACAAAAACGCCATCGTCTCCTGCTTGCA
GGCCTGCGGGGGCAACATCTCCTTCACCCGGCGCTACCTGCTCTTCCACCGCGGGGTGAACTTTCCCCGCAACA
TCTTGCATTACTACCGTCACCTCCACAGCCCCTACTACTTCCAAGAAGAGGCAGCAGCAGCAGAAAAAGACCAG
CAGAAAACCAGCAGCTAGAAAATCCACAGCGGCGGCAGCAGGTGGACTGAGGATCGCGGCGAACGAGCCGGCGC
AAACCCGGGAGCTGAGGAACCGGATCTTTCCCACCCTCTATGCCATCTTCCAGCAGAGTCGGGGGCAGGAGCAG
GAACTGAAAGTCAAGAACCGTTCTCTGCGCTCGCTCACCCGCAGTTGTCTGTATCACAAGAGCGAAGACCAACT
TCAGCGCACTCTCGAGGACGCCGAGGCTCTCTTCAACAAGTACTGCGCGCTCACTCTTAAAGAGTAGCCCGCGC
CCGCCCAGTCGCAGAAAAAGGCGGGAATTACGTCACCTGTGCCCTTCGCCCTAGCCGCCTCCACCCATCATCAT
GAGCAAAGAGATTCCCACGCCTTACATGTGGAGCTACCAGCCCCAGATGGGCCTGGCCGCCGGTGCCGCCCAGG
ACTACTCCACCCGCATGAATTGGCTCAGCGCCGGGCCCGCGATGATCTCACGGGTGAATGACATCCGCGCCCAC
CGAAACCAGATACTCCTAGAACAGTCAGCGCTCACCGCCACGCCCCGCAATCACCTCAATCCGCGTAATTGGCC
CGCCGCCCTGGTGTACCAGGAAATTCCCCAGCCCACGACCGTACTACTTCCGCGAGACGCCCAGGCCGAAGTCC
AGCTGACTAACTCAGGTGTCCAGCTGGCGGGCGGCGCCACCCTGTGTCGTCACCGCCCCGCTCAGGGTATAAAG
CGGCTGGTGATCCGGGGCAGAGGCACACAGCTCAACGACGAGGTGGTGAGCTCTTCGCTGGGTCTGCGACCTGA
CGGAGTCTTCCAACTCGCCGGATCGGGGAGATCTTCCTTCACGCCTCGTCAGGCCGTCCTGACTTTGGAGAGTT
CGTCCTCGCAGCCCCGCTCGGGTGGCATCGGCACTCTCCAGTTCGTGGAGGAGTTCACTCCCTCGGTCTACTTC
AACCCCTTCTCCGGCTCCCCCGGCCACTACCCGGACGAGTTCATCCCGAACTTCGACGCCATCAGCGAGTCGGT
GGACGGCTACGATTGAATGTCCCATGGTGGCGCAGCTGACCTAGCTCGGCTTCGACACCTGGACCACTGCCGCC
GCTTCCGCTGCTTCGCTCGGGATCTCGCCGAGTTTGCCTACTTTGAGCTGCCCGAGGAGCACCCTCAGGGCCCG
GCCCACGGAGTGCGGATCGTCGTCGAAGGGGGCCTCGACTCCCACCTGCTTCGGATCTTCAGCCAGCGTCCGAT
CCTGGTCGAGCGCGAGCAAGGACAGACCCTTCTGACTCTGTACTGCATCTGCAACCACCCCGGCCTGCATGAAA
GTCTTTGTTGTCTGCTGTGTACTGAGTATAATAAAAGCTGAGATCAGCGACTACTCCGGACTTCCGTGTGTTCC
TGAATCCATCAACCAGTCTTTGTTCTTCACCGGGAACGAGACCGAGCTCCAGCTCCAGTGTAAGCCCCACAAGA
AGTACCTCACCTGGCTGTTCCAGGGCTCCCCGATCGCCGTTGTCAACCACTGCGACAACGACGGAGTCCTGCTG
AGCGGCCCTGCCAACCTTACTTTTTCCACCCGCAGAAGCAAGCTCCAGCTCTTCCAACCCTTCCTCCCCGGGAC
CTATCAGTGCGTCTCGGGACCCTGCCATCACACCTTCCACCTGATCCCGAATACCACAGCGTCGCTCCCCGCTA
CTAACAACCAAACTAACCTCCACCAACGCCACCGTCGCGACGGCCACAATACATGCCCATATTAGACTATGAGG
CCGAGCCACAGCGACCCATGCTCCCCGCTATTAGTTACTTCAATCTAACCGGCGGAGATGACTGACCCACTGGC
CAACAACAACGTCAACGACCTTCTCCTGGACATGGACGGCCGCGCCTCGGAGCAGCGACTCGCCCAACTTCGCA
TTCGCCAGCAGCAGGAGAGAGCCGTCAAGGAGCTGCAGGATGCGGTGGCCATCCACCAGTGCAAGAGAGGCATC
TTCTGCCTGGTGAAACAGGCCAAGATCTCCTACGAGGTCACTCCAAACGACCATCGCCTCTCCTACGAGCTCCT
GCAGCAGCGCCAGAAGTTCACCTGCCTGGTCGGAGTCAACCCCATCGTCATCACCCAGCAGTCTGGCGATACCA
AGGGGTGCATCCACTGCTCCTGCGACTCCCCCGACTGCGTCCACACTCTGATCAAGACCCTCTGCGGCCTCCGC

2026201462 26 Feb 2026

GACCTCCTCCCCATGAACTAATCACCCCCTTATCCAGTGAAATAAAGATCATATTGATGATGATTTTACAGAAA
TAAAAAATAATCATTTGATTTGAAATAAAGATACAATCATATTGATGATTTGAGTTTAACAAAAAAATAAAGAA
TCACTTACTTGAAATCTGATACCAGGTCTCTGTCCATGTTTTCTGCCAACACCACTTCACTCCCCTCTTCCCAG
CTCTGGTACTGCAGGCCCCGGCGGGCTGCAAACTTCCTCCACACGCTGAAGGGGATGTCAAATTCCTCCTGTCC
CTCAATCTTCATTTTATCTTCTATCAGATGTCCAAAAAGCGCGTCCGGGTGGATGATGACTTCGACCCCGTCTA
CCCCTACGATGCAGACAACGCACCGACCGTGCCCTTCATCAACCCCCCCTTCGTCTCTTCAGATGGATTCCAAG
AGAAGCCCCTGGGGGGTGTTGTCCCTGCGACTGGCCGACCCCGTCACCACCAAGAACGGGGAAATCACCCTCAAG
CTGGGAGAGGGGGTGGACCTCGATTCCTCGGGAAAACTCATCTCCAACACGGCCACCAAGGCCGCCGCCCCTCT
CAGTTTTTCCAACAACACCATTTCCCTTAACATGGATCACCCCTTTTACACTAAAGATGGAAAATTATCCTTAC
AAGTTTCTCCACCATTAAATATACTGAGAACAAGCATTCTAAACACACTAGCTTTAGGTTTTGGATCAGGTTTA
GGACTCCGTGGCTCTGCCTTGGCAGTACAGTTAGTCTCTCCACTTACATTTGATACTGATGGAAACATAAAGCT
TACCTTAGACAGAGGTTTGCATGTTACAACAGGAGATGCAATTGAAAGCAACATAAGCTGGGCTAAAGGTTTAA
AATTTGAAGATGGAGCCATAGCAACCAACATTGGAAATGGGTTAGAGTTTGGAAGCAGTAGTACAGAAACAGGT
GTTGATGATGCTTACCCAATCCAAGTTAAACTTGGATCTGGCCTTAGCTTTGACAGTACAGGAGCCATAATGGC
TGGTAACAAAGAAGACGATAAACTCACTTTGTGGACAACACCTGATCCATCACCAAACTGTCAAATACTCGCAG
AAAATGATGCAAAACTAACACTTTGCTTGACTAAATGTGGTAGTCAAATACTGGCCACTGTGTCAGTCTTAGTT
GTAGGAAGTGGAAACCTAAACCCCATTACTGGCACCGTAAGCAGTGCTCAGGTGTTTCTACGTTTTGATGCAAA
CGGTGTTCTTTTAACAGAACATTCTACACTAAAAAAATACTGGGGGTATAGGCAGGGAGATAGCATAGATGGCA
CTCCATATACCAATGCTGTAGGATTCATGCCCAATTTAAAAGCTTATCCAAAGTCACAAAGTTCTACTACTAAA
AATAATATAGTAGGGCAAGTATACATGAATGGAGATGTTTCAAAACCTATGCTTCTCACTATAACCCTCAATGG
TACTGATGACAGCAACAGTACATATTCAATGTCATTTTCATACACCTGGACTAATGGAAGCTATGTTGGAGCAA
CATTTGGGGCTAACTCTTATACCTTCTCATACATCGCCCAAGAATGAACACTGTATCCCACCCTGCATGCCAAC
CCTTCCCACCCCACTCTGTGGAACAAACTCTGAAACACAAAATAAAATAAAGTTCAAGTGTTTTATTGATTCAA
CAGTTTTACAGGATTCGAGCAGTTATTTTTCCTCCACCCTCCCAGGACATGGAATACACCACCCTCTCCCCCCG
CACAGCCTTGAACATCTGAATGCCATTGGTGATGGACATGCTTTTGGTCTCCACGTTCCACACAGTTTCAGAGC
GAGCCAGTCTCGGGTCGGTCAGGGAGATGAAACCCTCCGGGCACTCCCGCATCTGCACCTCACAGCTCAACAGC
TGAGGATTGTCCTCGGTGGTCGGGATCACGGTTATCTGGAAGAAGCAGAAGAGCGGCGGTGGGAATCATAGTCC
GCGAACGGGATCGGCCGGTGGTGTCGCATCAGGCCCCGCAGCAGTCGCTGCCGCCGCCGCTCCGTCAAGCTGCT
GCTCAGGGGGTCCGGGTCCAGGGACTCCCTCAGCATGATGCCCACGGCCCTCAGCATCAGTCGTCTGGTGCGGC
GGGCGCAGCAGCGCATGCGGATCTCGCTCAGGTCGCTGCAGTACGTGCAACACAGAACCACCAGGTTGTTCAAC
AGTCCATAGTTCAACACGCTCCAGCCGAAACTCATCGCGGGAAGGATGCTACCCACGTGGCCGTCGTACCAGAT
CCTCAGGTAAATCAAGTGGTGCCCCCTCCAGAACACGCTGCCCACGTACATGATCTCCTTGGGCATGTGGCGGT
TCACCACCTCCCGGTACCACATCACCCTCTGGTTGAACATGCAGCCCCGGATGATCCTGCGGAACCACAGGGCC
AGCACCGCCCCGCCCGCCATGCAGCGAAGAGACCCCGGGTCCCGGCAATGGCAATGGAGGACCCACCGCTCGTA
CCCGTGGATCATCTGGGAGCTGAACAAGTCTATGTTGGCACAGCACAGGCATATGCTCATGCATCTCTTCAGCA
CTCTCAACTCCTCGGGGGTCAAAACCATATCCCAGGGCACGGGGAACTCTTGCAGGACAGCGAACCCCGCAGAA
CAGGGCAATCCTCGCACAGAACTTACATTGTGCATGGACAGGGTATCGCAATCAGGCAGCACCGGGTGATCCTC
CACCAGAGAAGCGCGGGTCTCGGTCTCCTCACAGCGTGGTAAGGGGGCCGGCCGATACGGGTGATGGCGGGACG
CGGCTGATCGTGTTCGCGACCGTGTCATGATGCAGTTGCTTTCGGACATTTTCGTACTTGCTGTAGCAGAACCT
GGTCCGGGCGCTGCACACCGATCGCCGGCGGCGGTCTCGGCGCTTGGAACGCTCGGTGTTGAAATTGTAAAACA
GCCACTCTCTCAGACCGTGCAGCAGATCTAGGGCCTCAGGAGTGATGAAGATCCCATCATGCCTGATGGCTCTG
ATCACATCGACCACCGTGGAATGGGCCAGACCCAGCCAGATGATGCAATTTTGTTGGGTTTCGGTGACGGCGGG
GGAGGGAAGAACAGGAAGAACCATGATTAACTTTTAATCCAAACGGTCTCGGAGTACTTCAAAATGAAGATCGC
GGAGATGGCACCTCTCGCCCCCGCTGTGTTGGTGGAAAATAACAGCCAGGTCAAAGGTGATACGGTTCTCGAGA
TGTTCCACGGTGGCTTCCAGCAAAGCCTCCACGCGCACATCCAGAAACAAGACAATAGCGAAAGCGGGAGGGTT
CTCTAATTCCTCAATCATCATGTTACACTCCTGCACCATCCCCAGATAATTTTCATTTTTCCAGCCTTGAATGA
TTCGAACTAGTTCGTGAGGTAAATCCAAGCCAGCCATGATAAAGAGCTCGCGCAGAGCGCCCTCCACCGGCATT
CTTAAGCACACCCTCATAATTCCAAGATATTCTGCTCCTGGTTCACCTGCAGCAGATTGACAAGCGGAATATCA
AAATCTCTGCCGCGATCCCTGAGCTCCTCCCTCAGCAATAACTGTAAGTACTCTTTCATATCCTCTCCGAAATT
TTTAGCCATAGGACCACCAGGAATAAGATTAGGGCAAGCCACAGTACAGATAAACCGAAGTCCTCCCCAGTGAG
CATTGCCAAATGCAAGACTGCTATAAGCATGCTGGCTAGACCCGGTGATATCTTCCAGATAACTGGACAGAAAA
TCGCCCAGGCAATTTTTAAGAAAATCAACAAAAGAAAAATCCTCCAGGTGGACGTTTAGAGCCTCGGGAACAAC
GATGAAGTAAATGCAAGCGGTGCGTTCCAGCATGGTTAGTTAGCTGATCTGTAGAAAAAACAAAAATGAACATT
AAACCATGCTAGCCTGGCGAACAGGTGGGTAAATCGTTCTCTCCAGCACCAGGCAGGCCACGGGGTCTCCGGCG
CGACCCTCGTAAAAATTGTCGCTATGATTGAAAACCATCACAGAGAGACGTTCCCGGTGGCCGGCGTGAATGAT
TCGACAAGATGAATACACCCCCGGAACATTGGCGTCCGCGAGTGAAAAAAAGCGCCCGAGGAAGCAATAAGGCA
CTACAATGCTCAGTCTCAAGTCCAGCAAAGCGATGCCATGCGGATGAAGCACAAAATTCTCAGGTGCGTACAAA
ATGTAATTACTCCCCTCCTGCACAGGCAGCAAAGCCCCCGATCCCTCCAGGTACACATACAAAGCCTCAGCGTC
CATAGCTTACCGAGCAGCAGCACACAACAGGCGCAAGAGTCAGAGAAAGGCTGAGCTCTAACCTGTCCACCCGC
TCTCTGCTCAATATATAGCCCAGATCTACACTGACGTAAAGGCCAAAGTCTAAAAATACCCGCCAAATAATCAC

2026201462 26 Feb 2026

ACACGCCCAGCACACGCCCAGAAACCGGTGACACACTCAAAAAAATACGCGCACTTCCTCAAACGCCCAAAACT
GCCGTCATTTCCGGGTTCCCACGCTACGTCATCAAAACACGACTTTCAAATTCCGTCGACCGTTAAAAACGTCA
CCCGCCCCGCCCCTAACGGTCGCCCGTCTCTCAGCCAATCAGCGCCCCGCATCCCCAAATTCAAACACCTCATT
TGCATATTAACGCGCACAAAAAGTTTGAGGTATATTATTGATGATGG

ChAdV68.4WTnt.MAG25mer (SEQ ID NO:12); AC_000011.1 with E1 (nt 577 to 3403) and E3 (nt 27,816- 31,332) sequences deleted; corresponding ATCC VR-594 nucleotides substituted at four positions; model neoantigen cassette under the control of the CMV promoter/enhancer inserted in place of deleted E1

CCATCTTCAATAATATACCTCAAACTTTTTGTGCGCGTTAATATGCAAATGAGGCGTTTGAATTTGGGGAGGAA
GGGCGGTGATTGGTCGAGGGATGAGCGACCGTTAGGGGCGGGGCGAGTGACGTTTTGATGACGTGGTTGCGAGG
AGGAGCCAGTTTGCAAGTTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTTGAACACGGAAATACTCAAT
TTTCCCGCGCTCTCTGACAGGAAATGAGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGCCATTTTCGCGCGAA
AACTGAATGAGGAAGTGAAAATCTGAGTAATTTCGCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGCCGAGTA
GACTTTGACCGATTACGTGGGGGTTTCGATTACCGTGTTTTTCACCTAAATTTCCGCGTACGGTGTCAAAGTCC
GGTGTTTTTACGTAGGTGTCAGCTGATCGCCAGGGTATTTAAACCTGCGCTCTCCAGTCAAGAGGCCACTCTTG
AGTGCCAGCGAGAAGAGTTTTCTCCTCCGCGCCGCGAGTCAGATCTACACTTTGAAAGTAGGGATAACAGGGTA
ATgacattgattattgactagttGttaaTAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGT
TCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATA
ATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAAC
TGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCCTATTGACGTCAATGACGGTAAATGGC
CCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATC
GCTATTACCATGgTGATGCGGTTTTGGCAGTACACCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCC
AAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ATAACCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAgcTCGTTTA
GTGAACCGTCAGATCGCCTGGAACGCCATCCACGCTGTTTTGACCTCCATAGAAGACAGCGATCGCGccaccAT
GGCCGGGATGTTCCAGGCACTGTCCGAAGGCTGCACACCCTATGATATTAACCAGATGCTGAATGTCCTGGGAG
ACCACCAGGTCTCTGGCCTGGAGCAGCTGGAGAGCATCATCAACTTCGAGAAGCTGACCGAGTGGACAAGCTCC
AATGTGATGCCTATCCTGTCCCCACTGACCAAGGGCATCCTGGGCTTCGTGTTTACCCTGACAGTGCCTTCTGA
GCGGGGCCTGTCTTGCATCAGCGAGGCAGACGCAACCACACCAGAGTCCGCCAATCTGGGCGAGGAGATCCTGT
CTCAGCTGTACCTGTGGCCCCGGGTGACATATCACTCCCCTTCTTACGCCTATCACCAGTTCGAGCGGAGAGCC
AAGTACAAGAGACACTTCCCAGGCTTTGGCCAGTCTCTGCTGTTCGGCTACCCCGTGTACGTGTTCGGCGATTG
CGTGCAGGGCGACTGGGATGCCATCCGGTTTAGATACTGCGCACCACCTGGATATGCACTGCTGAGGTGTAACG
ACACCAATTATTCCGCCCTGCTGGCAGTGGGCGCCCTGGAGGGCCCTCGCAATCAGGATTGGCTGGGCGTGCCA
AGGCAGCTGGTGACACGCATGCAGGCCATCCAGAACGCAGGCCTGTGCACCCTGGTGGCAATGCTGGAGGAGAC
AATCTTCTGGCTGCAGGCCTTTCTGATGGCCCTGACCGACAGCGGCCCCAAGACAAACATCATCGTGGATTCCC
AGTACGTGATGGGCATCTCCAAGCCTTCTTTCCAGGAGTTTGTGGACTGGGAGAACGTGAGCCCAGAGCTGAAT
TCCACCGATCAGCCATTCTGGCAGGCAGGAATCCTGGCAAGGAACCTGGTGCCTATGGTGGCCACAGTGCAGGG
CCAGAATCTGAAGTACCAGGGCCAGAGCCTGGTCATCAGCGCCTCCATCATCGTGTTTAACCTGCTGGAGCTGG
AGGGCGACTATCGGGACGATGGCAACGTGTGGGTGCACACCCCACTGAGCCCCAGAACACTGAACGCCTGGGTG
AAGGCCGTGGAGGAGAAGAAGGGCATCCCAGTGCACCTGGAGCTGGCCTCCATGACCAATATGGAGCTGATGTC
TAGCATCGTGCACCAGCAGGTGAGGACATACGGACCCGTGTTCATGTGCCTGGGAGGCCTGCTGACCATGGTGG
CAGGAGCCGTGTGGCTGACAGTGCGGGTGCTGGAGCTGTTCAGAGCCGCCCAGCTGGCCAACGATGTGGTGCTG
CAGATCATGGAGCTGTGCGGAGCAGCCTTTCGCCAGGTGTGCCACACCACAGTGCCATGGCCCAATGCCTCCCT
GACCCCCAAGTGGAACAATGAGACAACACAGCCTCAGATCGCCAACTGTAGCGTGTACGACTTCTTCGTGTGGC
TGCACTACTATAGCGTGAGGGATACCCTGTGGCCCCGCGTGACATACCACATGAATAAGTACGCCTATCACATG
CTGGAGAGGCGCGCCAAGTATAAGAGAGGCCCTGGCCCAGGCGCAAAGTTTGTGGCAGCATGGACCCTGAAGGC
CGCCGCCGGCCCCGGCCCCGGCCAGTATATCAAGGCTAACAGTAAGTTCATTGGAATCACAGAGCTGGGACCCG
GACCTGGATAATGAGTTTAAACTCCCATTTAAATGTGAGGGTTAATGCTTCGAGCAGACATGATAAGATACATT
GATGAGTTTGGACAAACCACAACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGC
TTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTC
AGGGGGAGATGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTAAAATAACTATAACGGTCCTA
AGGTAGCGAGTGAGTAGTGTTCTGGGGCGGGGGAGGACCTGCATGAGGGCCAGAATAACTGAAATCTGTGCTTT
TCTGTGTGTTGCAGCAGCATGAGCGGAAGCGGCTCCTTTGAGGGAGGGGTATTCAGCCCTTATCTGACGGGGCG
TCTCCCCTCCTGGGCGGGAGTGCGTCAGAATGTGATGGGATCCACGGTGGACGGCCGGCCCGTGCAGCCCGCGA
ACTCTTCAACCCTGACCTATGCAACCCTGAGCTCTTCGTCGTTGGACGCAGCTGCCGCCGCAGCTGCTGCATCT
GCCGCCAGCGCCGTGCGCGGAATGGCCATGGGCGCCGGCTACTACGGCACTCTGGTGGCCAACTCGAGTTCCAC
CAATAATCCCGCCAGCCTGAACGAGGAGAAGCTGTTGCTGCTGATGGCCCAGCTCGAGGCCTTGACCCAGCGCC
TGGGCGAGCTGACCCAGCAGGTGGCTCAGCTGCAGGAGCAGACGCGGGCCGCGGTTGCCACGGTGAAATCCAAA
TAAAAAATGAATCAATAAATAAACGGAGACGGTTGTTGATTTTAACACAGAGTCTGAATCTTTATTTGATTTTT

2026201462 26 Feb 2026

CGCGCGCGGTAGGCCCTGGACCACCGGTCTCGATCATTGAGCACCCGGTGGATCTTTTCCAGGACCCGGTAGAG
GTGGGCTTGGATGTTGAGGTACATGGGCATGAGCCCGTCCCGGGGGTGGAGGTAGCTCCATTGCAGGGCCTCGT
GCTCGGGGGTGGTGTTGTAAATCACCCAGTCATAGCAGGGGCGCAGGGCATGGTGTTGCACAATATCTTTGAGG
AGGAGACTGATGGCCACGGGCAGCCCTTTGGTGTAGGTGTTTACAAATCTGTTGAGCTGGGAGGGATGCATGCG
GGGGGAGATGAGGTGCATCTTGGCCTGGATCTTGAGATTGGCGATGTTACCGCCCAGATCCCGCCTGGGGTTCA
TGTTGTGCAGGACCACCAGCACGGTGTATCCGGTGCACTTGGGGAATTTATCATGCAACTTGGAAGGGAAGGCG
TGAAAGAATTTGGCGACGCCTTTGTGCCCGCCCAGGTTTTCCATGCACTCATCCATGATGATGGCGATGGGCCC
GTGGGCGGCGGCCTGGGCAAAGACGTTTCGGGGGTCGGACACATCATAGTTGTGGTCCTGGGTGAGGTCATCAT
AGGCCATTTTAATGAATTTGGGGCGGAGGGTGCCGGACTGGGGGACAAAGGTACCCTCGATCCCGGGGGCGTAG
TTCCCCTCACAGATCTGCATCTCCCAGGCTTTGAGCTCGGAGGGGGGGATCATGTCCACCTGCGGGGCGATAAA
GAACACGGTTTCCGGGGCGGGGGAGATGAGCTGGGCCGAAAGCAAGTTCCGGAGCAGCTGGGACTTGCCGCAGC
CGGTGGGGCCGTAGATGACCCCGATGACCGGCTGCAGGTGGTAGTTGAGGGAGAGACAGCTGCCGTCCTCCCGG
AGGAGGGGGGCCACCTCGTTCATCATCTCGCGCACGTGCATGTTCTCGCGCACCAGTTCCGCCAGGAGGCGCTC
TCCCCCCAGGGATAGGAGCTCCTGGAGCGAGGCGAAGTTTTTCAGCGGCTTGAGTCCGTCGGCCATGGGCATTT
TGGAGAGGGTTTGTTGCAAGAGTTCCAGGCGGTCCCAGAGCTCGGTGATGTGCTCTACGGCATCTCGATCCAGC
AGACCTCCTCGTTTCGCGGGTTGGGACGGCTGCGGGAGTAGGGCACCAGACGATGGGCGTCCAGCGCAGCCAGG
GTCCGGTCCTTCCAGGGTCGCAGCGTCCGCGTCAGGGTGGTCTCCGTCACGGTGAAGGGGTGCGCGCCGGGCTG
GGCGCTTGCGAGGGTGCGCTTCAGGCTCATCCGGCTGGTCGAAAACCGCTCCCGATCGGCGCCCTGCGCGTCGG
CCAGGTAGCAATTGACCATGAGTTCGTAGTTGAGCGCCTCGGCCGCGTGGCCTTTGGCGCGGAGCTTACCTTTG
GAAGTCTGCCCGCAGGCGGGACAGAGGAGGGACTTGAGGGCGTAGAGCTTGGGGGCGAGGAAGACGGACTCGGG
GGCGTAGGCGTCCGCGCCGCAGTGGGCGCAGACGGTCTCGCACTCCACGAGCCAGGTGAGGTCGGGCTGGTCGG
GGTCAAAAACCAGTTTCCCGCCGTTCTTTTTGATGCGTTTCTTACCTTTGGTCTCCATGAGCTCGTGTCCCCGC
TGGGTGACAAAGAGGCTGTCCGTGTCCCCGTAGACCGACTTTATGGGCCGGTCCTCGAGCGGTGTGCCGCGGTC
CTCCTCGTAGAGGAACCCCGCCCACTCCGAGACGAAAGCCCGGGTCCAGGCCAGCACGAAGGAGGCCACGTGGG
ACGGGTAGCGGTCGTTGTCCACCAGCGGGTCCACCTTTTCCAGGGTATGCAAACACATGTCCCCCTCGTCCACA
TCCAGGAAGGTGATTGGCTTGTAAGTGTAGGCCACGTGACCGGGGGTCCCGGCCGGGGGGGTATAAAAGGGTGC
GGGTCCCTGCTCGTCCTCACTGTCTTCCGGATCGCTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATTCCCTCT
CGAAGGCGGGCATGACCTCGGCACTCAGGTTGTCAGTTTCTAGAAACGAGGAGGATTTGATATTGACGGTGCCG
GCGGAGATGCCTTTCAAGAGCCCCTCGTCCATCTGGTCAGAAAAGACGATCTTTTTGTTGTCGAGCTTGGTGGC
GAAGGAGCCGTAGAGGGCGTTGGAGAGGAGCTTGGCGATGGAGCGCATGGTCTGGTTTTTTTCCTTGTCGGCGC
GCTCCTTGGCGGCGATGTTGAGCTGCACGTACTCGCGCGCCACGCACTTCCATTCGGGGAAGACGGTGGTCAGC
TCGTCGGGCACGATTCTGACCTGCCAGCCCCGATTATGCAGGGTGATGAGGTCCACACTGGTGGCCACCTCGCC
GCGCAGGGGCTCATTAGTCCAGCAGAGGCGTCCGCCCTTGCGCGAGCAGAAGGGGGGCAGGGGGTCCAGCATGA
CCTCGTCGGGGGGGTCGGCATCGATGGTGAAGATGCCGGGCAGGAGGTCGGGGTCAAAGTAGCTGATGGAAGTG
GCCAGATCGTCCAGGGCAGCTTGCCATTCGCGCACGGCCAGCGCGCtCTCGTAGGGACTGAGGGGCGTGCCCCA
GGGCATGGGATGGGTAAGCGCGGAGGCGTACATGCCGCAGATGTCGTAGACGTAGAGGGGCTCCTCGAGGATGC
CGATGTAGGTGGGGTAGCAGCGCCCCCCGCGGATGCTGGCGCGCACGTAGTCATACAGCTCGTGCGAGGGGGCG
AGGAGCCCCGGGCCCAGGTTGGTGCGACTGGGCTTTTCGGCGCGGTAGACGATCTGGCGGAAAATGGCATGCGA
GTTGGAGGAGATGGTGGGCCTTTGGAAGATGTTGAAGTGGGCGTGGGGCAGTCCGACCGAGTCGCGGATGAAGT
GGGCGTAGGAGTCTTGCAGCTTGGCGACGAGCTCGGCGGTGACTAGGACGTCCAGAGCGCAGTAGTCGAGGGTC
TCCTGGATGATGTCATACTTGAGCTGTCCCTTTTGTTTCCACAGCTCGCGGTTGAGAAGGAACTCTTCGCGGTC
CTTCCAGTACTCTTCGAGGGGGAACCCGTCCTGATCTGCACGGTAAGAGCCTAGCATGTAGAACTGGTTGACGG
CCTTGTAGGCGCAGCAGCCCTTCTCCACGGGGAGGGCGTAGGCCTGGGCGGCCTTGCGCAGGGAGGTGTGCGTG
AGGGCGAAAGTGTCCCTGACCATGACCTTGAGGAACTGGTGCTTGAAGTCGATATCGTCGCAGCCCCCCTGCTC
CCAGAGCTGGAAGTCCGTGCGCTTCTTGTAGGCGGGGTTGGGCAAAGCGAAAGTAACATCGTTGAAGAGGATCT
TGCCCGCGCGGGGCATAAAGTTGCGAGTGATGCGGAAAGGTTGGGGCACCTCGGCCCGGTTGTTGATGACCTGG
GCGGCGAGCACGATCTCGTCGAAGCCGTTGATGTTGTGGCCCACGATGTAGAGTTCCACGAATCGCGGACGGCC
CTTGACGTGGGGCAGTTTCTTGAGCTCCTCGTAGGTGAGCTCGTCGGGGTCGCTGAGCCCGTGCTGCTCGAGCG
CCCAGTCGGCGAGATGGGGGTTGGCGCGGAGGAAGGAAGTCCAGAGATCCACGGCCAGGGCGGTTTGCAGACGG
TCCCGGTACTGACGGAACTGCTGCCCGACGGCCATTTTTTCGGGGGTGACGCAGTAGAAGGTGCGGGGGTCCCC
GTGCCAGCGATCCCATTTGAGCTGGAGGGCGAGATCGAGGGCGAGCTCGACGAGCCGGTCGTCCCCGGAGAGTT
TCATGACCAGCATGAAGGGGACGAGCTGCTTGCCGAAGGACCCCATCCAGGTGTAGGTTTCCACATCGTAGGTG
AGGAAGAGCCTTTCGGTGCGAGGATGCGAGCCGATGGGGAAGAACTGGATCTCCTGCCACCAATTGGAGGAATG
GCTGTTGATGTGATGGAAGTAGAAATGCCGACGGCGCGCCGAACACTCGTGCTTGTGTTTATACAAGCGGCCAC
AGTGCTCGCAACGCTGCACGGGATGCACGTGCTGCACGAGCTGTACCTGAGTTCCTTTGACGAGGAATTTCAGT
GGGAAGTGGAGTCGTGGCGCCTGCATCTCGTGCTGTACTACGTCGTGGTGGTCGGCCTGGCCCTCTTCTGCCTC
GATGGTGGTCATGCTGACGAGCCCGCGCGGGAGGCAGGTCCAGACCTCGGCGCGAGCGGGTCGGAGAGCGAGGA
CGAGGGCGCGCAGGCCGGAGCTGTCCAGGGTCCTGAGACGCTGCGGAGTCAGGTCAGTGGGCAGCGGCGGCGCG
CGGTTGACTTGCAGGAGTTTTTCCAGGGCGCGCGGGAGGTCCAGATGGTACTTGATCTCCACCGCGCCATTGGT
GGCGACGTCGATGGCTTGCAGGGTCCCGTGCCCCTGGGGTGTGACCACCGTCCCCCGTTTCTTCTTGGGCGGCT

2026201462 26 Feb 2026

GGGGCGACGGGGGCGGTGCCTCTTCCATGGTTAGAAGCGGCGGCGAGGACGCGCGCCGGGCGGCAGGGGCGGCT
CGGGGCCCGGAGGCAGGGGCGGCAGGGGCACGTCGGCGCCGCGCGCGGGTAGGTTCTGGTACTGCGCCCGGAGA
AGACTGGCGTGAGCGACGACGCGACGGTTGACGTCCTGGATCTGACGCCTCTGGGTGAAGGCCACGGGACCCGT
GAGTTTGAACCTGAAAGAGAGTTCGACAGAATCAATCTCGGTATCGTTGACGGCGGCCTGCCGCAGGATCTCTT
GCACGTCGCCCGAGTTGTCCTGGTAGGCGATCTCGGTCATGAACTGCTCGATCTCCTCCTCTTGAAGGTCTCCG
CGGCCGGCGCGCTCCACGGTGGCCGCGAGGTCGTTGGAGATGCGGCCCATGAGCTGCGAGAAGGCGTTCATGCC
CGCCTCGTTCCAGACGCGGCTGTAGACCACGACGCCCTCGGGATCGCgGGCGCGCATGACCACCTGGGCGAGGT
TGAGCTCCACGTGGCGCGTGAAGACCGCGTAGTTGCAGAGGCGCTGGTAGAGGTAGTTGAGCGTGGTGGCGATG
TGCTCGGTGACGAAGAAATACATGATCCAGCGGCGGAGCGGCATCTCGCTGACGTCGCCCAGCGCCTCCAAACG
TTCCATGGCCTCGTAAAAGTCCACGGCGAAGTTGAAAAACTGGGAGTTGCGCGCCGAGACGGTCAACTCCTCCT
CCAGAAGACGGATGAGCTCGGCGATGGTGGCGCGCACCTCGCGCTCGAAGGCCCCCGGGAGTTCCTCCACTTCC
TCTTCTTCCTCCTCCACTAACATCTCTTCTACTTCCTCCTCAGGCGGCAGTGGTGGCGGGGGAGGGGGCCTGCG
TCGCCGGCGGCGCACGGGCAGACGGTCGATGAAGCGCTCGATGGTCTCGCCGCGCCGGCGTCGCATGGTCTCGG
TGACGGCGCGCCCGTCCTCGCGGGGCCGCAGCGTGAAGACGCCGCCGCGCATCTCCAGGTGGCCGGGGGGGTCC
CCGTTGGGCAGGGAGAGGGCGCTGACGATGCATCTTATCAATTGCCCCGTAGGGACTCCGCGCAAGGACCTGAG
CGTCTCGAGATCCACGGGATCTGAAAACCGCTGAACGAAGGCTTCGAGCCAGTCGCAGTCGCAAGGTAGGCTGA
GCACGGTTTCTTCTGGCGGGTCATGTTGGTTGGGAGCGGGGCGGGCGATGCTGCTGGTGATGAAGTTGAAATAG
GCGGTTCTGAGACGGCGGATGGTGGCGAGGAGCACCAGGTCTTTGGGCCCGGCTTGCTGGATGCGCAGACGGTC
GGCCATGCCCCAGGCGTGGTCCTGACACCTGGCCAGGTCCTTGTAGTAGTCCTGCATGAGCCGCTCCACGGGCA
CCTCCTCCTCGCCCGCGCGGCCGTGCATGCGCGTGAGCCCGAAGCCGCGCTGGGGCTGGACGAGCGCCAGGTCG
GCGACGACGCGCTCGGCGAGGATGGCTTGCTGGATCTGGGTGAGGGTGGTCTGGAAGTCATCAAAGTCGACGAA
GCGGTGGTAGGCTCCGGTGTTGATGGTGTAGGAGCAGTTGGCCATGACGGACCAGTTGACGGTCTGGTGGCCCG
GACGCACGAGCTCGTGGTACTTGAGGCGCGAGTAGGCGCGCGTGTCGAAGATGTAGTCGTTGCAGGTGCGCACC
AGGTACTGGTAGCCGATGAGGAAGTGCGGCGGCGGCTGGCGGTAGAGCGGCCATCGCTCGGTGGCGGGGGCGCC
GGGCGCGAGGTCCTCGAGCATGGTGCGGTGGTAGCCGTAGATGTACCTGGACATCCAGGTGATGCCGGCGGCGG
TGGTGGAGGCGCGCGGGAACTCGCGGACGCGGTTCCAGATGTTGCGCAGCGGCAGGAAGTAGTTCATGGTGGGC
ACGGTCTGGCCCGTGAGGCGCGCGCAGTCGTGGATGCTCTATACGGGCAAAAACGAAAGCGGTCAGCGGCTCGA
CTCCGTGGCCTGGAGGCTAAGCGAACGGGTTGGGCTGCGCGTGTACCCCGGTTCGAATCTCGAATCAGGCTGGA
GCCGCAGCTAACGTGGTATTGGCACTCCCGTCTCGACCCAAGCCTGCACCAACCCTCCAGGATACGGAGGCGGG
TCGTTTTGCAACTTTTTTTTGGAGGCCGGATGAGACTAGTAAGCGCGGAAAGCGGCCGACCGCGATGGCTCGCT
GCCGTAGTCTGGAGAAGAATCGCCAGGGTTGCGTTGCGGTGTGCCCCGGTTCGAGGCCGGCCGGATTCCGCGGC
TAACGAGGGCGTGGCTGCCCCGTCGTTTCCAAGACCCCATAGCCAGCCGACTTCTCCAGTTACGGAGCGAGCCC
CTCTTTTGTTTTGTTTGTTTTTGCCAGATGCATCCCGTACTGCGGCAGATGCGCCCCCACCACCCTCCACCGCA
ACAACAGCCCCCTCCACAGCCGGCGCTTCTGCCCCCGCCCCAGCAGCAACTTCCAGCCACGACCGCCGCGGCCG
CCGTGAGCGGGGCTGGACAGAGTTATGATCACCAGCTGGCCTTGGAAGAGGGCGAGGGGCTGGCGCGCCTGGGG
GCGTCGTCGCCGGAGCGGCACCCGCGCGTGCAGATGAAAAGGGACGCTCGCGAGGCCTACGTGCCCAAGCAGAA
CCTGTTCAGAGACAGGAGCGGCGAGGAGCCCGAGGAGATGCGCGCGGCCCGGTTCCACGCGGGGCGGGAGCTGC
GGCGCGGCCTGGACCGAAAGAGGGTGCTGAGGGACGAGGATTTCGAGGCGGACGAGCTGACGGGGATCAGCCCC
GCGCGCGCGCACGTGGCCGCGGCCAACCTGGTCACGGCGTACGAGCAGACCGTGAAGGAGGAGAGCAACTTCCA
AAAATCCTTCAACAACCACGTGCGCACCCTGATCGCGCGCGAGGAGGTGACCCTGGGCCTGATGCACCTGTGGG
ACCTGCTGGAGGCCATCGTGCAGAACCCCACCAGCAAGCCGCTGACGGCGCAGCTGTTCCTGGTGGTGCAGCAT
AGTCGGGACAACGAAGCGTTCAGGGAGGCGCTGCTGAATATCACCGAGCCCGAGGGCCGCTGGCTCCTGGACCT
GGTGAACATTCTGCAGAGCATCGTGGTGCAGGAGCGCGGGCTGCCGCTGTCCGAGAAGCTGGCGGCCATCAACT
TCTCGGTGCTGAGTTTGGGCAAGTACTACGCTAGGAAGATCTACAAGACCCCGTACGTGCCCATAGACAAGGAG
GTGAAGATCGACGGGTTTTACATGCGCATGACCCTGAAAGTGCTGACCCTGAGCGACGATCTGGGGGTGTACCG
CAACGACAGGATGCACCGTGCGGTGAGCGCCAGCAGGCGGCGCGAGCTGAGCGACCAGGAGCTGATGCATAGTC
TGCAGCGGGCCCTGACCGGGGCCGGGACCGAGGGGGAGAGCTACTTTGACATGGGCGCGGACCTGCACTGGCAG
CCCAGCCGCCGGGCCTTGGAGGCGGCGGCAGGACCCTACGTAGAAGAGGTGGACGATGAGGTGGACGAGGAGGG
CGAGTACCTGGAAGACTGATGGCGCGACCGTATTTTTGCTAGATGCAACAACAACAGCCACCTCCTGATCCCGC
GATGCGGGCGGCGCTGCAGAGCCAGCCGTCCGGCATTAACTCCTCGGACGATTGGACCCAGGCCATGCAACGCA
TCATGGCGCTGACGACCCGCAACCCCGAAGCCTTTAGACAGCAGCCCCAGGCCAACCGGCTCTCGGCCATCCTG
GAGGCCGTGGTGCCCTCGCGCTCCAACCCCACGCACGAGAAGGTCCTGGCCATCGTGAACGCGCTGGTGGAGAA
CAAGGCCATCCGCGGCGACGAGGCCGGCCTGGTGTACAACGCGCTGCTGGAGCGCGTGGCCCGCTACAACAGCA
CCAACGTGCAGACCAACCTGGACCGCATGGTGACCGACGTGCGCGAGGCCGTGGCCCAGCGCGAGCGGTTCCAC
CGCGAGTCCAACCTGGGATCCATGGTGGCGCTGAACGCCTTCCTCAGCACCCAGCCCGCCAACGTGCCCCGGGG
CCAGGAGGACTACACCAACTTCATCAGCGCCCTGCGCCTGATGGTGACCGAGGTGCCCCAGAGCGAGGTGTACC
AGTCCGGGCCGGACTACTTCTTCCAGACCAGTCGCCAGGGCTTGCAGACCGTGAACCTGAGCCAGGCTTTCAAG
AACTTGCAGGGCCTGTGGGGCGTGCAGGCCCCGGTCGGGGACCGCGCGACGGTGTCGAGCCTGCTGACGCCGAA
CTCGCGCCTGCTGCTGCTGCTGGTGGCCCCCTTCACGGACAGCGGCAGCATCAACCGCAACTCGTACCTGGGCT
ACCTGATTAACCTGTACCGCGAGGCCATCGGCCAGGCGCACGTGGACGAGCAGACCTACCAGGAGATCACCCAC

2026201462 26 Feb 2026

GTGAGCCGCGCCCTGGGCCAGGACGACCCGGGCAACCTGGAAGCCACCCTGAACTTTTTGCTGACCAACCGGTC
GCAGAAGATCCCGCCCCAGTACGCGCTCAGCACCGAGGAGGAGCGCATCCTGCGTTACGTGCAGCAGAGCGTGG
GCCTGTTCCTGATGCAGGAGGGGGCCACCCCCAGCGCCGCGCTCGACATGACCGCGCGCAACATGGAGCCCAGC
ATGTACGCCAGCAACCGCCCGTTCATCAATAAACTGATGGACTACTTGCATCGGGCGGCCGCCATGAACTCTGA
CTATTTCACCAACGCCATCCTGAATCCCCACTGGCTCCCGCCGCCGGGGTTCTACACGGGCGAGTACGACATGC
CCGACCCCAATGACGGGTTCCTGTGGGACGATGTGGACAGCAGCGTGTTCTCCCCCCGACCGGGTGCTAACGAG
CGCCCCTTGTGGAAGAAGGAAGGCAGCGACCGACGCCCGTCCTCGGCGCTGTCCGGCCGCGAGGGTGCTGCCGC
GGCGGTGCCCGAGGCCGCCAGTCCTTTCCCGAGCTTGCCCTTCTCGCTGAACAGTATCCGCAGCAGCGAGCTGG
GCAGGATCACGCGCCCGCGCTTGCTGGGCGAAGAGGAGTACTTGAATGACTCGCTGTTGAGACCCGAGCGGGAG
AAGAACTTCCCCAATAACGGGATAGAAAGCCTGGTGGACAAGATGAGCCGCTGGAAGACGTATGCGCAGGAGCA
CAGGGACGATCCCCGGGCGTCGCAGGGGGCCACGAGCCGGGGCAGCGCCGCCCGTAAACGCCGGTGGCACGACA
GGCAGCGGGGACAGATGTGGGACGATGAGGACTCCGCCGACGACAGCAGCGTGTTGGACTTGGGTGGGAGTGGT
AACCCGTTCGCTCACCTGCGCCCCCGTATCGGGCGCATGATGTAAGAGAAACCGAAAATAAATGATACTCACCA
AGGCCATGGCGACCAGCGTGCGTTCGTTTCTTCTCTGTTGTTGTTGTATCTAGTATGATGAGGCGTGCGTACCC
GGAGGGTCCTCCTCCCTCGTACGAGAGCGTGATGCAGCAGGCGATGGCGGCGGCGGCGATGCAGCCCCCGCTGG
AGGCTCCTTACGTGCCCCCGCGGTACCTGGCGCCTACGGAGGGGCGGAACAGCATTCGTTACTCGGAGCTGGCA
CCCTTGTACGATACCACCCGGTTGTACCTGGTGGACAACAAGTCGGCGGACATCGCCTCGCTGAACTACCAGAA
CGACCACAGCAACTTCCTGACCACCGTGGTGCAGAACAATGACTTCACCCCCACGGAGGCCAGCACCCAGACCA
TCAACTTTGACGAGCGCTCGCGGTGGGGCGGCCAGCTGAAAACCATCATGCACACCAACATGCCCAACGTGAAC
GAGTTCATGTACAGCAACAAGTTCAAGGCGCGGGTGATGGTCTCCCGCAAGACCCCCAATGGGGTGACAGTGAC
AGAGGATTATGATGGTAGTCAGGATGAGCTGAAGTATGAATGGGTGGAATTTGAGCTGCCCGAAGGCAACTTCT
CGGTGACCATGACCATCGACCTGATGAACAACGCCATCATCGACAATTACTTGGCGGTGGGGCGGCAGAACGGG
GTGCTGGAGAGCGACATCGGCGTGAAGTTCGACACTAGGAACTTCAGGCTGGGCTGGGACCCCGTGACCGAGCT
GGTCATGCCCGGGGTGTACACCAACGAGGCTTTCCATCCCGATATTGTCTTGCTGCCCGGCTGCGGGGTGGACT
TCACCGAGAGCCGCCTCAGCAACCTGCTGGGCATTCGCAAGAGGCAGCCCTTCCAGGAAGGCTTCCAGATCATG
TACGAGGATCTGGAGGGGGGCAACATCCCCGCGCTCCTGGATGTCGACGCCTATGAGAAAAGCAAGGAGGATGC
AGCAGCTGAAGCAACTGCAGCCGTAGCTACCGCCTCTACCGAGGTCAGGGGCGATAATTTTGCAAGCGCCGCAG
CAGTGGCAGCGGCCGAGGCGGCTGAAACCGAAAGTAAGATAGTCATTCAGCCGGTGGAGAAGGATAGCAAGAAC
AGGAGCTACAACGTACTACCGGACAAGATAAACACCGCCTACCGCAGCTGGTACCTAGCCTACAACTATGGCGA
CCCCGAGAAGGGCGTGCGCTCCTGGACGCTGCTCACCACCTCGGACGTCACCTGCGGCGTGGAGCAAGTCTACT
GGTCGCTGCCCGACATGATGCAAGACCCGGTCACCTTCCGCTCCACGCGTCAAGTTAGCAACTACCCGGTGGTG
GGCGCCGAGCTCCTGCCCGTCTACTCCAAGAGCTTCTTCAACGAGCAGGCCGTCTACTCGCAGCAGCTGCGCGC
CTTCACCTCGCTTACGCACGTCTTCAACCGCTTCCCCGAGAACCAGATCCTCGTCCGCCCGCCCGCGCCCACCA
TTACCACCGTCAGTGAAAACGTTCCTGCTCTCACAGATCACGGGACCCTGCCGCTGCGCAGCAGTATCCGGGGA
GTCCAGCGCGTGACCGTTACTGACGCCAGACGCCGCACCTGCCCCTACGTCTACAAGGCCCTGGGCATAGTCGC
GCCGCGCGTCCTCTCGAGCCGCACCTTCTAAATGTCCATTCTCATCTCGCCCAGTAATAACACCGGTTGGGGCC
TGCGCGCGCCCAGCAAGATGTACGGAGGCGCTCGCCAACGCTCCACGCAACACCCCGTGCGCGTGCGCGGGCAC
TTCCGCGCTCCCTGGGGCGCCCTCAAGGGCCGCGTGCGGTCGCGCACCACCGTCGACGACGTGATCGACCAGGT
GGTGGCCGACGCGCGCAACTACACCCCCGCCGCCGCGCCCGTCTCCACCGTGGACGCCGTCATCGACAGCGTGG
TGGCcGACGCGCGCCGGTACGCCCGCGCCAAGAGCCGGCGGCGGCGCATCGCCCGGCGGCACCGGAGCACCCCC
GCCATGCGCGCGGCGCGAGCCTTGCTGCGCAGGGCCAGGCGCACGGGACGCAGGGCCATGCTCAGGGCGGCCAG
ACGCGCGGCTTCAGGCGCCAGCGCCGGCAGGACCCGGAGACGCGCGGCCACGGCGGCGGCAGCGGCCATCGCCA
GCATGTCCCGCCCGCGGCGAGGGAACGTGTACTGGGTGCGCGACGCCGCCACCGGTGTGCGCGTGCCCGTGCGC
ACCCGCCCCCCTCGCACTTGAAGATGTTCACTTCGCGATGTTGATGTGTCCCAGCGGCGAGGAGGATGTCCAAG
CGCAAATTCAAGGAAGAGATGCTCCAGGTCATCGCGCCTGAGATCTACGGCCCTGCGGTGGTGAAGGAGGAAAG
AAAGCCCCGCAAAATCAAGCGGGTCAAAAAGGACAAAAAGGAAGAAGAAAGTGATGTGGACGGATTGGTGGAGT
TTGTGCGCGAGTTCGCCCCCCGGCGGCGCGTGCAGTGGCGCGGGCGGAAGGTGCAACCGGTGCTGAGACCCGGC
ACCACCGTGGTCTTCACGCCCGGCGAGCGCTCCGGCACCGCTTCCAAGCGCTCCTACGACGAGGTGTACGGGGA
TGATGATATTCTGGAGCAGGCGGCCGAGCGCCTGGGCGAGTTTGCTTACGGCAAGCGCAGCCGTTCCGCACCGA
AGGAAGAGGCGGTGTCCATCCCGCTGGACCACGGCAACCCCACGCCGAGCCTCAAGCCCGTGACCTTGCAGCAG
GTGCTGCCGACCGCGGCGCCGCGCCGGGGGTTCAAGCGCGAGGGCGAGGATCTGTACCCCACCATGCAGCTGAT
GGTGCCCAAGCGCCAGAAGCTGGAAGACGTGCTGGAGACCATGAAGGTGGACCCGGACGTGCAGCCCGAGGTCA
AGGTGCGGCCCATCAAGCAGGTGGCCCCGGGCCTGGGCGTGCAGACCGTGGACATCAAGATTCCCACGGAGCCC
ATGGAAACGCAGACCGAGCCCATGATCAAGCCCAGCACCAGCACCATGGAGGTGCAGACGGATCCCTGGATGCC
ATCGGCTCCTAGTCGAAGACCCCGGCGCAAGTACGGCGCGGCCAGCCTGCTGATGCCCAACTACGCGCTGCATC
CTTCCATCATCCCCACGCCGGGCTACCGCGGCACGCGCTTCTACCGCGGTCATACCAGCAGCCGCCGCCGCAAG
ACCACCACTCGCCGCCGCCGTCGCCGCACCGCCGCTGCAACCACCCCTGCCGCCCTGGTGCGGAGAGTGTACCG
CCGCGGCCGCGCACCTCTGACCCTGCCGCGCGCGCGCTACCACCCGAGCATCGCCATTTAAACTTTCGCCtGCT
TTGCAGATCAATGGCCCTCACATGCCGCCTTCGCGTTCCCATTACGGGCTACCGAGGAAGAAAACCGCGCCGTA
GAAGGCTGGCGGGGAACGGGATGCGTCGCCACCACCACCGGCGGCGGCGCGCCATCAGCAAGCGGTTGGGGGGA

2026201462 26 Feb 2026

GGCTTCCTGCCCGCGCTGATCCCCATCATCGCCGCGGCGATCGGGGCGATCCCCGGCATTGCTTCCGTGGCGGT
GCAGGCCTCTCAGCGCCACTGAGACACACTTGGAAACATCTTGTAATAAACCaATGGACTCTGACGCTCCTGGT
CCTGTGATGTGTTTTCGTAGACAGATGGAAGACATCAATTTTTCGTCCCTGGCTCCGCGACACGGCACGCGGCC
GTTCATGGGCACCTGGAGCGACATCGGCACCAGCCAACTGAACGGGGGCGCCTTCAATTGGAGCAGTCTCTGGA
GCGGGCTTAAGAATTTCGGGTCCACGCTTAAAACCTATGGCAGCAAGGCGTGGAACAGCACCACAGGGCAGGCG
CTGAGGGATAAGCTGAAAGAGCAGAACTTCCAGCAGAAGGTGGTCGATGGGCTCGCCTCGGGCATCAACGGGGT
GGTGGACCTGGCCAACCAGGCCGTGCAGCGGCAGATCAACAGCCGCCTGGACCCGGTGCCGCCCGCCGGCTCCG
TGGAGATGCCGCAGGTGGAGGAGGAGCTGCCTCCCCTGGACAAGCGGGGCGAGAAGCGACCCCGCCCCGATGCG
GAGGAGACGCTGCTGACGCACACGGACGAGCCGCCCCCGTACGAGGAGGCGGTGAAACTGGGTCTGCCCACCAC
GCGGCCCATCGCGCCCCTGGCCACCGGGGTGCTGAAACCCGAAAAGCCCGCGACCCTGGACTTGCCTCCTCCCC
AGCCTTCCCGCCCCTCTACAGTGGCTAAGCCCCTGCCGCCGGTGGCCGTGGCCCGCGCGCGACCCGGGGGCACC
GCCCGCCCTCATGCGAACTGGCAGAGCACTCTGAACAGCATCGTGGGTCTGGGAGTGCAGAGTGTGAAGCGCCG
CCGCTGCTATTAAACCTACCGTAGCGCTTAACTTGCTTGTCTGTGTGTGTATGTATTATGTCGCCGCCGCCGCT
GTCCACCAGAAGGAGGAGTGAAGAGGCGCGTCGCCGAGTTGCAAGATGGCCACCCCATCGATGCTGCCCCAGTG
GGCGTACATGCACATCGCCGGACAGGACGCTTCGGAGTACCTGAGTCCGGGTCTGGTGCAGTTTGCCCGCGCCA
CAGACACCTACTTCAGTCTGGGGAACAAGTTTAGGAACCCCACGGTGGCGCCCACGCACGATGTGACCACCGAC
CGCAGCCAGCGGCTGACGCTGCGCTTCGTGCCCGTGGACCGCGAGGACAACACCTACTCGTACAAAGTGCGCTA
CACGCTGGCCGTGGGCGACAACCGCGTGCTGGACATGGCCAGCACCTACTTTGACATCCGCGGCGTGCTGGATC
GGGGCCCTAGCTTCAAACCCTACTCCGGCACCGCCTACAACAGTCTGGCCCCCAAGGGAGCACCCAACACTTGT
CAGTGGACATATAAAGCCGATGGTGAAACTGCCACAGAAAAAACCTATACATATGGAAATGCACCCGTGCAGGG
CATTAACATCACAAAAGATGGTATTCAACTTGGAACTGACACCGATGATCAGCCAATCTACGCAGATAAAACCT
ATCAGCCTGAACCTCAAGTGGGTGATGCTGAATGGCATGACATCACTGGTACTGATGAAAAGTATGGAGGCAGA
GCTCTTAAGCCTGATACCAAAATGAAGCCTTGTTATGGTTCTTTTGCCAAGCCTACTAATAAAGAAGGAGGTCA
GGCAAATGTGAAAACAGGAACAGGCACTACTAAAGAATATGACATAGACATGGCTTTCTTTGACAACAGAAGTG
CGGCTGCTGCTGGCCTAGCTCCAGAAATTGTTTTGTATACTGAAAATGTGGATTTGGAAACTCCAGATACCCAT
ATTGTATACAAAGCAGGCACAGATGACAGCAGCTCTTCTATTAATTTGGGTCAGCAAGCCATGCCCAACAGACC
TAACTACATTGGTTTCAGAGACAACTTTATCGGGCTCATGTACTACAACAGCACTGGCAATATGGGGGTGCTGG
CCGGTCAGGCTTCTCAGCTGAATGCTGTGGTTGACTTGCAAGACAGAAACACCGAGCTGTCCTACCAGCTCTTG
CTTGACTCTCTGGGTGACAGAACCCGGTATTTCAGTATGTGGAATCAGGCGGTGGACAGCTATGATCCTGATGT
GCGCATTATTGAAAATCATGGTGTGGAGGATGAACTTCCCAACTATTGTTTCCCTCTGGATGCTGTTGGCAGAA
CAGATACTTATCAGGGAATTAAGGCTAATGGAACTGATCAAACCACATGGACCAAAGATGACAGTGTCAATGAT
GCTAATGAGATAGGCAAGGGTAATCCATTCGCCATGGAAATCAACATCCAAGCCAACCTGTGGAGGAACTTCCT
CTACGCCAACGTGGCCCTGTACCTGCCCGACTCTTACAAGTACACGCCGGCCAATGTTACCCTGCCCACCAACA
CCAACACCTACGATTACATGAACGGCCGGGTGGTGGCGCCCTCGCTGGTGGACTCCTACATCAACATCGGGGCG
CGCTGGTCGCTGGATCCCATGGACAACGTGAACCCCTTCAACCACCACCGCAATGCGGGGCTGCGCTACCGCTC
CATGCTCCTGGGCAACGGGCGCTACGTGCCCTTCCACATCCAGGTGCCCCAGAAATTTTTCGCCATCAAGAGCC
TCCTGCTCCTGCCCGGGTCCTACACCTACGAGTGGAACTTCCGCAAGGACGTCAACATGATCCTGCAGAGCTCC
CTCGGCAACGACCTGCGCACGGACGGGGCCTCCATCTCCTTCACCAGCATCAACCTCTACGCCACCTTCTTCCC
CATGGCGCACAACACGGCCTCCACGCTCGAGGCCATGCTGCGCAACGACACCAACGACCAGTCCTTCAACGACT
ACCTCTCGGCGGCCAACATGCTCTACCCCATCCCGGCCAACGCCACCAACGTGCCCATCTCCATCCCCTCGCGC
AACTGGGCCGCCTTCCGCGGCTGGTCCTTCACGCGTCTCAAGACCAAGGAGACGCCCTCGCTGGGCTCCGGGTT
CGACCCCTACTTCGTCTACTCGGGCTCCATCCCCTACCTCGACGGCACCTTCTACCTCAACCACACCTTCAAGA
AGGTCTCCATCACCTTCGACTCCTCCGTCAGCTGGCCCGGCAACGACCGGCTCCTGACGCCCAACGAGTTCGAA
ATCAAGCGCACCGTCGACGGCGAGGGCTACAACGTGGCCCAGTGCAACATGACCAAGGACTGGTTCCTGGTCCA
GATGCTGGCCCACTACAACATCGGCTACCAGGGCTTCTACGTGCCCGAGGGCTACAAGGACCGCATGTACTCCT
TCTTCCGCAACTTCCAGCCCATGAGCCGCCAGGTGGTGGACGAGGTCAACTACAAGGACTACCAGGCCGTCACC
CTGGCCTACCAGCACAACAACTCGGGCTTCGTCGGCTACCTCGCGCCCACCATGCGCCAGGGCCAGCCCTACCC
CGCCAACTACCCCTACCCGCTCATCGGCAAGAGCGCCGTCACCAGCGTCACCCAGAAAAAGTTCCTCTGCGACA
GGGTCATGTGGCGCATCCCCTTCTCCAGCAACTTCATGTCCATGGGCGCGCTCACCGACCTCGGCCAGAACATG
CTCTATGCCAACTCCGCCCACGCGCTAGACATGAATTTCGAAGTCGACCCCATGGATGAGTCCACCCTTCTCTA
TGTTGTCTTCGAAGTCTTCGACGTCGTCCGAGTGCACCAGCCCCACCGCGGCGTCATCGAGGCCGTCTACCTGC
GCACCCCCTTCTCGGCCGGTAACGCCACCACCTAAGCTCTTGCTTCTTGCAAGCCATGGCCGCGGGCTCCGGCG
AGCAGGAGCTCAGGGCCATCATCCGCGACCTGGGCTGCGGGCCCTACTTCCTGGGCACCTTCGATAAGCGCTTC
CCGGGATTCATGGCCCCGCACAAGCTGGCCTGCGCCATCGTCAACACGGCCGGCCGCGAGACCGGGGGCGAGCA
CTGGCTGGCCTTCGCCTGGAACCCGCGCTCGAACACCTGCTACCTCTTCGACCCCTTCGGGTTCTCGGACGAGC
GCCTCAAGCAGATCTACCAGTTCGAGTACGAGGGCCTGCTGCGCCGCAGCGCCCTGGCCACCGAGGACCGCTGC
GTCACCCTGGAAAAGTCCACCCAGACCGTGCAGGGTCCGCGCTCGGCCGCCTGCGGGCTCTTCTGCTGCATGTT
CCTGCACGCCTTCGTGCACTGGCCCGACCGCCCCATGGACAAGAACCCCACCATGAACTTGCTGACGGGGGTGC
CCAACGGCATGCTCCAGTCGCCCCAGGTGGAACCCACCCTGCGCCGCAACCAGGAGGCGCTCTACCGCTTCCTC
AACTCCCACTCCGCCTACTTTCGCTCCCACCGCGCGCGCATCGAGAAGGCCACCGCCTTCGACCGCATGAATCA

2026201462 26 Feb 2026

AGACATGTAAACCGTGTGTGTATGTTAAATGTCTTTAATAAACAGCACTTTCATGTTACACATGCATCTGAGAT
GATTTATTTAGAAATCGAAAGGGTTCTGCCGGGTCTCGGCATGGCCCGCGGGCAGGGACACGTTGCGGAACTGG
TACTTGGCCAGCCACTTGAACTCGGGGATCAGCAGTTTGGGCAGCGGGGTGTCGGGGAAGGAGTCGGTCCACAG
CTTCCGCGTCAGTTGCAGGGCGCCCAGCAGGTCGGGCGCGGAGATCTTGAAATCGCAGTTGGGACCCGCGTTCT
GCGCGCGGGAGTTGCGGTACACGGGGTTGCAGCACTGGAACACCATCAGGGCCGGGTGCTTCACGCTCGCCAGC
ACCGTCGCGTCGGTGATGCTCTCCACGTCGAGGTCCTCGGCGTTGGCCATCCCGAAGGGGGTCATCTTGCAGGT
CTGCCTTCCCATGGTGGGCACGCACCCGGGCTTGTGGTTGCAATCGCAGTGCAGGGGGATCAGCATCATCTGGG
CCTGGTCGGCGTTCATCCCCGGGTACATGGCCTTCATGAAAGCCTCCAATTGCCTGAACGCCTGCTGGGCCTTG
GCTCCCTCGGTGAAGAAGACCCCGCAGGACTTGCTAGAGAACTGGTTGGTGGCGCACCCGGCGTCGTGCACGCA
GCAGCGCGCGTCGTTGTTGGCCAGCTGCACCACGCTGCGCCCCCAGCGGTTCTGGGTGATCTTGGCCCGGTCGG
GGTTCTCCTTCAGCGCGCGCTGCCCGTTCTCGCTCGCCACATCCATCTCGATCATGTGCTCCTTCTGGATCATG
GTGGTCCCGTGCAGGCACCGCAGCTTGCCCTCGGCCTCGGTGCACCCGTGCAGCCACAGCGCGCACCCGGTGCA
CTCCCAGTTCTTGTGGGCGATCTGGGAATGCGCGTGCACGAAGCCCTGCAGGAAGCGGCCCATCATGGTGGTCA
GGGTCTTGTTGCTAGTGAAGGTCAGCGGAATGCCGCGGTGCTCCTCGTTGATGTACAGGTGGCAGATGCGGCGG
TACACCTCGCCCTGCTCGGGCATCAGCTGGAAGTTGGCTTTCAGGTCGGTCTCCACGCGGTAGCGGTCCATCAG
CATAGTCATGATTTCCATACCCTTCTCCCAGGCCGAGACGATGGGCAGGCTCATAGGGTTCTTCACCATCATCT
TAGCGCTAGCAGCCGCGGCCAGGGGGTCGCTCTCGTCCAGGGTCTCAAAGCTCCGCTTGCCGTCCTTCTCGGTG
ATCCGCACCGGGGGGTAGCTGAAGCCCACGGCCGCCAGCTCCTCCTCGGCCTGTCTTTCGTCCTCGCTGTCCTG
GCTGACGTCCTGCAGGACCACATGCTTGGTCTTGCGGGGTTTCTTCTTGGGCGGCAGCGGCGGCGGAGATGTTG
GAGATGGCGAGGGGGAGCGCGAGTTCTCGCTCACCACTACTATCTCTTCCTCTTCTTGGTCCGAGGCCACGCGG
CGGTAGGTATGTCTCTTCGGGGGCAGAGGCGGAGGCGACGGGCTCTCGCCGCCGCGACTTGGCGGATGGCTGGC
AGAGCCCCTTCCGCGTTCGGGGGTGCGCTCCCGGCGGCGCTCTGACTGACTTCCTCCGCGGCCGGCCATTGTGT
TCTCCTAGGGAGGAACAACAAGCATGGAGACTCAGCCATCGCCAACCTCGCCATCTGCCCCCACCGCCGACGAG
AAGCAGCAGCAGCAGAATGAAAGCTTAACCGCCCCGCCGCCCAGCCCCGCCACCTCCGACGCGGCCGTCCCAGA
CATGCAAGAGATGGAGGAATCCATCGAGATTGACCTGGGCTATGTGACGCCCGCGGAGCACGAGGAGGAGCTGG
CAGTGCGCTTTTCACAAGAAGAGATACACCAAGAACAGCCAGAGCAGGAAGCAGAGAATGAGCAGAGTCAGGCT
GGGCTCGAGCATGACGGCGACTACCTCCACCTGAGCGGGGGGGAGGACGCGCTCATCAAGCATCTGGCCCGGCA
GGCCACCATCGTCAAGGATGCGCTGCTCGACCGCACCGAGGTGCCCCTCAGCGTGGAGGAGCTCAGCCGCGCCT
ACGAGTTGAACCTCTTCTCGCCGCGCGTGCCCCCCAAGCGCCAGCCCAATGGCACCTGCGAGCCCAACCCGCGC
CTCAACTTCTACCCGGTCTTCGCGGTGCCCGAGGCCCTGGCCACCTACCACATCTTTTTCAAGAACCAAAAGAT
CCCCGTCTCCTGCCGCGCCAACCGCACCCGCGCCGACGCCCTTTTCAACCTGGGTCCCGGCGCCCGCCTACCTG
ATATCGCCTCCTTGGAAGAGGTTCCCAAGATCTTCGAGGGTCTGGGCAGCGACGAGACTCGGGCCGCGAACGCT
CTGCAAGGAGAAGGAGGAGAGCATGAGCACCACAGCGCCCTGGTCGAGTTGGAAGGCGACAACGCGCGGCTGGC
GGTGCTCAAACGCACGGTCGAGCTGACCCATTTCGCCTACCCGGCTCTGAACCTGCCCCCCAAAGTCATGAGCG
CGGTCATGGACCAGGTGCTCATCAAGCGCGCGTCGCCCATCTCCGAGGACGAGGGCATGCAAGACTCCGAGGAG
GGCAAGCCCGTGGTCAGCGACGAGCAGCTGGCCCGGTGGCTGGGTCCTAATGCTAGTCCCCAGAGTTTGGAAGA
GCGGCGCAAACTCATGATGGCCGTGGTCCTGGTGACCGTGGAGCTGGAGTGCCTGCGCCGCTTCTTCGCCGACG
CGGAGACCCTGCGCAAGGTCGAGGAGAACCTGCACTACCTCTTCAGGCACGGGTTCGTGCGCCAGGCCTGCAAG
ATCTCCAACGTGGAGCTGACCAACCTGGTCTCCTACATGGGCATCTTGCACGAGAACCGCCTGGGGCAGAACGT
GCTGCACACCACCCTGCGCGGGGAGGCCCGGCGCGACTACATCCGCGACTGCGTCTACCTCTACCTCTGCCACA
CCTGGCAGACGGGCATGGGCGTGTGGCAGCAGTGTCTGGAGGAGCAGAACCTGAAAGAGCTCTGCAAGCTCCTG
CAGAAGAACCTCAAGGGTCTGTGGACCGGGTTCGACGAGCGCACCACCGCCTCGGACCTGGCCGACCTCATTTT
CCCCGAGCGCCTCAGGCTGACGCTGCGCAACGGCCTGCCCGACTTTATGAGCCAAAGCATGTTGCAAAACTTTC
GCTCTTTCATCCTCGAACGCTCCGGAATCCTGCCCGCCACCTGCTCCGCGCTGCCCTCGGACTTCGTGCCGCTG
ACCTTCCGCGAGTGCCCCCCGCCGCTGTGGAGCCACTGCTACCTGCTGCGCCTGGCCAACTACCTGGCCTACCA
CTCGGACGTGATCGAGGACGTCAGCGGCGAGGGCCTGCTCGAGTGCCACTGCCGCTGCAACCTCTGCACGCCGC
ACCGCTCCCTGGCCTGCAACCCCCAGCTGCTGAGCGAGACCCAGATCATCGGCACCTTCGAGTTGCAAGGGCCC
AGCGAAGGCGAGGGTTCAGCCGCCAAGGGGGGTCTGAAACTCACCCCGGGGCTGTGGACCTCGGCCTACTTGCG
CAAGTTCGTGCCCGAGGACTACCATCCCTTCGAGATCAGGTTCTACGAGGACCAATCCCATCCGCCCAAGGCCG
AGCTGTCGGCCTGCGTCATCACCCAGGGGGCGATCCTGGCCCAATTGCAAGCCATCCAGAAATCCCGCCAAGAA
TTCTTGCTGAAAAAGGGCCGCGGGGTCTACCTCGACCCCCAGACCGGTGAGGAGCTCAACCCCGGCTTCCCCCA
GGATGCCCCGAGGAAACAAGAAGCTGAAAGTGGAGCTGCCGCCCGTGGAGGATTTGGAGGAAGACTGGGAGAAC
AGCAGTCAGGCAGAGGAGGAGGAGATGGAGGAAGACTGGGACAGCACTCAGGCAGAGGAGGACAGCCTGCAAGA
CAGTCTGGAGGAAGACGAGGAGGAGGCAGAGGAGGAGGTGGAAGAAGCAGCCGCCGCCAGACCGTCGTCCTCGG
CGGGGGAGAAAGCAAGCAGCACGGATACCATCTCCGCTCCGGGTCGGGGTCCCGCTCGACCACACAGTAGATGG
GACGAGACCGGACGATTCCCGAACCCCACCACCCAGACCGGTAAGAAGGAGCGGCAGGGATACAAGTCCTGGCG
GGGGCACAAAAACGCCATCGTCTCCTGCTTGCAGGCCTGCGGGGGCAACATCTCCTTCACCCGGCGCTACCTGC
TCTTCCACCGCGGGGTGAACTTTCCCCGCAACATCTTGCATTACTACCGTCACCTCCACAGCCCCTACTACTTC
CAAGAAGAGGCAGCAGCAGCAGAAAAAGACCAGCAGAAAACCAGCAGCTAGAAAATCCACAGCGGCGGCAGCAG
GTGGACTGAGGATCGCGGCGAACGAGCCGGCGCAAACCCGGGAGCTGAGGAACCGGATCTTTCCCACCCTCTAT

2026201462 26 Feb 2026

GCCATCTTCCAGCAGAGTCGGGGGCAGGAGCAGGAACTGAAAGTCAAGAACCGTTCTCTGCGCTCGCTCACCCG
CAGTTGTCTGTATCACAAGAGCGAAGACCAACTTCAGCGCACTCTCGAGGACGCCGAGGCTCTCTTCAACAAGT
ACTGCGCGCTCACTCTTAAAGAGTAGCCCGCGCCCGCCCAGTCGCAGAAAAAGGCGGGAATTACGTCACCTGTG
CCCTTCGCCCTAGCCGCCTCCACCCATCATCATGAGCAAAGAGATTCCCACGCCTTACATGTGGAGCTACCAGC
CCCAGATGGGCCTGGCCGCCGGTGCCGCCCAGGACTACTCCACCCGCATGAATTGGCTCAGCGCCGGGCCCGCG
ATGATCTCACGGGTGAATGACATCCGCGCCCACCGAAACCAGATACTCCTAGAACAGTCAGCGCTCACCGCCAC
GCCCCGCAATCACCTCAATCCGCGTAATTGGCCCGCCGCCCTGGTGTACCAGGAAATTCCCCAGCCCACGACCG
TACTACTTCCGCGAGACGCCCAGGCCGAAGTCCAGCTGACTAACTCAGGTGTCCAGCTGGCGGGCGGCGCCACC
CTGTGTCGTCACCGCCCCGCTCAGGGTATAAAGCGGCTGGTGATCCGGGGCAGAGGCACACAGCTCAACGACGA
GGTGGTGAGCTCTTCGCTGGGTCTGCGACCTGACGGAGTCTTCCAACTCGCCGGATCGGGGAGATCTTCCTTCA
CGCCTCGTCAGGCCGTCCTGACTTTGGAGAGTTCGTCCTCGCAGCCCCGCTCGGGTGGCATCGGCACTCTCCAG
TTCGTGGAGGAGTTCACTCCCTCGGTCTACTTCAACCCCTTCTCCGGCTCCCCCGGCCACTACCCGGACGAGTT
CATCCCGAACTTCGACGCCATCAGCGAGTCGGTGGACGGCTACGATTGAATGTCCCATGGTGGCGCAGCTGACC
TAGCTCGGCTTCGACACCTGGACCACTGCCGCCGCTTCCGCTGCTTCGCTCGGGATCTCGCCGAGTTTGCCTAC
TTTGAGCTGCCCGAGGAGCACCCTCAGGGCCCGGCCCACGGAGTGCGGATCGTCGTCGAAGGGGGCCTCGACTC
CCACCTGCTTCGGATCTTCAGCCAGCGTCCGATCCTGGTCGAGCGCGAGCAAGGACAGACCCTTCTGACTCTGT
ACTGCATCTGCAACCACCCCGGCCTGCATGAAAGTCTTTGTTGTCTGCTGTGTACTGAGTATAATAAAAGCTGA
GATCAGCGACTACTCCGGACTTCCGTGTGTTCCTGAATCCATCAACCAGTCTTTGTTCTTCACCGGGAACGAGA
CCGAGCTCCAGCTCCAGTGTAAGCCCCACAAGAAGTACCTCACCTGGCTGTTCCAGGGCTCCCCGATCGCCGTT
GTCAACCACTGCGACAACGACGGAGTCCTGCTGAGCGGCCCTGCCAACCTTACTTTTTCCACCCGCAGAAGCAA
GCTCCAGCTCTTCCAACCCTTCCTCCCCGGGACCTATCAGTGCGTCTCGGGACCCTGCCATCACACCTTCCACC
TGATCCCGAATACCACAGCGTCGCTCCCCGCTACTAACAACCAAACTAACCTCCACCAACGCCACCGTCGCGAC
GGCCACAATACATGCCCATATTAGACTATGAGGCCGAGCCACAGCGACCCATGCTCCCCGCTATTAGTTACTTC
AATCTAACCGGCGGAGATGACTGACCCACTGGCCAACAACAACGTCAACGACCTTCTCCTGGACATGGACGGCC
GCGCCTCGGAGCAGCGACTCGCCCAACTTCGCATTCGCCAGCAGCAGGAGAGAGCCGTCAAGGAGCTGCAGGAT
GCGGTGGCCATCCACCAGTGCAAGAGAGGCATCTTCTGCCTGGTGAAACAGGCCAAGATCTCCTACGAGGTCAC
TCCAAACGACCATCGCCTCTCCTACGAGCTCCTGCAGCAGCGCCAGAAGTTCACCTGCCTGGTCGGAGTCAACC
CCATCGTCATCACCCAGCAGTCTGGCGATACCAAGGGGTGCATCCACTGCTCCTGCGACTCCCCCGACTGCGTC
CACACTCTGATCAAGACCCTCTGCGGCCTCCGCGACCTCCTCCCCATGAACTAATCACCCCCTTATCCAGTGAA
ATAAAGATCATATTGATGATGATTTTACAGAAATAAAAAATAATCATTTGATTTGAAATAAAGATACAATCATA
TTGATGATTTGAGTTTAACAAAAAAATAAAGAATCACTTACTTGAAATCTGATACCAGGTCTCTGTCCATGTTT
TCTGCCAACACCACTTCACTCCCCTCTTCCCAGCTCTGGTACTGCAGGCCCCGGCGGGCTGCAAACTTCCTCCA
CACGCTGAAGGGGATGTCAAATTCCTCCTGTCCCTCAATCTTCATTTTATCTTCTATCAGATGTCCAAAAAGCG
CGTCCGGGTGGATGATGACTTCGACCCCGTCTACCCCTACGATGCAGACAACGCACCGACCGTGCCCTTCATCA
ACCCCCCCTTCGTCTCTTCAGATGGATTCCAAGAGAAGCCCCTGGGGGTGTTGTCCCTGCGACTGGCCGACCCC
GTCACCACCAAGAACGGGGAAATCACCCTCAAGCTGGGAGAGGGGGTGGACCTCGATTCCTCGGGAAAACTCAT
CTCCAACACGGCCACCAAGGCCGCCGCCCCTCTCAGTTTTTCCAACAACACCATTTCCCTTAACATGGATCACC
CCTTTTACACTAAAGATGGAAAATTATCCTTACAAGTTTCTCCACCATTAAATATACTGAGAACAAGCATTCTA
AACACACTAGCTTTAGGTTTTGGATCAGGTTTAGGACTCCGTGGCTCTGCCTTGGCAGTACAGTTAGTCTCTCC
ACTTACATTTGATACTGATGGAAACATAAAGCTTACCTTAGACAGAGGTTTGCATGTTACAACAGGAGATGCAA
TTGAAAGCAACATAAGCTGGGCTAAAGGTTTAAAATTTGAAGATGGAGCCATAGCAACCAACATTGGAAATGGG
TTAGAGTTTGGAAGCAGTAGTACAGAAACAGGTGTTGATGATGCTTACCCAATCCAAGTTAAACTTGGATCTGG
CCTTAGCTTTGACAGTACAGGAGCCATAATGGCTGGTAACAAAGAAGACGATAAACTCACTTTGTGGACAACAC
CTGATCCATCACCAAACTGTCAAATACTCGCAGAAAATGATGCAAAACTAACACTTTGCTTGACTAAATGTGGT
AGTCAAATACTGGCCACTGTGTCAGTCTTAGTTGTAGGAAGTGGAAACCTAAACCCCATTACTGGCACCGTAAG
CAGTGCTCAGGTGTTTCTACGTTTTGATGCAAACGGTGTTCTTTTAACAGAACATTCTACACTAAAAAAATACT
GGGGGTATAGGCAGGGAGATAGCATAGATGGCACTCCATATACCAATGCTGTAGGATTCATGCCCAATTTAAAA
GCTTATCCAAAGTCACAAAGTTCTACTACTAAAAATAATATAGTAGGGCAAGTATACATGAATGGAGATGTTTC
AAAACCTATGCTTCTCACTATAACCCTCAATGGTACTGATGACAGCAACAGTACATATTCAATGTCATTTTCAT
ACACCTGGACTAATGGAAGCTATGTTGGAGCAACATTTGGGGCTAACTCTTATACCTTCTCATACATCGCCCAA
GAATGAACACTGTATCCCACCCTGCATGCCAACCCTTCCCACCCCACTCTGTGGAACAAACTCTGAAACACAAA
ATAAAATAAAGTTCAAGTGTTTTATTGATTCAACAGTTTTACAGGATTCGAGCAGTTATTTTTCCTCCACCCTC
CCAGGACATGGAATACACCACCCTCTCCCCCCGCACAGCCTTGAACATCTGAATGCCATTGGTGATGGACATGC
TTTTGGTCTCCACGTTCCACACAGTTTCAGAGCGAGCCAGTCTCGGGTCGGTCAGGGAGATGAAACCCTCCGGG
CACTCCCGCATCTGCACCTCACAGCTCAACAGCTGAGGATTGTCCTCGGTGGTCGGGATCACGGTTATCTGGAA
GAAGCAGAAGAGCGGCGGTGGGAATCATAGTCCGCGAACGGGATCGGCCGGTGGTGTCGCATCAGGCCCCGCAG
CAGTCGCTGCCGCCGCCGCTCCGTCAAGCTGCTGCTCAGGGGGTCCGGGTCCAGGGACTCCCTCAGCATGATGC
CCACGGCCCTCAGCATCAGTCGTCTGGTGCGGCGGGCGCAGCAGCGCATGCGGATCTCGCTCAGGTCGCTGCAG
TACGTGCAACACAGAACCACCAGGTTGTTCAACAGTCCATAGTTCAACACGCTCCAGCCGAAACTCATCGCGGG
AAGGATGCTACCCACGTGGCCGTCGTACCAGATCCTCAGGTAAATCAAGTGGTGCCCCCTCCAGAACACGCTGC

2026201462 26 Feb 2026

CCACGTACATGATCTCCTTGGGCATGTGGCGGTTCACCACCTCCCGGTACCACATCACCCTCTGGTTGAACATG
CAGCCCCGGATGATCCTGCGGAACCACAGGGCCAGCACCGCCCCGCCCGCCATGCAGCGAAGAGACCCCGGGTC
CCGGCAATGGCAATGGAGGACCCACCGCTCGTACCCGTGGATCATCTGGGAGCTGAACAAGTCTATGTTGGCAC
AGCACAGGCATATGCTCATGCATCTCTTCAGCACTCTCAACTCCTCGGGGGTCAAAACCATATCCCAGGGCACG
GGGAACTCTTGCAGGACAGCGAACCCCGCAGAACAGGGCAATCCTCGCACAGAACTTACATTGTGCATGGACAG
GGTATCGCAATCAGGCAGCACCGGGTGATCCTCCACCAGAGAAGCGCGGGTCTCGGTCTCCTCACAGCGTGGTA
AGGGGGCCGGCCGATACGGGTGATGGCGGGACGCGGCTGATCGTGTTCGCGACCGTGTCATGATGCAGTTGCTT
TCGGACATTTTCGTACTTGCTGTAGCAGAACCTGGTCCGGGCGCTGCACACCGATCGCCGGCGGCGGTCTCGGC
GCTTGGAACGCTCGGTGTTGAAATTGTAAAACAGCCACTCTCTCAGACCGTGCAGCAGATCTAGGGCCTCAGGA
GTGATGAAGATCCCATCATGCCTGATGGCTCTGATCACATCGACCACCGTGGAATGGGCCAGACCCAGCCAGAT
GATGCAATTTTGTTGGGTTTCGGTGACGGCGGGGGAGGGAAGAACAGGAAGAACCATGATTAACTTTTAATCCA
AACGGTCTCGGAGTACTTCAAAATGAAGATCGCGGAGATGGCACCTCTCGCCCCCGCTGTGTTGGTGGAAAATA
ACAGCCAGGTCAAAGGTGATACGGTTCTCGAGATGTTCCACGGTGGCTTCCAGCAAAGCCTCCACGCGCACATC
CAGAAACAAGACAATAGCGAAAGCGGGAGGGTTCTCTAATTCCTCAATCATCATGTTACACTCCTGCACCATCC
CCAGATAATTTTCATTTTTCCAGCCTTGAATGATTCGAACTAGTTCGTGAGGTAAATCCAAGCCAGCCATGATA
AAGAGCTCGCGCAGAGCGCCCTCCACCGGCATTCTTAAGCACACCCTCATAATTCCAAGATATTCTGCTCCTGG
TTCACCTGCAGCAGATTGACAAGCGGAATATCAAAATCTCTGCCGCGATCCCTGAGCTCCTCCCTCAGCAATAA
CTGTAAGTACTCTTTCATATCCTCTCCGAAATTTTTAGCCATAGGACCACCAGGAATAAGATTAGGGCAAGCCA
CAGTACAGATAAACCGAAGTCCTCCCCAGTGAGCATTGCCAAATGCAAGACTGCTATAAGCATGCTGGCTAGAC
CCGGTGATATCTTCCAGATAACTGGACAGAAAATCGCCCAGGCAATTTTTAAGAAAATCAACAAAAGAAAAATC
CTCCAGGTGGACGTTTAGAGCCTCGGGAACAACGATGAAGTAAATGCAAGCGGTGCGTTCCAGCATGGTTAGTT
AGCTGATCTGTAGAAAAAACAAAAATGAACATTAAACCATGCTAGCCTGGCGAACAGGTGGGTAAATCGTTCTC
TCCAGCACCAGGCAGGCCACGGGGTCTCCGGCGCGACCCTCGTAAAAATTGTCGCTATGATTGAAAACCATCAC
AGAGAGACGTTCCCGGTGGCCGGCGTGAATGATTCGACAAGATGAATACACCCCCGGAACATTGGCGTCCGCGA
GTGAAAAAAAGCGCCCGAGGAAGCAATAAGGCACTACAATGCTCAGTCTCAAGTCCAGCAAAGCGATGCCATGC
GGATGAAGCACAAAATTCTCAGGTGCGTACAAAATGTAATTACTCCCCTCCTGCACAGGCAGCAAAGCCCCCGA
TCCCTCCAGGTACACATACAAAGCCTCAGCGTCCATAGCTTACCGAGCAGCAGCACACAACAGGCGCAAGAGTC
AGAGAAAGGCTGAGCTCTAACCTGTCCACCCGCTCTCTGCTCAATATATAGCCCAGATCTACACTGACGTAAAG
GCCAAAGTCTAAAAATACCCGCCAAATAATCACACACGCCCAGCACACGCCCAGAAACCGGTGACACACTCAAA
AAAATACGCGCACTTCCTCAAACGCCCAAAACTGCCGTCATTTCCGGGTTCCCACGCTACGTCATCAAAACACG
ACTTTCAAATTCCGTCGACCGTTAAAAACGTCACCCGCCCCGCCCCTAACGGTCGCCCGTCTCTCAGCCAATCA
GCGCCCCGCATCCCCAAATTCAAACACCTCATTTGCATATTAACGCGCACAAAAAGTTTGAGGTATATTATTGA
TGATGG

ChAdV68.5WTnt.GFP (SEQ ID NO:13); AC_000011.1 with E1 (nt 577 to 3403) and E3 (nt 27,125- 31,825) sequences deleted; corresponding ATCC VR-594 nucleotides substituted at five positions; GFP reporter under the control of the CMV promoter/enhancer inserted in place of deleted E1

CCATCTTCAATAATATACCTCAAACTTTTTGTGCGCGTTAATATGCAAATGAGGCGTTTGAATTTGGGGAGGAA
GGGCGGTGATTGGTCGAGGGATGAGCGACCGTTAGGGGCGGGGCGAGTGACGTTTTGATGACGTGGTTGCGAGG
AGGAGCCAGTTTGCAAGTTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTTGAACACGGAAATACTCAAT
TTTCCCGCGCTCTCTGACAGGAAATGAGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGCCATTTTCGCGCGAA
AACTGAATGAGGAAGTGAAAATCTGAGTAATTTCGCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGCCGAGTA
GACTTTGACCGATTACGTGGGGGTTTCGATTACCGTGTTTTTCACCTAAATTTCCGCGTACGGTGTCAAAGTCC
GGTGTTTTTACGTAGGTGTCAGCTGATCGCCAGGGTATTTAAACCTGCGCTCTCCAGTCAAGAGGCCACTCTTG
AGTGCCAGCGAGAAGAGTTTTCTCCTCCGCGCCGCGAGTCAGATCTACACTTTGAAAGTAGGGATAACAGGGTA
ATgacattgattattgactagttGttaaTAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGT
TCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATA
ATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAAC
TGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCCTATTGACGTCAATGACGGTAAATGGC
CCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATC
GCTATTACCATGgTGATGCGGTTTTGGCAGTACACCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCC
AAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ATAACCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAgcTCGTTTA
GTGAACCGTCAGATCGCCTGGAACGCCATCCACGCTGTTTTGACCTCCATAGAAGACAGCGATCGCGccaccAT
GGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCC
ACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC
ACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTA
CCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCT
TCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATC
GAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCA

2026201462 26 Feb 2026

CAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGG
ACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC
AACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGA
GTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTtTACAAGTAGtgaGTTTAAACTCCCATTTAAA
TGTGAGGGTTAATGCTTCGAGCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAG
TGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACA
AGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGATGTGGGAGGTTTTTTAAAGCAAGT
AAAACCTCTACAAATGTGGTAAAATAACTATAACGGTCCTAAGGTAGCGAGTGAGTAGTGTTCTGGGGCGGGGG
AGGACCTGCATGAGGGCCAGAATAACTGAAATCTGTGCTTTTCTGTGTGTTGCAGCAGCATGAGCGGAAGCGGC
TCCTTTGAGGGAGGGGTATTCAGCCCTTATCTGACGGGGCGTCTCCCCTCCTGGGCGGGAGTGCGTCAGAATGT
GATGGGATCCACGGTGGACGGCCGGCCCGTGCAGCCCGCGAACTCTTCAACCCTGACCTATGCAACCCTGAGCT
CTTCGTCGTTGGACGCAGCTGCCGCCGCAGCTGCTGCATCTGCCGCCAGCGCCGTGCGCGGAATGGCCATGGGC
GCCGGCTACTACGGCACTCTGGTGGCCAACTCGAGTTCCACCAATAATCCCGCCAGCCTGAACGAGGAGAAGCT
GTTGCTGCTGATGGCCCAGCTCGAGGCCTTGACCCAGCGCCTGGGCGAGCTGACCCAGCAGGTGGCTCAGCTGC
AGGAGCAGACGCGGGCCGCGGTTGCCACGGTGAAATCCAAATAAAAAATGAATCAATAAATAAACGGAGACGGT
TGTTGATTTTAACACAGAGTCTGAATCTTTATTTGATTTTTCGCGCGCGGTAGGCCCTGGACCACCGGTCTCGA
TCATTGAGCACCCGGTGGATCTTTTCCAGGACCCGGTAGAGGTGGGCTTGGATGTTGAGGTACATGGGCATGAG
CCCGTCCCGGGGGTGGAGGTAGCTCCATTGCAGGGCCTCGTGCTCGGGGGTGGTGTTGTAAATCACCCAGTCAT
AGCAGGGGCGCAGGGCATGGTGTTGCACAATATCTTTGAGGAGGAGACTGATGGCCACGGGCAGCCCTTTGGTG
TAGGTGTTTACAAATCTGTTGAGCTGGGAGGGATGCATGCGGGGGGAGATGAGGTGCATCTTGGCCTGGATCTT
GAGATTGGCGATGTTACCGCCCAGATCCCGCCTGGGGTTCATGTTGTGCAGGACCACCAGCACGGTGTATCCGG
TGCACTTGGGGAATTTATCATGCAACTTGGAAGGGAAGGCGTGAAAGAATTTGGCGACGCCTTTGTGCCCGCCC
AGGTTTTCCATGCACTCATCCATGATGATGGCGATGGGCCCGTGGGCGGCGGCCTGGGCAAAGACGTTTCGGGG
GTCGGACACATCATAGTTGTGGTCCTGGGTGAGGTCATCATAGGCCATTTTAATGAATTTGGGGCGGAGGGTGC
CGGACTGGGGGACAAAGGTACCCTCGATCCCGGGGGCGTAGTTCCCCTCACAGATCTGCATCTCCCAGGCTTTG
AGCTCGGAGGGGGGGATCATGTCCACCTGCGGGGCGATAAAGAACACGGTTTCCGGGGCGGGGGAGATGAGCTG
GGCCGAAAGCAAGTTCCGGAGCAGCTGGGACTTGCCGCAGCCGGTGGGGCCGTAGATGACCCCGATGACCGGCT
GCAGGTGGTAGTTGAGGGAGAGACAGCTGCCGTCCTCCCGGAGGAGGGGGGCCACCTCGTTCATCATCTCGCGC
ACGTGCATGTTCTCGCGCACCAGTTCCGCCAGGAGGCGCTCTCCCCCCAGGGATAGGAGCTCCTGGAGCGAGGC
GAAGTTTTTCAGCGGCTTGAGTCCGTCGGCCATGGGCATTTTGGAGAGGGTTTGTTGCAAGAGTTCCAGGCGGT
CCCAGAGCTCGGTGATGTGCTCTACGGCATCTCGATCCAGCAGACCTCCTCGTTTCGCGGGTTGGGACGGCTGC
GGGAGTAGGGCACCAGACGATGGGCGTCCAGCGCAGCCAGGGTCCGGTCCTTCCAGGGTCGCAGCGTCCGCGTC
AGGGTGGTCTCCGTCACGGTGAAGGGGTGCGCGCCGGGCTGGGCGCTTGCGAGGGTGCGCTTCAGGCTCATCCG
GCTGGTCGAAAACCGCTCCCGATCGGCGCCCTGCGCGTCGGCCAGGTAGCAATTGACCATGAGTTCGTAGTTGA
GCGCCTCGGCCGCGTGGCCTTTGGCGCGGAGCTTACCTTTGGAAGTCTGCCCGCAGGCGGGACAGAGGAGGGAC
TTGAGGGCGTAGAGCTTGGGGGCGAGGAAGACGGACTCGGGGGCGTAGGCGTCCGCGCCGCAGTGGGCGCAGAC
GGTCTCGCACTCCACGAGCCAGGTGAGGTCGGGCTGGTCGGGGTCAAAAACCAGTTTCCCGCCGTTCTTTTTGA
TGCGTTTCTTACCTTTGGTCTCCATGAGCTCGTGTCCCCGCTGGGTGACAAAGAGGCTGTCCGTGTCCCCGTAG
ACCGACTTTATGGGCCGGTCCTCGAGCGGTGTGCCGCGGTCCTCCTCGTAGAGGAACCCCGCCCACTCCGAGAC
GAAAGCCCGGGTCCAGGCCAGCACGAAGGAGGCCACGTGGGACGGGTAGCGGTCGTTGTCCACCAGCGGGTCCA
CCTTTTCCAGGGTATGCAAACACATGTCCCCCTCGTCCACATCCAGGAAGGTGATTGGCTTGTAAGTGTAGGCC
ACGTGACCGGGGGTCCCGGCCGGGGGGGTATAAAAGGGTGCGGGTCCCTGCTCGTCCTCACTGTCTTCCGGATC
GCTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATTCCCTCTCGAAGGCGGGCATGACCTCGGCACTCAGGTTGT
CAGTTTCTAGAAACGAGGAGGATTTGATATTGACGGTGCCGGCGGAGATGCCTTTCAAGAGCCCCTCGTCCATC
TGGTCAGAAAAGACGATCTTTTTGTTGTCGAGCTTGGTGGCGAAGGAGCCGTAGAGGGCGTTGGAGAGGAGCTT
GGCGATGGAGCGCATGGTCTGGTTTTTTTCCTTGTCGGCGCGCTCCTTGGCGGCGATGTTGAGCTGCACGTACT
CGCGCGCCACGCACTTCCATTCGGGGAAGACGGTGGTCAGCTCGTCGGGCACGATTCTGACCTGCCAGCCCCGA
TTATGCAGGGTGATGAGGTCCACACTGGTGGCCACCTCGCCGCGCAGGGGCTCATTAGTCCAGCAGAGGCGTCC
GCCCTTGCGCGAGCAGAAGGGGGGCAGGGGGTCCAGCATGACCTCGTCGGGGGGGTCGGCATCGATGGTGAAGA
TGCCGGGCAGGAGGTCGGGGTCAAAGTAGCTGATGGAAGTGGCCAGATCGTCCAGGGCAGCTTGCCATTCGCGC
ACGGCCAGCGCGCGCTCGTAGGGACTGAGGGGCGTGCCCCAGGGCATGGGATGGGTAAGCGCGGAGGCGTACAT
GCCGCAGATGTCGTAGACGTAGAGGGGCTCCTCGAGGATGCCGATGTAGGTGGGGTAGCAGCGCCCCCCGCGGA
TGCTGGCGCGCACGTAGTCATACAGCTCGTGCGAGGGGGCGAGGAGCCCCGGGCCCAGGTTGGTGCGACTGGGC
TTTTCGGCGCGGTAGACGATCTGGCGGAAAATGGCATGCGAGTTGGAGGAGATGGTGGGCCTTTGGAAGATGTT
GAAGTGGGCGTGGGGCAGTCCGACCGAGTCGCGGATGAAGTGGGCGTAGGAGTCTTGCAGCTTGGCGACGAGCT
CGGCGGTGACTAGGACGTCCAGAGCGCAGTAGTCGAGGGTCTCCTGGATGATGTCATACTTGAGCTGTCCCTTT
TGTTTCCACAGCTCGCGGTTGAGAAGGAACTCTTCGCGGTCCTTCCAGTACTCTTCGAGGGGGAACCCGTCCTG
ATCTGCACGGTAAGAGCCTAGCATGTAGAACTGGTTGACGGCCTTGTAGGCGCAGCAGCCCTTCTCCACGGGGA
GGGCGTAGGCCTGGGCGGCCTTGCGCAGGGAGGTGTGCGTGAGGGCGAAAGTGTCCCTGACCATGACCTTGAGG
AACTGGTGCTTGAAGTCGATATCGTCGCAGCCCCCCTGCTCCCAGAGCTGGAAGTCCGTGCGCTTCTTGTAGGC

2026201462 26 Feb 2026

GGGGTTGGGCAAAGCGAAAGTAACATCGTTGAAGAGGATCTTGCCCGCGCGGGGCATAAAGTTGCGAGTGATGC
GGAAAGGTTGGGGCACCTCGGCCCGGTTGTTGATGACCTGGGCGGCGAGCACGATCTCGTCGAAGCCGTTGATG
TTGTGGCCCACGATGTAGAGTTCCACGAATCGCGGACGGCCCTTGACGTGGGGCAGTTTCTTGAGCTCCTCGTA
GGTGAGCTCGTCGGGGTCGCTGAGCCCGTGCTGCTCGAGCGCCCAGTCGGCGAGATGGGGGTTGGCGCGGAGGA
AGGAAGTCCAGAGATCCACGGCCAGGGCGGTTTGCAGACGGTCCCGGTACTGACGGAACTGCTGCCCGACGGCC
ATTTTTTCGGGGGTGACGCAGTAGAAGGTGCGGGGGTCCCCGTGCCAGCGATCCCATTTGAGCTGGAGGGCGAG
ATCGAGGGCGAGCTCGACGAGCCGGTCGTCCCCGGAGAGTTTCATGACCAGCATGAAGGGGACGAGCTGCTTGC
CGAAGGACCCCATCCAGGTGTAGGTTTCCACATCGTAGGTGAGGAAGAGCCTTTCGGTGCGAGGATGCGAGCCG
ATGGGGAAGAACTGGATCTCCTGCCACCAATTGGAGGAATGGCTGTTGATGTGATGGAAGTAGAAATGCCGACG
GCGCGCCGAACACTCGTGCTTGTGTTTATACAAGCGGCCACAGTGCTCGCAACGCTGCACGGGATGCACGTGCT
GCACGAGCTGTACCTGAGTTCCTTTGACGAGGAATTTCAGTGGGAAGTGGAGTCGTGGCGCCTGCATCTCGTGC
TGTACTACGTCGTGGTGGTCGGCCTGGCCCTCTTCTGCCTCGATGGTGGTCATGCTGACGAGCCCGCGCGGGAG
GCAGGTCCAGACCTCGGCGCGAGCGGGTCGGAGAGCGAGGACGAGGGCGCGCAGGCCGGAGCTGTCCAGGGTCC
TGAGACGCTGCGGAGTCAGGTCAGTGGGCAGCGGCGGCGCGCGGTTGACTTGCAGGAGTTTTTCCAGGGCGCGC
GGGAGGTCCAGATGGTACTTGATCTCCACCGCGCCATTGGTGGCGACGTCGATGGCTTGCAGGGTCCCGTGCCC
CTGGGGTGTGACCACCGTCCCCCGTTTCTTCTTGGGCGGCTGGGGCGACGGGGGCGGTGCCTCTTCCATGGTTA
GAAGCGGCGGCGAGGACGCGCGCCGGGCGGCAGGGGCGGCTCGGGGCCCGGAGGCAGGGGCGGCAGGGGCACGT
CGGCGCCGCGCGCGGGTAGGTTCTGGTACTGCGCCCGGAGAAGACTGGCGTGAGCGACGACGCGACGGTTGACG
TCCTGGATCTGACGCCTCTGGGTGAAGGCCACGGGACCCGTGAGTTTGAACCTGAAAGAGAGTTCGACAGAATC
AATCTCGGTATCGTTGACGGCGGCCTGCCGCAGGATCTCTTGCACGTCGCCCGAGTTGTCCTGGTAGGCGATCT
CGGTCATGAACTGCTCGATCTCCTCCTCTTGAAGGTCTCCGCGGCCGGCGCGCTCCACGGTGGCCGCGAGGTCG
TTGGAGATGCGGCCCATGAGCTGCGAGAAGGCGTTCATGCCCGCCTCGTTCCAGACGCGGCTGTAGACCACGAC
GCCCTCGGGATCGCgGGCGCGCATGACCACCTGGGCGAGGTTGAGCTCCACGTGGCGCGTGAAGACCGCGTAGT
TGCAGAGGCGCTGGTAGAGGTAGTTGAGCGTGGTGGCGATGTGCTCGGTGACGAAGAAATACATGATCCAGCGG
CGGAGCGGCATCTCGCTGACGTCGCCCAGCGCCTCCAAACGTTCCATGGCCTCGTAAAAGTCCACGGCGAAGTT
GAAAAACTGGGAGTTGCGCGCCGAGACGGTCAACTCCTCCTCCAGAAGACGGATGAGCTCGGCGATGGTGGCGC
GCACCTCGCGCTCGAAGGCCCCCGGGAGTTCCTCCACTTCCTCTTCTTCCTCCTCCACTAACATCTCTTCTACT
TCCTCCTCAGGCGGCAGTGGTGGCGGGGGAGGGGGCCTGCGTCGCCGGCGGCGCACGGGCAGACGGTCGATGAA
GCGCTCGATGGTCTCGCCGCGCCGGCGTCGCATGGTCTCGGTGACGGCGCGCCCGTCCTCGCGGGGCCGCAGCG
TGAAGACGCCGCCGCGCATCTCCAGGTGGCCGGGGGGGTCCCCGTTGGGCAGGGAGAGGGCGCTGACGATGCAT
CTTATCAATTGCCCCGTAGGGACTCCGCGCAAGGACCTGAGCGTCTCGAGATCCACGGGATCTGAAAACCGCTG
AACGAAGGCTTCGAGCCAGTCGCAGTCGCAAGGTAGGCTGAGCACGGTTTCTTCTGGCGGGTCATGTTGGTTGG
GAGCGGGGCGGGCGATGCTGCTGGTGATGAAGTTGAAATAGGCGGTTCTGAGACGGCGGATGGTGGCGAGGAGC
ACCAGGTCTTTGGGCCCGGCTTGCTGGATGCGCAGACGGTCGGCCATGCCCCAGGCGTGGTCCTGACACCTGGC
CAGGTCCTTGTAGTAGTCCTGCATGAGCCGCTCCACGGGCACCTCCTCCTCGCCCGCGCGGCCGTGCATGCGCG
TGAGCCCGAAGCCGCGCTGGGGCTGGACGAGCGCCAGGTCGGCGACGACGCGCTCGGCGAGGATGGCTTGCTGG
ATCTGGGTGAGGGTGGTCTGGAAGTCATCAAAGTCGACGAAGCGGTGGTAGGCTCCGGTGTTGATGGTGTAGGA
GCAGTTGGCCATGACGGACCAGTTGACGGTCTGGTGGCCCGGACGCACGAGCTCGTGGTACTTGAGGCGCGAGT
AGGCGCGCGTGTCGAAGATGTAGTCGTTGCAGGTGCGCACCAGGTACTGGTAGCCGATGAGGAAGTGCGGCGGC
GGCTGGCGGTAGAGCGGCCATCGCTCGGTGGCGGGGGCGCCGGGCGCGAGGTCCTCGAGCATGGTGCGGTGGTA
GCCGTAGATGTACCTGGACATCCAGGTGATGCCGGCGGCGGTGGTGGAGGCGCGCGGGAACTCGCGGACGCGGT
TCCAGATGTTGCGCAGCGGCAGGAAGTAGTTCATGGTGGGCACGGTCTGGCCCGTGAGGCGCGCGCAGTCGTGG
ATGCTCTATACGGGCAAAAACGAAAGCGGTCAGCGGCTCGACTCCGTGGCCTGGAGGCTAAGCGAACGGGTTGG
GCTGCGCGTGTACCCCGGTTCGAATCTCGAATCAGGCTGGAGCCGCAGCTAACGTGGTATTGGCACTCCCGTCT
CGACCCAAGCCTGCACCAACCCTCCAGGATACGGAGGCGGGTCGTTTTGCAACTTTTTTTTGGAGGCCGGATGA
GACTAGTAAGCGCGGAAAGCGGCCGACCGCGATGGCTCGCTGCCGTAGTCTGGAGAAGAATCGCCAGGGTTGCG
TTGCGGTGTGCCCCGGTTCGAGGCCGGCCGGATTCCGCGGCTAACGAGGGCGTGGCTGCCCCGTCGTTTCCAAG
ACCCCATAGCCAGCCGACTTCTCCAGTTACGGAGCGAGCCCCTCTTTTGTTTTGTTTGTTTTTGCCAGATGCAT
CCCGTACTGCGGCAGATGCGCCCCCACCACCCTCCACCGCAACAACAGCCCCCTCCACAGCCGGCGCTTCTGCC
CCCGCCCCAGCAGCAACTTCCAGCCACGACCGCCGCGGCCGCCGTGAGCGGGGCTGGACAGAGTTATGATCACC
AGCTGGCCTTGGAAGAGGGCGAGGGGCTGGCGCGCCTGGGGGCGTCGTCGCCGGAGCGGCACCCGCGCGTGCAG
ATGAAAAGGGACGCTCGCGAGGCCTACGTGCCCAAGCAGAACCTGTTCAGAGACAGGAGCGGCGAGGAGCCCGA
GGAGATGCGCGCGGCCCGGTTCCACGCGGGGCGGGAGCTGCGGCGCGGCCTGGACCGAAAGAGGGTGCTGAGGG
ACGAGGATTTCGAGGCGGACGAGCTGACGGGGATCAGCCCCGCGCGCGCGCACGTGGCCGCGGCCAACCTGGTC
ACGGCGTACGAGCAGACCGTGAAGGAGGAGAGCAACTTCCAAAAATCCTTCAACAACCACGTGCGCACCCTGAT
CGCGCGCGAGGAGGTGACCCTGGGCCTGATGCACCTGTGGGACCTGCTGGAGGCCATCGTGCAGAACCCCACCA
GCAAGCCGCTGACGGCGCAGCTGTTCCTGGTGGTGCAGCATAGTCGGGACAACGAAGCGTTCAGGGAGGCGCTG
CTGAATATCACCGAGCCCGAGGGCCGCTGGCTCCTGGACCTGGTGAACATTCTGCAGAGCATCGTGGTGCAGGA
GCGCGGGCTGCCGCTGTCCGAGAAGCTGGCGGCCATCAACTTCTCGGTGCTGAGTTTGGGCAAGTACTACGCTA
GGAAGATCTACAAGACCCCGTACGTGCCCATAGACAAGGAGGTGAAGATCGACGGGTTTTACATGCGCATGACC

2026201462 26 Feb 2026

CTGAAAGTGCTGACCCTGAGCGACGATCTGGGGGTGTACCGCAACGACAGGATGCACCGTGCGGTGAGCGCCAG
CAGGCGGCGCGAGCTGAGCGACCAGGAGCTGATGCATAGTCTGCAGCGGGCCCTGACCGGGGCCGGGACCGAGG
GGGAGAGCTACTTTGACATGGGCGCGGACCTGCACTGGCAGCCCAGCCGCCGGGCCTTGGAGGCGGCGGCAGGA
CCCTACGTAGAAGAGGTGGACGATGAGGTGGACGAGGAGGGCGAGTACCTGGAAGACTGATGGCGCGACCGTAT
TTTTGCTAGATGCAACAACAACAGCCACCTCCTGATCCCGCGATGCGGGCGGCGCTGCAGAGCCAGCCGTCCGG
CATTAACTCCTCGGACGATTGGACCCAGGCCATGCAACGCATCATGGCGCTGACGACCCGCAACCCCGAAGCCT
TTAGACAGCAGCCCCAGGCCAACCGGCTCTCGGCCATCCTGGAGGCCGTGGTGCCCTCGCGCTCCAACCCCACG
CACGAGAAGGTCCTGGCCATCGTGAACGCGCTGGTGGAGAACAAGGCCATCCGCGGCGACGAGGCCGGCCTGGT
GTACAACGCGCTGCTGGAGCGCGTGGCCCGCTACAACAGCACCAACGTGCAGACCAACCTGGACCGCATGGTGA
CCGACGTGCGCGAGGCCGTGGCCCAGCGCGAGCGGTTCCACCGCGAGTCCAACCTGGGATCCATGGTGGCGCTG
AACGCCTTCCTCAGCACCCAGCCCGCCAACGTGCCCCGGGGCCAGGAGGACTACACCAACTTCATCAGCGCCCT
GCGCCTGATGGTGACCGAGGTGCCCCAGAGCGAGGTGTACCAGTCCGGGCCGGACTACTTCTTCCAGACCAGTC
GCCAGGGCTTGCAGACCGTGAACCTGAGCCAGGCTTTCAAGAACTTGCAGGGCCTGTGGGGCGTGCAGGCCCCG
GTCGGGGACCGCGCGACGGTGTCGAGCCTGCTGACGCCGAACTCGCGCCTGCTGCTGCTGCTGGTGGCCCCCTT
CACGGACAGCGGCAGCATCAACCGCAACTCGTACCTGGGCTACCTGATTAACCTGTACCGCGAGGCCATCGGCC
AGGCGCACGTGGACGAGCAGACCTACCAGGAGATCACCCACGTGAGCCGCGCCCTGGGCCAGGACGACCCGGGC
AACCTGGAAGCCACCCTGAACTTTTTGCTGACCAACCGGTCGCAGAAGATCCCGCCCCAGTACGCGCTCAGCAC
CGAGGAGGAGCGCATCCTGCGTTACGTGCAGCAGAGCGTGGGCCTGTTCCTGATGCAGGAGGGGGCCACCCCCA
GCGCCGCGCTCGACATGACCGCGCGCAACATGGAGCCCAGCATGTACGCCAGCAACCGCCCGTTCATCAATAAA
CTGATGGACTACTTGCATCGGGCGGCCGCCATGAACTCTGACTATTTCACCAACGCCATCCTGAATCCCCACTG
GCTCCCGCCGCCGGGGTTCTACACGGGCGAGTACGACATGCCCGACCCCAATGACGGGTTCCTGTGGGACGATG
TGGACAGCAGCGTGTTCTCCCCCCGACCGGGTGCTAACGAGCGCCCCTTGTGGAAGAAGGAAGGCAGCGACCGA
CGCCCGTCCTCGGCGCTGTCCGGCCGCGAGGGTGCTGCCGCGGCGGTGCCCGAGGCCGCCAGTCCTTTCCCGAG
CTTGCCCTTCTCGCTGAACAGTATCCGCAGCAGCGAGCTGGGCAGGATCACGCGCCCGCGCTTGCTGGGCGAAG
AGGAGTACTTGAATGACTCGCTGTTGAGACCCGAGCGGGAGAAGAACTTCCCCAATAACGGGATAGAAAGCCTG
GTGGACAAGATGAGCCGCTGGAAGACGTATGCGCAGGAGCACAGGGACGATCCCCGGGCGTCGCAGGGGGCCAC
GAGCCGGGGCAGCGCCGCCCGTAAACGCCGGTGGCACGACAGGCAGCGGGGACAGATGTGGGACGATGAGGACT
CCGCCGACGACAGCAGCGTGTTGGACTTGGGTGGGAGTGGTAACCCGTTCGCTCACCTGCGCCCCCGTATCGGG
CGCATGATGTAAGAGAAACCGAAAATAAATGATACTCACCAAGGCCATGGCGACCAGCGTGCGTTCGTTTCTTC
TCTGTTGTTGTTGTATCTAGTATGATGAGGCGTGCGTACCCGGAGGGTCCTCCTCCCTCGTACGAGAGCGTGAT
GCAGCAGGCGATGGCGGCGGCGGCGATGCAGCCCCCGCTGGAGGCTCCTTACGTGCCCCCGCGGTACCTGGCGC
CTACGGAGGGGCGGAACAGCATTCGTTACTCGGAGCTGGCACCCTTGTACGATACCACCCGGTTGTACCTGGTG
GACAACAAGTCGGCGGACATCGCCTCGCTGAACTACCAGAACGACCACAGCAACTTCCTGACCACCGTGGTGCA
GAACAATGACTTCACCCCCACGGAGGCCAGCACCCAGACCATCAACTTTGACGAGCGCTCGCGGTGGGGCGGCC
AGCTGAAAACCATCATGCACACCAACATGCCCAACGTGAACGAGTTCATGTACAGCAACAAGTTCAAGGCGCGG
GTGATGGTCTCCCGCAAGACCCCCAATGGGGTGACAGTGACAGAGGATTATGATGGTAGTCAGGATGAGCTGAA
GTATGAATGGGTGGAATTTGAGCTGCCCGAAGGCAACTTCTCGGTGACCATGACCATCGACCTGATGAACAACG
CCATCATCGACAATTACTTGGCGGTGGGGCGGCAGAACGGGGTGCTGGAGAGCGACATCGGCGTGAAGTTCGAC
ACTAGGAACTTCAGGCTGGGCTGGGACCCCGTGACCGAGCTGGTCATGCCCGGGGTGTACACCAACGAGGCTTT
CCATCCCGATATTGTCTTGCTGCCCGGCTGCGGGGTGGACTTCACCGAGAGCCGCCTCAGCAACCTGCTGGGCA
TTCGCAAGAGGCAGCCCTTCCAGGAAGGCTTCCAGATCATGTACGAGGATCTGGAGGGGGGCAACATCCCCGCG
CTCCTGGATGTCGACGCCTATGAGAAAAGCAAGGAGGATGCAGCAGCTGAAGCAACTGCAGCCGTAGCTACCGC
CTCTACCGAGGTCAGGGGCGATAATTTTGCAAGCGCCGCAGCAGTGGCAGCGGCCGAGGCGGCTGAAACCGAAA
GTAAGATAGTCATTCAGCCGGTGGAGAAGGATAGCAAGAACAGGAGCTACAACGTACTACCGGACAAGATAAAC
ACCGCCTACCGCAGCTGGTACCTAGCCTACAACTATGGCGACCCCGAGAAGGGCGTGCGCTCCTGGACGCTGCT
CACCACCTCGGACGTCACCTGCGGCGTGGAGCAAGTCTACTGGTCGCTGCCCGACATGATGCAAGACCCGGTCA
CCTTCCGCTCCACGCGTCAAGTTAGCAACTACCCGGTGGTGGGCGCCGAGCTCCTGCCCGTCTACTCCAAGAGC
TTCTTCAACGAGCAGGCCGTCTACTCGCAGCAGCTGCGCGCCTTCACCTCGCTTACGCACGTCTTCAACCGCTT
CCCCGAGAACCAGATCCTCGTCCGCCCGCCCGCGCCCACCATTACCACCGTCAGTGAAAACGTTCCTGCTCTCA
CAGATCACGGGACCCTGCCGCTGCGCAGCAGTATCCGGGGAGTCCAGCGCGTGACCGTTACTGACGCCAGACGC
CGCACCTGCCCCTACGTCTACAAGGCCCTGGGCATAGTCGCGCCGCGCGTCCTCTCGAGCCGCACCTTCTAAAT
GTCCATTCTCATCTCGCCCAGTAATAACACCGGTTGGGGCCTGCGCGCGCCCAGCAAGATGTACGGAGGCGCTC
GCCAACGCTCCACGCAACACCCCGTGCGCGTGCGCGGGCACTTCCGCGCTCCCTGGGGCGCCCTCAAGGGCCGC
GTGCGGTCGCGCACCACCGTCGACGACGTGATCGACCAGGTGGTGGCCGACGCGCGCGCAACTACACCCCCGCCGC
CGCGCCCGTCTCCACCGTGGACGCCGTCATCGACAGCGTGGTGGCcGACGCGCGCCGGTACGCCCGCGCCAAGA
GCCGGCGGCGGCGCATCGCCCGGCGGCACCGGAGCACCCCCGCCATGCGCGCGGCGCGAGCCTTGCTGCGCAGG
GCCAGGCGCACGGGACGCAGGGCCATGCTCAGGGCGGCCAGACGCGCGGCTTCAGGCGCCAGCGCCGGCAGGAC
CCGGAGACGCGCGGCCACGGCGGCGGCAGCGGCCATCGCCAGCATGTCCCGCCCGCGGCGAGGGAACGTGTACT
GGGTGCGCGACGCCGCCACCGGTGTGCGCGTGCCCGTGCGCACCCGCCCCCCTCGCACTTGAAGATGTTCACTT
CGCGATGTTGATGTGTCCCAGCGGCGAGGAGGATGTCCAAGCGCAAATTCAAGGAAGAGATGCTCCAGGTCATC

2026201462 26 Feb 2026

GCGCCTGAGATCTACGGCCCTGCGGTGGTGAAGGAGGAAAGAAAGCCCCGCAAAATCAAGCGGGTCAAAAAGGA
CAAAAAGGAAGAAGAAAGTGATGTGGACGGATTGGTGGAGTTTGTGCGCGAGTTCGCCCCCCGGCGGCGCGTGC
AGTGGCGCGGGCGGAAGGTGCAACCGGTGCTGAGACCCGGCACCACCGTGGTCTTCACGCCCGGCGAGCGCTCC
GGCACCGCTTCCAAGCGCTCCTACGACGAGGTGTACGGGGATGATGATATTCTGGAGCAGGCGGCCGAGCGCCT
GGGCGAGTTTGCTTACGGCAAGCGCAGCCGTTCCGCACCGAAGGAAGAGGCGGTGTCCATCCCGCTGGACCACG
GCAACCCCACGCCGAGCCTCAAGCCCGTGACCTTGCAGCAGGTGCTGCCGACCGCGGCGCCGCGCCGGGGGTTC
AAGCGCGAGGGCGAGGATCTGTACCCCACCATGCAGCTGATGGTGCCCAAGCGCCAGAAGCTGGAAGACGTGCT
GGAGACCATGAAGGTGGACCCGGACGTGCAGCCCGAGGTCAAGGTGCGGCCCATCAAGCAGGTGGCCCCGGGCC
TGGGCGTGCAGACCGTGGACATCAAGATTCCCACGGAGCCCATGGAAACGCAGACCGAGCCCATGATCAAGCCC
AGCACCAGCACCATGGAGGTGCAGACGGATCCCTGGATGCCATCGGCTCCTAGTCGAAGACCCCGGCGCAAGTA
CGGCGCGGCCAGCCTGCTGATGCCCAACTACGCGCTGCATCCTTCCATCATCCCCACGCCGGGCTACCGCGGCA
CGCGCTTCTACCGCGGTCATACCAGCAGCCGCCGCCGCAAGACCACCACTCGCCGCCGCCGTCGCCGCACCGCC
GCTGCAACCACCCCTGCCGCCCTGGTGCGGAGAGTGTACCGCCGCGGCCGCGCACCTCTGACCCTGCCGCGCGC
GCGCTACCACCCGAGCATCGCCATTTAAACTTTCGCCtGCTTTGCAGATCAATGGCCCTCACATGCCGCCTTCG
CGTTCCCATTACGGGCTACCGAGGAAGAAAACCGCGCCGTAGAAGGCTGGCGGGGAACGGGATGCGTCGCCACC
ACCACCGGCGGCGGCGCGCCATCAGCAAGCGGTTGGGGGGAGGCTTCCTGCCCGCGCTGATCCCCATCATCGCC
GCGGCGATCGGGGCGATCCCCGGCATTGCTTCCGTGGCGGTGCAGGCCTCTCAGCGCCACTGAGACACACTTGG
AAACATCTTGTAATAAACCaATGGACTCTGACGCTCCTGGTCCTGTGATGTGTTTTCGTAGACAGATGGAAGAC
ATCAATTTTTCGTCCCTGGCTCCGCGACACGGCACGCGGCCGTTCATGGGCACCTGGAGCGACATCGGCACCAG
CCAACTGAACGGGGGCGCCTTCAATTGGAGCAGTCTCTGGAGCGGGCTTAAGAATTTCGGGTCCACGCTTAAAA
CCTATGGCAGCAAGGCGTGGAACAGCACCACAGGGCAGGCGCTGAGGGATAAGCTGAAAGAGCAGAACTTCCAG
CAGAAGGTGGTCGATGGGCTCGCCTCGGGCATCAACGGGGTGGTGGACCTGGCCAACCAGGCCGTGCAGCGGCA
GATCAACAGCCGCCTGGACCCGGTGCCGCCCGCCGGCTCCGTGGAGATGCCGCAGGTGGAGGAGGAGCTGCCTC
CCCTGGACAAGCGGGGCGAGAAGCGACCCCGCCCCGATGCGGAGGAGACGCTGCTGACGCACACGGACGAGCCG
CCCCCGTACGAGGAGGCGGTGAAACTGGGTCTGCCCACCACGCGGCCCATCGCGCCCCTGGCCACCGGGGTGCT
GAAACCCGAAAAGCCCGCGACCCTGGACTTGCCTCCTCCCCAGCCTTCCCGCCCCTCTACAGTGGCTAAGCCCC
TGCCGCCGGTGGCCGTGGCCCGCGCGCGACCCGGGGGCACCGCCCGCCCTCATGCGAACTGGCAGAGCACTCTG
AACAGCATCGTGGGTCTGGGAGTGCAGAGTGTGAAGCGCCGCCGCTGCTATTAAACCTACCGTAGCGCTTAACT
TGCTTGTCTGTGTGTGTATGTATTATGTCGCCGCCGCCGCTGTCCACCAGAAGGAGGAGTGAAGAGGCGCGTCG
CCGAGTTGCAAGATGGCCACCCCATCGATGCTGCCCCAGTGGGCGTACATGCACATCGCCGGACAGGACGCTTC
GGAGTACCTGAGTCCGGGTCTGGTGCAGTTTGCCCGCGCCACAGACACCTACTTCAGTCTGGGGAACAAGTTTA
GGAACCCCACGGTGGCGCCCACGCACGATGTGACCACCGACCGCAGCCAGCGGCTGACGCTGCGCTTCGTGCCC
GTGGACCGCGAGGACAACACCTACTCGTACAAAGTGCGCTACACGCTGGCCGTGGGCGACAACCGCGTGCTGGA
CATGGCCAGCACCTACTTTGACATCCGCGGCGTGCTGGATCGGGGCCCTAGCTTCAAACCCTACTCCGGCACCG
CCTACAACAGTCTGGCCCCCAAGGGAGCACCCAACACTTGTCAGTGGACATATAAAGCCGATGGTGAAACTGCC
ACAGAAAAAACCTATACATATGGAAATGCACCCGTGCAGGGCATTAACATCACAAAAGATGGTATTCAACTTGG
AACTGACACCGATGATCAGCCAATCTACGCAGATAAAACCTATCAGCCTGAACCTCAAGTGGGTGATGCTGAAT
GGCATGACATCACTGGTACTGATGAAAAGTATGGAGGCAGAGCTCTTAAGCCTGATACCAAAATGAAGCCTTGT
TATGGTTCTTTTGCCAAGCCTACTAATAAAGAAGGAGGTCAGGCAAATGTGAAAACAGGAACAGGCACTACTAA
AGAATATGACATAGACATGGCTTTCTTTGACAACAGAAGTGCGGCTGCTGCTGGCCTAGCTCCAGAAATTGTTT
TGTATACTGAAAATGTGGATTTGGAAACTCCAGATACCCATATTGTATACAAAGCAGGCACAGATGACAGCAGC
TCTTCTATTAATTTGGGTCAGCAAGCCATGCCCAACAGACCTAACTACATTGGTTTCAGAGACAACTTTATCGG
GCTCATGTACTACAACAGCACTGGCAATATGGGGGTGCTGGCCGGTCAGGCTTCTCAGCTGAATGCTGTGGTTG
ACTTGCAAGACAGAAACACCGAGCTGTCCTACCAGCTCTTGCTTGACTCTCTGGGTGACAGAACCCGGTATTTC
AGTATGTGGAATCAGGCGGTGGACAGCTATGATCCTGATGTGCGCATTATTGAAAATCATGGTGTGGAGGATGA
ACTTCCCAACTATTGTTTCCCTCTGGATGCTGTTGGCAGAACAGATACTTATCAGGGAATTAAGGCTAATGGAA
CTGATCAAACCACATGGACCAAAGATGACAGTGTCAATGATGCTAATGAGATAGGCAAGGGTAATCCATTCGCC
ATGGAAATCAACATCCAAGCCAACCTGTGGAGGAACTTCCTCTACGCCAACGTGGCCCTGTACCTGCCCGACTC
TTACAAGTACACGCCGGCCAATGTTACCCTGCCCACCAACACCAACACCTACGATTACATGAACGGCCGGGTGG
TGGCGCCCTCGCTGGTGGACTCCTACATCAACATCGGGGCGCGCTGGTCGCTGGATCCCATGGACAACGTGAAC
CCCTTCAACCACCACCGCAATGCGGGGCTGCGCTACCGCTCCATGCTCCTGGGCAACGGGCGCTACGTGCCCTT
CCACATCCAGGTGCCCCAGAAATTTTTCGCCATCAAGAGCCTCCTGCTCCTGCCCGGGTCCTACACCTACGAGT
GGAACTTCCGCAAGGACGTCAACATGATCCTGCAGAGCTCCCTCGGCAACGACCTGCGCACGGACGGGGCCTCC
ATCTCCTTCACCAGCATCAACCTCTACGCCACCTTCTTCCCCATGGCGCACAACACGGCCTCCACGCTCGAGGC
CATGCTGCGCAACGACACCAACGACCAGTCCTTCAACGACTACCTCTCGGCGGCCAACATGCTCTACCCCATCC
CGGCCAACGCCACCAACGTGCCCATCTCCATCCCCTCGCGCAACTGGGCCGCCTTCCGCGGCTGGTCCTTCACG
CGTCTCAAGACCAAGGAGACGCCCTCGCTGGGCTCCGGGTTCGACCCCTACTTCGTCTACTCGGGCTCCATCCC
CTACCTCGACGGCACCTTCTACCTCAACCACACCTTCAAGAAGGTCTCCATCACCTTCGACTCCTCCGTCAGCT
GGCCCGGCAACGACCGGCTCCTGACGCCCAACGAGTTCGAAATCAAGCGCACCGTCGACGGCGAGGGCTACAAC
GTGGCCCAGTGCAACATGACCAAGGACTGGTTCCTGGTCCAGATGCTGGCCCACTACAACATCGGCTACCAGGG

2026201462 26 Feb 2026

CTTCTACGTGCCCGAGGGCTACAAGGACCGCATGTACTCCTTCTTCCGCAACTTCCAGCCCATGAGCCGCCAGG
TGGTGGACGAGGTCAACTACAAGGACTACCAGGCCGTCACCCTGGCCTACCAGCACAACAACTCGGGCTTCGTC
GGCTACCTCGCGCCCACCATGCGCCAGGGCCAGCCCTACCCCGCCAACTACCCCTACCCGCTCATCGGCAAGAG
CGCCGTCACCAGCGTCACCCAGAAAAAGTTCCTCTGCGACAGGGTCATGTGGCGCATCCCCTTCTCCAGCAACT
TCATGTCCATGGGCGCGCTCACCGACCTCGGCCAGAACATGCTCTATGCCAACTCCGCCCACGCGCTAGACATG
AATTTCGAAGTCGACCCCATGGATGAGTCCACCCTTCTCTATGTTGTCTTCGAAGTCTTCGACGTCGTCCGAGT
GCACCAGCCCCACCGCGGCGTCATCGAGGCCGTCTACCTGCGCACCCCCTTCTCGGCCGGTAACGCCACCACCT
AAGCTCTTGCTTCTTGCAAGCCATGGCCGCGGGCTCCGGCGAGCAGGAGCTCAGGGCCATCATCCGCGACCTGG
GCTGCGGGCCCTACTTCCTGGGCACCTTCGATAAGCGCTTCCCGGGATTCATGGCCCCGCACAAGCTGGCCTGC
GCCATCGTCAACACGGCCGGCCGCGAGACCGGGGGCGAGCACTGGCTGGCCTTCGCCTGGAACCCGCGCTCGAA
CACCTGCTACCTCTTCGACCCCTTCGGGTTCTCGGACGAGCGCCTCAAGCAGATCTACCAGTTCGAGTACGAGG
GCCTGCTGCGCCGCAGCGCCCTGGCCACCGAGGACCGCTGCGTCACCCTGGAAAAGTCCACCCAGACCGTGCAG
GGTCCGCGCTCGGCCGCCTGCGGGCTCTTCTGCTGCATGTTCCTGCACGCCTTCGTGCACTGGCCCGACCGCCC
CATGGACAAGAACCCCACCATGAACTTGCTGACGGGGGTGCCCAACGGCATGCTCCAGTCGCCCCAGGTGGAAC
CCACCCTGCGCCGCAACCAGGAGGCGCTCTACCGCTTCCTCAACTCCCACTCCGCCTACTTTCGCTCCCACCGC
GCGCGCATCGAGAAGGCCACCGCCTTCGACCGCATGAATCAAGACATGTAAACCGTGTGTGTATGTTAAATGTC
TTTAATAAACAGCACTTTCATGTTACACATGCATCTGAGATGATTTATTTAGAAATCGAAAGGGTTCTGCCGGG
TCTCGGCATGGCCCGCGGGCAGGGACACGTTGCGGAACTGGTACTTGGCCAGCCACTTGAACTCGGGGATCAGC
AGTTTGGGCAGCGGGGTGTCGGGGAAGGAGTCGGTCCACAGCTTCCGCGTCAGTTGCAGGGCGCCCAGCAGGTC
GGGCGCGGAGATCTTGAAATCGCAGTTGGGACCCGCGTTCTGCGCGCGGGAGTTGCGGTACACGGGGTTGCAGC
ACTGGAACACCATCAGGGCCGGGTGCTTCACGCTCGCCAGCACCGTCGCGTCGGTGATGCTCTCCACGTCGAGG
TCCTCGGCGTTGGCCATCCCGAAGGGGGTCATCTTGCAGGTCTGCCTTCCCATGGTGGGCACGCACCCGGGCTT
GTGGTTGCAATCGCAGTGCAGGGGGATCAGCATCATCTGGGCCTGGTCGGCGTTCATCCCCGGGTACATGGCCT
TCATGAAAGCCTCCAATTGCCTGAACGCCTGCTGGGCCTTGGCTCCCTCGGTGAAGAAGACCCCGCAGGACTTG
CTAGAGAACTGGTTGGTGGCGCACCCGGCGTCGTGCACGCAGCAGCGCGCGTCGTTGTTGGCCAGCTGCACCAC
GCTGCGCCCCCAGCGGTTCTGGGTGATCTTGGCCCGGTCGGGGTTCTCCTTCAGCGCGCGCTGCCCGTTCTCGC
TCGCCACATCCATCTCGATCATGTGCTCCTTCTGGATCATGGTGGTCCCGTGCAGGCACCGCAGCTTGCCCTCG
GCCTCGGTGCACCCGTGCAGCCACAGCGCGCACCCGGTGCACTCCCAGTTCTTGTGGGCGATCTGGGAATGCGC
GTGCACGAAGCCCTGCAGGAAGCGGCCCATCATGGTGGTCAGGGTCTTGTTGCTAGTGAAGGTCAGCGGAATGC
CGCGGTGCTCCTCGTTGATGTACAGGTGGCAGATGCGGCGGTACACCTCGCCCTGCTCGGGCATCAGCTGGAAG
TTGGCTTTCAGGTCGGTCTCCACGCGGTAGCGGTCCATCAGCATAGTCATGATTTCCATACCCTTCTCCCAGGC
CGAGACGATGGGCAGGCTCATAGGGTTCTTCACCATCATCTTAGCGCTAGCAGCCGCGGCCAGGGGGTCGCTCT
CGTCCAGGGTCTCAAAGCTCCGCTTGCCGTCCTTCTCGGTGATCCGCACCGGGGGGTAGCTGAAGCCCACGGCC
GCCAGCTCCTCCTCGGCCTGTCTTTCGTCCTCGCTGTCCTGGCTGACGTCCTGCAGGACCACATGCTTGGTCTT
GCGGGGTTTCTTCTTGGGCGGCAGCGGCGGCGGAGATGTTGGAGATGGCGAGGGGGAGCGCGAGTTCTCGCTCA
CCACTACTATCTCTTCCTCTTCTTGGTCCGAGGCCACGCGGCGGTAGGTATGTCTCTTCGGGGGCAGAGGCGGA
GGCGACGGGCTCTCGCCGCCGCGACTTGGCGGATGGCTGGCAGAGCCCCTTCCGCGTTCGGGGGTGCGCTCCCG
GCGGCGCTCTGACTGACTTCCTCCGCGGCCGGCCATTGTGTTCTCCTAGGGAGGAACAACAAGCATGGAGACTC
AGCCATCGCCAACCTCGCCATCTGCCCCCACCGCCGACGAGAAGCAGCAGCAGCAGAATGAAAGCTTAACCGCC
CCGCCGCCCAGCCCCGCCACCTCCGACGCGGCCGTCCCAGACATGCAAGAGATGGAGGAATCCATCGAGATTGA
CCTGGGCTATGTGACGCCCGCGGAGCACGAGGAGGAGCTGGCAGTGCGCTTTTCACAAGAAGAGATACACCAAG
AACAGCCAGAGCAGGAAGCAGAGAATGAGCAGAGTCAGGCTGGGCTCGAGCATGACGGCGACTACCTCCACCTG
AGCGGGGGGGAGGACGCGCTCATCAAGCATCTGGCCCGGCAGGCCACCATCGTCAAGGATGCGCTGCTCGACCG
CACCGAGGTGCCCCTCAGCGTGGAGGAGCTCAGCCGCGCCTACGAGTTGAACCTCTTCTCGCCGCGCGTGCCCC
CCAAGCGCCAGCCCAATGGCACCTGCGAGCCCAACCCGCGCCTCAACTTCTACCCGGTCTTCGCGGTGCCCGAG
GCCCTGGCCACCTACCACATCTTTTTCAAGAACCAAAAGATCCCCGTCTCCTGCCGCGCCAACCGCACCCGCGC
CGACGCCCTTTTCAACCTGGGTCCCGGCGCCCGCCTACCTGATATCGCCTCCTTGGAAGAGGTTCCCAAGATCT
TCGAGGGTCTGGGCAGCGACGAGACTCGGGCCGCGAACGCTCTGCAAGGAGAAGGAGGAGAGCATGAGCACCAC
AGCGCCCTGGTCGAGTTGGAAGGCGACAACGCGCGGCTGGCGGTGCTCAAACGCACGGTCGAGCTGACCCATTT
CGCCTACCCGGCTCTGAACCTGCCCCCCAAAGTCATGAGCGCGGTCATGGACCAGGTGCTCATCAAGCGCGCGT
CGCCCATCTCCGAGGACGAGGGCATGCAAGACTCCGAGGAGGGCAAGCCCGTGGTCAGCGACGAGCAGCTGGCC
CGGTGGCTGGGTCCTAATGCTAGTCCCCAGAGTTTGGAAGAGCGGCGCAAACTCATGATGGCCGTGGTCCTGGT
GACCGTGGAGCTGGAGTGCCTGCGCCGCTTCTTCGCCGACGCGGAGACCCTGCGCAAGGTCGAGGAGAACCTGC
ACTACCTCTTCAGGCACGGGTTCGTGCGCCAGGCCTGCAAGATCTCCAACGTGGAGCTGACCAACCTGGTCTCC
TACATGGGCATCTTGCACGAGAACCGCCTGGGGCAGAACGTGCTGCACACCACCCTGCGCGGGGAGGCCCGGCG
CGACTACATCCGCGACTGCGTCTACCTCTACCTCTGCCACACCTGGCAGACGGGCATGGGCGTGTGGCAGCAGT
GTCTGGAGGAGCAGAACCTGAAAGAGCTCTGCAAGCTCCTGCAGAAGAACCTCAAGGGTCTGTGGACCGGGTTC
GACGAGCGCACCACCGCCTCGGACCTGGCCGACCTCATTTTCCCCGAGCGCCTCAGGCTGACGCTGCGCAACGG
CCTGCCCGACTTTATGAGCCAAAGCATGTTGCAAAACTTTCGCTCTTTCATCCTCGAACGCTCCGGAATCCTGC
CCGCCACCTGCTCCGCGCTGCCCTCGGACTTCGTGCCGCTGACCTTCCGCGAGTGCCCCCCGCCGCTGTGGAGC

2026201462 26 Feb 2026

CACTGCTACCTGCTGCGCCTGGCCAACTACCTGGCCTACCACTCGGACGTGATCGAGGACGTCAGCGGCGAGGG
CCTGCTCGAGTGCCACTGCCGCTGCAACCTCTGCACGCCGCACCGCTCCCTGGCCTGCAACCCCCAGCTGCTGA
GCGAGACCCAGATCATCGGCACCTTCGAGTTGCAAGGGCCCAGCGAAGGCGAGGGTTCAGCCGCCAAGGGGGGT
CTGAAACTCACCCCGGGGCTGTGGACCTCGGCCTACTTGCGCAAGTTCGTGCCCGAGGACTACCATCCCTTCGA
GATCAGGTTCTACGAGGACCAATCCCATCCGCCCAAGGCCGAGCTGTCGGCCTGCGTCATCACCCAGGGGGCGA
TCCTGGCCCAATTGCAAGCCATCCAGAAATCCCGCCAAGAATTCTTGCTGAAAAAGGGCCGCGGGGTCTACCTC
GACCCCCAGACCGGTGAGGAGCTCAACCCCGGCTTCCCCCAGGATGCCCCGAGGAAACAAGAAGCTGAAAGTGG
AGCTGCCGCCCGTGGAGGATTTGGAGGAAGACTGGGAGAACAGCAGTCAGGCAGAGGAGGAGGAGATGGAGGAA
GACTGGGACAGCACTCAGGCAGAGGAGGACAGCCTGCAAGACAGTCTGGAGGAAGACGAGGAGGAGGCAGAGGA
GGAGGTGGAAGAAGCAGCCGCCGCCAGACCGTCGTCCTCGGCGGGGGAGAAAGCAAGCAGCACGGATACCATCT
CCGCTCCGGGTCGGGGTCCCGCTCGACCACACAGTAGATGGGACGAGACCGGACGATTCCCGAACCCCACCACC
CAGACCGGTAAGAAGGAGCGGCAGGGATACAAGTCCTGGCGGGGGCACAAAAACGCCATCGTCTCCTGCTTGCA
GGCCTGCGGGGGCAACATCTCCTTCACCCGGCGCTACCTGCTCTTCCACCGCGGGGTGAACTTTCCCCGCAACA
TCTTGCATTACTACCGTCACCTCCACAGCCCCTACTACTTCCAAGAAGAGGCAGCAGCAGCAGAAAAAGACCAG
CAGAAAACCAGCAGCTAGAAAATCCACAGCGGCGGCAGCAGGTGGACTGAGGATCGCGGCGAACGAGCCGGCGC
AAACCCGGGAGCTGAGGAACCGGATCTTTCCCACCCTCTATGCCATCTTCCAGCAGAGTCGGGGGCAGGAGCAG
GAACTGAAAGTCAAGAACCGTTCTCTGCGCTCGCTCACCCGCAGTTGTCTGTATCACAAGAGCGAAGACCAACT
TCAGCGCACTCTCGAGGACGCCGAGGCTCTCTTCAACAAGTACTGCGCGCTCACTCTTAAAGAGTAGCCCGCGC
CCGCCCAGTCGCAGAAAAAGGCGGGAATTACGTCACCTGTGCCCTTCGCCCTAGCCGCCTCCACCCATCATCAT
GAGCAAAGAGATTCCCACGCCTTACATGTGGAGCTACCAGCCCCAGATGGGCCTGGCCGCCGGTGCCGCCCAGG
ACTACTCCACCCGCATGAATTGGCTCAGCGCCGGGCCCGCGATGATCTCACGGGTGAATGACATCCGCGCCCAC
CGAAACCAGATACTCCTAGAACAGTCAGCGCTCACCGCCACGCCCCGCAATCACCTCAATCCGCGTAATTGGCC
CGCCGCCCTGGTGTACCAGGAAATTCCCCAGCCCACGACCGTACTACTTCCGCGAGACGCCCAGGCCGAAGTCC
AGCTGACTAACTCAGGTGTCCAGCTGGCGGGCGGCGCCACCCTGTGTCGTCACCGCCCCGCTCAGGGTATAAAG
CGGCTGGTGATCCGGGGCAGAGGCACACAGCTCAACGACGAGGTGGTGAGCTCTTCGCTGGGTCTGCGACCTGA
CGGAGTCTTCCAACTCGCCGGATCGGGGAGATCTTCCTTCACGCCTCGTCAGGCCGTCCTGACTTTGGAGAGTT
CGTCCTCGCAGCCCCGCTCGGGTGGCATCGGCACTCTCCAGTTCGTGGAGGAGTTCACTCCCTCGGTCTACTTC
AACCCCTTCTCCGGCTCCCCCGGCCACTACCCGGACGAGTTCATCCCGAACTTCGACGCCATCAGCGAGTCGGT
GGACGGCTACGATTGAAACTAATCACCCCCTTATCCAGTGAAATAAAGATCATATTGATGATGATTTTACAGAA
ATAAAAAATAATCATTTGATTTGAAATAAAGATACAATCATATTGATGATTTGAGTTTAACAAAAAAATAAAGA
ATCACTTACTTGAAATCTGATACCAGGTCTCTGTCCATGTTTTCTGCCAACACCACTTCACTCCCCTCTTCCCA
GCTCTGGTACTGCAGGCCCCGGCGGGCTGCAAACTTCCTCCACACGCTGAAGGGGATGTCAAATTCCTCCTGTC
CCTCAATCTTCATTTTATCTTCTATCAGATGTCCAAAAAGCGCGTCCGGGTGGATGATGACTTCGACCCCGTCT
ACCCCTACGATGCAGACAACGCACCGACCGTGCCCTTCATCAACCCCCCCTTCGTCTCTTCAGATGGATTCCAA
GAGAAGCCCCTGGGGGTGTTGTCCCTGCGACTGGCCGACCCCGTCACCACCAAGAACGGGGAAATCACCCTCAA
GCTGGGAGAGGGGGTGGACCTCGATTCCTCGGGAAAACTCATCTCCAACACGGCCACCAAGGCCGCCGCCCCTC
TCAGTTTTTCCAACAACACCATTTCCCTTAACATGGATCACCCCTTTTACACTAAAGATGGAAAATTATCCTTA
CAAGTTTCTCCACCATTAAATATACTGAGAACAAGCATTCTAAACACACTAGCTTTAGGTTTTGGATCAGGTTT
AGGACTCCGTGGCTCTGCCTTGGCAGTACAGTTAGTCTCTCCACTTACATTTGATACTGATGGAAACATAAAGC
TTACCTTAGACAGAGGTTTGCATGTTACAACAGGAGATGCAATTGAAAGCAACATAAGCTGGGCTAAAGGTTTA
AAATTTGAAGATGGAGCCATAGCAACCAACATTGGAAATGGGTTAGAGTTTGGAAGCAGTAGTACAGAAACAGG
TGTTGATGATGCTTACCCAATCCAAGTTAAACTTGGATCTGGCCTTAGCTTTGACAGTACAGGAGCCATAATGG
CTGGTAACAAAGAAGACGATAAACTCACTTTGTGGACAACACCTGATCCATCACCAAACTGTCAAATACTCGCA
GAAAATGATGCAAAACTAACACTTTGCTTGACTAAATGTGGTAGTCAAATACTGGCCACTGTGTCAGTCTTAGT
TGTAGGAAGTGGAAACCTAAACCCCATTACTGGCACCGTAAGCAGTGCTCAGGTGTTTCTACGTTTTGATGCAA
ACGGTGTTCTTTTAACAGAACATTCTACACTAAAAAAATACTGGGGGTATAGGCAGGGAGATAGCATAGATGGC
ACTCCATATACCAATGCTGTAGGATTCATGCCCAATTTAAAAGCTTATCCAAAGTCACAAAGTTCTACTACTAA
AAATAATATAGTAGGGCAAGTATACATGAATGGAGATGTTTCAAAACCTATGCTTCTCACTATAACCCTCAATG
GTACTGATGACAGCAACAGTACATATTCAATGTCATTTTCATACACCTGGACTAATGGAAGCTATGTTGGAGCA
ACATTTGGGGCTAACTCTTATACCTTCTCATACATCGCCCAAGAATGAACACTGTATCCCACCCTGCATGCCAA
CCCTTCCCACCCCACTCTGTGGAACAAACTCTGAAACACAAAATAAAATAAAGTTCAAGTGTTTTATTGATTCA
ACAGTTTTACAGGATTCGAGCAGTTATTTTTCCTCCACCCTCCCAGGACATGGAATACACCACCCTCTCCCCCC
GCACAGCCTTGAACATCTGAATGCCATTGGTGATGGACATGCTTTTGGTCTCCACGTTCCACACAGTTTCAGAG
CGAGCCAGTCTCGGGTCGGTCAGGGAGATGAAACCCTCCGGGCACTCCCGCATCTGCACCTCACAGCTCAACAG
CTGAGGATTGTCCTCGGTGGTCGGGATCACGGTTATCTGGAAGAAGCAGAAGAGCGGCGGTGGGAATCATAGTC
CGCGAACGGGATCGGCCGGTGGTGTCGCATCAGGCCCCGCAGCAGTCGCTGCCGCCGCCGCTCCGTCAAGCTGC
TGCTCAGGGGGTCCGGGTCCAGGGACTCCCTCAGCATGATGCCCACGGCCCTCAGCATCAGTCGTCTGGTGCGG
CGGGCGCAGCAGCGCATGCGGATCTCGCTCAGGTCGCTGCAGTACGTGCAACACAGAACCACCAGGTTGTTCAA
CAGTCCATAGTTCAACACGCTCCAGCCGAAACTCATCGCGGGAAGGATGCTACCCACGTGGCCGTCGTACCAGA
TCCTCAGGTAAATCAAGTGGTGCCCCCTCCAGAACACGCTGCCCACGTACATGATCTCCTTGGGCATGTGGCGG

2026201462 26 Feb 2026

```
TTCACCACCTCCCGGTACCACATCACCCTCTGGTTGAACATGCAGCCCCGGATGATCCTGCGGAACCACAGGGC
CAGCACCGCCCCGCCCGCCATGCAGCGAAGAGACCCCGGGTCCCGGCAATGGCAATGGAGGACCCACCGCTCGT
ACCCGTGGATCATCTGGGAGCTGAACAAGTCTATGTTGGCACAGCACAGGCATATGCTCATGCATCTCTTCAGC
ACTCTCAACTCCTCGGGGGTCAAAACCATATCCCAGGGCACGGGGAACTCTTGCAGGACAGCGAACCCCGCAGA
ACAGGGCAATCCTCGCACAGAACTTACATTGTGCATGGACAGGGTATCGCAATCAGGCAGCACCGGGTGATCCT
CCACCAGAGAAGCGCGGGTCTCGGTCTCCTCACAGCGTGGTAAGGGGGCCGGCCGATACGGGTGATGGCGGGAC
GCGGCTGATCGTGTTCGCGACCGTGTCATGATGCAGTTGCTTTCGGACATTTTCGTACTTGCTGTAGCAGAACC
TGGTCCGGGCGCTGCACACCGATCGCCGGCGGCGGTCTCGGCGCTTGGAACGCTCGGTGTTGAAATTGTAAAAC
AGCCACTCTCTCAGACCGTGCAGCAGATCTAGGGCCTCAGGAGTGATGAAGATCCCATCATGCCTGATGGCTCT
GATCACATCGACCACCGTGGAATGGGCCAGACCCAGCCAGATGATGCAATTTTGTTGGGTTTCGGTGACGGCGG
GGGAGGGAAGAACAGGAAGAACCATGATTAACTTTTAATCCAAACGGTCTCGGAGTACTTCAAAATGAAGATCG
CGGAGATGGCACCTCTCGCCCCCGCTGTGTTGGTGGAAAATAACAGCCAGGTCAAAGGTGATACGGTTCTCGAG
ATGTTCCACGGTGGCTTCCAGCAAAGCCTCCACGCGCACATCCAGAAACAAGACAATAGCGAAAGCGGGAGGGT
TCTCTAATTCCTCAATCATCATGTTACACTCCTGCACCATCCCCAGATAATTTTCATTTTTCCAGCCTTGAATG
ATTCGAACTAGTTCcTGAGGTAAATCCAAGCCAGCCATGATAAAGAGCTCGCGCAGAGCGCCCTCCACCGGCAT
TCTTAAGCACACCCTCATAATTCCAAGATATTCTGCTCCTGGTTCACCTGCAGCAGATTGACAAGCGGAATATC
AAAATCTCTGCCGCGATCCCTGAGCTCCTCCCTCAGCAATAACTGTAAGTACTCTTTCATATCCTCTCCGAAAT
TTTTAGCCATAGGACCACCAGGAATAAGATTAGGGCAAGCCACAGTACAGATAAACCGAAGTCCTCCCCAGTGA
GCATTGCCAAATGCAAGACTGCTATAAGCATGCTGGCTAGACCCGGTGATATCTTCCAGATAACTGGACAGAAA
ATCGCCCAGGCAATTTTTAAGAAAATCAACAAAAGAAAAATCCTCCAGGTGGACGTTTAGAGCCTCGGGAACAA
CGATGAAGTAAATGCAAGCGGTGCGTTCCAGCATGGTTAGTTAGCTGATCTGTAGAAAAAACAAAAATGAACAT
TAAACCATGCTAGCCTGGCGAACAGGTGGGTAAATCGTTCTCTCCAGCACCAGGCAGGCCACGGGGTCTCCGGC
GCGACCCTCGTAAAAATTGTCGCTATGATTGAAAACCATCACAGAGAGACGTTCCCGGTGGCCGGCGTGAATGA
TTCGACAAGATGAATACACCCCCGGAACATTGGCGTCCGCGAGTGAAAAAAAGCGCCCGAGGAAGCAATAAGGC
ACTACAATGCTCAGTCTCAAGTCCAGCAAAGCGATGCCATGCGGATGAAGCACAAAATTCTCAGGTGCGTACAA
AATGTAATTACTCCCCTCCTGCACAGGCAGCAAAGCCCCCGATCCCTCCAGGTACACATACAAAGCCTCAGCGT
CCATAGCTTACCGAGCAGCAGCACACAACAGGCGCAAGAGTCAGAGAAAGGCTGAGCTCTAACCTGTCCACCCG
CTCTCTGCTCAATATATAGCCCAGATCTACACTGACGTAAAGGCCAAAGTCTAAAAATACCCGCCAAATAATCA
CACACGCCCAGCACACGCCCAGAAACCGGTGACACACTCAAAAAAATACGCGCACTTCCTCAAACGCCCAAAAC
TGCCGTCATTTCCGGGTTCCCACGCTACGTCATCAAAACACGACTTTCAAATTCCGTCGACCGTTAAAAACGTC
ACCCGCCCCGCCCCTAACGGTCGCCCGTCTCTCAGCCAATCAGCGCCCCGCATCCCCAAATTCAAACACCTCAT
TTGCATATTAACGCGCACAAAAAGTTTGAGGTATATTATTGATGATGG
```

XV.B. ChAd Neoantigen Cassette Delivery Vector Testing

XV.B.1. ChAd Vector Evaluation Methods and Materials

Transfection of HEK293A cells using lipofectamine

[00812] DNA for the ChAdV68 constructs (ChAdV68.4WTnt.GFP, ChAdV68.5WTnt.GFP, ChAdV68.4WTnt.MAG25mer and ChAdV68.5WTnt.MAG25mer) was prepared and transfected into HEK293A cells using the following protocol.

[00813] 10 ug of plasmid DNA was digested with PacI to liberate the viral genome. DNA was then purified using GeneJet DNA cleanup Micro columns (Thermo Fisher) according to manufacturer's instructions for long DNA fragments, and eluted in 20 ul of pre-heated water; columns were left at 37 degrees for 0.5-1 hours before the elution step.

[00814] HEK293A cells were introduced into 6-well plates at a cell density of 10^6 cells/well 14-18 hours prior to transfection. Cells were overlaid with 1 ml of fresh medium (DMEM-10% hiFBS with pen/strep and glutamate) per well. 1-2 ug of purified DNA was used per well in a transfection with twice the ul volume (2-4 ul) of Lipofectamine2000, according to the

2026201462 26 Feb 2026

manufacturer's protocol. 0.5 ml of OPTI-MEM medium containing the transfection mix was added to the 1 ml of normal growth medium in each well, and left on cells overnight.

[00815] Transfected cell cultures were incubated at 37^0C for at least 5-7 days. If viral plaques were not visible by day 7 post-transfection, cells were split 1:4 or 1:6, and incubated at 37^0C to monitor for plaque development. Alternatively, transfected cells were harvested and subjected to 3 cycles of freezing and thawing and the cell lysates were used to infect HEK293A cells and the cells were incubated until virus plaques were observed.

Transfection of ChAdV68 vectors into HEK293A cells using calcium phosphate and generation of the tertiary viral stock

[00816] DNA for the ChAdV68 constructs (ChAdV68.4WTnt.GFP, ChAdV68.5WTnt.GFP, ChAdV68.4WTnt.MAG25mer, ChAdV68.5WTnt.MAG25mer) was prepared and transfected into HEK293A cells using the following protocol.

[00817] HEK293A cells were seeded one day prior to the transfection at 10^6 cells/ well of a 6 well plate in 5% BS/DMEM/ 1XP/S, 1XGlutamax. Two wells are needed per transfection. Two to four hours prior to transfection the media was changed to fresh media. The ChAdV68.4WTnt.GFP plasmid was linearized with PacI. The linearized DNA was then phenol chloroform extracted and precipitated using one tenth volume of 3M Sodium acetate pH 5.3 and two volumes of 100% ethanol. The precipitated DNA was pelleted by centrifugation at 12,000xg for 5 min before washing 1X with 70% ethanol. The pellet was air dried and re-suspended in 50 µL of sterile water. The DNA concentration was determined using a NanoDrop™ (ThermoFisher) and the volume adjusted to 5 µg of DNA/50 µL.

[00818] 169 µL of sterile water was added to a microfuge tube. 5 µL of 2M $CaCl_2$ was then added to the water and mixed gently by pipetting. 50 µL of DNA was added dropwise to the $CaCl_2$ water solution. Twenty six µL of 2M $CaCl_2$ was then added and mixed gently by pipetting twice with a micro-pipetor. This final solution should consist of 5 µg of DNA in 250 µL of 0.25M $CaCl_2$. A second tube was then prepared containing 250 µL of 2XHBS (Hepes buffered solution). Using a 2 mL sterile pipette attached to a Pipet-Aid air was slowly bubbled through the 2XHBS solution. At the same time the DNA solution in the 0.25M $CaCl_2$ solution was added in a dropwise fashion. Bubbling was continued for approximately 5 seconds after addition of the final DNA droplet. The solution was then incubated at room temperature for up to 20 minutes before adding to 293A cells. 250 µL of the DNA/Calcium phosphate solution was added dropwise to a monolayer of 293A cells that had been seeded one day prior at 10^6

2026201462 26 Feb 2026

cells per well of a 6 well plate. The cells were returned to the incubator and incubated overnight. The media was changed 24h later. After 72h the cells were split 1:6 into a 6 well plate. The monolayers were monitored daily by light microscopy for evidence of cytopathic effect (CPE). 7-10 days post transfection viral plaques were observed and the monolayer harvested by pipetting the media in the wells to lift the cells. The harvested cells and media were transferred to a 50 mL centrifuge tube followed by three rounds of freeze thawing (at -80 °C and 37 °C). The subsequent lysate, called the primary virus stock was clarified by centrifugation at full speed on a bench top centrifuge (4300Xg) and a proportion of the lysate 10-50%) used to infect 293A cells in a T25 flask. The infected cells were incubated for 48h before harvesting cells and media at complete CPE. The cells were once again harvested, freeze thawed and clarified before using this secondary viral stock to infect a T150 flask seeded at 1.5x 10^7 cells per flask. Once complete CPE was achieved at 72h the media and cells were harvested and treated as with earlier viral stocks to generate a tertiary stock.

Production in 293F cells

[00819] ChAdV68 virus production was performed in 293F cells grown in 293 FreeStyle^M (ThermoFisher) media in an incubator at 8% $C0_2$. On the day of infection cells were diluted to 10^6 cells per mL, with 98% viability and 400 mL were used per production run in 1L Shake flasks (Corning). 4 mL of the tertiary viral stock with a target MOI of >3.3 was used per infection. The cells were incubated for 48-72h until the viability was <70% as measured by Trypan blue. The infected cells were then harvested by centrifugation, full speed bench top centrifuge and washed in 1XPBS, re-centrifuged and then re-suspended in 20 mL of 10mM Tris pH7.4. The cell pellet was lysed by freeze thawing 3X and clarified by centrifugation at 4,300Xg for 5 minutes.

Purification by CsCl centrifugation

[00820] Viral DNA was purified by CsCl centrifugation. Two discontinuous gradient runs were performed. The first to purify virus from cellular components and the second to further refine separation from cellular components and separate defective from infectious particles.

[00821] 10 mL of 1.2 (26.8g CsCl dissolved in 92 mL of 10 mM Tris pH 8.0) CsCl was added to polyallomer tubes. Then 8 mL of 1.4 CsCl (53g CsCl dissolved in 87 mL of 10 mM Tris pH 8.0) was carefully added using a pipette delivering to the bottom of the tube. The clarified virus was carefully layered on top of the 1.2 layer. If needed more 10 mM Tris was added to balance the tubes. The tubes were then placed in a SW-32Ti rotor and centrifuged for 2h 30 min at 10^0C. The tube was then removed to a laminar flow cabinet and the virus band

2026201462 26 Feb 2026

pulled using an 18 guage needle and a 10 mL syringe. Care was taken not to remove contaminating host cell DNA and protein. The band was then diluted at least 2X with 10 mM Tris pH 8.0 and layered as before on a discontinuous gradient as described above. The run was performed as described before except that this time the run was performed overnight. The next day the band was pulled with care to avoid pulling any of the defective particle band. The virus was then dialyzed using a Slide-a-LyzerT^M Cassette (Pierce) against ARM buffer (20 mM Tris pH 8.0, 25 mM NaCl, 2.5% Glycerol). This was performed 3X, 1h per buffer exchange. The virus was then aliquoted for storage at -80°C.

Viral assays

[00822] VP concentration was performed by using an OD 260 assay based on the extinction coefficient of 1.1x 10^{12} viral particles (VP) is equivalent to an Absorbance value of 1 at OD260 nm. Two dilutions (1:5 and 1:10) of adenovirus were made in a viral lysis buffer (0.1% SDS, 10 mM Tris pH 7.4, 1mM EDTA). OD was measured in duplicate at both dilutions and the VP concentration/ mL was measured by multiplying the OD260 value X dilution factor X 1.1x 10^{12}VP.

[00823] An infectious unit (IU) titer was calculated by a limiting dilution assay of the viral stock. The virus was initially diluted 100X in DMEM/5% NS/ 1X PS and then subsequently diluted using 10-fold dilutions down to 1x 10^{-7}. 100 µL of these dilutions were then added to 293A cells that were seeded at least an hour before at 3e5 cells/ well of a 24 well plate. This was performed in duplicate. Plates were incubated for 48h in a CO2 (5%) incubator at 37 ^{0}C. The cells were then washed with 1XPBS and were then fixed with 100% cold methanol (-20 °C). The plates were then incubated at -20 ^{0}C for a minimum of 20 minutes. The wells were washed with 1XPBS then blocked in 1XPBS/0.1% BSA for 1 h at room temperature. A rabbit anti-Ad antibody (Abcam, Cambridge, MA) was added at 1:8,000 dilution in blocking buffer (0.25 ml per well) and incubated for 1 h at room temperature. The wells were washed 4X with 0.5 mL PBS per well. A HRP conjugated Goat anti-Rabbit antibody (Bethyl Labs, Montgomery Texas) diluted 1000X was added per well and incubated for 1h prior to a final round of washing. 5 PBS washes were performed and the plates were developed using DAB (Diaminobenzidine tetrahydrochloride) substrate in Tris buffered saline (0.67 mg/mL DAB in 50 mM Tris pH 7.5, 150 mM NaCl) with 0.01% H_2O_2. Wells were developed for 5 min prior to counting. Cells were counted under a 10X objective using a dilution that gave between 4-40 stained cells per field of view. The field of view that was used was a 0.32 mm^2 grid of which there are equivalent to 625 per field of view on a 24 well plate. The number of infectious

2026201462 26 Feb 2026

viruses/ mL can be determined by the number of stained cells per grid multiplied by the number of grids per field of view multiplied by a dilution factor 10. Similarly, when working with GFP expressing cells florescent can be used rather than capsid staining to determine the number of GFP expressing virions per mL.

Immunizations

[00824] C57BL/6J female mice and Balb/c female mice were injected with $1x10^8$ viral particles (VP) of ChAdV68.5WTnt.MAG25mer in 100 uL volume, bilateral intramuscular injection (50 uL per leg).

Splenocyte dissociation

[00825] Spleen and lymph nodes for each mouse were pooled in 3 mL of complete RPMI (RPMI, 10% FBS, penicillin/streptomycin). Mechanical dissociation was performed using the gentleMACS Dissociator (Miltenyi Biotec), following manufacturer's protocol. Dissociated cells were filtered through a 40 micron filter and red blood cells were lysed with ACK lysis buffer (150mM NH_4Cl, 10mM $KHCO_3$, 0.1mM Na_2EDTA). Cells were filtered again through a 30 micron filter and then resuspended in complete RPMI. Cells were counted on the Attune NxT flow cytometer (Thermo Fisher) using propidium iodide staining to exclude dead and apoptotic cells. Cell were then adjusted to the appropriate concentration of live cells for subsequent analysis.

Ex vivo enzyme-linked immunospot (ELISPOT) analysis

[00826] ELISPOT analysis was performed according to ELISPOT harmonization guidelines {DOI: 10.1038/nprot.2015.068} with the mouse IFNg ELISpotPLUS kit (MABTECH). $5x10^4$ splenocytes were incubated with 10uM of the indicated peptides for 16 hours in 96-well IFNg antibody coated plates. Spots were developed using alkaline phosphatase. The reaction was timed for 10 minutes and was terminated by running plate under tap water. Spots were counted using an AID vSpot Reader Spectrum. For ELISPOT analysis, wells with saturation >50% were recorded as "too numerous to count". Samples with deviation of replicate wells > 10% were excluded from analysis. Spot counts were then corrected for well confluency using the formula: spot count + 2 x (spot count x %confluence /[100% - %confluence]). Negative background was corrected by subtraction of spot counts in the negative peptide stimulation wells from the antigen stimulated wells. Finally, wells labeled too numerous to count were set to the highest observed corrected value, rounded up to the nearest hundred.

2026201462 26 Feb 2026

XV.B.2. Production of ChAdV68 Viral Delivery Particles after DNA Transfection

[00827] In one example, ChAdV68.4WTnt.GFP (Fig. 21) and ChAdV68.5WTnt.GFP (Fig. 22) DNA was transfected into HEK293A cells and virus replication (viral plaques) was observed 7-10 days after transfection. ChAdV68 viral plaques were visualized using light (Fig. 21 A and 22A) and fluorescent microscopy (Fig. 21 B-C and Fig. 22 B-C). GFP denotes productive ChAdV68 viral delivery particle production.

XV.B.3. ChAdV68 Viral Delivery Particles Expansion

[00828] In one example, ChAdV68.4WTnt.GFP, ChAdV68.5WTnt.GFP, and ChAdV68.5WTnt.MAG25mer viruses were expanded in HEK293F cells and a purified virus stock produced 18 days after transfection (Fig 23). Viral particles were quantified in the purified ChAdV68 virus stocks and compared to adenovirus type 5 (Ad5) and ChAdVY25 (a closely related ChAdV; Dicks, 2012, PloS ONE 7, e40385) viral stocks produced using the same protocol. ChAdV68 viral titers were comparable to Ad5 and ChAdVY25 (Table 7).

Table 7. Adenoviral vector production in 293F suspension cells

Construct	Average VP/cell+/- SD
Ad5-Vectors (Multiple vectors)	2.96e4+/- 2.26e4
Ad5-GFP	3.89e4
chAdY25-GFP	1.75e3+/-6.03e1
ChAdV68.4WTnt.GFP	1.2e4 +/-6.5e3
ChAdV68.5WTnt.GFP	1.8e3
ChAdV68.5WTnt.MAG25mer	1.39e3+/-1.1e3

*SD is only reported where multiple Production runs have been performed

XV.B.4. Evaluation of Immunogenicity in Tumor Models

[00829] C68 vector expressing mouse tumor antigens were evaluated in mouse immunogenicity studies to demonstrate the C68 vector elicits T-cell responses. T-cell responses to the MHC class I epitope SIINFEKL were measured in C57BL/6J female mice and the MHC class I epitope AH1-A5 (Slansky et al., 2000, Immunity13:529-538) measured in Balb/c mice. As shown in Fig 29, strong T-cell responses relative to control were measured after immunization of mice with ChAdV68.5WTnt.MAG25mer. Mean cellular immune responses of 8957 or 4019 spot forming cells (SFCs) per 10^6 splenocytes were observed in ELISpot assays when C57BL/6J or Balb/c mice were immunized with ChAdV68.5WTnt.MAG25mer, respectively, 10 days after immunization.

2026201462 26 Feb 2026

XVI. Alphavirus Neoantigen Cassette Delivery Vector

XVI.A. Alphavirus Delivery Vector Evaluation Materials and Methods

In vitro transcription to generate RNA

[00830] ***For in vitro testing***: plasmid DNA was linearized by restriction digest with PmeI, column purified following manufacturer's protocol (GeneJet DNA cleanup kit, Thermo) and used as template. *In vitro* transcription was performed using the RiboMAX Large Scale RNA production System (Promega) with the m^7G cap analog (Promega) according to manufacturer's protocol. mRNA was purified using the RNeasy kit (Qiagen) according to manufacturer's protocol.

[00831] ***For in vivo studies***: RNA was generated and purified by TriLInk Biotechnologies and capped with Enzymatic Cap1.

Transfection of RNA

[00832] HEK293A cells were seeded at 6e4 cells/well for 96 wells and 2e5 cells/well for 24 wells, ~16 hours prior to transfection. Cells were transfected with mRNA using MessengerMAX lipofectamine (Invitrogen) and following manufacturer's protocol. For 96-wells, 0.15 uL of lipofectamine and 10 ng of mRNA was used per well, and for 24-wells, 0.75 uL of lipofectamine and 150 ng of mRNA was used per well. A GFP expressing mRNA (TriLink Biotechnologies) was used as a transfection control.

Luciferase assay

[00833] Luciferase reporter assay was performed in white-walled 96-well plates with each condition in triplicate using the ONE-Glo luciferase assay (Promega) following manufacturer's protocol. Luminescence was measured using the SpectraMax.

qRT-PCR

[00834] Transfected cells were rinsed and replaced with fresh media 2 hours post transfection to remove any untransfected mRNA. Cells were then harvested at various timepoints in RLT plus lysis buffer (Qiagen), homogenized using a QiaShredder (Qiagen) and RNA was extracted using the RNeasy kit (Qiagen), all according to manufacturer's protocol. Total RNA was quantified using a Nanodrop (Thermo Scientific). qRT-PCR was performed using the Quantitect Probe One-Step RT-PCR kit (Qiagen) on the $qTower^3$ (Analytik Jena) according to manufacturer's protocol, using 20 ng of total RNA per reaction. Each sample was run in triplicate for each probe. Actin or GusB were used as reference genes. Custom primer/probes were generated by IDT (Table 8).

2026201462 26 Feb 2026

Table 8. qPCR primers/probes

Target		
Luci	Primer1	GTGGTGTGCAGCGAGAATAG
	Primer2	CGCTCGTTGTAGATGTCGTTAG
	Probe	/56-FAM/TTGCAGTTC/ZEN/TTCATGCCCGTGTTG/3IABkFQ/
GusB	Primer1	GTTTTTGATCCAGACCCAGATG
	Primer2	GCCCATTATTCAGAGCGAGTA
	Probe	/56-FAM/TGCAGGGTT/ZEN/TCACCAGGATCCAC/3IABkFQ/
ActB	Primer1	CCTTGCACATGCCGGAG
	Primer2	ACAGAGCCTCGCCTTTG
	Probe	/56-FAM/TCATCCATG/ZEN/GTGAGCTGGCGG/3IABkFQ/
MAG-25mer	Primer1	CTGAAAGCTCGGTTTGCTAATG
Set1	Primer2	CCATGCTGGAAGAGACAATCT
	Probe	/56-FAM/CGTTTCTGA/ZEN/TGGCGCTGACCGATA/3IABkFQ/
MAG-25mer	Primer1	TATGCCTATCCTGTCTCCTCTG
Set2	Primer2	GCTAATGCAGCTAAGTCCTCTC
	Probe	/56-FAM/TGTTTACCC/ZEN/TGACCGTGCCTTCTG/3IABkFQ/

B16-OVA tumor model

[00835] C57BL/6J mice were injected in the lower left abdominal flank with 10^5 B16-OVA cells/animal. Tumors were allowed to grow for 3 days prior to immunization.

CT26 tumor model

[00836] Balb/c mice were injected in the lower left abdominal flank with 10^6 CT26 cells/animal. Tumors were allowed to grow for 7 days prior to immunization.

Immunizations

[00837] For srRNA vaccine, mice were injected with 10 ug of RNA in 100 uL volume, bilateral intramuscular injection (50 uL per leg). For Ad5 vaccine, mice were injected with $5x10^{10}$ viral particles (VP) in 100 uL volume, bilateral intramuscular injection (50 uL per leg). Animals were injected with anti-CTLA-4 (clone 9D9, BioXcell), anti-PD-1 (clone RMP1-14, BioXcell) or anti-IgG (clone MPC-11, BioXcell), 250 ug dose, 2 times per week, via intraperitoneal injection.

In vivo bioluminescent imaging

2026201462 26 Feb 2026

[00838] At each timepoint mice were injected with 150 mg/kg luciferin substrate via intraperitoneal injection and bioluminescence was measured using the IVIS In vivo imaging system (PerkinElmer) 10-15 minutes after injection.

Splenocyte dissociation

[00839] Spleen and lymph nodes for each mouse were pooled in 3 mL of complete RPMI (RPMI, 10% FBS, penicillin/streptomycin). Mechanical dissociation was performed using the gentleMACS Dissociator (Miltenyi Biotec), following manufacturer's protocol. Dissociated cells were filtered through a 40 micron filter and red blood cells were lysed with ACK lysis buffer (150mM NH_4Cl, 10mM $KHCO_3$, 0.1mM Na_2EDTA). Cells were filtered again through a 30 micron filter and then resuspended in complete RPMI. Cells were counted on the Attune NxT flow cytometer (Thermo Fisher) using propidium iodide staining to exclude dead and apoptotic cells. Cell were then adjusted to the appropriate concentration of live cells for subsequent analysis.

Ex vivo enzyme-linked immunospot (ELISPOT) analysis

[00840] ELISPOT analysis was performed according to ELISPOT harmonization guidelines {DOI: 10.1038/nprot.2015.068} with the mouse IFNg ELISpotPLUS kit (MABTECH). $5x10^4$ splenocytes were incubated with 10uM of the indicated peptides for 16 hours in 96-well IFNg antibody coated plates. Spots were developed using alkaline phosphatase. The reaction was timed for 10 minutes and was terminated by running plate under tap water. Spots were counted using an AID vSpot Reader Spectrum. For ELISPOT analysis, wells with saturation >50% were recorded as "too numerous to count". Samples with deviation of replicate wells > 10% were excluded from analysis. Spot counts were then corrected for well confluency using the formula: spot count + 2 x (spot count x %confluence /[100% - %confluence]). Negative background was corrected by subtraction of spot counts in the negative peptide stimulation wells from the antigen stimulated wells. Finally, wells labeled too numerous to count were set to the highest observed corrected value, rounded up to the nearest hundred.

XVI.B. Alphavirus Vector

XVI.B.1. Alphavirus Vector *in vitro* Evaluation

[00841] In one implementation of the present invention, a RNA alphavirus backbone for the neoantigen expression system was generated from a Venezuelan Equine Encephalitis (VEE) (Kinney, 1986, Virology 152: 400-413) based self-replicating RNA (srRNA) vector. In one example, the sequences encoding the structural proteins of VEE located 3' of the 26S sub-

2026201462 26 Feb 2026

genomic promoter were deleted (VEE sequences 7544 to 11,175 deleted; numbering based on Kinney *et al* 1986; SEQ ID NO:6) and replaced by antigen sequences (SEQ ID NO:14 and SEQ ID NO:4) or a luciferase reporter (e.g., VEE-Luciferase, SEQ ID NO:15) (Fig. 24). RNA was transcribed from the srRNA DNA vector *in vitro*, transfected into HEK293A cells and luciferase reporter expression was measured. In addition, an (non-replicating) mRNA encoding luciferase was transfected for comparison. An ~30,000-fold increase in srRNA reporter signal was observed for VEE-Luciferase srRNA when comparing the 23 hour measurement vs the 2 hour measurement (Table 9). In contrast, the mRNA reporter exhibited a less than 10-fold increase in signal over the same time period (Table 9).

Table 9. Expression of luciferase from VEE self-replicating vector increases over time. HEK293A cells transfected with 10 ng of VEE-Luciferase srRNA or 10 ng of non-replicating luciferase mRNA (TriLink L-6307) per well in 96 wells. Luminescence was measured at various times post transfection. Luciferase expression is reported as relative luminescence units (RLU). Each data point is the mean +/- SD of 3 transfected wells.

Construct	Timepoint (hr)	Mean RLU	Standard Dev (triplicate wells)
mRNA	2	878.6666667	120.7904522
mRNA	5	1847.333333	978.515372
mRNA	9	4847	868.3271273
mRNA	23	8639.333333	751.6816702
SRRNA	2	27	15
SRRNA	5	4884.333333	2955.158935
SRRNA	9	182065.5	16030.81784
SRRNA	23	783658.3333	68985.05538

[00842] In another example, replication of the srRNA was confirmed directly by measuring RNA levels after transfection of either the luciferase encoding srRNA (VEE-Luciferase) or an srRNA encoding a multi-epitope cassette (VEE-MAG25mer) using quantitative reverse transcription polymerase chain reaction (qRT-PCR). An ~150-fold increase in RNA was observed for the VEE-luciferase srRNA (Table 10), while a 30-50-fold increase in RNA was observed for the VEE-MAG25mer srRNA (Table 11). These data confirm that the VEE srRNA vectors replicate when transfected into cells.

26 Feb 2026
2026201462

Table 10. Direct measurement of RNA replication in VEE-Luciferase srRNA transfected cells. HEK293A cells transfected with VEE-Luciferase srRNA (150 ng per well, 24-well) and RNA levels quantified by qRT-PCR at various times after transfection. Each measurement was normalized based on the Actin reference gene and fold-change relative to the 2 hour timepoint is presented.

Timepoint (hr)	Luciferase Ct	Actin Ct	dCt	Ref dCt	ddCt	Relative Fold change
2	20.51	18.14	2.38	2.38	0.00	1.00
4	20.09	18.39	1.70	2.38	-0.67	1.59
6	15.50	18.19	-2.69	2.38	-5.07	33.51
8	13.51	18.36	-4.85	2.38	-7.22	149.43

Table 11. Direct measurement of RNA replication in VEE-MAG25mer srRNA transfected cells. HEK293 cells transfected with VEE-MAG25mer srRNA (150 ng per well, 24-well) and RNA levels quantified by qRT-PCR at various times after transfection. Each measurement was normalized based on the GusB reference gene and fold-change relative to the 2 hour timepoint is presented. Different lines on the graph represent 2 different qPCR primer/probe sets, both of which detect the epitope cassette region of the srRNA.

Primer/ probe	Timepoint (hr)	Ct	GusB Ct	dCt	Ref dCt	ddCt	Relative Fold-Change
Set1	2	18.96	22.41	-3.45	-3.45	0.00	1.00
Set1	4	17.46	22.27	-4.81	-3.45	-1.37	2.58
Set1	6	14.87	22.04	-7.17	-3.45	-3.72	13.21
Set1	8	14.16	22.19	-8.02	-3.45	-4.58	23.86
Set1	24	13.16	22.01	-8.86	-3.45	-5.41	42.52
Set1	36	13.53	22.63	-9.10	-3.45	-5.66	50.45
Set2	2	17.75	22.41	-4.66	-4.66	0.00	1.00
Set2	4	16.66	22.27	-5.61	-4.66	-0.94	1.92
Set2	6	14.22	22.04	-7.82	-4.66	-3.15	8.90
Set2	8	13.18	22.19	-9.01	-4.66	-4.35	20.35
Set2	24	12.22	22.01	-9.80	-4.66	-5.13	35.10
Set2	36	13.08	22.63	-9.55	-4.66	-4.89	29.58

XVI.B.2. Alphavirus Vector *in vivo* Evaluation

[00843] In another example, VEE-Luciferase reporter expression was evaluated *in vivo*. Mice were injected with 10 ug of VEE-Luciferase srRNA encapsulated in lipid nanoparticle (MC3) and imaged at 24 and 48 hours, and 7 and 14 days post injection to determine

2026201462 26 Feb 2026

bioluminescent signal. Luciferase signal was detected at 24 hours post injection and increased over time and appeared to peak at 7 days after srRNA injection (Fig. 25).

XVI.B.3. Alphavirus Vector Tumor Model Evaluation

[00844] In one implementation, to determine if the VEE srRNA vector directs antigen-specific immune responses *in vivo*, a VEE srRNA vector was generated (VEE-UbAAY, SEQ ID NO:14) that expresses 2 different MHC class I mouse tumor epitopes, SIINFEKL and AH1-A5 (Slansky et al., 2000, Immunity 13:529-538). The SFL (SIINFEKL) epitope is expressed by the B16-OVA melanoma cell line, and the AH1-A5 (SPSYAYHQF; Slansky et al., 2000, Immunity) epitope induces T cells targeting a related epitope (AH1/ SPSYVYHQF; Huang et al., 1996, Proc Natl Acad Sci USA 93:9730-9735) that is expressed by the CT26 colon carcinoma cell line. In one example, for *in vivo* studies, VEE-UbAAY srRNA was generated by *in vitro* transcription using T7 polymerase (TriLink Biotechnologies) and encapsulated in a lipid nanoparticle (MC3).

[00845] A strong antigen-specific T-cell response targeting SFL, relative to control, was observed two weeks after immunization of B16-OVA tumor bearing mice with MC3 formulated VEE-UbAAY srRNA. In one example, a median of 3835 spot forming cells (SFC) per 10^6 splenocytes was measured after stimulation with the SFL peptide in ELISpot assays (Fig. 26A, Table 12) and 1.8% (median) of CD8 T-cells were SFL antigen-specific as measured by pentamer staining (Fig. 26B, Table 12). In another example, co-administration of an anti-CTLA-4 monoclonal antibody (mAb) with the VEE srRNA vaccine resulted in a moderate increase in overall T-cell responses with a median of 4794.5 SFCs per 10^6 splenocytes measured in the ELISpot assay (Fig. 26A, Table 12).

2026201462 26 Feb 2026

Table 12. Results of ELISPOT and MHCI-pentamer staining assays 14 days post VEE srRNA immunization in B16-OVA tumor bearing C57BL/6J mice.

Group	Mouse	SFC/1e6 splenocytes	Pentamer positive (% of CD8)	Group	Mouse	SFC/1e6 splenocytes	Pentamer positive (% of CD8)
Control	1	47	0.22	Vax	1	6774	4.92
	2	80	0.32		2	2323	1.34
	3	0	0.27		3	2997	1.52
	4	0	0.29		4	4492	1.86
	5	0	0.27		5	4970	3.7
	6	0	0.25		6		4.13
	7	0	0.23		7	3835	1.66
	8	87	0.25		8	3119	1.64
aCTLA4	1	0	0.24	Vax + aCTLA4	1	6232	2.16
	2	0	0.26		2	4242	0.82
	3	0	0.39		3	5347	1.57
	4	0	0.28		4	6568	2.33
	5	0	0.28		5	6269	1.55
	6	0	0.28		6	4056	1.74
	7	0	0.31		7	4163	1.14
	8	6	0.26		8	3667	1.01

***** *Note that results from mouse #6 in the Vax group were excluded from analysis due to high variability between triplicate wells.*

[00846] In another implementation, to mirror a clinical approach, a heterologous prime/boost in the B16-OVA and CT26 mouse tumor models was performed, where tumor bearing mice were immunized first with adenoviral vector expressing the same antigen cassette (Ad5-UbAAY), followed by a boost immunization with the VEE-UbAAY srRNA vaccine 14 days after the Ad5-UbAAY prime. In one example, an antigen-specific immune response was induced by the Ad5-UbAAY vaccine resulting in 7330 (median) SFCs per 10^6 splenocytes measured in the ELISpot assay (Fig. 27A, Table 13) and 2.9% (median) of CD8 T-cells targeting the SFL antigen as measured by pentamer staining (Fig. 27C, Table 13). In another example, the T-cell response was maintained 2 weeks after the VEE-UbAAY srRNA boost in the B16-OVA model with 3960 (median) SFL-specific SFCs per 10^6 splenocytes measured in the ELISpot assay (Fig. 27B, Table 13) and 3.1% (median) of CD8 T-cells targeting the SFL antigen as measured by pentamer staining (Fig. 27D, Table 13).

2026201462 26 Feb 2026

Table 13. Immune monitoring of B16-OVA mice following heterologous prime/boost with Ad5 vaccine prime and srRNA boost.

Day 14

Group	Mouse	SFC/1e6 splenocytes	Pentamer positive (% of CD8)	Group	Mouse	SFC/1e6 splenocytes	Pentamer positive (% of CD8)
Control	1	0	0.10	Vax	1	8514	1.87
	2	0	0.09		2	7779	1.91
	3	0	0.11		3	6177	3.17
	4	46	0.18		4	7945	3.41
	5	0	0.11		5	8821	4.51
	6	16	0.11		6	6881	2.48
	7	0	0.24		7	5365	2.57
	8	37	0.10		8	6705	3.98
aCTLA4	1	0	0.08	Vax + aCTLA4	1	9416	2.35
	2	29	0.10		2	7918	3.33
	3	0	0.09		3	10153	4.50
	4	29	0.09		4	7212	2.98
	5	0	0.10		5	11203	4.38
	6	49	0.10		6	9784	2.27
	7	0	0.10		8	7267	2.87
	8	31	0.14				

Day 28

Group	Mouse	SFC/1e6 splenocytes	Pentamer positive (% of CD8)	Group	Mouse	SFC/1e6 splenocytes	Pentamer positive (% of CD8)
Control	2	0	0.17	Vax	1	5033	2.61
	4	0	0.15		2	3958	3.08
	6	20	0.17		4	3960	3.58
aCTLA4	1	7	0.23	Vax + aCTLA4	4	3460	2.44
	2	0	0.18		5	5670	3.46
	3	0	0.14				

[00847] In another implementation, similar results were observed after an Ad5-UbAAY prime and VEE-UbAAY srRNA boost in the CT26 mouse model. In one example, an AH1 antigen-specific response was observed after the Ad5-UbAAY prime (day 14) with a mean of 5187 SFCs per 10^6 splenocytes measured in the ELISpot assay (Fig. 28A, Table 14) and 3799 SFCs per 10^6 splenocytes measured in the ELISpot assay after the VEE-UbAAY srRNA boost (day 28) (Fig. 28B, Table 14).

2026201462 26 Feb 2026

Table 14. Immune monitoring after heterologous prime/boost in CT26 tumor mouse model.

Day 12			Day 21		
Group	**Mouse**	**SFC/1e6 splenocytes**	**Group**	**Mouse**	**SFC/1e6 splenocytes**
Control	1	1799	Control	9	167
	2	1442		10	115
	3	1235		11	347
aPD1	1	737	aPD1	8	511
	2	5230		11	758
	3	332	Vax	9	3133
Vax	1	6287		10	2036
	2	4086		11	6227
Vax + aPD1	1	5363	Vax + aPD1	8	3844
	2	6500		9	2071
				11	4888

XVII. ChAdV/srRNA Combination Tumor Model Evaluation

[00848] Various dosing protocols using ChAdV68 and self-replicating RNA (srRNA) were evaluated in murine CT26 tumor models.

XVII.A ChAdV/srRNA Combination Tumor Model Evaluation Methods and Materials

Tumor Injection

[00849] Balb/c mice were injected with the CT26 tumor cell line. 7 days after tumor cell injection, mice were randomized to the different study arms (28-40 mice per group) and treatment initiated. Balb/c mice were injected in the lower left abdominal flank with 10^6 CT26 cells/animal. Tumors were allowed to grow for 7 days prior to immunization. The study arms are described in detail in Table 15.

2026201462 26 Feb 2026

Table 15 - ChAdV/srRNA Combination Tumor Model Evaluation Study Arms

Group	N	Treatment	Dose	Volume	Schedule	Route
1	40	chAd68 control	1e11 vp	2x 50 uL	day 0	IM
		srRNA control	10 ug	50 uL	day 14, 28, 42	IM
		Anti-PD1	250 ug	100 uL	2x / week (start day 0)	IP
2	40	chAd68 control	1e11 vp	2x 50 uL	day 0	IM
		srRNA control	10 ug	50 uL	day 14, 28, 42	IM
		Anti-IgG	250 ug	100 uL	2x / week (start day 0)	IP
3	28	chAd68 vaccine	1e11 vp	2x 50 uL	day 0	IM
		srRNA vaccine	10 ug	50 uL	day 14, 28, 42	IM
		Anti-PD1	250 ug	100 uL	2x / week (start day 0)	IP
4	28	chAd68 vaccine	1e11 vp	2x 50 uL	day 0	IM
		srRNA vaccine	10 ug	50 uL	day 14, 28, 42	IM
		Anti-IgG	250 ug	100 uL	2x / week (start day 0)	IP
5	28	srRNA vaccine	10 ug	50 uL	day 0, 28, 42	IM
		chAd68 vaccine	1e11 vp	2x 50 uL	day 14	IM
		Anti-PD1	250 ug	100 uL	2x / week (start day 0)	IP
6	28	srRNA vaccine	10 ug	50 uL	day 0, 28, 42	IM
		chAd68 vaccine	1e11 vp	2x 50 uL	day 14	IM
		Anti-IgG	250 ug	100 uL	2x / week (start day 0)	IP
7	40	srRNA vaccine	10 ug	50 uL	day 0, 14, 28, 42	IM
		Anti-PD1	250 ug	100 uL	2x / week (start day 0)	IP
8	40	srRNA vaccine	10 ug	50 uL	day 0, 14, 28, 42	IM
		Anti-IgG	250 ug	100 uL	2x / week (start day 0)	IP

Immunizations

[00850] For srRNA vaccine, mice were injected with 10 ug of VEE-MAG25mer srRNA in 100 uL volume, bilateral intramuscular injection (50 uL per leg). For C68 vaccine, mice were injected with $1x10^{11}$ viral particles (VP) of ChAdV68.5WTnt.MAG25mer in 100 uL volume, bilateral intramuscular injection (50 uL per leg). Animals were injected with anti-PD-1 (clone RMP1-14, BioXcell) or anti-IgG (clone MPC-11, BioXcell), 250 ug dose, 2 times per week, via intraperitoneal injection.

Splenocyte dissociation

[00851] Spleen and lymph nodes for each mouse were pooled in 3 mL of complete RPMI (RPMI, 10% FBS, penicillin/streptomycin). Mechanical dissociation was performed using the gentleMACS Dissociator (Miltenyi Biotec), following manufacturer's protocol. Dissociated cells were filtered through a 40 micron filter and red blood cells were lysed with ACK lysis

26 Feb 2026
2026201462

buffer (150mM NH_4Cl, 10mM $KHCO_3$, 0.1mM Na_2EDTA). Cells were filtered again through a 30 micron filter and then resuspended in complete RPMI. Cells were counted on the Attune NxT flow cytometer (Thermo Fisher) using propidium iodide staining to exclude dead and apoptotic cells. Cell were then adjusted to the appropriate concentration of live cells for subsequent analysis.

Ex vivo enzyme-linked immunospot (ELISPOT) analysis

[00852] ELISPOT analysis was performed according to ELISPOT harmonization guidelines {DOI: 10.1038/nprot.2015.068} with the mouse IFNg ELISpotPLUS kit (MABTECH). $5x10^4$ splenocytes were incubated with 10uM of the indicated peptides for 16 hours in 96-well IFNg antibody coated plates. Spots were developed using alkaline phosphatase. The reaction was timed for 10 minutes and was terminated by running plate under tap water. Spots were counted using an AID vSpot Reader Spectrum. For ELISPOT analysis, wells with saturation >50% were recorded as "too numerous to count". Samples with deviation of replicate wells > 10% were excluded from analysis. Spot counts were then corrected for well confluency using the formula: spot count + 2 x (spot count x %confluence /[100% - %confluence]). Negative background was corrected by subtraction of spot counts in the negative peptide stimulation wells from the antigen stimulated wells. Finally, wells labeled too numerous to count were set to the highest observed corrected value, rounded up to the nearest hundred.

XVII.B ChAdV/srRNA Combination Evaluation in a CT26 Tumor Model

[00853] The immunogenicity and efficacy of the ChAdV68.5WTnt.MAG25mer/ VEE-MAG25mer srRNA heterologous prime/boost or VEE-MAG25mer srRNA homologous prime/boost vaccines were evaluated in the CT26 mouse tumor model. Balb/c mice were injected with the CT26 tumor cell line. 7 days after tumor cell injection, mice were randomized to the different study arms and treatment initiated. The study arms are described in detail in Table 15 and more generally in Table 16.

2026201462 26 Feb 2026

Table 16 – Prime/Boost Study Arms

Group	Prime	Boost
1	Control	Control
2	Control + anti-PD-1	Control + anti-PD-1
3	ChAdV68.5WTnt.MAG25mer	VEE-MAG25mer srRNA
4	ChAdV68.5WTnt.MAG25mer + anti-PD-1	VEE-MAG25mer srRNA + anti-PD-1
5	VEE-MAG25mer srRNA	ChAdV68.5WTnt.MAG25mer
6	VEE-MAG25mer srRNA + anti-PD-1	ChAdV68.5WTnt.MAG25mer + anti-PD-1
7	VEE-MAG25mer srRNA	VEE-MAG25mer srRNA
8	VEE-MAG25mer srRNA + anti-PD-1	VEE-MAG25mer srRNA + anti-PD-1

[00854] Spleens were harvested 14 days after the prime vaccination for immune monitoring. Tumor and body weight measurements were taken twice a week and survival was monitored. Strong immune responses relative to control were observed in all active vaccine groups.

[00855] Median cellular immune responses of 10,630, 12,976, 3319, or 3745 spot forming cells (SFCs) per 10^6 splenocytes were observed in ELISpot assays in mice immunized with ChAdV68.5WTnt.MAG25mer (ChAdV/group 3), ChAdV68.5WTnt.MAG25mer + anti-PD-1 (ChAdV + PD-1/group 4), VEE-MAG25mer srRNA (srRNA/median for groups 5 & 7 combined), or VEE-MAG25mer srRNA + anti-PD-1 (srRNA + PD-1/median for groups 6 & 8 combined), respectively, 14 days after the first immunization (Fig. 30 and Table 17). In contrast, the vaccine control (group 1) or vaccine control with anti-PD-1 (group 2) exhibited median cellular immune responses of 296 or 285 SFC per 10^6 splenocytes, respectively.

2026201462 26 Feb 2026

Table 17 – Cellular immune responses in a CT26 tumor model

Treatment	Median SFC/10^6 Splenocytes
Control	296
PD1	285
ChAdV68.5WTnt.MAG25mer (ChAdV)	10630
ChAdV68.5WTnt.MAG25mer + PD1 (ChAdV + PD-1)	12976
VEE-MAG25mer srRNA (srRNA)	3319
VEE-MAG25mer srRNA + PD-1 (srRNA + PD1)	3745

[00856] Consistent with the ELISpot data, 5.6, 7.8, 1.8 or 1.9% of CD8 T cells (median) exhibited antigen-specific responses in intracellular cytokine staining (ICS) analyses for mice immunized with ChAdV68.5WTnt.MAG25mer (ChAdV/group 3), ChAdV68.5WTnt.MAG25mer + anti-PD-1 (ChAdV + PD-1/group 4), VEE-MAG25mer srRNA (srRNA/median for groups 5 & 7 combined), or VEE-MAG25mer srRNA + anti-PD-1 (srRNA + PD-1/median for groups 6 & 8 combined), respectively, 14 days after the first immunization (Fig. 31 and Table 18). Mice immunized with the vaccine control or vaccine control combined with anti-PD-1 showed antigen-specific CD8 responses of 0.2 and 0.1%, respectively.

Table 18 - CD8 T-Cell responses in a CT26 tumor model

Treatment	Median % CD8 IFN-gamma Positive
Control	0.21
PD1	0.1
ChAdV68.5WTnt.MAG25mer (ChAdV)	5.6
ChAdV68.5WTnt.MAG25mer + PD1 (ChAdV + PD-1)	7.8
VEE-MAG25mer srRNA (srRNA)	1.8
VEE-MAG25mer srRNA + PD-1 (srRNA + PD1)	1.9

[00857] Tumor growth was measured in the CT26 colon tumor model for all groups, and tumor growth up to 21 days after treatment initiation (28 days after injection of CT-26 tumor cells) is presented. Mice were sacrificed 21 days after treatment initiation based on large tumor

2026201462 26 Feb 2026

sizes (>2500 mm^3); therefore, only the first 21 days are presented to avoid analytical bias. Mean tumor volumes at 21 days were 1129, 848, 2142, 1418, 2198 and 1606 mm^3 for ChAdV68.5WTnt.MAG25mer prime/ VEE-MAG25mer srRNA boost (group 3), ChAdV68.5WTnt.MAG25mer prime/ VEE-MAG25mer srRNA boost + anti-PD-1 (group 4), VEE-MAG25mer srRNA prime/ ChAdV68.5WTnt.MAG25mer boost (group 5), VEE-MAG25mer srRNA prime / ChAdV68.5WTnt.MAG25mer boost + anti-PD-1 (group 6), VEE-MAG25mer srRNA prime/ VEE-MAG25mer srRNA boost (group 7) and VEE-MAG25mer srRNA prime/ VEE-MAG25mer srRNA boost + anti-PD-1 (group 8), respectively (Fig. 32 and Table 19). The mean tumor volumes in the vaccine control or vaccine control combined with anti-PD-1 were 2361 or 2067 mm^3, respectively. Based on these data, vaccine treatment with ChAdV68.5WTnt.MAG25mer / VEE-MAG25mer srRNA (group 3), ChAdV68.5WTnt.MAG25mer / VEE-MAG25mer srRNA + anti-PD-1 (group 4), VEE-MAG25mer srRNA/ ChAdV68.5WTnt.MAG25mer + anti-PD-1 (group 6) and VEE-MAG25mer srRNA/ VEE-MAG25mer srRNA + anti-PD-1 (group 8) resulted in a reduction of tumor growth at 21 days that was significantly different from the control (group 1).

Table 19 - Tumor size at day 21 measured in the CT26 model

Treatment	**Tumor Size (mm^3)**	**SEM**
Control	2361	235
PD1	2067	137
chAdV/srRNA	1129	181
chAdV/srRNA + PD1	848	182
srRNA/chAdV	2142	233
srRNA/chAdV + PD1	1418	220
srRNA	2198	134
srRNA + PD1	1606	210

[00858] Survival was monitored for 35 days after treatment initiation in the CT-26 tumor model (42 days after injection of CT-26 tumor cells). Improved survival was observed after vaccination of mice with 4 of the combinations tested. After vaccination, 64%, 46%, 41% and 36% of mice survived with ChAdV68.5WTnt.MAG25mer prime/ VEE-MAG25mer srRNA boost in combination with anti-PD-1 (group 4; $P<0.0001$ relative to control group 1), VEE-MAG25mer srRNA prime/ VEE-MAG25mer srRNA boost in combination with anti-PD-1 (group 8; $P=0.0006$ relative to control group 1), ChAdV68.5WTnt.MAG25mer prime/ VEE-

2026201462 26 Feb 2026

MAG25mer srRNA boost (group 3; P=0.0003 relative to control group 1) and VEE-MAG25mer srRNA prime/ ChAdV68.5WTnt.MAG25mer boost in combination with anti-PD-1 (group 6; P=0.0016 relative to control group 1), respectively (Fig. 33 and Table 20). Survival was not significantly different from the control group 1 (≤14%) for the remaining treatment groups [VEE-MAG25mer srRNAprime/ ChAdV68.5WTnt.MAG25mer boost (group 5), VEE-MAG25mer srRNA prime/ VEE-MAG25mer srRNA boost (group 7) and anti-PD-1 alone (group 2)].

Table 20 - Survival in the CT26 model

Timepoint	Control	PD1	chAdV/ srRNA	chAdV/ srRNA + PD1	srRNA/ chAdV	srRNA/ chAdV + PD1	srRNA	srRNA + PD1
0	100	100	100	100.00	100.00	100	100	100
21	96	100	100	100	100	95	100	100
24	54	64	91	100	68	82	68	71
28	21	32	68	86	45	68	21	64
31	7	14	41	64	14	36	11	46
35	7	14	41	64	14	36	11	46

[00859] In conclusion, ChAdV68.5WTnt.MAG25mer and VEE-MAG25mer srRNA elicited strong T-cell responses to mouse tumor antigens encoded by the vaccines, relative to control. Administration of a ChAdV68.5WTnt.MAG25mer prime and VEE-MAG25mer srRNA boost with or without co-administration of anti-PD-1, VEE-MAG25mer srRNA prime and ChAdV68.5WTnt.MAG25mer boost in combination with anti-PD-1 or administration of VEE-MAG25mer srRNA as a homologous prime boost immunization in combination with anti-PD-1 to tumor bearing mice resulted in improved survival.

XVIII. Non-Human Primate Studies

[00860] Various dosing protocols using ChAdV68 and self-replicating RNA (srRNA) were evaluated in non-human primates (NHP).

Materials and Methods

[00861] A priming vaccine was injected intramuscularly (IM) in each NHP to initiate the study (vaccine prime). One or more boosting vaccines (vaccine boost) were also injected

2026201462 26 Feb 2026

intramuscularly in each NHP. Bilateral injections per dose were administered according to groups outlined in tables and summarized below.

Immunizations

[00862] Mamu-A*01 Indian rhesus macaques were immunized bilaterally with $1x10^{12}$ viral particles ($5x10^{11}$ viral particles per injection) of ChAdV68.5WTnt.MAG25mer, 30 ug of VEE-MAG25MER srRNA, 100 ug of VEE-MAG25mer srRNA or 300 ug of VEE-MAG25mer srRNA formulated in LNP-1 or LNP-2. Vaccine boosts of 30 ug, 100 ug or 300 ug VEE-MAG25mer srRNA were administered intramuscularly at the indicated time after prime vaccination.

Immune Monitoring

[00863] PBMCs were isolated at indicated times after prime vaccination using Lymphocyte Separation Medium (LSM, MP Biomedicals) and LeucoSep separation tubes (Greiner Bio-One) and resuspended in RPMI containing 10% FBS and penicillin/streptomycin. Cells were counted on the Attune NxT flow cytometer (Thermo Fisher) using propidium iodide staining to exclude dead and apoptotic cells. Cell were then adjusted to the appropriate concentration of live cells for subsequent analysis. For each monkey in the studies, T cell responses were measured using ELISpot or flow cytometry methods. T cell responses to 6 different rhesus macaque Mamu-A*01 class I epitopes encoded in the vaccines were monitored from PBMCs by measuring induction of cytokines, such as IFN-gamma, using ex vivo enzyme-linked immunospot (ELISpot) analysis. ELISpot analysis was performed according to ELISPOT harmonization guidelines {DOI: 10.1038/nprot.2015.068} with the monkey IFNg ELISpotPLUS kit (MABTECH). 200,000 PBMCs were incubated with 10uM of the indicated peptides for 16 hours in 96-well IFNg antibody coated plates. Spots were developed using alkaline phosphatase. The reaction was timed for 10 minutes and was terminated by running plate under tap water. Spots were counted using an AID vSpot Reader Spectrum. For ELISPOT analysis, wells with saturation >50% were recorded as “too numerous to count”. Samples with deviation of replicate wells > 10% were excluded from analysis. Spot counts were then corrected for well confluency using the formula: spot count + 2 x (spot count x %confluence /[100% - %confluence]). Negative background was corrected by subtraction of spot counts in the negative peptide stimulation wells from the antigen stimulated wells. Finally, wells labeled too numerous to count were set to the highest observed corrected value, rounded up to the nearest hundred.

2026201462 26 Feb 2026

[00864] Specific CD4 and CD8 T cell responses to 6 different rhesus macaque Mamu-A*01 class I epitopes encoded in the vaccines were monitored from PBMCs by measuring induction of intracellular cytokines, such as IFN-gamma, using flow cytometry. The results from both methods indicate that cytokines were induced in an antigen-specific manner to epitopes.

Immunogenicity in rhesus macaques

[00865] This study was designed to (a) evaluate the immunogenicity and preliminary safety of VEE-MAG25mer srRNA 30 µg and 100 µg doses as a homologous prime/boost or heterologous prime/boost in combination with ChAdV68.5WTnt.MAG25mer; (b) compare the immune responses of VEE-MAG25mer srRNA in lipid nanoparticles using LNP1 versus LNP2; (c) evaluate the kinetics of T-cell responses to VEE-MAG25mer srRNA and ChAdV68.5WTnt.MAG25mer immunizations.

[00866] The study arm was conducted in Mamu-A*01 Indian rhesus macaques to demonstrate immunogenicity. Select antigens used in this study are only recognized in Rhesus macaques, specifically those with a Mamu-A*01 MHC class I haplotype. Mamu-A*01 Indian rhesus macaques were randomized to the different study arms (6 macaques per group) and administered an IM injection bilaterally with either ChAdV68.5WTnt.MAG25mer or VEE-MAG25mer srRNA vector encoding model antigens that includes multiple Mamu-A*01 restricted epitopes. The study arms were as described below.

[00867] **Table 21:** Non-GLP immunogenicity study in Indian Rhesus Macaques

2026201462 26 Feb 2026

Group	Prime	Boost 1	Boost 2
1	VEE-MAG25mer srRNA -LNP1(30 µg)	VEE-MAG25mer srRNA -LNP1 (30 µg)	VEE-MAG25mer srRNA -LNP1 (30 µg)
2	VEE-MAG25mer srRNA -LNP1 (100 µg)	VEE-MAG25mer srRNA -LNP1 (100 µg)	VEE-MAG25mer srRNA -LNP1 (100 µg)
3	VEE-MAG25mer srRNA -LNP2 (100 µg)	VEE-MAG25mer srRNA -LNP2 (100 µg)	VEE-MAG25mer srRNA -LNP2 (100 µg)
4	ChAdV68.5WTnt .MAG25mer	VEE-MAG25mer srRNA -LNP1 (100 µg)	VEE-MAG25mer srRNA -LNP1 (100 µg)

[00868] PBMCs were collected prior to immunization and on weeks 1, 2, 3, 4, 5, 6, 8, 9, and 10 after the initial immunization for immune monitoring.

Results

[00869] Antigen-specific cellular immune responses in peripheral blood mononuclear cells (PBMCs) were measured to six different Mamu-A*01 restricted epitopes prior to immunization and 1, 2, 3, 4, 5, 6, 8, 9, and 10 weeks after the initial immunization. Animals received a boost immunization with VEE-MAG25mer srRNA on weeks 4 and 8 with either 30 µg or 100 µg doses, and either formulated with LNP1 or LNP2, as described in Table 21. Combined immune responses to all six epitopes were plotted for each immune monitoring timepoint (FIG. 34A-D and Tables 22-25).

[00870] Combined antigen-specific immune responses were observed at all measurements with 170, 14, 15, 11, 7, 8, 14, 17, 12 SFCs per 10^6 PBMCs (six epitopes combined) 1, 2, 3, 4, 5, 6, 8, 9, or 10 weeks after an initial VEE-MAG25mer srRNA-LNP1(30 µg) prime immunization, respectively (FIG. 34A). Combined antigen-specific immune responses were observed at all measurements with 108, -3, 14, 1, 37, 4, 105, 17, 25 SFCs per 10^6 PBMCs (six epitopes combined) 1, 2, 3, 4, 5, 6, 8, 9, or 10 weeks after an initial VEE-MAG25mer srRNA-LNP1(100 µg) prime immunization, respectively (FIG. 34B). Combined antigen-specific

2026201462 26 Feb 2026

immune responses were observed at all measurements with -17, 38, 14, -2, 87, 21, 104, 129, 89 SFCs per 10^6 PBMCs (six epitopes combined) 1, 2, 3, 4, 5, 6, 8, 9, or 10 weeks after an initial VEE-MAG25mer srRNA-LNP2(100 μg) prime immunization, respectively (FIG. 34C). Negative values are a result of normalization to pre-bleed values for each epitope/animal.

[00871] Combined antigen-specific immune responses were observed at all measurements with 1218, 1784, 1866, 973, 1813, 747, 797, 1249, and 547 SFCs per 10^6 PBMCs (six epitopes combined) 1, 2, 3, 4, 5, 6, 8, 9, or 10 weeks after an initial ChAdV68.5WTnt.MAG25mer prime immunization, respectively (FIG. 34D). The immune response showed the expected profile with peak immune responses measured ~2-3 weeks after the prime immunization followed by a contraction in the immune response after 4 weeks. Combined antigen-specific cellular immune responses of 1813 SFCs per 10^6 PBMCs (six epitopes combined) were measured 5 weeks after the initial immunization with ChAdV68.5WTnt.MAG25mer (i.e., 1 week after the first boost with VEE-MAG25mer srRNA). The immune response measured 1 week after the first boost with VEE-MAG25mer srRNA (week 5) was comparable to the peak immune response measured for the ChAdV68.5WTnt.MAG25mer prime immunization (week 3) (FIG. 34D). Combined antigen-specific cellular immune responses of 1249 SFCs per 10^6 PBMCs (six epitopes combined) was measured 9 weeks after the initial immunization with ChAdV68.5WTnt.MAG25mer, respectivley (i.e., 1 week after the second boost with VEE-MAG25mer srRNA). The immune responses measured 1 week after the second boost with VEE-MAG25mer srRNA (week 9) was ~2-fold higher than that measured just before the boost immunization (FIG. 34D).

2026201462 26 Feb 2026

[00872] **Table 22**: Mean spot forming cells (SFC) per 10^6 PBMCs for each epitope ± SEM for VEE-MAG25mer srRNA-LNP1(30 μg) (Group 1)

Wk	Antigen					
	Env CL9	Env TL9	Gag CM9	Gag LW9	Pol SV9	Tat TL8
1	0±0	0±0	0±0	0±0	0±0	0±0
2	39.7±22.7	35.4±25.1	3.2±3.6	33±28.1	30.9±20.3	28.3±17.5
3	2±2.4	0.2±1.8	1.8±2.4	3.7±1.9	1.7±2.8	4.9±2.3
4	1±1.8	0.3±1.2	5.5±3.6	2.3±2.2	5.7±2.7	0.8±0.8
5	0.5±0.9	1.4±3.8	3.1±1.6	2.3±2.7	1.9±2	1.4±1.2
6	1.9±1.8	-0.3±3	1.7±1.2	1.4±1.4	0.8±1.1	1.1±1
8	-0.4±0.8	-0.9±2.9	0.5±1.3	3±1.1	2.2±2.1	3.7±2
9	1±1.7	1.2±4.2	7.2±3.9	0.5±0.7	1.6±3	3±1
10	3.8±1.8	11±5	-1.1±1.1	1.9±0.9	1.3±1.6	0.2±0.5

[00873] **Table 23**: Mean spot forming cells (SFC) per 10^6 PBMCs for each epitope ± SEM for VEE-MAG25mer srRNA-LNP1(100 μg) (Group 2)

Wk	Antigen					
	Env CL9	Env TL9	Gag CM9	Gag LW9	Pol SV9	Tat TL8
1	0±0	0±0	0±0	0±0	0±0	0±0
2	7.9±17.2	23.2±17.4	11.4±4.9	41.7±16.5	15±13.5	8.9±6.2
3	-3.1±4.6	-7.2±6.5	2.3±2.3	-0.3±2.7	2.7±5.1	2.2±1.4
4	1.9±3.8	-6.2±7.6	10.5±4.1	1.2±2.9	5.6±4.9	1.1±0.8
5	-2.6±7	-8±5.9	1.5±1.7	6.4±2.3	0.7±4.3	3.3±1.3
6	6.3±6.3	4.4±8.3	6.6±4.4	5.2±5.2	3.9±5	10.8±6.9
8	-3.6±7.2	-6.8±7.3	-0.8±1.2	3.4±4.2	6.4±7.5	5.7±2.7
9	8.1±2.4	20.6±23.4	18.9±5.7	8.1±8.9	9±11.2	40±17.6
10	3.1±8	-3.9±8.5	3.3±1.8	0.6±2.9	7.4±6.4	6.1±2.5

2026201462 26 Feb 2026

[00874] **Table 24**: Mean spot forming cells (SFC) per 10^6 PBMCs for each epitope ± SEM for VEE-MAG25mer srRNA-LNP2(100 μg) (Group 3)

Wk	Antigen					
	Env CL9	Env TL9	Gag CM9	Gag LW9	Pol SV9	Tat TL8
1	0±0	0±0	0±0	0±0	0±0	0±0
2	-5.9±3.8	-0.3±0.5	-0.5±1.5	-5.7±6.1	-1±1.3	-3.2±5.5
3	0.7±5.2	3.4±2.4	4.2±4.6	18.3±15.5	11.9±5.1	-0.4±8.2
4	-3.8±5.5	2.3±1.8	11.3±6.1	-3.1±5.6	8.5±4	-1.5±6.1
5	-3.7±5.7	-0.1±0.7	-0.2±1.6	3.4±8.5	3±3.1	-4.6±5
6	12.3±15	7.8±4.9	24.7±19.8	23.2±22.5	18.7±15.8	0.5±6.2
8	5.9±12.3	-0.1±0.7	-0.5±1.3	8.8±14.4	8.7±8	-1.3±4
9	16.1±13.4	16.5±4	22.9±4.2	13±13.2	16.4±7.8	19.6±9.2
10	29.9±21.8	22±19.5	0.5±2.6	22.2±22.6	35.3±15.8	19.4±17.3

[00875] **Table 25**: Mean spot forming cells (SFC) per 10^6 PBMCs for each epitope ± SEM for ChAdV68.5WTnt.MAG25mer prime

Wk	Antigen					
	Env CL9	Env TL9	Gag CM9	Gag LW9	Pol SV9	Tat TL8
1	178±68.7	206.5±94.8	221.2±120	15.4±16.7	33.3±25.9	563.5±174.4
2	311.2±165.5	278.8±100.9	344.6±110.8	46.3±13.5	181.6±76.8	621.4±220.9
3	277.3±101.1	359.6±90.5	468.2±106.6	41.7±11.1	169.8±57.8	549.4±115.7
4	140±46.5	169.6±46.8	239.4±37	26.5±11.4	75±31.6	322.2±50.7
5	155.6±62.1	406.7±96.4	542.7±143.3	35.1±16.6	134.2±53.7	538.5±91.9
6	78.9±42.5	95.5±29.4	220.9±75.3	-1.4±5.3	43.4±19.6	308.1±42.6
8	88.4±30.4	162.1±30.3	253.4±78.6	21.4±11.2	53.7±22.3	217.8±45.2
9	158.5±69	322.3±87.2	338.2±137.1	5.6±12.4	109.2±17.9	314.8±43.4
10	97.3±32.5	133.2±27	154.9±59.2	10±6	26±16.7	125.5±27.7

2026201462 26 Feb 2026

Non-GLP RNA dose ranging study (higher doses) in Indian rhesus macaques

[00876] This study was designed to (a) evaluate the immunogenicity of VEE-MAG25mer srRNAat a dose of 300 µg as a homologous prime/boost or heterologous prime/boost in combination with ChAdV68.5WTnt.MAG25mer; (b) compare the immune responses of VEE-MAG25mer srRNA in lipid nanoparticles using LNP1 versus LNP2 at the 300µg dose; and (c) evaluate the kinetics of T-cell responses to VEE-MAG25mer srRNA and ChAdV68.5WTnt.MAG25mer immunizations.

[00877] The study arm was conducted in Mamu-A*01 Indian rhesus macaques to demonstrate immunogenicity. Vaccine immunogenicity in nonhuman primate species, such as Rhesus, is the best predictor of vaccine potency in humans. Furthermore, select antigens used in this study are only recognized in Rhesus macaques, specifically those with a Mamu-A*01 MHC class I haplotype. Mamu-A*01 Indian rhesus macaques were randomized to the different study arms (6 macaques per group) and administered an IM injection bilaterally with either ChAdV68.5-WTnt.MAG25mer or VEE-MAG25mer srRNA encoding model antigens that includes multiple Mamu-A*01 restricted antigens. The study arms were as described below.

[00878] PBMCs were collected prior to immunization and 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 or 24 weeks after the initial immunization for immune monitoring for group 1 (heterologous prime/boost). PBMCs were collected prior to immunization and 4, 5, 7, 8, 10, 11, 12, 13, 14, or 15 weeks after the initial immunization for immune monitoring for groups 2 and 3 (homologous prime/boost).

[00879] **Table 26:** Non-GLP immunogenicity study in Indian Rhesus Macaques

Group	Prime	Boost 1	Boost 2	Boost 3
1	ChAdV68.5WTnt .MAG25mer	VEE-MAG25mer srRNA -LNP2 (300 µg)	VEE-MAG25mer srRNA -LNP2 (300 µg)	VEE-MAG25mer srRNA -LNP2 (300 µg)
2	VEE-MAG25mer srRNA -LNP2 (300 µg)	VEE-MAG25mer srRNA -LNP2 (300 µg)	VEE-MAG25mer srRNA -LNP2 (300 µg)	
3	VEE-MAG25mer srRNA -LNP1 (300 µg)	VEE-MAG25mer srRNA -LNP1 (300 µg)	VEE-MAG25mer srRNA -LNP1 (300 µg)	

2026201462 26 Feb 2026

Results

[00880] Mamu-A*01 Indian rhesus macaques were immunized with ChAdV68.5-WTnt.MAG25mer. Antigen-specific cellular immune responses in peripheral blood mononuclear cells (PBMCs) were measured to six different Mamu-A*01 restricted epitopes prior to immunization and 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 or 24 weeks after the initial immunization (FIG. 35 and Table 27). Animals received boost immunizations with VEE-MAG25mer srRNA using the LNP2 formulation on weeks 4, 12, and 20. Combined antigen-specific immune responses of 1750, 4225, 1100, 2529, 3218, 1915, 1708, 1561, 5077, 4543, 4920, 5820, 3395, 2728, 1996, 1465, 4730, 2984, 2828, or 3043 SFCs per 10^6 PBMCs (six epitopes combined) were measured 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 or 24 weeks after the initial immunization with ChAdV68.5WTnt.MAG25mer (FIG. 35). Immune responses measured 1 week after the second boost immunization (week 13) with VEE-MAG25mer srRNA were ~3-fold higher than that measured just before the boost immunization (week 12). Immune responses measured 1 week after the third boost immunization (week 21) with VEE-MAG25mer srRNA, were ~3-fold higher than that measured just before the boost immunization (week 20), similar to the response observed for the second boost.

[00881] Mamu-A*01 Indian rhesus macaques were also immunized with VEE-MAG25mer srRNA using two different LNP forumulations (LNP1 and LNP2). Antigen-specific cellular immune responses in peripheral blood mononuclear cells (PBMCs) were measured to six different Mamu-A*01 restricted epitopes prior to immunization and 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, or 15 weeks after the initial immunization (FIGS. 36 and 37, Tables 28 and 29). Animals received boost immunizations with VEE-MAG25mer srRNA using the respective LNP1 or LNP2 formulation on weeks 4 and 12. Combined antigen-specific immune responses of 168, 204, 103, 126, 140, 145, 330, 203, and 162 SFCs per 106 PBMCs (six epitopes combined) were measured 4, 5, 7, 8, 10, 11, 13, 14, 15 weeks after the immunization with VEE-MAG25mer srRNA-LNP2 (FIG. 36). Combined antigen-specific immune responses of 189, 185, 349, 437, 492, 570, 233, 886, 369, and 381 SFCs per 10^6 PBMCs (six epitopes combined) were measured 4, 5, 7, 8, 10, 11, 12, 13, 14, 15 weeks after the immunization with VEE-MAG25mer srRNA-LNP1 (FIG. 37).

2026201462 26 Feb 2026

[00882] **Table 27:** Mean spot forming cells (SFC) per 10^6 PBMCs for each epitope ± SEM for priming vaccination with ChAdV68.5WTnt.MAG25mer (Group 1)

Wk	Antigen					
	Env CL9	Env TL9	Gag CM9	Gag LW9	Pol SV9	Tat TL8
4	173±41.6	373.5±87.3	461.4±74.2	38.4±26.1	94.5±26	609.2±121.9
5	412.7±138.4	987.8±283.3	1064.4±266.9	85.6±31.2	367.2±135.2	1306.8±332.8
6	116.2±41.2	231.1±46.3	268.3±90.7	86.1±42	174.3±61	223.9±38.1
7	287.4±148.7	588.9±173.9	693.2±224.8	92.1±33.5	172.9±55.6	694.6±194.8
8	325.4±126.6	735.8±212	948.9±274.5	211.3±62.7	179.1±50	817.3±185.2
10	312±129.7	543.2±188.4	618.6±221.7	-5.7±4.1	136.5±51.3	309.9±85.6
11	248.5±81.1	348.7±129.8	581.1±205.5	-3.1±4.4	119±51.2	413.7±144.8
12	261.9±68.2	329.9±83	486.5±118.6	-1.2±5.1	132.8±31.8	350.9±69.3
13	389.3±167.7	1615.8±418.3	1244.3±403.6	1.3±8.1	522.5±155	1303.3±385.6
14	406.3±121.6	1616±491.7	1142.3±247.2	6.6±11.1	322.7±94.1	1048.6±215.6
15	446.8±138.7	1700.8±469.1	1306.3±294.4	43±24.5	421.2±87.9	1001.5±236.4
16	686.8±268.8	1979.5±541.7	1616.8±411.8	2.4±7.8	381.9±116.4	1152.8±352.7
17	375.8±109.3	1378.6±561.2	773.1±210.3	-1.4±4.3	177.6±93.7	691.7±245
18	255.9±99.7	1538.4±498.1	498.7±152.3	-5.3±3.3	26.2±13.4	413.9±164.8
19	133±62.6	955.9±456.8	491.1±121.8	-5.7±4.1	50.3±25.4	371.2±123.7
20	163.7±55.8	641.7±313.5	357.9±91.1	2.6±7.5	41.4±24.2	257.8±68.9
21	319.9±160.5	2017.1±419.9	1204.8±335.2	-3.7±5.1	268.1±109.6	924.1±301
22	244.7±105.6	1370.9±563.5	780.3±390	-3.6±5.1	118.2±68.1	473.3±249.3
23	176.7±81.8	1263.7±527.3	838.6±367.9	-5.7±4.1	73.6±49	480.9±163.9
24	236.5±92	1324.7±589.3	879.7±321	-0.4±5.7	104±53.1	498±135.8

2026201462 26 Feb 2026

[00883] **Table 28:** Mean spot forming cells (SFC) per 10^6 PBMCs for each epitope ± SEM for priming vaccination with VEE-MAG25mer srRNA-LNP2 (300 µg) (Group 2)

Wk	Antigen					
	Env CL9	Env TL9	Gag CM9	Gag LW9	Pol SV9	Tat TL8
4	46±27.1	18.4±6.8	58.3±45.8	29.9±20.8	4.9±2.3	10.7±4
5	85.4±54	5.2±5.8	52.4±51.2	34.5±35	11.8±12.2	14.4±7.9
7	18.6±32.5	1.9±1.7	59.4±55.7	9.3±10.7	3.3±3	10.7±6.1
8	36.6±39.4	6.3±3.9	48.7±39.9	13.5±8.8	3.8±3.6	17.2±9.7
10	69.1±59.1	4.4±1.9	39.3±38	14.7±10.8	4.4±5.3	8.5±5.3
11	43±38.8	22.6±21.1	30.2±26.2	3.3±2.2	5.8±3.5	40.3±25.5
13	120.4±78.3	68.2±43.9	54.2±36.8	21.8±7.4	17.7±6.1	47.4±27.3
14	76±44.8	28±19.5	65.9±64.3	-0.3±1.3	2.5±2	31.1±26.5
15	58.9±41.4	19.5±15.1	55.4±51	2.5±2	5.5±3.6	20.1±15.7

[00884] **Table 29:** Mean spot forming cells (SFC) per 10^6 PBMCs for each epitope ± SEM for priming vaccination with VEE-MAG25mer srRNA-LNP1 (300 µg) (Group 3)

Wk	Antigen					
	Env CL9	Env TL9	Gag CM9	Gag LW9	Pol SV9	Tat TL8
4	19.5±8.7	13.3±13.1	16.5±15.3	10.5±7.3	35.9±24.8	92.9±91.6
5	87.9±43.9	12.7±11.7	37.2±31.9	21.1±23.8	13.2±13.7	12.6±13.7
7	21.1±13.3	48.8±48.4	51.7±39.5	9.1±10.5	58.6±55.8	159.4±159
8	47.7±21.7	66.4±52.2	59.8±57.4	49.4±28	79.4±63	133.8±132.1
10	49±30.2	42.2±41.1	139.3±139.3	51.6±51.2	78.2±75.8	131.7±131.6
11	42±26.8	20.9±21.4	177.1±162	-6.3±4.3	104.3±104.1	231.5±230.1
12	40.2±19	20.3±11.9	42.2±46.7	3.7±6.7	57±44.7	70±69.2
13	81.2±48.9	38.2±37.6	259.4±222.2	-4±4.1	164.1±159.3	347.3±343.5
14	34.5±31.8	5.3±11.6	138.6±137.3	-4.7±5.2	52.3±52.9	142.6±142.6
15	49±24	6.7±9.8	167.1±163.8	-6.4±4.2	47.8±42.3	116.6±114.5

2026201462 26 Feb 2026

srRNA Dose Ranging Study

[00885] In one implementation of the present invention, an srRNA dose ranging study can be conducted in mamu A01 Indian rhesus macaques to identify which srRNA dose to progress to NHP immunogenicity studies. In one example, Mamu A01 Indian rhesus macaques can be administered with an srRNA vector encoding model antigens that includes multiple mamu A01 restricted epitopes by IM injection. In another example, an anti-CTLA-4 monoclonal antibody can be administered SC proximal to the site of IM vaccine injection to target the vaccine draining lymph node in one group of animals. PBMCs can be collected every 2 weeks after the initial vaccination for immune monitoring. The study arms are described in below (Table 30).

Table 30: Non-GLP RNA dose ranging study in Indian Rhesus Macaques

Group	Prime	Boost 1	Boost 2
1	srRNA-LNP (Low Dose)	srRNA-LNP (Low Dose)	srRNA-LNP (Low Dose)
2	srRNA-LNP (Mid Dose)	srRNA-LNP (Mid Dose)	srRNA-LNP (Mid Dose)
3	srRNA-LNP (High Dose)	srRNA-LNP (High Dose)	srRNA-LNP (High Dose)
4	srRNA-LNP (High Dose) + anti-CTLA-4	srRNA-LNP (High Dose) + anti-CTLA-4	srRNA-LNP (High Dose) + anti-CTLA-4

* Dose range of srRNA to be determined with the high dose ≤300 μg.

Immunogenicity Study in Indian Rhesus Macaques

[00886] In one implementation of the present invention, vaccine studies can be conducted in mamu A01 Indian rhesus macaques to demonstrate immunogenicity. In one example, Mamu A01 Indian rhesus macaques can be administered an IM injection with a ChAdV and/or srRNA vector encoding model antigens that includes multiple mamu A01 restricted antigens. In another example, an anti-CTLA-4 monoclonal antibody will be administered SC proximal to the site of IM vaccine injection to some of the groups. PBMCs can be collected every 2 weeks after the initial vaccination for immune monitoring. The study arms are described in below (Table 31).

2026201462 26 Feb 2026

Table 31: Non-GLP immunogenicity study in Indian Rhesus Macaques

Group	Prime	Boost 1	Boost 2
1	ChAdV	srRNA-LNP*	srRNA-LNP
2	srRNA-LNP	ChAdV	srRNA-LNP
3	srRNA-LNP	srRNA-LNP	ChAdV
4	srRNA-LNP + anti-CTLA-4	srRNA-LNP + anti-CTLA-4	srRNA-LNP + anti-CTLA-4
5	ChAdV + anti-CTLA-4	srRNA-LNP + anti-CTLA-4	srRNA-LNP + anti-CTLA-4
6	srRNA-LNP + anti-CTLA-4	ChAdV + anti-CTLA-4	srRNA-LNP + anti-CTLA-4

*srRNA dose to be determined based on srRNA dose range study.

XIX. Identification of MHC/peptide target-reactive T cells and TCRs

[00887] T cells can be isolated from blood, lymph nodes, or tumors of patients. T cells can be enriched for antigen-specific T cells, e.g., by sorting antigen -MHC tetramer binding cells or by sorting activated cells stimulated in an *in vitro* co-culture of T cells and antigen -pulsed antigen presenting cells. Various reagents are known in the art for antigen-specific T cell identification including antigen-loaded tetramers and other MHC-based reagents.

[00888] Antigen-relevant alpha-beta (or gamma-delta) TCR dimers can be identified by single cell sequencing of TCRs of antigen-specific T cells. Alternatively, bulk TCR sequencing of antigen-specific T cells can be performed and alpha-beta pairs with a high probability of matching can be determined using a TCR pairing method known in the art.

[00889] Alternatively or in addition, antigen-specific T cells can be obtained through *in vitro* priming of naïve T cells from healthy donors. T cells obtained from PBMCs, lymph nodes, or cord blood can be repeatedly stimulated by antigen-pulsed antigen presenting cells to prime differentiation of antigen-experienced T cells. TCRs can then be identified similarly as described above for antigen-specific T cells from patients.

2026201462 26 Feb 2026

Certain Sequences

[00890] Sequences for vectors, cassettes, and antibodies are shown below.

Tremelimumab VL (SEQ ID NO:16)
PSSLSASVGDRVTITCRASQSINSYLDWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTI SSLQPEDFATYYCQQYYSTPFTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV
Tremelimumab VH (SEQ ID NO:17)
GVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDPRGATLYYYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALG CLVKDYFPEPVTVSWNSGALTSGVH
Tremelimumab VH CDR1 (SEQ ID NO:18)
GFTFSSYGMH
Tremelimumab VH CDR2 (SEQ ID NO:19)
VIWYDGSNKYYADSV
Tremelimumab VH CDR3 (SEQ ID NO:20)
DPRGATLYYYYYGMDV
Tremelimumab VL CDR1 (SEQ ID NO:21)
RASQSINSYLD
Tremelimumab VL CDR2 (SEQ ID NO:22)
AASSLQS
Tremelimumab VL CDR3 (SEQ ID NO:23)
QQYYSTPFT
Durvalumab (MEDI4736) VL (SEQ ID NO:24)
EIVLTQSPGTLSLSPGERATLSCRASQRVSSSYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGSGTDFTL TISRLEPEDFAVYYCQQYGSLPWTFGQGTKVEIK
MEDI4736 VH (SEQ ID NO:25)
EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDN AKNSLYLQMNSLRAEDTAVYYCAREGGWFGELAFDYWGQGTLVTVSS
MEDI4736 VH CDR1 (SEQ ID NO:26)
RYWMS
MEDI4736 VH CDR2 (SEQ ID NO:27)
NIKQDGSEKYYVDSVKG
MEDI4736 VH CDR3 (SEQ ID NO:28)
EGGWFGELAFDY
MEDI4736 VL CDR1 (SEQ ID NO:29)
RASQRVSSSYLA
MEDI4736 VL CDR2 (SEQ ID NO:30)
DASSRAT
MEDI4736 VL CDR3 (SEQ ID NO:31)
QQYGSLPWT
UbA76-25merPDTT nucleotide (SEQ ID NO:32)
GCCCGGGCATTTAAATGCGATCGCATCGATtacgactctagaatagtctagtccgcaggccaccatgC AGATCTTCGTGAAGACCCTGACCGGCAAGACCATCACCCTAGAGGTGGAGCCCAGTGACACCATCGAGAACGTG AAGGCCAAGATCCAGGATAAAGAGGGCATCCCCCCTGACCAGCAGAGGCTGATCTTTGCCGGCAAGCAGCTGGA AGATGGCCGCACCCTCTCTGATTACAACATCCAGAAGGAGTCAACCCTGCACCTGGTCCTTCGCCTGAGAGGTG cCatgtttcaggcgctgagcgaaggctgcaccccgtatgatattaaccagatgctgaacgtgctgggcgatcat caggtctcaggccttgagcagcttgagagtataatcaactttgaaaaactgactgaatggaccagttctaatgt tatgCCTATCCTGTCTCCTCTGACAAAGGGCATCCTGGGCTTCGTGTTTACCCTGACCGTGCCTTCTGAGAGAG GACTTagctgcattagcgaagcggatgcgaccaccccggaaagcgcgaacctgggcgaagaaattctgagccag ctgtatctttggccaagggtgacctaccattcccctagttatgcttaccaccaatttgaaagacgagccaaata taaaagaCACTTCCCCGGCTTTGGCCAGAGCCTGCTGTTTGGCTACCCTGTGTACGTGTTCGGCGATTGCGTGC AGGGCGATtgggatgcgattcgctttcgctattgcgcgccgccgggctatgcgctgctgcgctgcaacgatacc aactatagcgctctgctggctgtgggggccctagaaggacccaggaatcaggactggcttggtgtcccaagaca acttgtaactCGGATGCAGGCTATTCAGAATGCCGGCCTGTGTACCCTGGTGGCCATGCTGGAAGAGACAATCT TCTGGCTGCAAgcgtttctgatggcgctgaccgatagcggcccgaaaaccaacattattgtggatagccagtat

2026201462 26 Feb 2026

gtgatgggcattagcaaaccgagctttcaggaatttgtggattgggaaaacgtgagcccggaactgaacagcac
cgatcagccgtttTGGCAAGCCGGAATCCTGGCCAGAAATCTGGTGCCTATGGTGGCCACAGTGCAGGGCCAGA
ACCTGAAGTACCAGggtcagtcactagtcatctctgcttctatcattgtcttcaacctgCtggaactggaaggt
gattatcgagatgatggcaacgtgtgggtgcataccccgctgagcccgcgcaccctgaacgcgtgggtgaaagc
ggtggaagaaaaaaaaggtattccagttcacctagagctggccagtatgaccaacaTggagctcatgagcagta
ttgtgcatcagcaggtcAGAACATACGGCCCCGTGTTCATGTGTCTCGGCGGACTGCTTACAATGGTGGCTGGT
GCTGTGTGGCTGACAGTGcgagtgctcgagctgttccgggccgcgcagctggccaacgacgtggtcctccagat
catggagctttgtggtgcagcgtttcgccaggtgtgccataccaccgtgccgtggccgaacgcgagcctgaccc
cgaaatggaacaacgaaaccacccagccccagatcgccaactgcagcgtgtatgacttttttgtgtggctccat
tattattctgttcgagacacactttggccaagggtgacctaccatatgaacaaatatgcgtatcatatgctgga
aagacgagccaaatataaaagaGGACCAGGACCTGGCGCTAAATTTGTGGCCGCCTGGACACTGAAAGCCGCTG
CTGGTCCTGGACCTGGCCAGTACATCAAGGCCAACAGCAAGTTCATCGGCATCACCGAACTCGGACCCGGACCA
GGCTGATGATTTCGAAATTTAAATAAGCTTGCGGCCGCTAGGGATAACAGGGTAATtatcacgcccaaacattt
acagccgcggtgtcaaaaaccgcgtgg

UbA76-25merPDTT polypeptide (SEQ ID NO:33)

MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLH
LVLRLRGAMFQALSEGCTPYDINQMLNVLGDHQVSGLEQLESIINFEKLTEWTSSNVMPILSPLTKGILGFVFT
LTVPSERGLSCISEADATTPESANLGEEILSQLYLWPRVTYHSPSYAYHQFERRAKYKRHFPGFGQSLLFGYPV
YVFGDCVQGDWDAIRFRYCAPPGYALLRCNDTNYSALLAVGALEGPRNQDWLGVPRQLVTRMQAIQNAGLCTLV
AMLEETIFWLQAFLMALTDSGPKTNIIVDSQYVMGISKPSFQEFVDWENVSPELNSTDQPFWQAGILARNLVPM
VATVQGQNLKYQGQSLVISASIIVFNLLELEGDYRDDGNVWVHTPLSPRTLNAWVKAVEEKKGIPVHLELASMT
NMELMSSIVHQQVRTYGPVFMCLGGLLTMVAGAVWLTVRVLELFRAAQLANDVVLQIMELCGAAFRQVCHTTVP
WPNASLTPKWNNETTQPQIANCSVYDFFVWLHYYSVRDTLWPRVTYHMNKYAYHMLERRAKYKRGPGPGAKFVA
AWTLKAAAGPGPGQYIKANSKFIGITELGPGPG

MAG-25merPDTT nucleotide (SEQ ID NO:34)

ATGGCCGGGATGTTCCAGGCACTGTCCGAAGGCTGCACACCCTATGATATTAACCAGATGCTGAATGTCCTGGG
AGACCACCAGGTCTCTGGCCTGGAGCAGCTGGAGAGCATCATCAACTTCGAGAAGCTGACCGAGTGGACAAGCT
CCAATGTGATGCCTATCCTGTCCCCACTGACCAAGGGCATCCTGGGCTTCGTGTTTACCCTGACAGTGCCTTCT
GAGCGGGGCCTGTCTTGCATCAGCGAGGCAGACGCAACCACACCAGAGTCCGCCAATCTGGGCGAGGAGATCCT
GTCTCAGCTGTACCTGTGGCCCCGGGTGACATATCACTCCCCTTCTTACGCCTATCACCAGTTCGAGCGGAGAG
CCAAGTACAAGAGACACTTCCCAGGCTTTGGCCAGTCTCTGCTGTTCGGCTACCCCGTGTACGTGTTCGGCGAT
TGCGTGCAGGGCGACTGGGATGCCATCCGGTTTAGATACTGCGCACCACCTGGATATGCACTGCTGAGGTGTAA
CGACACCAATTATTCCGCCCTGCTGGCAGTGGGCGCCCTGGAGGGCCCTCGCAATCAGGATTGGCTGGGCGTGC
CAAGGCAGCTGGTGACACGCATGCAGGCCATCCAGAACGCAGGCCTGTGCACCCTGGTGGCAATGCTGGAGGAG
ACAATCTTCTGGCTGCAGGCCTTTCTGATGGCCCTGACCGACAGCGGCCCCAAGACAAACATCATCGTGGATTC
CCAGTACGTGATGGGCATCTCCAAGCCTTCTTTCCAGGAGTTTGTGGACTGGGAGAACGTGAGCCCAGAGCTGA
ATTCCACCGATCAGCCATTCTGGCAGGCAGGAATCCTGGCAAGGAACCTGGTGCCTATGGTGGCCACAGTGCAG
GGCCAGAATCTGAAGTACCAGGGCCAGAGCCTGGTCATCAGCGCCTCCATCATCGTGTTTAACCTGCTGGAGCT
GGAGGGCGACTATCGGGACGATGGCAACGTGTGGGTGCACACCCCACTGAGCCCCAGAACACTGAACGCCTGGG
TGAAGGCCGTGGAGGAGAAGAAGGGCATCCCAGTGCACCTGGAGCTGGCCTCCATGACCAATATGGAGCTGATG
TCTAGCATCGTGCACCAGCAGGTGAGGACATACGGACCCGTGTTCATGTGCCTGGGAGGCCTGCTGACCATGGT
GGCAGGAGCCGTGTGGCTGACAGTGCGGGTGCTGGAGCTGTTCAGAGCCGCCCAGCTGGCCAACGATGTGGTGC
TGCAGATCATGGAGCTGTGCGGAGCAGCCTTTCGCCAGGTGTGCCACACCACAGTGCCATGGCCCAATGCCTCC
CTGACCCCCAAGTGGAACAATGAGACAACACAGCCTCAGATCGCCAACTGTAGCGTGTACGACTTCTTCGTGTG
GCTGCACTACTATAGCGTGAGGGATACCCTGTGGCCCCGCGTGACATACCACATGAATAAGTACGCCTATCACA
TGCTGGAGAGGCGCGCCAAGTATAAGAGAGGCCCTGGCCCAGGCGCAAAGTTTGTGGCAGCATGGACCCTGAAG
GCCGCCGCCGGCCCCGGCCCCGGCCAGTATATCAAGGCTAACAGTAAGTTCATTGGAATCACAGAGCTGGGACC
CGGACCTGGA

MAG-25merPDTT polypeptide (SEQ ID NO:35)

MAGMFQALSEGCTPYDINQMLNVLGDHQVSGLEQLESIINFEKLTEWTSSNVMPILSPLTKGILGFVF
TLTVPSERGLSCISEADATTPESANLGEEILSQLYLWPRVTYHSPSYAYHQFERRAKYKRHFPGFGQSLLFGYP
VYVFGDCVQGDWDAIRFRYCAPPGYALLRCNDTNYSALLAVGALEGPRNQDWLGVPRQLVTRMQAIQNAGLCTL
VAMLEETIFWLQAFLMALTDSGPKTNIIVDSQYVMGISKPSFQEFVDWENVSPELNSTDQPFWQAGILARNLVP
MVATVQGQNLKYQGQSLVISASIIVFNLLELEGDYRDDGNVWVHTPLSPRTLNAWVKAVEEKKGIPVHLELASM
TNMELMSSIVHQQVRTYGPVFMCLGGLLTMVAGAVWLTVRVLELFRAAQLANDVVLQIMELCGAAFRQVCHTTV
PWPNASLTPKWNNETTQPQIANCSVYDFFVWLHYYSVRDTLWPRVTYHMNKYAYHMLERRAKYKRGPGPGAKFV
AAWTLKAAAGPGPGQYIKANSKFIGITELGPGPG

2026201462 26 Feb 2026

Ub7625merPDTT_NoSFL nucleotide (SEQ ID NO:36)

GCCCGGGCATTTAAATGCGATCGCATCGATtacgactctagaatagtctagtccgcaggccaccatgC
AGATCTTCGTGAAGACCCTGACCGGCAAGACCATCACCCTAGAGGTGGAGCCCAGTGACACCATCGAGAACGTG
AAGGCCAAGATCCAGGATAAAGAGGGCATCCCCCCTGACCAGCAGAGGCTGATCTTTGCCGGCAAGCAGCTGGA
AGATGGCCGCACCCTCTCTGATTACAACATCCAGAAGGAGTCAACCCTGCACCTGGTCCTTCGCCTGAGAGGTG
cCatgtttcaggcgctgagcgaaggctgcaccccgtatgatattaaccagatgctgaacgtgctgggcgatcat
cagtttaagcacatcaaagcctttgaccggacatttgctaacaacccaggtcccatggttgtgtttgccacacc
tgggCCTATCCTGTCTCCTCTGACAAAGGGCATCCTGGGCTTCGTGTTTACCCTGACCGTGCCTTCTGAGAGAG
GACTTagctgcattagcgaagcggatgcgaccaccccggaaagcgcgaacctgggcgaagaaattctgagccag
ctgtatctttggccaagggtgacctaccattcccctagttatgcttaccaccaatttgaaagacgagccaaata
taaaagaCACTTCCCCGGCTTTGGCCAGAGCCTGCTGTTTGGCTACCCTGTGTACGTGTTCGGCGATTGCGTGC
AGGGCGATtgggatgcgattcgctttcgctattgcgcgccgccgggctatgcgctgctgcgctgcaacgatacc
aactatagcgctctgctggctgtgggggccctagaaggacccaggaatcaggactggcttggtgtcccaagaca
acttgtaactCGGATGCAGGCTATTCAGAATGCCGGCCTGTGTACCCTGGTGGCCATGCTGGAAGAGACAATCT
TCTGGCTGCAAgcgtttctgatggcgctgaccgatagcggcccgaaaaccaacattattgtggatagccagtat
gtgatgggcattagcaaaccgagctttcaggaatttgtggattgggaaaacgtgagcccggaactgaacagcac
cgatcagccgtttTGGCAAGCCGGAATCCTGGCCAGAAATCTGGTGCCTATGGTGGCCACAGTGCAGGGCCAGA
ACCTGAAGTACCAGggtcagtcactagtcatctctgcttctatcattgtcttcaacctgCtggaactggaaggt
gattatcgagatgatggcaacgtgtgggtgcataccccgctgagcccgcgcaccctgaacgcgtgggtgaaagc
ggtggaagaaaaaaaaggtattccagttcacctagagctggccagtatgaccaacaTggagctcatgagcagta
ttgtgcatcagcaggtcAGAACATACGGCCCCGTGTTCATGTGTCTCGGCGGACTGCTTACAATGGTGGCTGGT
GCTGTGTGGCTGACAGTGcgagtgctcgagctgttccgggccgcgcagctggccaacgacgtggtcctccagat
catggagctttgtggtgcagcgtttcgccaggtgtgccataccaccgtgccgtggccgaacgcgagcctgaccc
cgaaatggaacaacgaaaccacccagccccagatcgccaactgcagcgtgtatgacttttttgtgtggctccat
tattattctgttcgagacacactttggccaagggtgacctaccatatgaacaaatatgcgtatcatatgctgga
aagacgagccaaatataaaagaGGACCAGGACCTGGCGCTAAATTTGTGGCCGCCTGGACACTGAAAGCCGCTG
CTGGTCCTGGACCTGGCCAGTACATCAAGGCCAACAGCAAGTTCATCGGCATCACCGAACTCGGACCCGGACCA
GGCTGATGATTTCGAAATTTAAATAAGCTTGCGGCCGCTAGGGATAACAGGGTAATtatcacgcccaaacattt
acagccgcggtgtcaaaaaccgcgtgg

Ub7625merPDTT_NoSFL polypeptide (SEQ ID NO:37)

MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLH
LVLRLRGAMFQALSEGCTPYDINQMLNVLGDHQFKHIKAFDRTFANNPGPMVVFATPGPILSPLTKGILGFVFT
LTVPSERGLSCISEADATTPESANLGEEILSQLYLWPRVTYHSPSYAYHQFERRAKYKRHFPGFGQSLLFGYPV
YVFGDCVQGDWDAIRFRYCAPPGYALLRCNDTNYSALLAVGALEGPRNQDWLGVPRQLVTRMQAIQNAGLCTLV
AMLEETIFWLQAFLMALTDSGPKTNIIVDSQYVMGISKPSFQEFVDWENVSPELNSTDQPFWQAGILARNLVPM
VATVQGQNLKYQGQSLVISASIIVFNLLELEGDYRDDGNVWVHTPLSPRTLNAWVKAVEEKKGIPVHLELASMT
NMELMSSIVHQQVRTYGPVFMCLGGLLTMVAGAVWLTVRVLELFRAAQLANDVVLQIMELCGAAFRQVCHTTVP
WPNASLTPKWNNETTQPQIANCSVYDFFVWLHYYSVRDTLWPRVTYHMNKYAYHMLERRAKYKRGPGPGAKFVA
AWTLKAAAGPGPGQYIKANSKFIGITELGPGPG

ChAdV68.5WTnt.MAG25mer (SEQ ID NO:2); AC_000011.1 with E1 (nt 577 to 3403) and E3 (nt 27,125- 31,825) sequences deleted; corresponding ATCC VR-594 nucleotides substituted at five positions; model neoantigen cassette under the control of the CMV promoter/enhancer inserted in place of deleted E1; SV40 polyA 3′ of cassette

CCATCTTCAATAATATACCTCAAACTTTTTGTGCGCGTTAATATGCAAATGAGGCGTTTGAATTTGGG
GAGGAAGGGCGGTGATTGGTCGAGGGATGAGCGACCGTTAGGGGCGGGGCGAGTGACGTTTTGATGACGTGGTT
GCGAGGAGGAGCCAGTTTGCAAGTTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTTGAACACGGAAATA
CTCAATTTTCCCGCGCTCTCTGACAGGAAATGAGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGCCATTTTCG
CGCGAAAACTGAATGAGGAAGTGAAAATCTGAGTAATTTCGCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGC
CGAGTAGACTTTGACCGATTACGTGGGGGTTTCGATTACCGTGTTTTTCACCTAAATTTCCGCGTACGGTGTCA
AAGTCCGGTGTTTTTACGTAGGTGTCAGCTGATCGCCAGGGTATTTAAACCTGCGCTCTCCAGTCAAGAGGCCA
CTCTTGAGTGCCAGCGAGAAGAGTTTTCTCCTCCGCGCCGCGAGTCAGATCTACACTTTGAAAGTAGGGATAAC
AGGGTAATgacattgattattgactagttGttaaTAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATA
TGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACG
TCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACG
GTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCCTATTGACGTCAATGACGGTA
AATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGGCAGTACATCTACGTATTA
GTCATCGCTATTACCATGgTGATGCGGTTTTGGCAGTACACCAATGGGCGTGGATAGCGGTTTGACTCACGGGG
ATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAAT

2026201462 26 Feb 2026

GTCGTAATAACCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAgcT
CGTTTAGTGAACCGTCAGATCGCCTGGAACGCCATCCACGCTGTTTTGACCTCCATAGAAGACAGCGATCGCGc
caccATGGCCGGGATGTTCCAGGCACTGTCCGAAGGCTGCACACCCTATGATATTAACCAGATGCTGAATGTCC
TGGGAGACCACCAGGTCTCTGGCCTGGAGCAGCTGGAGAGCATCATCAACTTCGAGAAGCTGACCGAGTGGACA
AGCTCCAATGTGATGCCTATCCTGTCCCCACTGACCAAGGGCATCCTGGGCTTCGTGTTTACCCTGACAGTGCC
TTCTGAGCGGGGCCTGTCTTGCATCAGCGAGGCAGACGCAACCACACCAGAGTCCGCCAATCTGGGCGAGGAGA
TCCTGTCTCAGCTGTACCTGTGGCCCCGGGTGACATATCACTCCCCTTCTTACGCCTATCACCAGTTCGAGCGG
AGAGCCAAGTACAAGAGACACTTCCCAGGCTTTGGCCAGTCTCTGCTGTTCGGCTACCCCGTGTACGTGTTCGG
CGATTGCGTGCAGGGCGACTGGGATGCCATCCGGTTTAGATACTGCGCACCACCTGGATATGCACTGCTGAGGT
GTAACGACACCAATTATTCCGCCCTGCTGGCAGTGGGCGCCCTGGAGGGCCCTCGCAATCAGGATTGGCTGGGC
GTGCCAAGGCAGCTGGTGACACGCATGCAGGCCATCCAGAACGCAGGCCTGTGCACCCTGGTGGCAATGCTGGA
GGAGACAATCTTCTGGCTGCAGGCCTTTCTGATGGCCCTGACCGACAGCGGCCCCAAGACAAACATCATCGTGG
ATTCCCAGTACGTGATGGGCATCTCCAAGCCTTCTTTCCAGGAGTTTGTGGACTGGGAGAACGTGAGCCCAGAG
CTGAATTCCACCGATCAGCCATTCTGGCAGGCAGGAATCCTGGCAAGGAACCTGGTGCCTATGGTGGCCACAGT
GCAGGGCCAGAATCTGAAGTACCAGGGCCAGAGCCTGGTCATCAGCGCCTCCATCATCGTGTTTAACCTGCTGG
AGCTGGAGGGCGACTATCGGGACGATGGCAACGTGTGGGTGCACACCCCACTGAGCCCCAGAACACTGAACGCC
TGGGTGAAGGCCGTGGAGGAGAAGAAGGGCATCCCAGTGCACCTGGAGCTGGCCTCCATGACCAATATGGAGCT
GATGTCTAGCATCGTGCACCAGCAGGTGAGGACATACGGACCCGTGTTCATGTGCCTGGGAGGCCTGCTGACCA
TGGTGGCAGGAGCCGTGTGGCTGACAGTGCGGGTGCTGGAGCTGTTCAGAGCCGCCCAGCTGGCCAACGATGTG
GTGCTGCAGATCATGGAGCTGTGCGGAGCAGCCTTTCGCCAGGTGTGCCACACCACAGTGCCATGGCCCAATGC
CTCCCTGACCCCCAAGTGGAACAATGAGACAACACAGCCTCAGATCGCCAACTGTAGCGTGTACGACTTCTTCG
TGTGGCTGCACTACTATAGCGTGAGGGATACCCTGTGGCCCCGCGTGACATACCACATGAATAAGTACGCCTAT
CACATGCTGGAGAGGCGCGCCAAGTATAAGAGAGGCCCTGGCCCAGGCGCAAAGTTTGTGGCAGCATGGACCCT
GAAGGCCGCCGCCGGCCCCGGCCCCGGCCAGTATATCAAGGCTAACAGTAAGTTCATTGGAATCACAGAGCTGG
GACCCGGACCTGGATAATGAGTTTAAACTCCCATTTAAATGTGAGGGTTAATGCTTCGAGCAGACATGATAAGA
TACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGC
TATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTC
AGGTTCAGGGGGAGATGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTAAAATAACTATAACG
GTCCTAAGGTAGCGAGTGAGTAGTGTTCTGGGGCGGGGGAGGACCTGCATGAGGGCCAGAATAACTGAAATCTG
TGCTTTTCTGTGTGTTGCAGCAGCATGAGCGGAAGCGGCTCCTTTGAGGGAGGGGTATTCAGCCCTTATCTGAC
GGGGCGTCTCCCCTCCTGGGCGGGAGTGCGTCAGAATGTGATGGGATCCACGGTGGACGGCCGGCCCGTGCAGC
CCGCGAACTCTTCAACCCTGACCTATGCAACCCTGAGCTCTTCGTCGTTGGACGCAGCTGCCGCCGCAGCTGCT
GCATCTGCCGCCAGCGCCGTGCGCGGAATGGCCATGGGCGCCGGCTACTACGGCACTCTGGTGGCCAACTCGAG
TTCCACCAATAATCCCGCCAGCCTGAACGAGGAGAAGCTGTTGCTGCTGATGGCCCAGCTCGAGGCCTTGACCC
AGCGCCTGGGCGAGCTGACCCAGCAGGTGGCTCAGCTGCAGGAGCAGACGCGGGCCGCGGTTGCCACGGTGAAA
TCCAAATAAAAAATGAATCAATAAATAAACGGAGACGGTTGTTGATTTTAACACAGAGTCTGAATCTTTATTTG
ATTTTTCGCGCGCGGTAGGCCCTGGACCACCGGTCTCGATCATTGAGCACCCGGTGGATCTTTTCCAGGACCCG
GTAGAGGTGGGCTTGGATGTTGAGGTACATGGGCATGAGCCCGTCCCGGGGGGTGGAGGTAGCTCCATTGCAGGG
CCTCGTGCTCGGGGGTGGTGTTGTAAATCACCCAGTCATAGCAGGGGCGCAGGGCATGGTGTTGCACAATATCT
TTGAGGAGGAGACTGATGGCCACGGGCAGCCCTTTGGTGTAGGTGTTTACAAATCTGTTGAGCTGGGAGGGATG
CATGCGGGGGGAGATGAGGTGCATCTTGGCCTGGATCTTGAGATTGGCGATGTTACCGCCCAGATCCCGCCTGG
GGTTCATGTTGTGCAGGACCACCAGCACGGTGTATCCGGTGCACTTGGGGAATTTATCATGCAACTTGGAAGGG
AAGGCGTGAAAGAATTTGGCGACGCCTTTGTGCCCGCCCAGGTTTTCCATGCACTCATCCATGATGATGGCGAT
GGGCCCGTGGGCGGCGGCCTGGGCAAAGACGTTTCGGGGGTCGGACACATCATAGTTGTGGTCCTGGGTGAGGT
CATCATAGGCCATTTTAATGAATTTGGGGCGGAGGGTGCCGGACTGGGGGACAAAGGTACCCTCGATCCCGGGG
GCGTAGTTCCCCTCACAGATCTGCATCTCCCAGGCTTTGAGCTCGGAGGGGGGGATCATGTCCACCTGCGGGGC
GATAAAGAACACGGTTTCCGGGGCGGGGGAGATGAGCTGGGCCGAAAGCAAGTTCCGGAGCAGCTGGGACTTGC
CGCAGCCGGTGGGGCCGTAGATGACCCCGATGACCGGCTGCAGGTGGTAGTTGAGGGAGAGACAGCTGCCGTCC
TCCCGGAGGAGGGGGGCCACCTCGTTCATCATCTCGCGCACGTGCATGTTCTCGCGCACCAGTTCCGCCAGGAG
GCGCTCTCCCCCCAGGGATAGGAGCTCCTGGAGCGAGGCGAAGTTTTTCAGCGGCTTGAGTCCGTCGGCCATGG
GCATTTTGGAGAGGGTTTGTTGCAAGAGTTCCAGGCGGTCCCAGAGCTCGGTGATGTGCTCTACGGCATCTCGA
TCCAGCAGACCTCCTCGTTTCGCGGGTTGGGACGGCTGCGGGAGTAGGGCACCAGACGATGGGCGTCCAGCGCA
GCCAGGGTCCGGTCCTTCCAGGGTCGCAGCGTCCGCGTCAGGGTGGTCTCCGTCACGGTGAAGGGGTGCGCGCC
GGGCTGGGCGCTTGCGAGGGTGCGCTTCAGGCTCATCCGGCTGGTCGAAAACCGCTCCCGATCGGCGCCCTGCG
CGTCGGCCAGGTAGCAATTGACCATGAGTTCGTAGTTGAGCGCCTCGGCCGCGTGGCCTTTGGCGCGGAGCTTA
CCTTTGGAAGTCTGCCCGCAGGCGGGACAGAGGAGGGACTTGAGGGCGTAGAGCTTGGGGGCGAGGAAGACGGA
CTCGGGGGCGTAGGCGTCCGCGCCGCAGTGGGCGCAGACGGTCTCGCACTCCACGAGCCAGGTGAGGTCGGGCT
GGTCGGGGTCAAAAACCAGTTTCCCGCCGTTCTTTTTGATGCGTTTCTTACCTTTGGTCTCCATGAGCTCGTGT
CCCCGCTGGGTGACAAAGAGGCTGTCCGTGTCCCCGTAGACCGACTTTATGGGCCGGTCCTCGAGCGGTGTGCC
GCGGTCCTCCTCGTAGAGGAACCCCGCCCACTCCGAGACGAAAGCCCGGGTCCAGGCCAGCACGAAGGAGGCCA

2026201462 26 Feb 2026

CGTGGGACGGGTAGCGGTCGTTGTCCACCAGCGGGTCCACCTTTTCCAGGGTATGCAAACACATGTCCCCCTCG
TCCACATCCAGGAAGGTGATTGGCTTGTAAGTGTAGGCCACGTGACCGGGGGTCCCGGCCGGGGGGGTATAAAA
GGGTGCGGGTCCCTGCTCGTCCTCACTGTCTTCCGGATCGCTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATT
CCCTCTCGAAGGCGGGCATGACCTCGGCACTCAGGTTGTCAGTTTCTAGAAACGAGGAGGATTTGATATTGACG
GTGCCGGCGGAGATGCCTTTCAAGAGCCCCTCGTCCATCTGGTCAGAAAAGACGATCTTTTTGTTGTCGAGCTT
GGTGGCGAAGGAGCCGTAGAGGGCGTTGGAGAGGAGCTTGGCGATGGAGCGCATGGTCTGGTTTTTTTCCTTGT
CGGCGCGCTCCTTGGCGGCGATGTTGAGCTGCACGTACTCGCGCGCCACGCACTTCCATTCGGGGAAGACGGTG
GTCAGCTCGTCGGGCACGATTCTGACCTGCCAGCCCCGATTATGCAGGGTGATGAGGTCCACACTGGTGGCCAC
CTCGCCGCGCAGGGGCTCATTAGTCCAGCAGAGGCGTCCGCCCTTGCGCGAGCAGAAGGGGGGCAGGGGGTCCA
GCATGACCTCGTCGGGGGGGTCGGCATCGATGGTGAAGATGCCGGGCAGGAGGTCGGGGTCAAAGTAGCTGATG
GAAGTGGCCAGATCGTCCAGGGCAGCTTGCCATTCGCGCACGGCCAGCGCGCGCTCGTAGGGACTGAGGGGCGT
GCCCCAGGGCATGGGATGGGTAAGCGCGGAGGCGTACATGCCGCAGATGTCGTAGACGTAGAGGGGCTCCTCGA
GGATGCCGATGTAGGTGGGGTAGCAGCGCCCCCCGCGGATGCTGGCGCGCACGTAGTCATACAGCTCGTGCGAG
GGGGCGAGGAGCCCCGGGCCCAGGTTGGTGCGACTGGGCTTTTCGGCGCGGTAGACGATCTGGCGGAAAATGGC
ATGCGAGTTGGAGGAGATGGTGGGCCTTTGGAAGATGTTGAAGTGGGCGTGGGGCAGTCCGACCGAGTCGCGGA
TGAAGTGGGCGTAGGAGTCTTGCAGCTTGGCGACGAGCTCGGCGGTGACTAGGACGTCCAGAGCGCAGTAGTCG
AGGGTCTCCTGGATGATGTCATACTTGAGCTGTCCCTTTTGTTTCCACAGCTCGCGGTTGAGAAGGAACTCTTC
GCGGTCCTTCCAGTACTCTTCGAGGGGGAACCCGTCCTGATCTGCACGGTAAGAGCCTAGCATGTAGAACTGGT
TGACGGCCTTGTAGGCGCAGCAGCCCTTCTCCACGGGGAGGGCGTAGGCCTGGGCGGCCTTGCGCAGGGAGGTG
TGCGTGAGGGCGAAAGTGTCCCTGACCATGACCTTGAGGAACTGGTGCTTGAAGTCGATATCGTCGCAGCCCCC
CTGCTCCCAGAGCTGGAAGTCCGTGCGCTTCTTGTAGGCGGGGTTGGGCAAAGCGAAAGTAACATCGTTGAAGA
GGATCTTGCCCGCGCGGGGCATAAAGTTGCGAGTGATGCGGAAAGGTTGGGGCACCTCGGCCCGGTTGTTGATG
ACCTGGGCGGCGAGCACGATCTCGTCGAAGCCGTTGATGTTGTGGCCCACGATGTAGAGTTCCACGAATCGCGG
ACGGCCCTTGACGTGGGGCAGTTTCTTGAGCTCCTCGTAGGTGAGCTCGTCGGGGTCGCTGAGCCCGTGCTGCT
CGAGCGCCCAGTCGGCGAGATGGGGGTTGGCGCGGAGGAAGGAAGTCCAGAGATCCACGGCCAGGGCGGTTTGC
AGACGGTCCCGGTACTGACGGAACTGCTGCCCGACGGCCATTTTTTCGGGGGTGACGCAGTAGAAGGTGCGGGG
GTCCCCGTGCCAGCGATCCCATTTGAGCTGGAGGGCGAGATCGAGGGCGAGCTCGACGAGCCGGTCGTCCCCGG
AGAGTTTCATGACCAGCATGAAGGGGACGAGCTGCTTGCCGAAGGACCCCATCCAGGTGTAGGTTTCCACATCG
TAGGTGAGGAAGAGCCTTTCGGTGCGAGGATGCGAGCCGATGGGGAAGAACTGGATCTCCTGCCACCAATTGGA
GGAATGGCTGTTGATGTGATGGAAGTAGAAATGCCGACGGCGCGCCGAACACTCGTGCTTGTGTTTATACAAGC
GGCCACAGTGCTCGCAACGCTGCACGGGATGCACGTGCTGCACGAGCTGTACCTGAGTTCCTTTGACGAGGAAT
TTCAGTGGGAAGTGGAGTCGTGGCGCCTGCATCTCGTGCTGTACTACGTCGTGGTGGTCGGCCTGGCCCTCTTC
TGCCTCGATGGTGGTCATGCTGACGAGCCCGCGCGGGAGGCAGGTCCAGACCTCGGCGCGAGCGGGTCGGAGAG
CGAGGACGAGGGCGCGCAGGCCGGAGCTGTCCAGGGTCCTGAGACGCTGCGGAGTCAGGTCAGTGGGCAGCGGC
GGCGCGCGGTTGACTTGCAGGAGTTTTTCCAGGGCGCGCGGGAGGTCCAGATGGTACTTGATCTCCACCGCGCC
ATTGGTGGCGACGTCGATGGCTTGCAGGGTCCCGTGCCCCTGGGGTGTGACCACCGTCCCCCGTTTCTTCTTGG
GCGGCTGGGGCGACGGGGGCGGTGCCTCTTCCATGGTTAGAAGCGGCGGCGAGGACGCGCGCCGGGCGGCAGGG
GCGGCTCGGGGCCCGGAGGCAGGGGCGGCAGGGGCACGTCGGCGCCGCGCGCGGGTAGGTTCTGGTACTGCGCC
CGGAGAAGACTGGCGTGAGCGACGACGCGACGGTTGACGTCCTGGATCTGACGCCTCTGGGTGAAGGCCACGGG
ACCCGTGAGTTTGAACCTGAAAGAGAGTTCGACAGAATCAATCTCGGTATCGTTGACGGCGGCCTGCCGCAGGA
TCTCTTGCACGTCGCCCGAGTTGTCCTGGTAGGCGATCTCGGTCATGAACTGCTCGATCTCCTCCTCTTGAAGG
TCTCCGCGGCCGGCGCGCTCCACGGTGGCCGCGAGGTCGTTGGAGATGCGGCCCATGAGCTGCGAGAAGGCGTT
CATGCCCGCCTCGTTCCAGACGCGGCTGTAGACCACGACGCCCTCGGGATCGCgGGCGCGCATGACCACCTGGG
CGAGGTTGAGCTCCACGTGGCGCGTGAAGACCGCGTAGTTGCAGAGGCGCTGGTAGAGGTAGTTGAGCGTGGTG
GCGATGTGCTCGGTGACGAAGAAATACATGATCCAGCGGCGGAGCGGCATCTCGCTGACGTCGCCCAGCGCCTC
CAAACGTTCCATGGCCTCGTAAAAGTCCACGGCGAAGTTGAAAAACTGGGAGTTGCGCGCCGAGACGGTCAACT
CCTCCTCCAGAAGACGGATGAGCTCGGCGATGGTGGCGCGCACCTCGCGCTCGAAGGCCCCCGGGAGTTCCTCC
ACTTCCTCTTCTTCCTCCTCCACTAACATCTCTTCTACTTCCTCCTCAGGCGGCAGTGGTGGCGGGGGAGGGGG
CCTGCGTCGCCGGCGGCGCACGGGCAGACGGTCGATGAAGCGCTCGATGGTCTCGCCGCGCCGGCGTCGCATGG
TCTCGGTGACGGCGCGCCCGTCCTCGCGGGGCCGCAGCGTGAAGACGCCGCCGCGCATCTCCAGGTGGCCGGGG
GGGTCCCCGTTGGGCAGGGAGAGGGCGCTGACGATGCATCTTATCAATTGCCCCGTAGGGACTCCGCGCAAGGA
CCTGAGCGTCTCGAGATCCACGGGATCTGAAAACCGCTGAACGAAGGCTTCGAGCCAGTCGCAGTCGCAAGGTA
GGCTGAGCACGGTTTCTTCTGGCGGGTCATGTTGGTTGGGAGCGGGGCGGGCGATGCTGCTGGTGATGAAGTTG
AAATAGGCGGTTCTGAGACGGCGGATGGTGGCGAGGAGCACCAGGTCTTTGGGCCCGGCTTGCTGGATGCGCAG
ACGGTCGGCCATGCCCCAGGCGTGGTCCTGACACCTGGCCAGGTCCTTGTAGTAGTCCTGCATGAGCCGCTCCA
CGGGCACCTCCTCCTCGCCCGCGCGGCCGTGCATGCGCGTGAGCCCGAAGCCGCGCTGGGGCTGGACGAGCGCC
AGGTCGGCGACGACGCGCTCGGCGAGGATGGCTTGCTGGATCTGGGTGAGGGTGGTCTGGAAGTCATCAAAGTC
GACGAAGCGGTGGTAGGCTCCGGTGTTGATGGTGTAGGAGCAGTTGGCCATGACGGACCAGTTGACGGTCTGGT
GGCCCGGACGCACGAGCTCGTGGTACTTGAGGCGCGAGTAGGCGCGCGTGTCGAAGATGTAGTCGTTGCAGGTG
CGCACCAGGTACTGGTAGCCGATGAGGAAGTGCGGCGGCGGCTGGCGGTAGAGCGGCCATCGCTCGGTGGCGGG

2026201462 26 Feb 2026

GGCGCCGGGCGCGAGGTCCTCGAGCATGGTGCGGTGGTAGCCGTAGATGTACCTGGACATCCAGGTGATGCCGG
CGGCGGTGGTGGAGGCGCGCGGGAACTCGCGGACGCGGTTCCAGATGTTGCGCAGCGGCAGGAAGTAGTTCATG
GTGGGCACGGTCTGGCCCGTGAGGCGCGCGCAGTCGTGGATGCTCTATACGGGCAAAAACGAAAGCGGTCAGCG
GCTCGACTCCGTGGCCTGGAGGCTAAGCGAACGGGTTGGGCTGCGCGTGTACCCCGGTTCGAATCTCGAATCAG
GCTGGAGCCGCAGCTAACGTGGTATTGGCACTCCCGTCTCGACCCAAGCCTGCACCAACCCTCCAGGATACGGA
GGCGGGTCGTTTTGCAACTTTTTTTTGGAGGCCGGATGAGACTAGTAAGCGCGGAAAGCGGCCGACCGCGATGG
CTCGCTGCCGTAGTCTGGAGAAGAATCGCCAGGGTTGCGTTGCGGTGTGCCCCGGTTCGAGGCCGGCCGGATTC
CGCGGCTAACGAGGGCGTGGCTGCCCCGTCGTTTCCAAGACCCCATAGCCAGCCGACTTCTCCAGTTACGGAGC
GAGCCCCTCTTTTGTTTTGTTTGTTTTTGCCAGATGCATCCCGTACTGCGGCAGATGCGCCCCCACCACCCTCC
ACCGCAACAACAGCCCCCTCCACAGCCGGCGCTTCTGCCCCCGCCCCAGCAGCAACTTCCAGCCACGACCGCCG
CGGCCGCCGTGAGCGGGGCTGGACAGAGTTATGATCACCAGCTGGCCTTGGAAGAGGGCGAGGGGCTGGCGCGC
CTGGGGGCGTCGTCGCCGGAGCGGCACCCGCGCGTGCAGATGAAAAGGGACGCTCGCGAGGCCTACGTGCCCAA
GCAGAACCTGTTCAGAGACAGGAGCGGCGAGGAGCCCGAGGAGATGCGCGCGGCCCGGTTCCACGCGGGGCGGG
AGCTGCGGCGCGGCCTGGACCGAAAGAGGGTGCTGAGGGACGAGGATTTCGAGGCGGACGAGCTGACGGGGATC
AGCCCCGCGCGCGCGCACGTGGCCGCGGCCAACCTGGTCACGGCGTACGAGCAGACCGTGAAGGAGGAGAGCAA
CTTCCAAAAATCCTTCAACAACCACGTGCGCACCCTGATCGCGCGCGAGGAGGTGACCCTGGGCCTGATGCACC
TGTGGGACCTGCTGGAGGCCATCGTGCAGAACCCCACCAGCAAGCCGCTGACGGCGCAGCTGTTCCTGGTGGTG
CAGCATAGTCGGGACAACGAAGCGTTCAGGGAGGCGCTGCTGAATATCACCGAGCCCGAGGGCCGCTGGCTCCT
GGACCTGGTGAACATTCTGCAGAGCATCGTGGTGCAGGAGCGCGGGCTGCCGCTGTCCGAGAAGCTGGCGGCCA
TCAACTTCTCGGTGCTGAGTTTGGGCAAGTACTACGCTAGGAAGATCTACAAGACCCCGTACGTGCCCATAGAC
AAGGAGGTGAAGATCGACGGGTTTTACATGCGCATGACCCTGAAAGTGCTGACCCTGAGCGACGATCTGGGGGT
GTACCGCAACGACAGGATGCACCGTGCGGTGAGCGCCAGCAGGCGGCGCGAGCTGAGCGACCAGGAGCTGATGC
ATAGTCTGCAGCGGGCCCTGACCGGGGCCGGGACCGAGGGGGAGAGCTACTTTGACATGGGCGCGGACCTGCAC
TGGCAGCCCAGCCGCCGGGCCTTGGAGGCGGCGGCAGGACCCTACGTAGAAGAGGTGGACGATGAGGTGGACGA
GGAGGGCGAGTACCTGGAAGACTGATGGCGCGACCGTATTTTTGCTAGATGCAACAACAACAGCCACCTCCTGA
TCCCGCGATGCGGGCGGCGCTGCAGAGCCAGCCGTCCGGCATTAACTCCTCGGACGATTGGACCCAGGCCATGC
AACGCATCATGGCGCTGACGACCCGCAACCCCGAAGCCTTTAGACAGCAGCCCCAGGCCAACCGGCTCTCGGCC
ATCCTGGAGGCCGTGGTGCCCTCGCGCTCCAACCCCACGCACGAGAAGGTCCTGGCCATCGTGAACGCGCTGGT
GGAGAACAAGGCCATCCGCGGCGACGAGGCCGGCCTGGTGTACAACGCGCTGCTGGAGCGCGTGGCCCGCTACA
ACAGCACCAACGTGCAGACCAACCTGGACCGCATGGTGACCGACGTGCGCGAGGCCGTGGCCCAGCGCGAGCGG
TTCCACCGCGAGTCCAACCTGGGATCCATGGTGGCGCTGAACGCCTTCCTCAGCACCCAGCCCGCCAACGTGCC
CCGGGGCCAGGAGGACTACACCAACTTCATCAGCGCCCTGCGCCTGATGGTGACCGAGGTGCCCCAGAGCGAGG
TGTACCAGTCCGGGCCGGACTACTTCTTCCAGACCAGTCGCCAGGGCTTGCAGACCGTGAACCTGAGCCAGGCT
TTCAAGAACTTGCAGGGCCTGTGGGGCGTGCAGGCCCCGGTCGGGGACCGCGCGACGGTGTCGAGCCTGCTGAC
GCCGAACTCGCGCCTGCTGCTGCTGCTGGTGGCCCCCTTCACGGACAGCGGCAGCATCAACCGCAACTCGTACC
TGGGCTACCTGATTAACCTGTACCGCGAGGCCATCGGCCAGGCGCACGTGGACGAGCAGACCTACCAGGAGATC
ACCCACGTGAGCCGCGCCCTGGGCCAGGACGACCCGGGCAACCTGGAAGCCACCCTGAACTTTTTGCTGACCAA
CCGGTCGCAGAAGATCCCGCCCCAGTACGCGCTCAGCACCGAGGAGGAGCGCATCCTGCGTTACGTGCAGCAGA
GCGTGGGCCTGTTCCTGATGCAGGAGGGGGCCACCCCCAGCGCCGCGCTCGACATGACCGCGCGCAACATGGAG
CCCAGCATGTACGCCAGCAACCGCCCGTTCATCAATAAACTGATGGACTACTTGCATCGGGCGGCCGCCATGAA
CTCTGACTATTTCACCAACGCCATCCTGAATCCCCACTGGCTCCCGCCGCCGGGGTTCTACACGGGCGAGTACG
ACATGCCCGACCCCAATGACGGGTTCCTGTGGGACGATGTGGACAGCAGCGTGTTCTCCCCCCGACCGGGTGCT
AACGAGCGCCCCTTGTGGAAGAAGGAAGGCAGCGACCGACGCCCGTCCTCGGCGCTGTCCGGCCGCGAGGGTGC
TGCCGCGGCGGTGCCCGAGGCCGCCAGTCCTTTCCCGAGCTTGCCCTTCTCGCTGAACAGTATCCGCAGCAGCG
AGCTGGGCAGGATCACGCGCCCGCGCTTGCTGGGCGAAGAGGAGTACTTGAATGACTCGCTGTTGAGACCCGAG
CGGGAGAAGAACTTCCCCAATAACGGGATAGAAAGCCTGGTGGACAAGATGAGCCGCTGGAAGACGTATGCGCA
GGAGCACAGGGACGATCCCCGGGCGTCGCAGGGGGCCACGAGCCGGGGCAGCGCCGCCCGTAAACGCCGGTGGC
ACGACAGGCAGCGGGGACAGATGTGGGACGATGAGGACTCCGCCGACGACAGCAGCGTGTTGGACTTGGGTGGG
AGTGGTAACCCGTTCGCTCACCTGCGCCCCCGTATCGGGCGCATGATGTAAGAGAAACCGAAAATAAATGATAC
TCACCAAGGCCATGGCGACCAGCGTGCGTTCGTTTCTTCTCTGTTGTTGTTGTATCTAGTATGATGAGGCGTGC
GTACCCGGAGGGTCCTCCTCCCTCGTACGAGAGCGTGATGCAGCAGGCGATGGCGGCGGCGGCGATGCAGCCCC
CGCTGGAGGCTCCTTACGTGCCCCCGCGGTACCTGGCGCCTACGGAGGGGCGGAACAGCATTCGTTACTCGGAG
CTGGCACCCTTGTACGATACCACCCGGTTGTACCTGGTGGACAACAAGTCGGCGGACATCGCCTCGCTGAACTA
CCAGAACGACCACAGCAACTTCCTGACCACCGTGGTGCAGAACAATGACTTCACCCCCACGGAGGCCAGCACCC
AGACCATCAACTTTGACGAGCGCTCGCGGTGGGGCGGCCAGCTGAAAACCATCATGCACACCAACATGCCCAAC
GTGAACGAGTTCATGTACAGCAACAAGTTCAAGGCGCGGGTGATGGTCTCCCGCAAGACCCCCAATGGGGTGAC
AGTGACAGAGGATTATGATGGTAGTCAGGATGAGCTGAAGTATGAATGGGTGGAATTTGAGCTGCCCGAAGGCA
ACTTCTCGGTGACCATGACCATCGACCTGATGAACAACGCCATCATCGACAATTACTTGGCGGTGGGGCGGCAG
AACGGGGTGCTGGAGAGCGACATCGGCGTGAAGTTCGACACTAGGAACTTCAGGCTGGGCTGGGACCCCGTGAC
CGAGCTGGTCATGCCCGGGGTGTACACCAACGAGGCTTTCCATCCCGATATTGTCTTGCTGCCCGGCTGCGGGG

2026201462 26 Feb 2026

TGGACTTCACCGAGAGCCGCCTCAGCAACCTGCTGGGCATTCGCAAGAGGCAGCCCTTCCAGGAAGGCTTCCAG
ATCATGTACGAGGATCTGGAGGGGGGCAACATCCCCGCGCTCCTGGATGTCGACGCCTATGAGAAAAGCAAGGA
GGATGCAGCAGCTGAAGCAACTGCAGCCGTAGCTACCGCCTCTACCGAGGTCAGGGGCGATAATTTTGCAAGCG
CCGCAGCAGTGGCAGCGGCCGAGGCGGCTGAAACCGAAAGTAAGATAGTCATTCAGCCGGTGGAGAAGGATAGC
AAGAACAGGAGCTACAACGTACTACCGGACAAGATAAACACCGCCTACCGCAGCTGGTACCTAGCCTACAACTA
TGGCGACCCCGAGAAGGGCGTGCGCTCCTGGACGCTGCTCACCACCTCGGACGTCACCTGCGGCGTGGAGCAAG
TCTACTGGTCGCTGCCCGACATGATGCAAGACCCGGTCACCTTCCGCTCCACGCGTCAAGTTAGCAACTACCCG
GTGGTGGGCGCCGAGCTCCTGCCCGTCTACTCCAAGAGCTTCTTCAACGAGCAGGCCGTCTACTCGCAGCAGCT
GCGCGCCTTCACCTCGCTTACGCACGTCTTCAACCGCTTCCCCGAGAACCAGATCCTCGTCCGCCCGCCCGCGC
CCACCATTACCACCGTCAGTGAAAACGTTCCTGCTCTCACAGATCACGGGACCCTGCCGCTGCGCAGCAGTATC
CGGGGAGTCCAGCGCGTGACCGTTACTGACGCCAGACGCCGCACCTGCCCCTACGTCTACAAGGCCCTGGGCAT
AGTCGCGCCGCGCGTCCTCTCGAGCCGCACCTTCTAAATGTCCATTCTCATCTCGCCCAGTAATAACACCGGTT
GGGGCCTGCGCGCGCCCAGCAAGATGTACGGAGGCGCTCGCCAACGCTCCACGCAACACCCCGTGCGCGTGCGC
GGGCACTTCCGCGCTCCCTGGGGCGCCCTCAAGGGCCGCGTGCGGTCGCGCACCACCGTCGACGACGTGATCGA
CCAGGTGGTGGCCGACGCGCGCAACTACACCCCCGCCGCCGCGCCCGTCTCCACCGTGGACGCCGTCATCGACA
GCGTGGTGGCcGACGCGCGCCGGTACGCCCGCGCCAAGAGCCGGCGGCGGCGCATCGCCCGGCGGCACCGGAGC
ACCCCCGCCATGCGCGCGGCGCGAGCCTTGCTGCGCAGGGCCAGGCGCACGGGACGCAGGGCCATGCTCAGGGC
GGCCAGACGCGCGGCTTCAGGCGCCAGCGCCGGCAGGACCCGGAGACGCGCGGCCACGGCGGCGGCAGCGGCCA
TCGCCAGCATGTCCCGCCCGCGGCGAGGGAACGTGTACTGGGTGCGCGACGCCGCCACCGGTGTGCGCGTGCCC
GTGCGCACCCGCCCCCCTCGCACTTGAAGATGTTCACTTCGCGATGTTGATGTGTCCCAGCGGCGAGGAGGATG
TCCAAGCGCAAATTCAAGGAAGAGATGCTCCAGGTCATCGCGCCTGAGATCTACGGCCCTGCGGTGGTGAAGGA
GGAAAGAAAGCCCCGCAAAATCAAGCGGGTCAAAAAGGACAAAAAGGAAGAAGAAAGTGATGTGGACGGATTGG
TGGAGTTTGTGCGCGAGTTCGCCCCCCGGCGGCGCGTGCAGTGGCGCGGGCGGAAGGTGCAACCGGTGCTGAGA
CCCGGCACCACCGTGGTCTTCACGCCCGGCGAGCGCTCCGGCACCGCTTCCAAGCGCTCCTACGACGAGGTGTA
CGGGGATGATGATATTCTGGAGCAGGCGGCCGAGCGCCTGGGCGAGTTTGCTTACGGCAAGCGCAGCCGTTCCG
CACCGAAGGAAGAGGCGGTGTCCATCCCGCTGGACCACGGCAACCCCACGCCGAGCCTCAAGCCCGTGACCTTG
CAGCAGGTGCTGCCGACCGCGGCGCCGCGCCGGGGGTTCAAGCGCGAGGGCGAGGATCTGTACCCCACCATGCA
GCTGATGGTGCCCAAGCGCCAGAAGCTGGAAGACGTGCTGGAGACCATGAAGGTGGACCCGGACGTGCAGCCCG
AGGTCAAGGTGCGGCCCATCAAGCAGGTGGCCCCGGGCCTGGGCGTGCAGACCGTGGACATCAAGATTCCCACG
GAGCCCATGGAAACGCAGACCGAGCCCATGATCAAGCCCAGCACCAGCACCATGGAGGTGCAGACGGATCCCTG
GATGCCATCGGCTCCTAGTCGAAGACCCCGGCGCAAGTACGGCGCGGCCAGCCTGCTGATGCCCAACTACGCGC
TGCATCCTTCCATCATCCCCACGCCGGGCTACCGCGGCACGCGCTTCTACCGCGGTCATACCAGCAGCCGCCGC
CGCAAGACCACCACTCGCCGCCGCCGTCGCCGCACCGCCGCTGCAACCACCCCTGCCGCCCTGGTGCGGAGAGT
GTACCGCCGCGGCCGCGCACCTCTGACCCTGCCGCGCGCGCGCTACCACCCGAGCATCGCCATTTAAACTTTCG
CCtGCTTTGCAGATCAATGGCCCTCACATGCCGCCTTCGCGTTCCCATTACGGGCTACCGAGGAAGAAAACCGC
GCCGTAGAAGGCTGGCGGGGAACGGGATGCGTCGCCACCACCACCGGCGGCGGCGCGCCATCAGCAAGCGGTTG
GGGGGAGGCTTCCTGCCCGCGCTGATCCCCATCATCGCCGCGGCGATCGGGGCGATCCCCGGCATTGCTTCCGT
GGCGGTGCAGGCCTCTCAGCGCCACTGAGACACACTTGGAAACATCTTGTAATAAACCaATGGACTCTGACGCT
CCTGGTCCTGTGATGTGTTTTCGTAGACAGATGGAAGACATCAATTTTTCGTCCCTGGCTCCGCGACACGGCAC
GCGGCCGTTCATGGGCACCTGGAGCGACATCGGCACCAGCCAACTGAACGGGGGCGCCTTCAATTGGAGCAGTC
TCTGGAGCGGGCTTAAGAATTTCGGGTCCACGCTTAAAACCTATGGCAGCAAGGCGTGGAACAGCACCACAGGG
CAGGCGCTGAGGGATAAGCTGAAAGAGCAGAACTTCCAGCAGAAGGTGGTCGATGGGCTCGCCTCGGGCATCAA
CGGGGTGGTGGACCTGGCCAACCAGGCCGTGCAGCGGCAGATCAACAGCCGCCTGGACCCGGTGCCGCCCGCCG
GCTCCGTGGAGATGCCGCAGGTGGAGGAGGAGCTGCCTCCCCTGGACAAGCGGGGCGAGAAGCGACCCCGCCCC
GATGCGGAGGAGACGCTGCTGACGCACACGGACGAGCCGCCCCCGTACGAGGAGGCGGTGAAACTGGGTCTGCC
CACCACGCGGCCCATCGCGCCCCTGGCCACCGGGGTGCTGAAACCCGAAAAGCCCGCGACCCTGGACTTGCCTC
CTCCCCAGCCTTCCCGCCCCTCTACAGTGGCTAAGCCCCTGCCGCCGGTGGCCGTGGCCCGCGCGCGACCCGGG
GGCACCGCCCGCCCTCATGCGAACTGGCAGAGCACTCTGAACAGCATCGTGGGTCTGGGAGTGCAGAGTGTGAA
GCGCCGCCGCTGCTATTAAACCTACCGTAGCGCTTAACTTGCTTGTCTGTGTGTGTATGTATTATGTCGCCGCC
GCCGCTGTCCACCAGAAGGAGGAGTGAAGAGGCGCGTCGCCGAGTTGCAAGATGGCCACCCCATCGATGCTGCC
CCAGTGGGCGTACATGCACATCGCCGGACAGGACGCTTCGGAGTACCTGAGTCCGGGTCTGGTGCAGTTTGCCC
GCGCCACAGACACCTACTTCAGTCTGGGGAACAAGTTTAGGAACCCCACGGTGGCGCCCACGCACGATGTGACC
ACCGACCGCAGCCAGCGGCTGACGCTGCGCTTCGTGCCCGTGGACCGCGAGGACAACACCTACTCGTACAAAGT
GCGCTACACGCTGGCCGTGGGCGACAACCGCGTGCTGGACATGGCCAGCACCTACTTTGACATCCGCGGCGTGC
TGGATCGGGGCCCTAGCTTCAAACCCTACTCCGGCACCGCCTACAACAGTCTGGCCCCCAAGGGAGCACCCAAC
ACTTGTCAGTGGACATATAAAGCCGATGGTGAAACTGCCACAGAAAAAACCTATACATATGGAAATGCACCCGT
GCAGGGCATTAACATCACAAAAGATGGTATTCAACTTGGAACTGACACCGATGATCAGCCAATCTACGCAGATA
AAACCTATCAGCCTGAACCTCAAGTGGGTGATGCTGAATGGCATGACATCACTGGTACTGATGAAAAGTATGGA
GGCAGAGCTCTTAAGCCTGATACCAAAATGAAGCCTTGTTATGGTTCTTTTGCCAAGCCTACTAATAAAGAAGG
AGGTCAGGCAAATGTGAAAACAGGAACAGGCACTACTAAAGAATATGACATAGACATGGCTTTCTTTGACAACA

2026201462 26 Feb 2026

GAAGTGCGGCTGCTGCTGGCCTAGCTCCAGAAATTGTTTTGTATACTGAAAATGTGGATTTGGAAACTCCAGAT
ACCCATATTGTATACAAAGCAGGCACAGATGACAGCAGCTCTTCTATTAATTTGGGTCAGCAAGCCATGCCCAA
CAGACCTAACTACATTGGTTTCAGAGACAACTTTATCGGGCTCATGTACTACAACAGCACTGGCAATATGGGGG
TGCTGGCCGGTCAGGCTTCTCAGCTGAATGCTGTGGTTGACTTGCAAGACAGAAACACCGAGCTGTCCTACCAG
CTCTTGCTTGACTCTCTGGGTGACAGAACCCGGTATTTCAGTATGTGGAATCAGGCGGTGGACAGCTATGATCC
TGATGTGCGCATTATTGAAAATCATGGTGTGGAGGATGAACTTCCCAACTATTGTTTCCCTCTGGATGCTGTTG
GCAGAACAGATACTTATCAGGGAATTAAGGCTAATGGAACTGATCAAACCACATGGACCAAAGATGACAGTGTC
AATGATGCTAATGAGATAGGCAAGGGTAATCCATTCGCCATGGAAATCAACATCCAAGCCAACCTGTGGAGGAA
CTTCCTCTACGCCAACGTGGCCCTGTACCTGCCCGACTCTTACAAGTACACGCCGGCCAATGTTACCCTGCCCA
CCAACACCAACACCTACGATTACATGAACGGCCGGGTGGTGGCGCCCTCGCTGGTGGACTCCTACATCAACATC
GGGGCGCGCTGGTCGCTGGATCCCATGGACAACGTGAACCCCTTCAACCACCACCGCAATGCGGGGCTGCGCTA
CCGCTCCATGCTCCTGGGCAACGGGCGCTACGTGCCCTTCCACATCCAGGTGCCCCAGAAATTTTTCGCCATCA
AGAGCCTCCTGCTCCTGCCCGGGTCCTACACCTACGAGTGGAACTTCCGCAAGGACGTCAACATGATCCTGCAG
AGCTCCCTCGGCAACGACCTGCGCACGGACGGGGCCTCCATCTCCTTCACCAGCATCAACCTCTACGCCACCTT
CTTCCCCATGGCGCACAACACGGCCTCCACGCTCGAGGCCATGCTGCGCAACGACACCAACGACCAGTCCTTCA
ACGACTACCTCTCGGCGGCCAACATGCTCTACCCCATCCCGGCCAACGCCACCAACGTGCCCATCTCCATCCCC
TCGCGCAACTGGGCCGCCTTCCGCGGCTGGTCCTTCACGCGTCTCAAGACCAAGGAGACGCCCTCGCTGGGCTC
CGGGTTCGACCCCTACTTCGTCTACTCGGGCTCCATCCCCTACCTCGACGGCACCTTCTACCTCAACCACACCT
TCAAGAAGGTCTCCATCACCTTCGACTCCTCCGTCAGCTGGCCCGGCAACGACCGGCTCCTGACGCCCAACGAG
TTCGAAATCAAGCGCACCGTCGACGGCGAGGGCTACAACGTGGCCCAGTGCAACATGACCAAGGACTGGTTCCT
GGTCCAGATGCTGGCCCACTACAACATCGGCTACCAGGGCTTCTACGTGCCCGAGGGCTACAAGGACCGCATGT
ACTCCTTCTTCCGCAACTTCCAGCCCATGAGCCGCCAGGTGGTGGACGAGGTCAACTACAAGGACTACCAGGCC
GTCACCCTGGCCTACCAGCACAACAACTCGGGCTTCGTCGGCTACCTCGCGCCCACCATGCGCCAGGGCCAGCC
CTACCCCGCCAACTACCCCTACCCGCTCATCGGCAAGAGCGCCGTCACCAGCGTCACCCAGAAAAAGTTCCTCT
GCGACAGGGTCATGTGGCGCATCCCCTTCTCCAGCAACTTCATGTCCATGGGCGCGCTCACCGACCTCGGCCAG
AACATGCTCTATGCCAACTCCGCCCACGCGCTAGACATGAATTTCGAAGTCGACCCCATGGATGAGTCCACCCT
TCTCTATGTTGTCTTCGAAGTCTTCGACGTCGTCCGAGTGCACCAGCCCCACCGCGGCGTCATCGAGGCCGTCT
ACCTGCGCACCCCCTTCTCGGCCGGTAACGCCACCACCTAAGCTCTTGCTTCTTGCAAGCCATGGCCGCGGGCT
CCGGCGAGCAGGAGCTCAGGGCCATCATCCGCGACCTGGGCTGCGGGCCCTACTTCCTGGGCACCTTCGATAAG
CGCTTCCCGGGATTCATGGCCCCGCACAAGCTGGCCTGCGCCATCGTCAACACGGCCGGCCGCGAGACCGGGGG
CGAGCACTGGCTGGCCTTCGCCTGGAACCCGCGCTCGAACACCTGCTACCTCTTCGACCCCTTCGGGTTCTCGG
ACGAGCGCCTCAAGCAGATCTACCAGTTCGAGTACGAGGGCCTGCTGCGCCGCAGCGCCCTGGCCACCGAGGAC
CGCTGCGTCACCCTGGAAAAGTCCACCCAGACCGTGCAGGGTCCGCGCTCGGCCGCCTGCGGGCTCTTCTGCTG
CATGTTCCTGCACGCCTTCGTGCACTGGCCCGACCGCCCCATGGACAAGAACCCCACCATGAACTTGCTGACGG
GGGTGCCCAACGGCATGCTCCAGTCGCCCCAGGTGGAACCCACCCTGCGCCGCAACCAGGAGGCGCTCTACCGC
TTCCTCAACTCCCACTCCGCCTACTTTCGCTCCCACCGCGCGCGCATCGAGAAGGCCACCGCCTTCGACCGCAT
GAATCAAGACATGTAAACCGTGTGTGTATGTTAAATGTCTTTAATAAACAGCACTTTCATGTTACACATGCATC
TGAGATGATTTATTTAGAAATCGAAAGGGTTCTGCCGGGTCTCGGCATGGCCCGCGGGCAGGGACACGTTGCGG
AACTGGTACTTGGCCAGCCACTTGAACTCGGGGATCAGCAGTTTGGGCAGCGGGGTGTCGGGGAAGGAGTCGGT
CCACAGCTTCCGCGTCAGTTGCAGGGCGCCCAGCAGGTCGGGCGCGGAGATCTTGAAATCGCAGTTGGGACCCG
CGTTCTGCGCGCGGGAGTTGCGGTACACGGGGTTGCAGCACTGGAACACCATCAGGGCCGGGTGCTTCACGCTC
GCCAGCACCGTCGCGTCGGTGATGCTCTCCACGTCGAGGTCCTCGGCGTTGGCCATCCCGAAGGGGGTCATCTT
GCAGGTCTGCCTTCCCATGGTGGGCACGCACCCGGGCTTGTGGTTGCAATCGCAGTGCAGGGGGATCAGCATCA
TCTGGGCCTGGTCGGCGTTCATCCCCGGGTACATGGCCTTCATGAAAGCCTCCAATTGCCTGAACGCCTGCTGG
GCCTTGGCTCCCTCGGTGAAGAAGACCCCGCAGGACTTGCTAGAGAACTGGTTGGTGGCGCACCCGGCGTCGTG
CACGCAGCAGCGCGCGTCGTTGTTGGCCAGCTGCACCACGCTGCGCCCCCAGCGGTTCTGGGTGATCTTGGCCC
GGTCGGGGTTCTCCTTCAGCGCGCGCTGCCCGTTCTCGCTCGCCACATCCATCTCGATCATGTGCTCCTTCTGG
ATCATGGTGGTCCCGTGCAGGCACCGCAGCTTGCCCTCGGCCTCGGTGCACCCGTGCAGCCACAGCGCGCACCC
GGTGCACTCCCAGTTCTTGTGGGCGATCTGGGAATGCGCGTGCACGAAGCCCTGCAGGAAGCGGCCCATCATGG
TGGTCAGGGTCTTGTTGCTAGTGAAGGTCAGCGGAATGCCGCGGTGCTCCTCGTTGATGTACAGGTGGCAGATG
CGGCGGTACACCTCGCCCTGCTCGGGCATCAGCTGGAAGTTGGCTTTCAGGTCGGTCTCCACGCGGTAGCGGTC
CATCAGCATAGTCATGATTTCCATACCCTTCTCCCAGGCCGAGACGATGGGCAGGCTCATAGGGTTCTTCACCA
TCATCTTAGCGCTAGCAGCCGCGGCCAGGGGGTCGCTCTCGTCCAGGGTCTCAAAGCTCCGCTTGCCGTCCTTC
TCGGTGATCCGCACCGGGGGGTAGCTGAAGCCCACGGCCGCCAGCTCCTCCTCGGCCTGTCTTTCGTCCTCGCT
GTCCTGGCTGACGTCCTGCAGGACCACATGCTTGGTCTTGCGGGGTTTCTTCTTGGGCGGCAGCGGCGGCGGAG
ATGTTGGAGATGGCGAGGGGGAGCGCGAGTTCTCGCTCACCACTACTATCTCTTCCTCTTCTTGGTCCGAGGCC
ACGCGGCGGTAGGTATGTCTCTTCGGGGGCAGAGGCGGAGGCGACGGGCTCTCGCCGCCGCGACTTGGCGGATG
GCTGGCAGAGCCCCTTCCGCGTTCGGGGGTGCGCTCCCGGCGGCGCTCTGACTGACTTCCTCCGCGGCCGGCCA
TTGTGTTCTCCTAGGGAGGAACAACAAGCATGGAGACTCAGCCATCGCCAACCTCGCCATCTGCCCCCACCGCC
GACGAGAAGCAGCAGCAGCAGAATGAAAGCTTAACCGCCCCGCCGCCCAGCCCCGCCACCTCCGACGCGGCCGT

2026201462 26 Feb 2026

CCCAGACATGCAAGAGATGGAGGAATCCATCGAGATTGACCTGGGCTATGTGACGCCCGCGGAGCACGAGGAGG
AGCTGGCAGTGCGCTTTTCACAAGAAGAGATACACCAAGAACAGCCAGAGCAGGAAGCAGAGAATGAGCAGAGT
CAGGCTGGGCTCGAGCATGACGGCGACTACCTCCACCTGAGCGGGGGGGAGGACGCGCTCATCAAGCATCTGGC
CCGGCAGGCCACCATCGTCAAGGATGCGCTGCTCGACCGCACCGAGGTGCCCCTCAGCGTGGAGGAGCTCAGCC
GCGCCTACGAGTTGAACCTCTTCTCGCCGCGCGTGCCCCCCAAGCGCCAGCCCAATGGCACCTGCGAGCCCAAC
CCGCGCCTCAACTTCTACCCGGTCTTCGCGGTGCCCGAGGCCCTGGCCACCTACCACATCTTTTTCAAGAACCA
AAAGATCCCCGTCTCCTGCCGCGCCAACCGCACCCGCGCCGACGCCCTTTTCAACCTGGGTCCCGGCGCCCGCC
TACCTGATATCGCCTCCTTGGAAGAGGTTCCCAAGATCTTCGAGGGTCTGGGCAGCGACGAGACTCGGGCCGCG
AACGCTCTGCAAGGAGAAGGAGGAGAGCATGAGCACCACAGCGCCCTGGTCGAGTTGGAAGGCGACAACGCGCG
GCTGGCGGTGCTCAAACGCACGGTCGAGCTGACCCATTTCGCCTACCCGGCTCTGAACCTGCCCCCCAAAGTCA
TGAGCGCGGTCATGGACCAGGTGCTCATCAAGCGCGCGTCGCCCATCTCCGAGGACGAGGGCATGCAAGACTCC
GAGGAGGGCAAGCCCGTGGTCAGCGACGAGCAGCTGGCCCGGTGGCTGGGTCCTAATGCTAGTCCCCAGAGTTT
GGAAGAGCGGCGCAAACTCATGATGGCCGTGGTCCTGGTGACCGTGGAGCTGGAGTGCCTGCGCCGCTTCTTCG
CCGACGCGGAGACCCTGCGCAAGGTCGAGGAGAACCTGCACTACCTCTTCAGGCACGGGTTCGTGCGCCAGGCC
TGCAAGATCTCCAACGTGGAGCTGACCAACCTGGTCTCCTACATGGGCATCTTGCACGAGAACCGCCTGGGGCA
GAACGTGCTGCACACCACCCTGCGCGGGGAGGCCCGGCGCGACTACATCCGCGACTGCGTCTACCTCTACCTCT
GCCACACCTGGCAGACGGGCATGGGCGTGTGGCAGCAGTGTCTGGAGGAGCAGAACCTGAAAGAGCTCTGCAAG
CTCCTGCAGAAGAACCTCAAGGGTCTGTGGACCGGGTTCGACGAGCGCACCACCGCCTCGGACCTGGCCGACCT
CATTTTCCCCGAGCGCCTCAGGCTGACGCTGCGCAACGGCCTGCCCGACTTTATGAGCCAAAGCATGTTGCAAA
ACTTTCGCTCTTTCATCCTCGAACGCTCCGGAATCCTGCCCGCCACCTGCTCCGCGCTGCCCTCGGACTTCGTG
CCGCTGACCTTCCGCGAGTGCCCCCCGCCGCTGTGGAGCCACTGCTACCTGCTGCGCCTGGCCAACTACCTGGC
CTACCACTCGGACGTGATCGAGGACGTCAGCGGCGAGGGCCTGCTCGAGTGCCACTGCCGCTGCAACCTCTGCA
CGCCGCACCGCTCCCTGGCCTGCAACCCCCAGCTGCTGAGCGAGACCCAGATCATCGGCACCTTCGAGTTGCAA
GGGCCCAGCGAAGGCGAGGGTTCAGCCGCCAAGGGGGGTCTGAAACTCACCCCGGGGCTGTGGACCTCGGCCTA
CTTGCGCAAGTTCGTGCCCGAGGACTACCATCCCTTCGAGATCAGGTTCTACGAGGACCAATCCCATCCGCCCA
AGGCCGAGCTGTCGGCCTGCGTCATCACCCAGGGGGCGATCCTGGCCCAATTGCAAGCCATCCAGAAATCCCGC
CAAGAATTCTTGCTGAAAAAGGGCCGCGGGGTCTACCTCGACCCCCAGACCGGTGAGGAGCTCAACCCCGGCTT
CCCCCAGGATGCCCCGAGGAAACAAGAAGCTGAAAGTGGAGCTGCCGCCCGTGGAGGATTTGGAGGAAGACTGG
GAGAACAGCAGTCAGGCAGAGGAGGAGGAGATGGAGGAAGACTGGGACAGCACTCAGGCAGAGGAGGACAGCCT
GCAAGACAGTCTGGAGGAAGACGAGGAGGAGGCAGAGGAGGAGGTGGAAGAAGCAGCCGCCGCCAGACCGTCGT
CCTCGGCGGGGGAGAAAGCAAGCAGCACGGATACCATCTCCGCTCCGGGTCGGGGTCCCGCTCGACCACACAGT
AGATGGGACGAGACCGGACGATTCCCGAACCCCACCACCCAGACCGGTAAGAAGGAGCGGCAGGGATACAAGTC
CTGGCGGGGGCACAAAAACGCCATCGTCTCCTGCTTGCAGGCCTGCGGGGGCAACATCTCCTTCACCCGGCGCT
ACCTGCTCTTCCACCGCGGGGTGAACTTTCCCCGCAACATCTTGCATTACTACCGTCACCTCCACAGCCCCTAC
TACTTCCAAGAAGAGGCAGCAGCAGCAGAAAAAGACCAGCAGAAAACCAGCAGCTAGAAAATCCACAGCGGCGG
CAGCAGGTGGACTGAGGATCGCGGCGAACGAGCCGGCGCAAACCCGGGAGCTGAGGAACCGGATCTTTCCCACC
CTCTATGCCATCTTCCAGCAGAGTCGGGGGCAGGAGCAGGAACTGAAAGTCAAGAACCGTTCTCTGCGCTCGCT
CACCCGCAGTTGTCTGTATCACAAGAGCGAAGACCAACTTCAGCGCACTCTCGAGGACGCCGAGGCTCTCTTCA
ACAAGTACTGCGCGCTCACTCTTAAAGAGTAGCCCGCGCCCGCCCAGTCGCAGAAAAAGGCGGGAATTACGTCA
CCTGTGCCCTTCGCCCTAGCCGCCTCCACCCATCATCATGAGCAAAGAGATTCCCACGCCTTACATGTGGAGCT
ACCAGCCCCAGATGGGCCTGGCCGCCGGTGCCGCCCAGGACTACTCCACCCGCATGAATTGGCTCAGCGCCGGG
CCCGCGATGATCTCACGGGTGAATGACATCCGCGCCCACCGAAACCAGATACTCCTAGAACAGTCAGCGCTCAC
CGCCACGCCCCGCAATCACCTCAATCCGCGTAATTGGCCCGCCGCCCTGGTGTACCAGGAAATTCCCCAGCCCA
CGACCGTACTACTTCCGCGAGACGCCCAGGCCGAAGTCCAGCTGACTAACTCAGGTGTCCAGCTGGCGGGCGGC
GCCACCCTGTGTCGTCACCGCCCCGCTCAGGGTATAAAGCGGCTGGTGATCCGGGGCAGAGGCACACAGCTCAA
CGACGAGGTGGTGAGCTCTTCGCTGGGTCTGCGACCTGACGGAGTCTTCCAACTCGCCGGATCGGGGAGATCTT
CCTTCACGCCTCGTCAGGCCGTCCTGACTTTGGAGAGTTCGTCCTCGCAGCCCCGCTCGGGTGGCATCGGCACT
CTCCAGTTCGTGGAGGAGTTCACTCCCTCGGTCTACTTCAACCCCTTCTCCGGCTCCCCCGGCCACTACCCGGA
CGAGTTCATCCCGAACTTCGACGCCATCAGCGAGTCGGTGGACGGCTACGATTGAAACTAATCACCCCCTTATC
CAGTGAAATAAAGATCATATTGATGATGATTTTACAGAAATAAAAAATAATCATTTGATTTGAAATAAAGATAC
AATCATATTGATGATTTGAGTTTAACAAAAAAATAAAGAATCACTTACTTGAAATCTGATACCAGGTCTCTGTC
CATGTTTTCTGCCAACACCACTTCACTCCCCTCTTCCCAGCTCTGGTACTGCAGGCCCCGGCGGGCTGCAAACT
TCCTCCACACGCTGAAGGGGATGTCAAATTCCTCCTGTCCCTCAATCTTCATTTTATCTTCTATCAGATGTCCA
AAAAGCGCGTCCGGGTGGATGATGACTTCGACCCCGTCTACCCCTACGATGCAGACAACGCACCGACCGTGCCC
TTCATCAACCCCCCCTTCGTCTCTTCAGATGGATTCCAAGAGAAGCCCCTGGGGGGTGTTGTCCCTGCGACTGGC
CGACCCCGTCACCACCAAGAACGGGGAAATCACCCTCAAGCTGGGAGAGGGGGTGGACCTCGATTCCTCGGGAA
AACTCATCTCCAACACGGCCACCAAGGCCGCCGCCCCTCTCAGTTTTTCCAACAACACCATTTCCCTTAACATG
GATCACCCCTTTTACACTAAAGATGGAAAATTATCCTTACAAGTTTCTCCACCATTAAATATACTGAGAACAAG
CATTCTAAACACACTAGCTTTAGGTTTTGGATCAGGTTTAGGACTCCGTGGCTCTGCCTTGGCAGTACAGTTAG
TCTCTCCACTTACATTTGATACTGATGGAAACATAAAGCTTACCTTAGACAGAGGTTTGCATGTTACAACAGGA

2026201462 26 Feb 2026

GATGCAATTGAAAGCAACATAAGCTGGGCTAAAGGTTTAAAATTTGAAGATGGAGCCATAGCAACCAACATTGG
AAATGGGTTAGAGTTTGGAAGCAGTAGTACAGAAACAGGTGTTGATGATGCTTACCCAATCCAAGTTAAACTTG
GATCTGGCCTTAGCTTTGACAGTACAGGAGCCATAATGGCTGGTAACAAAGAAGACGATAAACTCACTTTGTGG
ACAACACCTGATCCATCACCAAACTGTCAAATACTCGCAGAAAATGATGCAAAACTAACACTTTGCTTGACTAA
ATGTGGTAGTCAAATACTGGCCACTGTGTCAGTCTTAGTTGTAGGAAGTGGAAACCTAAACCCCATTACTGGCA
CCGTAAGCAGTGCTCAGGTGTTTCTACGTTTTGATGCAAACGGTGTTCTTTTAACAGAACATTCTACACTAAAA
AAATACTGGGGGTATAGGCAGGGAGATAGCATAGATGGCACTCCATATACCAATGCTGTAGGATTCATGCCCAA
TTTAAAAGCTTATCCAAAGTCACAAAGTTCTACTACTAAAAATAATATAGTAGGGCAAGTATACATGAATGGAG
ATGTTTCAAAACCTATGCTTCTCACTATAACCCTCAATGGTACTGATGACAGCAACAGTACATATTCAATGTCA
TTTTCATACACCTGGACTAATGGAAGCTATGTTGGAGCAACATTTGGGGCTAACTCTTATACCTTCTCATACAT
CGCCCAAGAATGAACACTGTATCCCACCCTGCATGCCAACCCTTCCCACCCCACTCTGTGGAACAAACTCTGAA
ACACAAAATAAAATAAAGTTCAAGTGTTTTATTGATTCAACAGTTTTACAGGATTCGAGCAGTTATTTTTCCTC
CACCCTCCCAGGACATGGAATACACCACCCTCTCCCCCCGCACAGCCTTGAACATCTGAATGCCATTGGTGATG
GACATGCTTTTGGTCTCCACGTTCCACACAGTTTCAGAGCGAGCCAGTCTCGGGTCGGTCAGGGAGATGAAACC
CTCCGGGCACTCCCGCATCTGCACCTCACAGCTCAACAGCTGAGGATTGTCCTCGGTGGTCGGGATCACGGTTA
TCTGGAAGAAGCAGAAGAGCGGCGGTGGGAATCATAGTCCGCGAACGGGATCGGCCGGTGGTGTCGCATCAGGC
CCCGCAGCAGTCGCTGCCGCCGCCGCTCCGTCAAGCTGCTGCTCAGGGGGTCCGGGTCCAGGGACTCCCTCAGC
ATGATGCCCACGGCCCTCAGCATCAGTCGTCTGGTGCGGCGGGCGCAGCAGCGCATGCGGATCTCGCTCAGGTC
GCTGCAGTACGTGCAACACAGAACCACCAGGTTGTTCAACAGTCCATAGTTCAACACGCTCCAGCCGAAACTCA
TCGCGGGAAGGATGCTACCCACGTGGCCGTCGTACCAGATCCTCAGGTAAATCAAGTGGTGCCCCCTCCAGAAC
ACGCTGCCCACGTACATGATCTCCTTGGGCATGTGGCGGTTCACCACCTCCCGGTACCACATCACCCTCTGGTT
GAACATGCAGCCCCGGATGATCCTGCGGAACCACAGGGCCAGCACCGCCCCGCCCGCCATGCAGCGAAGAGACC
CCGGGTCCCGGCAATGGCAATGGAGGACCCACCGCTCGTACCCGTGGATCATCTGGGAGCTGAACAAGTCTATG
TTGGCACAGCACAGGCATATGCTCATGCATCTCTTCAGCACTCTCAACTCCTCGGGGGTCAAAACCATATCCCA
GGGCACGGGGAACTCTTGCAGGACAGCGAACCCCGCAGAACAGGGCAATCCTCGCACAGAACTTACATTGTGCA
TGGACAGGGTATCGCAATCAGGCAGCACCGGGTGATCCTCCACCAGAGAAGCGCGGGTCTCGGTCTCCTCACAG
CGTGGTAAGGGGGCCGGCCGATACGGGTGATGGCGGGACGCGGCTGATCGTGTTCGCGACCGTGTCATGATGCA
GTTGCTTTCGGACATTTTCGTACTTGCTGTAGCAGAACCTGGTCCGGGCGCTGCACACCGATCGCCGGCGGCGG
TCTCGGCGCTTGGAACGCTCGGTGTTGAAATTGTAAAACAGCCACTCTCTCAGACCGTGCAGCAGATCTAGGGC
CTCAGGAGTGATGAAGATCCCATCATGCCTGATGGCTCTGATCACATCGACCACCGTGGAATGGGCCAGACCCA
GCCAGATGATGCAATTTTGTTGGGTTTCGGTGACGGCGGGGGAGGGAAGAACAGGAAGAACCATGATTAACTTT
TAATCCAAACGGTCTCGGAGTACTTCAAAATGAAGATCGCGGAGATGGCACCTCTCGCCCCCGCTGTGTTGGTG
GAAAATAACAGCCAGGTCAAAGGTGATACGGTTCTCGAGATGTTCCACGGTGGCTTCCAGCAAAGCCTCCACGC
GCACATCCAGAAACAAGACAATAGCGAAAGCGGGAGGGTTCTCTAATTCCTCAATCATCATGTTACACTCCTGC
ACCATCCCCAGATAATTTTCATTTTTCCAGCCTTGAATGATTCGAACTAGTTCcTGAGGTAAATCCAAGCCAGC
CATGATAAAGAGCTCGCGCAGAGCGCCCTCCACCGGCATTCTTAAGCACACCCTCATAATTCCAAGATATTCTG
CTCCTGGTTCACCTGCAGCAGATTGACAAGCGGAATATCAAAATCTCTGCCGCGATCCCTGAGCTCCTCCCTCA
GCAATAACTGTAAGTACTCTTTCATATCCTCTCCGAAATTTTTAGCCATAGGACCACCAGGAATAAGATTAGGG
CAAGCCACAGTACAGATAAACCGAAGTCCTCCCCAGTGAGCATTGCCAAATGCAAGACTGCTATAAGCATGCTG
GCTAGACCCGGTGATATCTTCCAGATAACTGGACAGAAAATCGCCCAGGCAATTTTTAAGAAAATCAACAAAAG
AAAAATCCTCCAGGTGGACGTTTAGAGCCTCGGGAACAACGATGAAGTAAATGCAAGCGGTGCGTTCCAGCATG
GTTAGTTAGCTGATCTGTAGAAAAAACAAAAATGAACATTAAACCATGCTAGCCTGGCGAACAGGTGGGTAAAT
CGTTCTCTCCAGCACCAGGCAGGCCACGGGGTCTCCGGCGCGACCCTCGTAAAAATTGTCGCTATGATTGAAAA
CCATCACAGAGAGACGTTCCCGGTGGCCGGCGTGAATGATTCGACAAGATGAATACACCCCCGGAACATTGGCG
TCCGCGAGTGAAAAAAAGCGCCCGAGGAAGCAATAAGGCACTACAATGCTCAGTCTCAAGTCCAGCAAAGCGAT
GCCATGCGGATGAAGCACAAAATTCTCAGGTGCGTACAAAATGTAATTACTCCCCTCCTGCACAGGCAGCAAAG
CCCCCGATCCCTCCAGGTACACATACAAAGCCTCAGCGTCCATAGCTTACCGAGCAGCAGCACACAACAGGCGC
AAGAGTCAGAGAAAGGCTGAGCTCTAACCTGTCCACCCGCTCTCTGCTCAATATATAGCCCAGATCTACACTGA
CGTAAAGGCCAAAGTCTAAAAATACCCGCCAAATAATCACACACGCCCAGCACACGCCCAGAAACCGGTGACAC
ACTCAAAAAAATACGCGCACTTCCTCAAACGCCCAAAACTGCCGTCATTTCCGGGTTCCCACGCTACGTCATCA
AAACACGACTTTCAAATTCCGTCGACCGTTAAAAACGTCACCCGCCCCGCCCCTAACGGTCGCCCGTCTCTCAG
CCAATCAGCGCCCCGCATCCCCAAATTCAAACACCTCATTTGCATATTAACGCGCACAAAAAGTTTGAGG

Venezuelan equine encephalitis virus [VEE] (SEQ ID NO:3) GenBank: L01442.2

atgggcggcg catgagagaa gcccagacca attacctacc caaaatggag aaagttcacg
ttgacatcga ggaagacagc ccattcctca gagctttgca gcggagcttc ccgcagtttg
aggtagaagc caagcaggtc actgataatg accatgctaa tgccagagcg ttttcgcatc
tggcttcaaa actgatcgaa acggaggtgg acccatccga cacgatcctt gacattggaa
gtgcgcccgc ccgcagaatg tattctaagc acaagtatca ttgtatctgt ccgatgagat
gtgcggaaga tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgtaagg

2026201462 26 Feb 2026

aaataactga taaggaattg gacaagaaaa tgaaggagct cgccgccgtc atgagcgacc
ctgacctgga aactgagact atgtgcctcc acgacgacga gtcgtgtcgc tacgaagggc
aagtcgctgt ttaccaggat gtatacgcgg ttgacggacc gacaagtctc tatcaccaag
ccaataaggg agttagagtc gcctactgga taggctttga caccacccct tttatgttta
agaacttggc tggagcatat ccatcatact ctaccaactg ggccgacgaa accgtgttaa
cggctcgtaa cataggccta tgcagctctg acgttatgga gcggtcacgt agagggatgt
ccattcttag aaagaagtat ttgaaaccat ccaacaatgt tctattctct gttggctcga
ccatctacca cgagaagagg gacttactga ggagctggca cctgccgtct gtatttcact
tacgtggcaa gcaaaattac acatgtcggt gtgagactat agttagttgc gacgggtacg
tcgttaaaag aatagctatc agtccaggcc tgtatgggaa gccttcaggc tatgctgcta
cgatgcaccg cgagggattc ttgtgctgca aagtgacaga cacattgaac ggggagaggg
tctcttttcc cgtgtgcacg tatgtgccag ctacattgtg tgaccaaatg actggcatac
tggcaacaga tgtcagtgcg gacgacgcgc aaaaactgct ggttgggctc aaccagcgta
tagtcgtcaa cggtcgcacc cagagaaaca ccaataccat gaaaaattac cttttgcccg
tagtggccca ggcatttgct aggtgggcaa aggaatataa ggaagatcaa gaagatgaaa
ggccactagg actacgagat agacagttag tcatggggtg ttgttgggct tttagaaggc
acaagataac atctatttat aagcgcccgg atacccaaac catcatcaaa gtgaacagcg
atttccactc attcgtgctg cccaggatag gcagtaacac attggagatc gggctgagaa
caagaatcag gaaaatgtta gaggagcaca aggagccgtc acctctcatt accgccgagg
acgtacaaga agctaagtgc gcagccgatg aggctaagga ggtgcgtgaa gccgaggagt
tgcgcgcagc tctaccacct ttggcagctg atgttgagga gcccactctg gaagccgatg
tcgacttgat gttacaagag gctggggccg gctcagtgga gacacctcgt ggcttgataa
aggttaccag ctacgctggc gaggacaaga tcggctctta cgctgtgctt tctccgcagg
ctgtactcaa gagtgaaaaa ttatcttgca tccaccctct cgctgaacaa gtcatagtga
taacacactc tggccgaaaa gggcgttatg ccgtggaacc ataccatggt aaagtagtgg
tgccagaggg acatgcaata cccgtccagg actttcaagc tctgagtgaa agtgccacca
ttgtgtacaa cgaacgtgag ttcgtaaaca ggtacctgca ccatattgcc acacatggag
gagcgctgaa cactgatgaa gaatattaca aaactgtcaa gcccagcgag cacgacggcg
aatacctgta cgacatcgac aggaaacagt gcgtcaagaa agaactagtc actgggctag
ggctcacagg cgagctggtg gatcctccct tccatgaatt cgcctacgag agtctgagaa
cacgaccagc cgctccttac caagtaccaa ccataggggt gtatggcgtg ccaggatcag
gcaagtctgg catcattaaa agcgcagtca ccaaaaaaga tctagtggtg agcgccaaga
aagaaaactg tgcagaaatt ataagggacg tcaagaaaat gaaagggctg gacgtcaatg
ccagaactgt ggactcagtg ctcttgaatg gatgcaaaca ccccgtagag accctgtata
ttgacgaagc ttttgcttgt catgcaggta ctctcagagc gctcatagcc attataagac
ctaaaaaggc agtgctctgc ggggatccca aacagtgcgg ttttttaac atgatgtgcc
tgaaagtgca ttttaaccac gagatttgca cacaagtctt ccacaaaagc atctctcgcc
gttgcactaa atctgtgact tcggtcgtct caaccttgtt ttacgacaaa aaaatgagaa
cgacgaatcc gaaagagact aagattgtga ttgacactac cggcagtacc aaacctaagc
aggacgatct cattctcact tgtttcagag ggtgggtgaa gcagttgcaa atagattaca
aaggcaacga aataatgacg gcagctgcct ctcaagggct gacccgtaaa ggtgtgtatg
ccgttcggta caaggtgaat gaaaatcctc tgtacgcacc cacctcagaa catgtgaacg
tcctactgac ccgcacggag gaccgcatcg tgtggaaaac actagccggc gacccatgga
taaaaacact gactgccaag taccctggga atttcactgc cacgatagag gagtggcaag
cagagcatga tgccatcatg aggcacatct tggagagacc ggaccctacc gacgtcttcc
agaataaggc aaacgtgtgt tgggccaagg ctttagtgcc ggtgctgaag accgctggca
tagacatgac cactgaacaa tggaacactg tggattattt tgaaacggac aaagctcact
cagcagagat agtattgaac caactatgcg tgaggttctt tggactcgat ctggactccg
gtctattttc tgcacccact gttccgttat ccattaggaa taatcactgg gataactccc
cgtcgcctaa catgtacggg ctgaataaag aagtggtccg tcagctctct cgcaggtacc
cacaactgcc tcgggcagtt gccactggaa gagtctatga catgaacact ggtacactgc
gcaattatga tccgcgcata aacctagtac ctgtaaacag aagactgcct catgctttag
tcctccacca taatgaacac ccacagagtg acttttcttc attcgtcagc aaattgaagg
gcagaactgt cctggtggtc ggggaaaagt tgtccgtccc aggcaaaatg gttgactggt
tgtcagaccg gcctgaggct accttcagag ctcggctgga tttaggcatc ccaggtgatg
tgcccaaata tgacataata tttgttaatg tgaggacccc atataaatac catcactatc
agcagtgtga agaccatgcc attaagctta gcatgttgac caagaaagct tgtctgcatc
tgaatcccgg cggaacctgt gtcagcatag gttatggtta cgctgacagg gccagcgaaa
gcatcattgg tgctatagcg cggcagttca agttttcccg ggtatgcaaa ccgaaatcct
cacttgaaga gacggaagtt ctgtttgtat tcattgggta cgatcgcaag gcccgtacgc

2026201462 26 Feb 2026

acaatcctta caagctttca tcaaccttga ccaacattta tacaggttcc agactccacg
aagccggatg tgcaccctca tatcatgtgg tgcgagggga tattgccacg gccaccgaag
gagtgattat aaatgctgct aacagcaaag gacaacctgg cggaggggtg tgcggagcgc
tgtataagaa attcccggaa agcttcgatt tacagccgat cgaagtagga aaagcgcgac
tggtcaaagg tgcagctaaa catatcattc atgccgtagg accaaacttc aacaaagttt
cggaggttga aggtgacaaa cagttggcag aggcttatga gtccatcgct aagattgtca
acgataacaa ttacaagtca gtagcgattc cactgttgtc caccggcatc ttttccggga
acaaagatcg actaacccaa tcattgaacc atttgctgac agctttagac accactgatg
cagatgtagc catatactgc agggacaaga aatgggaaat gactctcaag gaagcagtgg
ctaggagaga agcagtggag gagatatgca tatccgacga ctcttcagtg acagaacctg
atgcagagct ggtgagggtg catccgaaga gttctttggc tggaaggaag ggctacagca
caagcgatgg caaaactttc tcatatttgg aagggaccaa gtttcaccag gcggccaagg
atatagcaga aattaatgcc atgtggcccg ttgcaacgga ggccaatgag caggtatgca
tgtatatcct cggagaaagc atgagcagta ttaggtcgaa atgccccgtc gaagagtcgg
aagcctccac accacctagc acgctgcctt gcttgtgcat ccatgccatg actccagaaa
gagtacagcg cctaaaagcc tcacgtccag aacaaattac tgtgtgctca tcctttccat
tgccgaagta tagaatcact ggtgtgcaga agatccaatg ctcccagcct atattgttct
caccgaaagt gcctgcgtat attcatccaa ggaagtatct cgtggaaaca ccaccggtag
acgagactcc ggagccatcg gcagagaacc aatccacaga ggggacacct gaacaaccac
cacttataac cgaggatgag accaggacta gaacgcctga gccgatcatc atcgaagagg
aagaagagga tagcataagt ttgctgtcag atggcccgac ccaccaggtg ctgcaagtcg
aggcagacat tcacgggccg ccctctgtat ctagctcatc ctggtccatt cctcatgcat
ccgactttga tgtggacagt ttatccatac ttgacaccct ggagggagct agcgtgacca
gcggggcaac gtcagccgag actaactctt acttcgcaaa gagtatggag tttctggcgc
gaccggtgcc tgcgcctcga acagtattca ggaaccctcc acatcccgct ccgcgcacaa
gaacaccgtc acttgcaccc agcagggcct gctcgagaac cagcctagtt tccacccgc
caggcgtgaa tagggtgatc actagagagg agctcgaggc gcttaccccg tcacgcactc
ctagcaggtc ggtctcgaga accagcctgg tctccaaccc gccaggcgta aatagggtga
ttacaagaga ggagtttgag gcgttcgtag cacaacaaca atgacggttt gatgcgggtg
catacatctt ttcctccgac accggtcaag ggcatttaca acaaaaatca gtaaggcaaa
cggtgctatc cgaagtggtg ttggagagga ccgaattgga gatttcgtat gccccgcgcc
tcgaccaaga aaaagaagaa ttactacgca agaaattaca gttaaatccc acacctgcta
acagaagcag ataccagtcc aggaaggtgg agaacatgaa agccataaca gctagacgta
ttctgcaagg cctagggcat tatttgaagg cagaaggaaa agtggagtgc taccgaaccc
tgcatcctgt tcctttgtat tcatctagtg tgaaccgtgc cttttcaagc cccaaggtcg
cagtggaagc ctgtaacgcc atgttgaaag agaactttcc gactgtggct tcttactgta
ttattccaga gtacgatgcc tatttggaca tggttgacgg agcttcatgc tgcttagaca
ctgccagttt ttgccctgca aagctgcgca gctttccaaa gaaacactcc tatttggaac
ccacaatacg atcggcagtg ccttcagcga tccagaacac gctccagaac gtcctggcag
ctgccacaaa aagaaattgc aatgtcacgc aaatgagaga attgcccgta ttggattcgg
cggcctttaa tgtggaatgc ttcaagaaat atgcgtgtaa taatgaatat tgggaaacgt
ttaaagaaaa ccccatcagg cttactgaag aaaacgtggt aaattacatt accaaattaa
aaggaccaaa agctgctgct ctttttgcga agacacataa tttgaatatg ttgcaggaca
taccaatgga caggtttgta atggacttaa agagagacgt gaaagtgact ccaggaacaa
aacatactga agaacggccc aaggtacagg tgatccaggc tgccgatccg ctagcaacag
cgtatctgtg cggaatccac cgagagctgg ttaggagatt aaatgcggtc ctgcttccga
acattcatac actgtttgat atgtcggctg aagactttga cgctattata gccgagcact
tccagcctgg ggattgtgtt ctggaaactg acatcgcgtc gtttgataaa agtgaggacg
acgccatggc tctgaccgcg ttaatgattc tggaagactt aggtgtggac gcagagctgt
tgacgctgat tgaggcggct ttcggcgaaa tttcatcaat acatttgccc actaaaacta
aatttaaatt cggagccatg atgaaatctg gaatgttcct cacactgttt gtgaacacag
tcattaacat tgtaatcgca agcagagtgt tgagagaacg gctaaccgga tcaccatgtg
cagcattcat tggagatgac aatatcgtga aaggagtcaa atcggacaaa ttaatggcag
acaggtgcgc cacctggttg aatatggaag tcaagattat agatgctgtg gtgggcgaga
aagcgcctta tttctgtgga gggtttattt tgtgtgactc cgtgaccggc acagcgtgcc
gtgtggcaga ccccctaaaa aggctgttta agcttggcaa acctctggca gcagacgatg
aacatgatga tgacaggaga agggcattgc atgaagagtc aacacgctgg aaccgagtgg
gtattctttc agagctgtgc aaggcagtag aatcaaggta tgaaaccgta ggaacttcca
tcatagttat ggccatgact actctagcta gcagtgttaa atcattcagc tacctgagag
gggcccctat aactctctac ggctaacctg aatggactac gacatagtct agtccgccaa

2026201462 26 Feb 2026

gatgttcccg ttccagccaa tgtatccgat gcagccaatg ccctatcgca acccgttcgc
ggccccgcgc aggccctggt tccccagaac cgacccttt ctggcgatgc aggtgcagga
attaacccgc tcgatggcta acctgacgtt caagcaacgc cgggacgcgc cacctgaggg
gccatccgct aagaaaccga agaaggaggc ctcgcaaaaa cagaaagggg gaggccaagg
gaagaagaag aagaaccaag ggaagaagaa ggctaagaca gggccgccta atccgaaggc
acagaatgga aacaagaaga agaccaacaa gaaaccaggc aagagacagc gcatggtcat
gaaattggaa tctgacaaga cgttcccaat catgttggaa gggaagataa acggctacgc
ttgtgtggtc ggagggaagt tattcaggcc gatgcatgtg gaaggcaaga tcgacaacga
cgttctggcc gcgcttaaga cgaagaaagc atccaaatac gatcttgagt atgcagatgt
gccacagaac atgcgggccg atacattcaa atacacccat gagaaacccc aaggctatta
cagctggcat catggagcag tccaatatga aaatgggcgt ttcacggtgc cgaaaggagt
tggggccaag ggagacagcg gacgacccat tctggataac cagggacggg tggtcgctat
tgtgctggga ggtgtgaatg aaggatctag gacagccctt tcagtcgtca tgtggaacga
gaagggagtt accgtgaagt atactccgga gaactgcgag caatggtcac tagtgaccac
catgtgtctg ctcgccaatg tgacgttccc atgtgctcaa ccaccaattt gctacgacag
aaaaccagca gagactttgg ccatgctcag cgttaacgtt gacaacccgg gctacgatga
gctgctggaa gcagctgtta agtgccccgg aaggaaaagg agatccaccg aggagctgtt
taaggagtat aagctaacgc gcccttacat ggccagatgc atcagatgtg cagttgggag
ctgccatagt ccaatagcaa tcgaggcagt aaagagcgac gggcacgacg gttatgttag
acttcagact tcctcgcagt atggcctgga ttcctccggc aacttaaagg gcaggaccat
gcggtatgac atgcacggga ccattaaaga gataccacta catcaagtgt cactccatac
atctcgcccg tgtcacattg tggatgggca cggttatttc ctgcttgcca ggtgcccggc
aggggactcc atcaccatgg aatttaagaa agattccgtc acacactcct gctcggtgcc
gtatgaagtg aaatttaatc ctgtaggcag agaactctat actcatcccc cagaacacgg
agtagagcaa gcgtgccaag tctacgcaca tgatgcacag aacagaggag cttatgtcga
gatgcacctc ccgggctcag aagtggacag cagtttggtt tccttgagcg gcagttcagt
caccgtgaca cctcctgttg ggactagcgc cctggtggaa tgcgagtgtg gcggcacaaa
gatctccgag accatcaaca agacaaaaca gttcagccag tgcacaaaga aggagcagtg
cagagcatat cggctgcaga acgataagtg ggtgtataat tctgacaaac tgcccaaagc
agcgggagcc accttaaaag gaaaactgca tgtcccattc ttgctggcag acggcaaatg
caccgtgcct ctagcaccag aacctatgat aacctttggt ttcagatcag tgtcactgaa
actgcaccct aagaatccca catatctaac cacccgccaa cttgctgatg agcctcacta
cacgcacgag ctcatatctg aaccagctgt taggaatttt accgtcaccg aaaaagggtg
ggagtttgta tggggaaacc acccgccgaa aaggttttgg gcacaggaaa cagcacccgg
aaatccacat gggctaccgc acgaggtgat aactcattat taccacagat accctatgtc
caccatcctg ggtttgtcaa tttgtgccgc cattgcaacc gtttccgttg cagcgtctac
ctggctgttt tgcagatcta gagttgcgtg cctaactcct taccggctaa cacctaacgc
taggatacca ttttgtctgg ctgtgctttg ctgcgcccgc actgcccggg ccgagaccac
ctgggagtcc ttggatcacc tatggaacaa taaccaacag atgttctgga ttcaattgct
gatccctctg gccgccttga tcgtagtgac tcgcctgctc aggtgcgtgt gctgtgtcgt
gccttttta gtcatggccg gcgccgcagg cgccggcgcc tacgagcacg cgaccacgat
gccgagccaa gcgggaatct cgtataacac tatagtcaac agagcaggct acgcaccact
ccctatcagc ataacaccaa caaagatcaa gctgatacct acagtgaact tggagtacgt
cacctgccac tacaaaacag gaatggattc accagccatc aaatgctgcg gatctcagga
atgcactcca acttacaggc ctgatgaaca gtgcaaagtc ttcacagggg tttacccgtt
catgtggggt ggtgcatatt gcttttgcga cactgagaac acccaagtca gcaaggccta
cgtaatgaaa tctgacgact gccttgcgga tcatgctgaa gcatataaag cgcacacagc
ctcagtgcag gcgttcctca acatcacagt gggagaacac tctattgtga ctaccgtgta
tgtgaatgga gaaactcctg tgaatttcaa tggggtcaaa ttaactgcag gtccgctttc
cacagcttgg acacccttg atcgcaaaat cgtgcagtat gccggggaga tctataatta
tgattttcct gagtatgggg caggacaacc aggagcattt ggagatatac aatccagaac
agtctcaagc tcagatctgt atgccaatac caacctagtg ctgcagagac ccaaagcagg
agcgatccac gtgccataca ctcaggcacc ttcgggtttt gagcaatgga agaaagataa
agctccatca ttgaaattta ccgccccttt cggatgcgaa atatatacaa accccattcg
cgccgaaaac tgtgctgtag ggtcaattcc attagccttt gacattcccg acgccttgtt
caccagggtg tcagaaacac cgacactttc agcggccgaa tgcactctta acgagtgcgt
gtattcttcc gactttggtg ggatcgccac ggtcaagtac tcggccagca agtcaggcaa
gtgcgcagtc catgtgccat cagggactgc taccctaaaa gaagcagcag tcgagctaac
cgagcaaggg tcggcgacta tccatttctc gaccgcaaat atccacccgg agttcaggct
ccaaatatgc acatcatatg ttacgtgcaa aggtgattgt caccccccga aagaccatat

tgtgacacac cctcagtatc acgcccaaac atttacagcc gcggtgtcaa aaaccgcgtg
gacgtggtta acatccctgc tgggaggatc agccgtaatt attataattg gcttggtgct
ggctactatt gtggccatgt acgtgctgac caaccagaaa cataattgaa tacagcagca
attggcaagc tgcttacata gaactcgcgg cgattggcat gccgccttaa aatttttatt
ttatttttttc ttttcttttc cgaatcggat tttgttttta atatttc

VEE-MAG25mer (SEQ ID NO:4); contains MAG-25merPDTT nucleotide (bases 30-1755)

atgggcggcgcatgagagaagcccagaccaattacctacccaaaatggagaaagttcacgttgacatc
gaggaagacagcccattcctcagagctttgcagcggagcttcccgcagtttgaggtagaagccaagcaggtcac
tgataatgaccatgctaatgccagagcgttttcgcatctggcttcaaaactgatcgaaacggaggtggacccat
ccgacacgatccttgacattggaagtgcgcccgcccgcagaatgtattctaagcacaagtatcattgtatctgt
ccgatgagatgtgcggaagatccggacagattgtataagtatgcaactaagctgaagaaaaactgtaaggaaat
aactgataaggaattggacaagaaaatgaaggagctcgccgccgtcatgagcgaccctgacctggaaactgaga
ctatgtgcctccacgacgacgagtcgtgtcgctacgaagggcaagtcgctgtttaccaggatgtatacgcggtt
gacggaccgacaagtctctatcaccaagccaataagggagttagagtcgcctactggataggctttgacaccac
ccctttatgtttaagaacttggctggagcatatccatcatactctaccaactgggccgacgaaaccgtgttaa
cggctcgtaacataggcctatgcagctctgacgttatggagcggtcacgtagagggatgtccattcttagaaag
aagtatttgaaaccatccaacaatgttctattctctgttggctcgaccatctaccacgagaagagggacttact
gaggagctggcacctgccgtctgtatttcacttacgtggcaagcaaaattacacatgtcggtgtgagactatag
ttagttgcgacgggtacgtcgttaaaagaatagctatcagtccaggcctgtatgggaagccttcaggctatgct
gctacgatgcaccgcgagggattcttgtgctgcaaagtgacagacacattgaacggggagagggtctcttttcc
cgtgtgcacgtatgtgccagctacattgtgtgaccaaatgactggcatactggcaacagatgtcagtgcggacg
acgcgcaaaaactgctggttgggctcaaccagcgtatagtcgtcaacggtcgcacccagagaaacaccaatacc
atgaaaaattacctttgcccgtagtggcccaggcatttgctaggtgggcaaaggaatataaggaagatcaaga
agatgaaaggccactaggactacgagatagacagttagtcatggggtgttgttgggcttttagaaggcacaaga
taacatctatttataagcgcccggatacccaaaccatcatcaaagtgaacagcgatttccactcattcgtgctg
cccaggataggcagtaacacattggagatcgggctgagaacaagaatcaggaaaatgttagaggagcacaagga
gccgtcacctctcattaccgccgaggacgtacaagaagctaagtgcgcagccgatgaggctaaggaggtgcgtg
aagccgaggagttgcgcgcagctctaccacctttggcagctgatgttgaggagcccactctggaagccgatgtc
gacttgatgttacaagaggctggggccggctcagtggagacacctcgtggcttgataaaggttaccagctacgc
tggcgaggacaagatcggctcttacgctgtgctttctccgcaggctgtactcaagagtgaaaaattatcttgca
tccaccctctcgctgaacaagtcatagtgataacacactctggccgaaaagggcgttatgccgtggaaccatac
catggtaaagtagtggtgccagagggacatgcaatacccgtccaggactttcaagctctgagtgaaagtgccac
cattgtgtacaacgaacgtgagttcgtaaacaggtacctgcaccatattgccacacatggaggagcgctgaaca
ctgatgaagaatattacaaaactgtcaagcccagcgagcacgacggcgaatacctgtacgacatcgacaggaaa
cagtgcgtcaagaaagaactagtcactgggctagggctcacaggcgagctggtggatcctcccttccatgaatt
cgcctacgagagtctgagaacacgaccagccgctccttaccaagtaccaaccataggggtgtatggcgtgccag
gatcaggcaagtctggcatcattaaaagcgcagtcaccaaaaaagatctagtggtgagcgccaagaaagaaaac
tgtgcagaaattataagggacgtcaagaaaatgaaagggctggacgtcaatgccagaactgtggactcagtgct
cttgaatggatgcaaacaccccgtagagaccctgtatattgacgaagcttttgcttgtcatgcaggtactctca
gagcgctcatagccattataagacctaaaaaggcagtgctctgcggggatcccaaacagtgcggtttttttaac
atgatgtgcctgaaagtgcattttaaccacgagatttgcacacaagtcttccacaaaagcatctctcgccgttg
cactaaatctgtgacttcggtcgtctcaaccttgttttacgacaaaaaaatgagaacgacgaatccgaaagaga
ctaagattgtgattgacactaccggcagtaccaaacctaagcaggacgatctcattctcacttgtttcagaggg
tgggtgaagcagttgcaaatagattacaaaggcaacgaaataatgacggcagctgcctctcaagggctgacccg
taaaggtgtgtatgccgttcggtacaaggtgaatgaaaatcctctgtacgcacccacctcagaacatgtgaacg
tcctactgacccgcacggaggaccgcatcgtgtggaaaacactagccggcgacccatggataaaaacactgact
gccaagtaccctgggaatttcactgccacgatagaggagtggcaagcagagcatgatgccatcatgaggcacat
cttggagagaccggaccctaccgacgtcttccagaataaggcaaacgtgtgttgggccaaggctttagtgccgg
tgctgaagaccgctggcatagacatgaccactgaacaatggaacactgtggattattttgaaacggacaaagct
cactcagcagagatagtattgaaccaactatgcgtgaggttctttggactcgatctggactccggtctattttc
tgcacccactgttccgttatccattaggaataatcactgggataactccccgtcgcctaacatgtacgggctga
ataaagaagtggtccgtcagctctctcgcaggtacccacaactgcctcgggcagttgccactggaagagtctat
gacatgaacactggtacactgcgcaattatgatccgcgcataaacctagtacctgtaaacagaagactgcctca
tgctttagtcctccaccataatgaacacccacagagtgacttttcttcattcgtcagcaaattgaagggcagaa
ctgtcctggtggtcggggaaaagttgtccgtcccaggcaaaatggttgactggttgtcagaccggcctgaggct
accttcagagctcggctggatttaggcatcccaggtgatgtgcccaaatatgacataatatttgttaatgtgag
gaccccatataaataccatcactatcagcagtgtgaagaccatgccattaagcttagcatgttgaccaagaaag
cttgtctgcatctgaatcccggcggaacctgtgtcagcataggttatggttacgctgacagggccagcgaaagc

2026201462 26 Feb 2026

atcattggtgctatagcgcggcagttcaagttttcccgggtatgcaaaccgaaatcctcacttgaagagacgga
agttctgtttgtattcattgggtacgatcgcaaggcccgtacgcacaatccttacaagctttcatcaaccttga
ccaacatttatacaggttccagactccacgaagccggatgtgcaccctcatatcatgtggtgcgaggggatatt
gccacggccaccgaaggagtgattataaatgctgctaacagcaaaggacaacctggcggaggggtgtgcggagc
gctgtataagaaattcccggaaagcttcgatttacagccgatcgaagtaggaaaagcgcgactggtcaaaggtg
cagctaaacatatcattcatgccgtaggaccaaacttcaacaaagtttcggaggttgaaggtgacaaacagttg
gcagaggcttatgagtccatcgctaagattgtcaacgataacaattacaagtcagtagcgattccactgttgtc
caccggcatcttttccgggaacaaagatcgactaacccaatcattgaaccatttgctgacagctttagacacca
ctgatgcagatgtagccatatactgcagggacaagaaatgggaaatgactctcaaggaagcagtggctaggaga
gaagcagtggaggagatatgcatatccgacgactcttcagtgacagaacctgatgcagagctggtgagggtgca
tccgaagagttctttggctggaaggaagggctacagcacaagcgatggcaaaactttctcatatttggaaggga
ccaagtttcaccaggcggccaaggatatagcagaaattaatgccatgtggcccgttgcaacggaggccaatgag
caggtatgcatgtatatcctcggagaaagcatgagcagtattaggtcgaaatgccccgtcgaagagtcggaagc
ctccacaccacctagcacgctgccttgcttgtgcatccatgccatgactccagaaagagtacagcgcctaaaag
cctcacgtccagaacaaattactgtgtgctcatcctttccattgccgaagtatagaatcactggtgtgcagaag
atccaatgctcccagcctatattgttctcaccgaaagtgcctgcgtatattcatccaaggaagtatctcgtgga
aacaccaccggtagacgagactccggagccatcggcagagaaccaatccacagaggggacacctgaacaaccac
cacttataaccgaggatgagaccaggactagaacgcctgagccgatcatcatcgaagaggaagaagaggatagc
ataagtttgctgtcagatggcccgacccaccaggtgctgcaagtcgaggcagacattcacgggccgccctctgt
atctagctcatcctggtccattcctcatgcatccgactttgatgtggacagtttatccatacttgacaccctgg
agggagctagcgtgaccagcggggcaacgtcagccgagactaactcttacttcgcaaagagtatggagtttctg
gcgcgaccggtgcctgcgcctcgaacagtattcaggaaccctccacatcccgctccgcgcacaagaacaccgtc
acttgcacccagcagggcctgctcgagaaccagcctagtttccaccccgccaggcgtgaatagggtgatcacta
gagaggagctcgaggcgcttaccccgtcacgcactcctagcaggtcggtctcgagaaccagcctggtctccaac
ccgccaggcgtaaatagggtgattacaagagaggagtttgaggcgttcgtagcacaacaacaatgacggtttga
tgcgggtgcatacatcttttcctccgacaccggtcaagggcatttacaacaaaaatcagtaaggcaaacggtgc
tatccgaagtggtgttggagaggaccgaattggagatttcgtatgccccgcgcctcgaccaagaaaaagaagaa
ttactacgcaagaaattacagttaaatcccacacctgctaacagaagcagataccagtccaggaaggtggagaa
catgaaagccataacagctagacgtattctgcaaggcctagggcattatttgaaggcagaaggaaaagtggagt
gctaccgaaccctgcatcctgttcctttgtattcatctagtgtgaaccgtgccttttcaagccccaaggtcgca
gtggaagcctgtaacgccatgttgaaagagaactttccgactgtggcttcttactgtattattccagagtacga
tgcctatttggacatggttgacggagcttcatgctgcttagacactgccagtttttgccctgcaaagctgcgca
gctttccaaagaaacactcctatttggaacccacaatacgatcggcagtgccttcagcgatccagaacacgctc
cagaacgtcctggcagctgccacaaaaagaaattgcaatgtcacgcaaatgagagaattgcccgtattggattc
ggcggcctttaatgtggaatgcttcaagaaatatgcgtgtaataatgaatattgggaaacgtttaaagaaaacc
ccatcaggcttactgaagaaaacgtggtaaattacattaccaaattaaaaggaccaaaagctgctgctcttttt
gcgaagacacataatttgaatatgttgcaggacataccaatggacaggtttgtaatggacttaaagagagacgt
gaaagtgactccaggaacaaaacatactgaagaacggcccaaggtacaggtgatccaggctgccgatccgctag
caacagcgtatctgtgcggaatccaccgagagctggttaggagattaaatgcggtcctgcttccgaacattcat
acactgtttgatatgtcggctgaagactttgacgctattatagccgagcacttccagcctggggattgtgttct
ggaaactgacatcgcgtcgtttgataaaagtgaggacgacgccatggctctgaccgcgttaatgattctggaag
acttaggtgtggacgcagagctgttgacgctgattgaggcggctttcggcgaaatttcatcaatacatttgccc
actaaaactaaatttaaattcggagccatgatgaaatctggaatgttcctcacactgtttgtgaacacagtcat
taacattgtaatcgcaagcagagtgttgagagaacggctaaccggatcaccatgtgcagcattcattggagatg
acaatatcgtgaaaggagtcaaatcggacaaattaatggcagacaggtgcgccacctggttgaatatggaagtc
aagattatagatgctgtggtgggcgagaaagcgccttatttctgtggagggtttattttgtgtgactccgtgac
cggcacagcgtgccgtgtggcagacccccctaaaaaggctgtttaagcttggcaaacctctggcagcagacgatg
aacatgatgatgacaggagaagggcattgcatgaagagtcaacacgctggaaccgagtgggtattctttcagag
ctgtgcaaggcagtagaatcaaggtatgaaaccgtaggaacttccatcatagttatggccatgactactctagc
tagcagtgttaaatcattcagctacctgagaggggcccctataactctctacggctaacctgaatggactacga
ctctagaatagtctttaatTAAGCCACCATGGCAGGCATGTTTCAGGCGCTGAGCGAAGGCTGCACCCCGTATG
ATATTAACCAGATGCTGAACGTGCTGGGCGATCATCAGGTCTCAGGCCTTGAGCAGCTTGAGAGTATAATCAAC
TTTGAAAAACTGACTGAATGGACCAGTTCTAATGTTATGCCTATCCTGTCTCCTCTGACAAAGGGCATCCTGGG
CTTCGTGTTTACCCTGACCGTGCCTTCTGAGAGAGGACTTAGCTGCATTAGCGAAGCGGATGCGACCACCCCGG
AAAGCGCGAACCTGGGCGAAGAAATTCTGAGCCAGCTGTATCTTTGGCCAAGGGTGACCTACCATTCCCCTAGT
TATGCTTACCACCAATTTGAAAGACGAGCCAAATATAAAAGACACTTCCCCGGCTTTGGCCAGAGCCTGCTGTT
TGGCTACCCTGTGTACGTGTTCGGCGATTGCGTGCAGGGCGATTGGGATGCGATTCGCTTTCGCTATTGCGCGC
CGCCGGGCTATGCGCTGCTGCGCTGCAACGATACCAACTATAGCGCTCTGCTGGCTGTGGGGGCCCTAGAAGGA
CCCAGGAATCAGGACTGGCTTGGTGTCCCAAGACAACTTGTAACTCGGATGCAGGCTATTCAGAATGCCGGCCT
GTGTACCCTGGTGGCCATGCTGGAAGAGACAATCTTCTGGCTGCAAGCGTTTCTGATGGCGCTGACCGATAGCG

2026201462 26 Feb 2026

GCCCGAAAACCAACATTATTGTGGATAGCCAGTATGTGATGGGCATTAGCAAACCGAGCTTTCAGGAATTTGTG
GATTGGGAAAACGTGAGCCCGGAACTGAACAGCACCGATCAGCCGTTTTGGCAAGCCGGAATCCTGGCCAGAAA
TCTGGTGCCTATGGTGGCCACAGTGCAGGGCCAGAACCTGAAGTACCAGGGTCAGTCACTAGTCATCTCTGCTT
CTATCATTGTCTTCAACCTGCTGGAACTGGAAGGTGATTATCGAGATGATGGCAACGTGTGGGTGCATACCCCG
CTGAGCCCGCGCACCCTGAACGCGTGGGTGAAAGCGGTGGAAGAAAAAAAAGGTATTCCAGTTCACCTAGAGCT
GGCCAGTATGACCAACATGGAGCTCATGAGCAGTATTGTGCATCAGCAGGTCAGAACATACGGCCCCGTGTTCA
TGTGTCTCGGCGGACTGCTTACAATGGTGGCTGGTGCTGTGTGGCTGACAGTGCGAGTGCTCGAGCTGTTCCGG
GCCGCGCAGCTGGCCAACGACGTGGTCCTCCAGATCATGGAGCTTTGTGGTGCAGCGTTTCGCCAGGTGTGCCA
TACCACCGTGCCGTGGCCGAACGCGAGCCTGACCCCGAAATGGAACAACGAAACCACCCAGCCCCAGATCGCCA
ACTGCAGCGTGTATGACTTTTTTGTGTGGCTCCATTATTATTCTGTTCGAGACACACTTTGGCCAAGGGTGACC
TACCATATGAACAAATATGCGTATCATATGCTGGAAAGACGAGCCAAATATAAAAGAGGACCAGGACCTGGCGC
TAAATTTGTGGCCGCCTGGACACTGAAAGCCGCTGCTGGTCCTGGACCTGGCCAGTACATCAAGGCCAACAGCA
AGTTCATCGGCATCACCGAACTCGGACCCGGACCAGGCTGATGATTcgaacggccgtatcacgcccaaacattt
acagccgcggtgtcaaaaaccgcgtggacgtggttaacatccctgctgggaggatcagccgtaattattataat
tggcttggtgctggctactattgtggccatgtacgtgctgaccaaccagaaacataattgaatacagcagcaat
tggcaagctgcttacatagaactcgcggcgattggcatgccgccttaaaatttttatttttatttttttcttttct
tttccgaatcggattttgtttttaatatttcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

Venezuelan equine encephalitis virus strain TC-83 [TC-83](SEQ ID NO:5)
GenBank: L01443.1

atgggcggcg catgagagaa gcccagacca attacctacc caaaatggag aaagttcacg
ttgacatcga ggaagacagc ccattcctca gagctttgca gcggagcttc ccgcagtttg
aggtagaagc caagcaggtc actgataatg accatgctaa tgccagagcg ttttcgcatc
tggcttcaaa actgatcgaa acggaggtgg acccatccga cacgatcctt gacattggaa
gtgcgcccgc ccgcagaatg tattctaagc acaagtatca ttgtatctgt ccgatgagat
gtgcggaaga tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgtaagg
aaataactga taaggaattg gacaagaaaa tgaaggagct cgccgccgtc atgagcgacc
ctgacctgga aactgagact atgtgcctcc acgacgacga gtcgtgtcgc tacgaagggc
aagtcgctgt ttaccaggat gtatacgcgg ttgacggacc gacaagtctc tatcaccaag
ccaataaggg agttagagtc gcctactgga taggctttga caccacccct tttatgttta
agaacttggc tggagcatat ccatcatact ctaccaactg ggccgacgaa accgtgttaa
cggctcgtaa cataggccta tgcagctctg acgttatgga gcggtcacgt agagggatgt
ccattcttag aaagaagtat ttgaaaccat ccaacaatgt tctattctct gttggctcga
ccatctacca cgagaagagg gacttactga ggagctggca cctgccgtct gtatttcact
tacgtggcaa gcaaaattac acatgtcggt gtgagactat agttagttgc gacgggtacg
tcgttaaaag aatagctatc agtccaggcc tgtatgggaa gccttcaggc tatgctgcta
cgatgcaccg cgagggattc ttgtgctgca aagtgacaga cacattgaac ggggagaggg
tctcttttcc cgtgtgcacg tatgtgccag ctacattgtg tgaccaaatg actggcatac
tggcaacaga tgtcagtgcg gacgacgcgc aaaaactgct ggttgggctc aaccagcgta
tagtcgtcaa cggtcgcacc cagagaaaca ccaataccat gaaaaattac cttttgcccg
tagtggccca ggcatttgct aggtgggcaa aggaatataa ggaagatcaa gaagatgaaa
ggccactagg actacgagat agacagttag tcatggggtg ttgttgggct tttagaaggc
acaagataac atctatttat aagcgcccgg atacccaaac catcatcaaa gtgaacagcg
atttccactc attcgtgctg cccaggatag gcagtaacac attggagatc gggctgagaa
caagaatcag gaaaatgtta gaggagcaca aggagccgtc acctctcatt accgccgagg
acgtacaaga agctaagtgc gcagccgatg aggctaagga ggtgcgtgaa gccgaggagt
tgcgcgcagc tctaccacct ttggcagctg atgttgagga gcccactctg gaagccgatg
tcgacttgat gttacaagag gctggggccg gctcagtgga gacacctcgt ggcttgataa
aggttaccag ctacgctggc gaggacaaga tcggctctta cgctgtgctt tctccgcagg
ctgtactcaa gagtgaaaaa ttatcttgca tccaccctct cgctgaacaa gtcatagtga
taacacactc tggccgaaaa gggcgttatg ccgtggaacc ataccatggt aaagtagtgg
tgccagaggg acatgcaata cccgtccagg actttcaagc tctgagtgaa agtgccacca
ttgtgtacaa cgaacgtgag ttcgtaaaca ggtacctgca ccatattgcc acacatggag
gagcgctgaa cactgatgaa gaatattaca aaactgtcaa gcccagcgag cacgacggcg
aatacctgta cgacatcgac aggaaacagt gcgtcaagaa agaactagtc actgggctag
ggctcacagg cgagctggtg gatcctccct tccatgaatt cgcctacgag agtctgagaa
cacgaccagc cgctccttac caagtaccaa ccataggggt gtatggcgtg ccaggatcag
gcaagtctgg catcattaaa agcgcagtca ccaaaaaaga tctagtggtg agcgccaaga
aagaaaactg tgcagaaatt ataagggacg tcaagaaaat gaaagggctg gacgtcaatg

2026201462 26 Feb 2026

ccagaactgt ggactcagtg ctcttgaatg gatgcaaaca ccccgtagag accctgtata
ttgacgaagc ttttgcttgt catgcaggta ctctcagagc gctcatagcc attataagac
ctaaaaaggc agtgctctgc ggggatccca aacagtgcgg ttttttaac atgatgtgcc
tgaaagtgca ttttaaccac gagatttgca cacaagtctt ccacaaaagc atctctcgcc
gttgcactaa atctgtgact tcggtcgtct caaccttgtt ttacgacaaa aaaatgagaa
cgacgaatcc gaaagagact aagattgtga ttgacactac cggcagtacc aaacctaagc
aggacgatct cattctcact tgtttcagag ggtgggtgaa gcagttgcaa atagattaca
aaggcaacga aataatgacg gcagctgcct ctcaagggct gacccgtaaa ggtgtgtatg
ccgttcggta caaggtgaat gaaaatcctc tgtacgcacc cacctcagaa catgtgaacg
tcctactgac ccgcacggag gaccgcatcg tgtggaaaac actagccggc gacccatgga
taaaaacact gactgccaag taccctggga atttcactgc cacgatagag gagtggcaag
cagagcatga tgccatcatg aggcacatct tggagagacc ggaccctacc gacgtcttcc
agaataaggc aaacgtgtgt tgggccaagg ctttagtgcc ggtgctgaag accgctggca
tagacatgac cactgaacaa tggaacactg tggattattt tgaaacggac aaagctcact
cagcagagat agtattgaac caactatgcg tgaggttctt tggactcgat ctggactccg
gtctattttc tgcacccact gttccgttat ccattaggaa taatcactgg gataactccc
cgtcgcctaa catgtacggg ctgaataaag aagtggtccg tcagctctct cgcaggtacc
cacaactgcc tcgggcagtt gccactggaa gagtctatga catgaacact ggtacactgc
gcaattatga tccgcgcata aacctagtac ctgtaaacag aagactgcct catgctttag
tcctccacca taatgaacac ccacagagtg acttttcttc attcgtcagc aaattgaagg
gcagaactgt cctggtggtc ggggaaaagt tgtccgtccc aggcaaaatg gttgactggt
tgtcagaccg gcctgaggct accttcagag ctcggctgga tttaggcatc ccaggtgatg
tgcccaaata tgacataata tttgttaatg tgaggacccc atataaatac catcactatc
agcagtgtga agaccatgcc attaagctta gcatgttgac caagaaagct tgtctgcatc
tgaatcccgg cggaacctgt gtcagcatag gttatggtta cgctgacagg gccagcgaaa
gcatcattgg tgctatagcg cggcagttca agttttcccg ggtatgcaaa ccgaaatcct
cacttgaaga gacggaagtt ctgtttgtat tcattgggta cgatcgcaag gcccgtacgc
acaatcctta caagctttca tcaaccttga ccaacattta tacaggttcc agactccacg
aagccggatg tgcaccctca tatcatgtgg tgcgagggga tattgccacg gccaccgaag
gagtgattat aaatgctgct aacagcaaag gacaacctgg cggaggggtg tgcggagcgc
tgtataagaa attcccggaa agcttcgatt tacagccgat cgaagtagga aaagcgcgac
tggtcaaagg tgcagctaaa catatcattc atgccgtagg accaaacttc aacaaagttt
cggaggttga aggtgacaaa cagttggcag aggcttatga gtccatcgct aagattgtca
acgataacaa ttacaagtca gtagcgattc cactgttgtc caccggcatc ttttccggga
acaaagatcg actaacccaa tcattgaacc atttgctgac agctttagac accactgatg
cagatgtagc catatactgc agggacaaga aatgggaaat gactctcaag gaagcagtgg
ctaggagaga agcagtggag gagatatgca tatccgacga ctcttcagtg acagaacctg
atgcagagct ggtgagggtg catccgaaga gttctttggc tggaaggaag ggctacagca
caagcgatgg caaaactttc tcatatttgg aagggaccaa gtttcaccag gcggccaagg
atatagcaga aattaatgcc atgtggcccg ttgcaacgga ggccaatgag caggtatgca
tgtatatcct cggagaaagc atgagcagta ttaggtcgaa atgccccgtc gaagagtcgg
aagcctccac accacctagc acgctgcctt gcttgtgcat ccatgccatg actccagaaa
gagtacagcg cctaaaagcc tcacgtccag aacaaattac tgtgtgctca tcctttccat
tgccgaagta tagaatcact ggtgtgcaga agatccaatg ctcccagcct atattgttct
caccgaaagt gcctgcgtat attcatccaa ggaagtatct cgtggaaaca ccaccggtag
acgagactcc ggagccatcg gcagagaacc aatccacaga ggggacacct gaacaaccac
cacttataac cgaggatgag accaggacta gaacgcctga gccgatcatc atcgaagagg
aagaagagga tagcataagt ttgctgtcag atggcccgac ccaccaggtg ctgcaagtcg
aggcagacat tcacgggccg ccctctgtat ctagctcatc ctggtccatt cctcatgcat
ccgactttga tgtggacagt ttatccatac ttgacaccct ggagggagct agcgtgacca
gcggggcaac gtcagccgag actaactctt acttcgcaaa gagtatggag tttctggcgc
gaccggtgcc tgcgcctcga acagtattca ggaaccctcc acatcccgct ccgcgcacaa
gaacaccgtc acttgcaccc agcagggcct gctcgagaac cagcctagtt tccacccccgc
caggcgtgaa tagggtgatc actagagagg agctcgaggc gcttaccccg tcacgcactc
ctagcaggtc ggtctcgaga accagcctgg tctccaaccc gccaggcgta aatagggtga
ttacaagaga ggagtttgag gcgttcgtag cacaacaaca atgacggttt gatgcgggtg
catacatctt ttcctccgac accggtcaag ggcatttaca acaaaaatca gtaaggcaaa
cggtgctatc cgaagtggtg ttggagagga ccgaattgga gatttcgtat gccccgcgcc
tcgaccaaga aaaagaagaa ttactacgca agaaattaca gttaaatccc acacctgcta
acagaagcag ataccagtcc aggaaggtgg agaacatgaa agccataaca gctagacgta

2026201462 26 Feb 2026

ttctgcaagg cctagggcat tatttgaagg cagaaggaaa agtggagtgc taccgaaccc
tgcatcctgt tcctttgtat tcatctagtg tgaaccgtgc cttttcaagc cccaaggtcg
cagtggaagc ctgtaacgcc atgttgaaag agaactttcc gactgtggct tcttactgta
ttattccaga gtacgatgcc tatttggaca tggttgacgg agcttcatgc tgcttagaca
ctgccagttt ttgccctgca aagctgcgca gctttccaaa gaaacactcc tatttggaac
ccacaatacg atcggcagtg ccttcagcga tccagaacac gctccagaac gtcctggcag
ctgccacaaa aagaaattgc aatgtcacgc aaatgagaga attgcccgta ttggattcgg
cggcctttaa tgtggaatgc ttcaagaaat atgcgtgtaa taatgaatat tgggaaacgt
ttaaagaaaa ccccatcagg cttactgaag aaaacgtggt aaattacatt accaaattaa
aaggaccaaa agctgctgct ctttttgcga agacacataa tttgaatatg ttgcaggaca
taccaatgga caggtttgta atggacttaa agagagacgt gaaagtgact ccaggaacaa
aacatactga agaacggccc aaggtacagg tgatccaggc tgccgatccg ctagcaacag
cgtatctgtg cggaatccac cgagagctgg ttaggagatt aaatgcggtc ctgcttccga
acattcatac actgtttgat atgtcggctg aagactttga cgctattata gccgagcact
tccagcctgg ggattgtgtt ctggaaactg acatcgcgtc gtttgataaa agtgaggacg
acgccatggc tctgaccgcg ttaatgattc tggaagactt aggtgtggac gcagagctgt
tgacgctgat tgaggcggct ttcggcgaaa tttcatcaat acatttgccc actaaaacta
aatttaaatt cggagccatg atgaaatctg gaatgttcct cacactgttt gtgaacacag
tcattaacat tgtaatcgca agcagagtgt tgagagaacg gctaaccgga tcaccatgtg
cagcattcat tggagatgac aatatcgtga aaggagtcaa atcggacaaa ttaatggcag
acaggtgcgc cacctggttg aatatggaag tcaagattat agatgctgtg gtgggcgaga
aagcgcctta tttctgtgga gggtttattt tgtgtgactc cgtgaccggc acagcgtgcc
gtgtggcaga ccccctaaaa aggctgttta agcttggcaa acctctggca gcagacgatg
aacatgatga tgacaggaga agggcattgc atgaagagtc aacacgctgg aaccgagtgg
gtattctttc agagctgtgc aaggcagtag aatcaaggta tgaaaccgta ggaacttcca
tcatagttat ggccatgact actctagcta gcagtgttaa atcattcagc tacctgagag
gggcccctat aactctctac ggctaacctg aatggactac gacatagtct agtccgccaa
gatgttcccg ttccagccaa tgtatccgat gcagccaatg ccctatcgca acccgttcgc
ggccccgcgc aggccctggt tccccagaac cgacccttt ctggcgatgc aggtgcagga
attaacccgc tcgatggcta acctgacgtt caagcaacgc cgggacgcgc cacctgaggg
gccatccgct aagaaaccga agaaggaggc ctcgcaaaaa cagaaagggg gaggccaagg
gaagaagaag aagaaccaag ggaagaagaa ggctaagaca gggccgccta atccgaaggc
acagaatgga aacaagaaga agaccaacaa gaaaccaggc aagagacagc gcatggtcat
gaaattggaa tctgacaaga cgttcccaat catgttggaa gggaagataa acggctacgc
ttgtgtggtc ggagggaagt tattcaggcc gatgcatgtg gaaggcaaga tcgacaacga
cgttctggcc gcgcttaaga cgaagaaagc atccaaatac gatcttgagt atgcagatgt
gccacagaac atgcgggccg atacattcaa atacacccat gagaaacccc aaggctatta
cagctggcat catggagcag tccaatatga aaatgggcgt ttcacggtgc cgaaaggagt
tggggccaag ggagacagcg gacgacccat tctggataac cagggacggg tggtcgctat
tgtgctggga ggtgtgaatg aaggatctag gacagccctt tcagtcgtca tgtggaacga
gaagggagtt accgtgaagt atactccgga gaactgcgag caatggtcac tagtgaccac
catgtgtctg ctcgccaatg tgacgttccc atgtgctcaa ccaccaattt gctacgacag
aaaaccagca gagactttgg ccatgctcag cgttaacgtt gacaacccgg gctacgatga
gctgctggaa gcagctgtta agtgccccgg aaggaaaagg agatccaccg aggagctgtt
taaggagtat aagctaacgc gcccttacat ggccagatgc atcagatgtg cagttgggag
ctgccatagt ccaatagcaa tcgaggcagt aaagagcgac gggcacgacg gttatgttag
acttcagact tcctcgcagt atggcctgga ttcctccggc aacttaaagg gcaggaccat
gcggtatgac atgcacggga ccattaaaga gataccacta catcaagtgt cactccatac
atctcgcccg tgtcacattg tggatgggca cggttatttc ctgcttgcca ggtgcccggc
aggggactcc atcaccatgg aatttaagaa agattccgtc acacactcct gctcggtgcc
gtatgaagtg aaatttaatc ctgtaggcag agaactctat actcatcccc cagaacacgg
agtagagcaa gcgtgccaag tctacgcaca tgatgcacag aacagaggag cttatgtcga
gatgcacctc ccgggctcag aagtggacag cagtttggtt tccttgagcg gcagttcagt
caccgtgaca cctcctgttg ggactagcgc cctggtggaa tgcgagtgtg gcggcacaaa
gatctccgag accatcaaca agacaaaaca gttcagccag tgcacaaaga aggagcagtg
cagagcatat cggctgcaga acgataagtg ggtgtataat tctgacaaac tgcccaaagc
agcgggagcc accttaaaag gaaaactgca tgtcccattc ttgctggcag acggcaaatg
caccgtgcct ctagcaccag aacctatgat aacctttggt ttcagatcag tgtcactgaa
actgcaccct aagaatccca catatctaac cacccgccaa cttgctgatg agcctcacta
cacgcacgag ctcatatctg aaccagctgt taggaatttt accgtcaccg aaaaagggtg

2026201462 26 Feb 2026

ggagtttgta tggggaaacc acccgccgaa aaggttttgg gcacaggaaa cagcacccgg
aaatccacat gggctaccgc acgaggtgat aactcattat taccacagat accctatgtc
caccatcctg ggtttgtcaa tttgtgccgc cattgcaacc gtttccgttg cagcgtctac
ctggctgttt tgcagatcta gagttgcgtg cctaactcct taccggctaa cacctaacgc
taggatacca ttttgtctgg ctgtgctttg ctgcgcccgc actgcccggg ccgagaccac
ctgggagtcc ttggatcacc tatggaacaa taaccaacag atgttctgga ttcaattgct
gatccctctg gccgccttga tcgtagtgac tcgcctgctc aggtgcgtgt gctgtgtcgt
gccttttta gtcatggccg gcgccgcagg cgccggcgcc tacgagcacg cgaccacgat
gccgagccaa gcgggaatct cgtataacac tatagtcaac agagcaggct acgcaccact
ccctatcagc ataacaccaa caaagatcaa gctgatacct acagtgaact tggagtacgt
cacctgccac tacaaaacag gaatggattc accagccatc aaatgctgcg gatctcagga
atgcactcca acttacaggc ctgatgaaca gtgcaaagtc ttcacagggg tttacccgtt
catgtggggt ggtgcatatt gcttttgcga cactgagaac acccaagtca gcaaggccta
cgtaatgaaa tctgacgact gccttgcgga tcatgctgaa gcatataaag cgcacacagc
ctcagtgcag gcgttcctca acatcacagt gggagaacac tctattgtga ctaccgtgta
tgtgaatgga gaaactcctg tgaatttcaa tggggtcaaa ttaactgcag gtccgctttc
cacagcttgg acacccttg atcgcaaaat cgtgcagtat gccggggaga tctataatta
tgattttcct gagtatgggg caggacaacc aggagcattt ggagatatac aatccagaac
agtctcaagc tcagatctgt atgccaatac caacctagtg ctgcagagac ccaaagcagg
agcgatccac gtgccataca ctcaggcacc ttcgggtttt gagcaatgga agaaagataa
agctccatca ttgaaattta ccgccccttt cggatgcgaa atatatacaa accccattcg
cgccgaaaac tgtgctgtag ggtcaattcc attagccttt gacattcccg acgccttgtt
caccagggtg tcagaaacac cgacactttc agcggccgaa tgcactctta acgagtgcgt
gtattcttcc gactttggtg ggatcgccac ggtcaagtac tcggccagca agtcaggcaa
gtgcgcagtc catgtgccat cagggactgc taccctaaaa gaagcagcag tcgagctaac
cgagcaaggg tcggcgacta tccatttctc gaccgcaaat atccacccgg agttcaggct
ccaaatatgc acatcatatg ttacgtgcaa aggtgattgt caccccccga aagaccatat
tgtgacacac cctcagtatc acgcccaaac atttacagcc gcggtgtcaa aaaccgcgtg
gacgtggtta acatccctgc tgggaggatc agccgtaatt attataattg gcttggtgct
ggctactatt gtggccatgt acgtgctgac caaccagaaa cataattgaa tacagcagca
attggcaagc tgcttacata gaactcgcgg cgattggcat gccgccttaa aatttttatt
ttatttttc ttttcttttc cgaatcggat tttgttttta atatttc

VEE Delivery Vector (SEQ ID NO:6); VEE genome with nucleotides 7544-11175 deleted [alphavirus structural proteins removed]

ATGggcggcgcatgagagaagcccagaccaattacctacccaaaATGGagaaagttcacgttgacatcgaggaa
gacagcccattcctcagagctttgcagcggagcttcccgcagtttgaggtagaagccaagcaggtcactgataa
tgaccatgctaatgccagagcgttttcgcatctggcttcaaaactgatcgaaacggaggtggacccatccgaca
cgatccttgacattggaagtgcgcccgcccgcagaatgtattctaagcacaagtatcattgtatctgtccgatg
agatgtgcggaagatccggacagattgtataagtatgcaactaagctgaagaaaaactgtaaggaaataactga
taaggaattggacaagaaaatgaaggagctcgccgccgtcatgagcgaccctgacctggaaactgagactatgt
gcctccacgacgacgagtcgtgtcgctacgaagggcaagtcgctgtttaccaggatgtatacgcggttgacgga
ccgacaagtctctatcaccaagccaataagggagttagagtcgcctactggataggctttgacaccacccctttt
tatgtttaagaacttggctggagcatatccatcatactctaccaactgggccgacgaaaccgtgttaacggctc
gtaacataggcctatgcagctctgacgttatggagcggtcacgtagagggatgtccattcttagaaagaagtat
ttgaaaccatccaacaatgttctattctctgttggctcgaccatctaccacgagaagagggacttactgaggag
ctggcacctgccgtctgtatttcacttacgtggcaagcaaaattacacatgtcggtgtgagactatagttagtt
gcgacgggtacgtcgttaaaagaatagctatcagtccaggcctgtatgggaagccttcaggctatgctgctacg
atgcaccgcgagggattcttgtgctgcaaagtgacagacacattgaacggggagagggtctcttttcccgtgtg
cacgtatgtgccagctacattgtgtgaccaaatgactggcatactggcaacagatgtcagtgcggacgacgcgc
aaaaactgctggttgggctcaaccagcgtatagtcgtcaacggtcgcacccagagaaacaccaataccatgaaa
aattacctttgcccgtagtggcccaggcatttgctaggtgggcaaaggaatataaggaagatcaagaagatga
aaggccactaggactacgagatagacagttagtcatggggtgttgttgggcttttagaaggcacaagataacat
ctatttataagcgcccggatacccaaaccatcatcaaagtgaacagcgatttccactcattcgtgctgcccagg
ataggcagtaacacattggagatcgggctgagaacaagaatcaggaaaatgttagaggagcacaaggagccgtc
acctctcattaccgccgaggacgtacaagaagctaagtgcgcagccgatgaggctaaggaggtgcgtgaagccg
aggagttgcgcgcagctctaccacctttggcagctgatgttgaggagcccactctggaagccgatgtcgacttg
atgttacaagaggctggggccggctcagtggagacacctcgtggcttgataaaggttaccagctacgctggcga
ggacaagatcggctcttacgctgtgctttctccgcaggctgtactcaagagtgaaaaattatcttgcatccacc
ctctcgctgaacaagtcatagtgataacacactctggccgaaaagggcgttatgccgtggaaccataccatggt
aaagtagtggtgccagagggacatgcaatacccgtccaggactttcaagctctgagtgaaagtgccaccattgt

2026201462 26 Feb 2026

gtacaacgaacgtgagttcgtaaacaggtacctgcaccatattgccacacatggaggagcgctgaacactgatg
aagaatattacaaaactgtcaagcccagcgagcacgacggcgaatacctgtacgacatcgacaggaaacagtgc
gtcaagaaagaactagtcactgggctagggctcacaggcgagctggtggatcctcccttccatgaattcgccta
cgagagtctgagaacacgaccagccgctccttaccaagtaccaaccataggggtgtatggcgtgccaggatcag
gcaagtctggcatcattaaaagcgcagtcaccaaaaaagatctagtggtgagcgccaagaaagaaaactgtgca
gaaattataagggacgtcaagaaaatgaaagggctggacgtcaatgccagaactgtggactcagtgctcttgaa
tggatgcaaacaccccgtagagaccctgtatattgacgaagcttttgcttgtcatgcaggtactctcagagcgc
tcatagccattataagacctaaaaaggcagtgctctgcggggatcccaaacagtgcggtttttttaacatgatg
tgcctgaaagtgcattttaaccacgagatttgcacacaagtcttccacaaaagcatctctcgccgttgcactaa
atctgtgacttcggtcgtctcaaccttgttttacgacaaaaaaatgagaacgacgaatccgaaagagactaaga
ttgtgattgacactaccggcagtaccaaacctaagcaggacgatctcattctcacttgtttcagagggtgggtg
aagcagttgcaaatagattacaaaggcaacgaaataatgacggcagctgcctctcaagggctgacccgtaaagg
tgtgtatgccgttcggtacaaggtgaatgaaaatcctctgtacgcacccacctcagaacatgtgaacgtcctac
tgacccgcacggaggaccgcatcgtgtggaaaacactagccggcgacccatggataaaaacactgactgccaag
taccctgggaatttcactgccacgatagaggagtggcaagcagagcatgatgccatcatgaggcacatcttgga
gagaccggaccctaccgacgtcttccagaataaggcaaacgtgtgttgggccaaggctttagtgccggtgctga
agaccgctggcatagacatgaccactgaacaatggaacactgtggattattttgaaacggacaaagctcactca
gcagagatagtattgaaccaactatgcgtgaggttctttggactcgatctggactccggtctattttctgcacc
cactgttccgttatccattaggaataatcactgggataactccccgtcgcctaacatgtacgggctgaataaag
aagtggtccgtcagctctctcgcaggtacccacaactgcctcgggcagttgccactggaagagtctatgacatg
aacactggtacactgcgcaattatgatccgcgcataaacctagtacctgtaaacagaagactgcctcatgcttt
agtcctccaccataatgaacacccacagagtgacttttcttcattcgtcagcaaattgaagggcagaactgtcc
tggtggtcggggaaaagttgtccgtcccaggcaaaatggttgactggttgtcagaccggcctgaggctaccttc
agagctcggctggatttaggcatcccaggtgatgtgcccaaatatgacataatatttgttaatgtgaggacccc
atataaataccatcactatcagcagtgtgaagaccatgccattaagcttagcatgttgaccaagaaagcttgtc
tgcatctgaatcccggcggaacctgtgtcagcataggttatggttacgctgacagggccagcgaaagcatcatt
ggtgctatagcgcggcagttcaagttttcccgggtatgcaaaccgaaatcctcacttgaagagacggaagttct
gtttgtattcattgggtacgatcgcaaggcccgtacgcacaatccttacaagctttcatcaaccttgaccaaca
tttatacaggttccagactccacgaagccggatgtgcaccctcatatcatgtggtgcgaggggatattgccacg
gccaccgaaggagtgattataaatgctgctaacagcaaaggacaacctggcggaggggtgtgcggagcgctgta
taagaaattcccggaaagcttcgatttacagccgatcgaagtaggaaaagcgcgactggtcaaaggtgcagcta
aacatatcattcatgccgtaggaccaaacttcaacaaagtttcggaggttgaaggtgacaaacagttggcagag
gcttatgagtccatcgctaagattgtcaacgataacaattacaagtcagtagcgattccactgttgtccaccgg
catcttttccgggaacaaagatcgactaacccaatcattgaaccatttgctgacagctttagacaccactgatg
cagatgtagccatatactgcagggacaagaaatgggaaatgactctcaaggaagcagtggctaggagagaagca
gtggaggagatatgcatatccgacgactcttcagtgacagaacctgatgcagagctggtgagggtgcatccgaa
gagttctttggctggaaggaagggctacagcacaagcgatggcaaaactttctcatatttggaagggaccaagt
ttcaccaggcggccaaggatatagcagaaattaatgccatgtggcccgttgcaacggaggccaatgagcaggta
tgcatgtatatcctcggagaaagcatgagcagtattaggtcgaaatgccccgtcgaagagtcggaagcctccac
accacctagcacgctgccttgcttgtgcatccatgccatgactccagaaagagtacagcgcctaaaagcctcac
gtccagaacaaattactgtgtgctcatcctttccattgccgaagtatagaatcactggtgtgcagaagatccaa
tgctcccagcctatattgttctcaccgaaagtgcctgcgtatattcatccaaggaagtatctcgtggaaacacc
accggtagacgagactccggagccatcggcagagaaccaatccacagaggggacacctgaacaaccaccactta
taaccgaggatgagaccaggactagaacgcctgagccgatcatcatcgaagaggaagaagaggatagcataagt
ttgctgtcagatggcccgacccaccaggtgctgcaagtcgaggcagacattcacgggccgccctctgtatctag
ctcatcctggtccattcctcatgcatccgactttgatgtggacagtttatccatacttgacaccctggagggag
ctagcgtgaccagcggggcaacgtcagccgagactaactcttacttcgcaaagagtatggagtttctggcgcga
ccggtgcctgcgcctcgaacagtattcaggaaccctccacatcccgctccgcgcacaagaacaccgtcacttgc
acccagcagggcctgctcgagaaccagcctagtttccaccccgccaggcgtgaatagggtgatcactagagagg
agctcgaggcgcttaccccgtcacgcactcctagcaggtcggtctcgagaaccagcctggtctccaacccgcca
ggcgtaaatagggtgattacaagagaggagtttgaggcgttcgtagcacaacaacaatgacggtttgatgcggg
tgcatacatcttttcctccgacaccggtcaagggcatttacaacaaaaatcagtaaggcaaacggtgctatccg
aagtggtgttggagaggaccgaattggagatttcgtatgccccgcgcctcgaccaagaaaaagaagaattacta
cgcaagaaattacagttaaatcccacacctgctaacagaagcagataccagtccaggaaggtggagaacatgaa
agccataacagctagacgtattctgcaaggcctagggcattatttgaaggcagaaggaaaagtggagtgctacc
gaaccctgcatcctgttccttttgtattcatctagtgtgaaccgtgccttttcaagccccaaggtcgcagtggaa
gcctgtaacgccatgttgaaagagaacttttccgactgtggcttcttactgtattattccagagtacgatgccta
tttggacatggttgacggagcttcatgctgcttagacactgccagtttttgccctgcaaagctgcgcagctttc
caaagaaacactcctatttggaacccacaatacgatcggcagtgccttcagcgatccagaacacgctccagaac
gtcctggcagctgccacaaaaagaaattgcaatgtcacgcaaatgagagaattgcccgtattggattcggcggc

2026201462 26 Feb 2026

ctttaatgtggaatgcttcaagaaatatgcgtgtaataatgaatattgggaaacgtttaaagaaaaccccatca
ggcttactgaagaaaacgtggtaaattacattaccaaattaaaaggaccaaaagctgctgctcttttgcgaag
acacataatttgaatatgttgcaggacataccaatggacaggtttgtaatggacttaaagagagacgtgaaagt
gactccaggaacaaaacatactgaagaacggcccaaggtacaggtgatccaggctgccgatccgctagcaacag
cgtatctgtgcggaatccaccgagagctggttaggagattaaatgcggtcctgcttccgaacattcatacactg
tttgatatgtcggctgaagactttgacgctattatagccgagcacttccagcctggggattgtgttctggaaac
tgacatcgcgtcgtttgataaaagtgaggacgacgccatggctctgaccgcgttaatgattctggaagacttag
gtgtggacgcagagctgttgacgctgattgaggcggctttcggcgaaatttcatcaatacatttgcccactaaa
actaaatttaaattcggagccatgatgaaatctggaatgttcctcacactgtttgtgaacacagtcattaacat
tgtaatcgcaagcagagtgttgagagaacggctaaccggatcaccatgtgcagcattcattggagatgacaata
tcgtgaaaggagtcaaatcggacaaattaatggcagacaggtgcgccacctggttgaatatggaagtcaagatt
atagatgctgtggtgggcgagaaagcgccttatttctgtggagggtttattttgtgtgactccgtgaccggcac
agcgtgccgtgtggcagacccccctaaaaaggctgtttaagcttggcaaacctctggcagcagacgatgaacatg
atgatgacaggagaagggcattgcatgaagagtcaacacgctggaaccgagtgggtattctttcagagctgtgc
aaggcagtagaatcaaggtatgaaaccgtaggaacttccatcatagttatggccatgactactctagctagcag
tgttaaatcattcagctacctgagaggggcccctataactctctacggcTAAcctgaatggactacgactatca
cgcccaaacatttacagccgcggtgtcaaaaaccgcgtggacgtggttaacatccctgctgggaggatcagccg
taattattataattggcttggtgctggctactattgtggccatgtacgtgctgaccaaccagaaacataattga
atacagcagcaattggcaagctgcttacatagaactcgcggcgattggcatgccgccttaaaatttttatttta
ttttttctttttctttccgaatcggattttgtttttaatatttcAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

TC-83 Delivery Vector(SEQ ID NO:7); TC-83 genome with nucleotides 7544-11175 deleted [alphavirus structural proteins removed]

ATAGGCGGCGCATGAGAGAAGCCCAGACCAATTACCTACCCAAAATGGAGAAAGTTCACGTTGACATCGAGGAA
GACAGCCCATTCCTCAGAGCTTTGCAGCGGAGCTTCCCGCAGTTTGAGGTAGAAGCCAAGCAGGTCACTGATAA
TGACCATGCTAATGCCAGAGCGTTTTCGCATCTGGCTTCAAAACTGATCGAAACGGAGGTGGACCCATCCGACA
CGATCCTTGACATTGGAAGTGCGCCCGCCCGCAGAATGTATTCTAAGCACAAGTATCATTGTATCTGTCCGATG
AGATGTGCGGAAGATCCGGACAGATTGTATAAGTATGCAACTAAGCTGAAGAAAAACTGTAAGGAAATAACTGA
TAAGGAATTGGACAAGAAAATGAAGGAGCTCGCCGCCGTCATGAGCGACCCTGACCTGGAAACTGAGACTATGT
GCCTCCACGACGACGAGTCGTGTCGCTACGAAGGGCAAGTCGCTGTTTACCAGGATGTATACGCGGTTGACGGA
CCGACAAGTCTCTATCACCAAGCCAATAAGGGAGTTAGAGTCGCCTACTGGATAGGCTTTGACACCACCCCTTT
TATGTTTAAGAACTTGGCTGGAGCATATCCATCATACTCTACCAACTGGGCCGACGAAACCGTGTTAACGGCTC
GTAACATAGGCCTATGCAGCTCTGACGTTATGGAGCGGTCACGTAGAGGGATGTCCATTCTTAGAAAGAAGTAT
TTGAAACCATCCAACAATGTTCTATTCTCTGTTGGCTCGACCATCTACCACGAGAAGAGGGACTTACTGAGGAG
CTGGCACCTGCCGTCTGTATTTCACTTACGTGGCAAGCAAAATTACACATGTCGGTGTGAGACTATAGTTAGTT
GCGACGGGTACGTCGTTAAAAGAATAGCTATCAGTCCAGGCCTGTATGGGAAGCCTTCAGGCTATGCTGCTACG
ATGCACCGCGAGGGATTCTTGTGCTGCAAAGTGACAGACACATTGAACGGGGAGAGGGTCTCTTTTCCCGTGTG
CACGTATGTGCCAGCTACATTGTGTGACCAAATGACTGGCATACTGGCAACAGATGTCAGTGCGGACGACGCGC
AAAAACTGCTGGTTGGGCTCAACCAGCGTATAGTCGTCAACGGTCGCACCCAGAGAAACACCAATACCATGAAA
AATTACCTTTTGCCCGTAGTGGCCCAGGCATTTGCTAGGTGGGCAAAGGAATATAAGGAAGATCAAGAAGATGA
AAGGCCACTAGGACTACGAGATAGACAGTTAGTCATGGGGTGTTGTTGGGCTTTTAGAAGGCACAAGATAACAT
CTATTTATAAGCGCCCGGATACCCAAACCATCATCAAAGTGAACAGCGATTTCCACTCATTCGTGCTGCCCAGG
ATAGGCAGTAACACATTGGAGATCGGGCTGAGAACAAGAATCAGGAAAATGTTAGAGGAGCACAAGGAGCCGTC
ACCTCTCATTACCGCCGAGGACGTACAAGAAGCTAAGTGCGCAGCCGATGAGGCTAAGGAGGTGCGTGAAGCCG
AGGAGTTGCGCGCAGCTCTACCACCTTTGGCAGCTGATGTTGAGGAGCCCACTCTGGAAGCCGATGTCGACTTG
ATGTTACAAGAGGCTGGGGCCGGCTCAGTGGAGACACCTCGTGGCTTGATAAAGGTTACCAGCTACGATGGCGA
GGACAAGATCGGCTCTTACGCTGTGCTTTCTCCGCAGGCTGTACTCAAGAGTGAAAAATTATCTTGCATCCACC
CTCTCGCTGAACAAGTCATAGTGATAACACACTCTGGCCGAAAAGGGCGTTATGCCGTGGAACCATACCATGGT
AAAGTAGTGGTGCCAGAGGGACATGCAATACCCGTCCAGGACTTTCAAGCTCTGAGTGAAAGTGCCACCATTGT
GTACAACGAACGTGAGTTCGTAAACAGGTACCTGCACCATATTGCCACACATGGAGGAGCGCTGAACACTGATG
AAGAATATTACAAAACTGTCAAGCCCAGCGAGCACGACGGCGAATACCTGTACGACATCGACAGGAAACAGTGC
GTCAAGAAAGAACTAGTCACTGGGCTAGGGCTCACAGGCGAGCTGGTGGATCCTCCCTTCCATGAATTCGCCTA
CGAGAGTCTGAGAACACGACCAGCCGCTCCTTACCAAGTACCAACCATAGGGGTGTATGGCGTGCCAGGATCAG
GCAAGTCTGGCATCATTAAAAGCGCAGTCACCAAAAAAGATCTAGTGGTGAGCGCCAAGAAAGAAAACTGTGCA
GAAATTATAAGGGACGTCAAGAAAATGAAAGGGCTGGACGTCAATGCCAGAACTGTGGACTCAGTGCTCTTGAA
TGGATGCAAACACCCCGTAGAGACCCTGTATATTGACGAAGCTTTTGCTTGTCATGCAGGTACTCTCAGAGCGC
TCATAGCCATTATAAGACCTAAAAAGGCAGTGCTCTGCGGGGATCCCAAACAGTGCGGTTTTTTTAACATGATG
TGCCTGAAAGTGCATTTTAACCACGAGATTTGCACACAAGTCTTCCACAAAAGCATCTCTCGCCGTTGCACTAA
ATCTGTGACTTCGGTCGTCTCAACCTTGTTTTACGACAAAAAAATGAGAACGACGAATCCGAAAGAGACTAAGA

2026201462 26 Feb 2026

TTGTGATTGACACTACCGGCAGTACCAAACCTAAGCAGGACGATCTCATTCTCACTTGTTTCAGAGGGTGGGTG
AAGCAGTTGCAAATAGATTACAAAGGCAACGAAATAATGACGGCAGCTGCCTCTCAAGGGCTGACCCGTAAAGG
TGTGTATGCCGTTCGGTACAAGGTGAATGAAAATCCTCTGTACGCACCCACCTCAGAACATGTGAACGTCCTAC
TGACCCGCACGGAGGACCGCATCGTGTGGAAAACACTAGCCGGCGACCCATGGATAAAAACACTGACTGCCAAG
TACCCTGGGAATTTCACTGCCACGATAGAGGAGTGGCAAGCAGAGCATGATGCCATCATGAGGCACATCTTGGA
GAGACCGGACCCTACCGACGTCTTCCAGAATAAGGCAAACGTGTGTTGGGCCAAGGCTTTAGTGCCGGTGCTGA
AGACCGCTGGCATAGACATGACCACTGAACAATGGAACACTGTGGATTATTTTGAAACGGACAAAGCTCACTCA
GCAGAGATAGTATTGAACCAACTATGCGTGAGGTTCTTTGGACTCGATCTGGACTCCGGTCTATTTTCTGCACC
CACTGTTCCGTTATCCATTAGGAATAATCACTGGGATAACTCCCCGTCGCCTAACATGTACGGGCTGAATAAAG
AAGTGGTCCGTCAGCTCTCTCGCAGGTACCCACAACTGCCTCGGGCAGTTGCCACTGGAAGAGTCTATGACATG
AACACTGGTACACTGCGCAATTATGATCCGCGCATAAACCTAGTACCTGTAAACAGAAGACTGCCTCATGCTTT
AGTCCTCCACCATAATGAACACCCACAGAGTGACTTTTCTTCATTCGTCAGCAAATTGAAGGGCAGAACTGTCC
TGGTGGTCGGGGAAAAGTTGTCCGTCCCAGGCAAAATGGTTGACTGGTTGTCAGACCGGCCTGAGGCTACCTTC
AGAGCTCGGCTGGATTTAGGCATCCCAGGTGATGTGCCCAAATATGACATAATATTTGTTAATGTGAGGACCCC
ATATAAATACCATCACTATCAGCAGTGTGAAGACCATGCCATTAAGCTTAGCATGTTGACCAAGAAAGCTTGTC
TGCATCTGAATCCCGGCGGAACCTGTGTCAGCATAGGTTATGGTTACGCTGACAGGGCCAGCGAAAGCATCATT
GGTGCTATAGCGCGGCAGTTCAAGTTTTCCCGGGTATGCAAACCGAAATCCTCACTTGAAGAGACGGAAGTTCT
GTTTGTATTCATTGGGTACGATCGCAAGGCCCGTACGCACAATCCTTACAAGCTTTCATCAACCTTGACCAACA
TTTATACAGGTTCCAGACTCCACGAAGCCGGATGTGCACCCTCATATCATGTGGTGCGAGGGGATATTGCCACG
GCCACCGAAGGAGTGATTATAAATGCTGCTAACAGCAAAGGACAACCTGGCGGAGGGGTGTGCGGAGCGCTGTA
TAAGAAATTCCCGGAAAGCTTCGATTTACAGCCGATCGAAGTAGGAAAAGCGCGACTGGTCAAAGGTGCAGCTA
AACATATCATTCATGCCGTAGGACCAAACTTCAACAAAGTTTCGGAGGTTGAAGGTGACAAACAGTTGGCAGAG
GCTTATGAGTCCATCGCTAAGATTGTCAACGATAACAATTACAAGTCAGTAGCGATTCCACTGTTGTCCACCGG
CATCTTTTCCGGGAACAAAGATCGACTAACCCAATCATTGAACCATTTGCTGACAGCTTTAGACACCACTGATG
CAGATGTAGCCATATACTGCAGGGACAAGAAATGGGAAATGACTCTCAAGGAAGCAGTGGCTAGGAGAGAAGCA
GTGGAGGAGATATGCATATCCGACGACTCTTCAGTGACAGAACCTGATGCAGAGCTGGTGAGGGTGCATCCGAA
GAGTTCTTTGGCTGGAAGGAAGGGCTACAGCACAAGCGATGGCAAAACTTTCTCATATTTGGAAGGGACCAAGT
TTCACCAGGCGGCCAAGGATATAGCAGAAATTAATGCCATGTGGCCCGTTGCAACGGAGGCCAATGAGCAGGTA
TGCATGTATATCCTCGGAGAAAGCATGAGCAGTATTAGGTCGAAATGCCCCGTCGAAGAGTCGGAAGCCTCCAC
ACCACCTAGCACGCTGCCTTGCTTGTGCATCCATGCCATGACTCCAGAAAGAGTACAGCGCCTAAAAGCCTCAC
GTCCAGAACAAATTACTGTGTGCTCATCCTTTCCATTGCCGAAGTATAGAATCACTGGTGTGCAGAAGATCCAA
TGCTCCCAGCCTATATTGTTCTCACCGAAAGTGCCTGCGTATATTCATCCAAGGAAGTATCTCGTGGAAACACC
ACCGGTAGACGAGACTCCGGAGCCATCGGCAGAGAACCAATCCACAGAGGGGACACCTGAACAACCACCACTTA
TAACCGAGGATGAGACCAGGACTAGAACGCCTGAGCCGATCATCATCGAAGAGGAAGAAGAGGATAGCATAAGT
TTGCTGTCAGATGGCCCGACCCACCAGGTGCTGCAAGTCGAGGCAGACATTCACGGGCCGCCCTCTGTATCTAG
CTCATCCTGGTCCATTCCTCATGCATCCGACTTTGATGTGGACAGTTTATCCATACTTGACACCCTGGAGGGAG
CTAGCGTGACCAGCGGGGCAACGTCAGCCGAGACTAACTCTTACTTCGCAAAGAGTATGGAGTTTCTGGCGCGA
CCGGTGCCTGCGCCTCGAACAGTATTCAGGAACCCTCCACATCCCGCTCCGCGCACAAGAACACCGTCACTTGC
ACCCAGCAGGGCCTGCTCGAGAACCAGCCTAGTTTCCACCCCGCCAGGCGTGAATAGGGTGATCACTAGAGAGG
AGCTCGAGGCGCTTACCCCGTCACGCACTCCTAGCAGGTCGGTCTCGAGAACCAGCCTGGTCTCCAACCCGCCA
GGCGTAAATAGGGTGATTACAAGAGAGGAGTTTGAGGCGTTCGTAGCACAACAACAATGACGGTTTGATGCGGG
TGCATACATCTTTTCCTCCGACACCGGTCAAGGGCATTTACAACAAAAATCAGTAAGGCAAACGGTGCTATCCG
AAGTGGTGTTGGAGAGGACCGAATTGGAGATTTCGTATGCCCCGCGCCTCGACCAAGAAAAAGAAGAATTACTA
CGCAAGAAATTACAGTTAAATCCCACACCTGCTAACAGAAGCAGATACCAGTCCAGGAAGGTGGAGAACATGAA
AGCCATAACAGCTAGACGTATTCTGCAAGGCCTAGGGCATTATTTGAAGGCAGAAGGAAAAGTGGAGTGCTACC
GAACCCTGCATCCTGTTCCTTTGTATTCATCTAGTGTGAACCGTGCCTTTTCAAGCCCCAAGGTCGCAGTGGAA
GCCTGTAACGCCATGTTGAAAGAGAACTTTCCGACTGTGGCTTCTTACTGTATTATTCCAGAGTACGATGCCTA
TTTGGACATGGTTGACGGAGCTTCATGCTGCTTAGACACTGCCAGTTTTTGCCCTGCAAAGCTGCGCAGCTTTC
CAAAGAAACACTCCTATTTGGAACCCACAATACGATCGGCAGTGCCTTCAGCGATCCAGAACACGCTCCAGAAC
GTCCTGGCAGCTGCCACAAAAAGAAATTGCAATGTCACGCAAATGAGAGAATTGCCCGTATTGGATTCGGCGGC
CTTTAATGTGGAATGCTTCAAGAAATATGCGTGTAATAATGAATATTGGGAAACGTTTAAAGAAAACCCCATCA
GGCTTACTGAAGAAAACGTGGTAAATTACATTACCAAATTAAAAGGACCAAAAGCTGCTGCTCTTTTTGCGAAG
ACACATAATTTGAATATGTTGCAGGACATACCAATGGACAGGTTTGTAATGGACTTAAAGAGAGACGTGAAAGT
GACTCCAGGAACAAAACATACTGAAGAACGGCCCAAGGTACAGGTGATCCAGGCTGCCGATCCGCTAGCAACAG
CGTATCTGTGCGGAATCCACCGAGAGCTGGTTAGGAGATTAAATGCGGTCCTGCTTCCGAACATTCATACACTG
TTTGATATGTCGGCTGAAGACTTTGACGCTATTATAGCCGAGCACTTCCAGCCTGGGGATTGTGTTCTGGAAAC
TGACATCGCGTCGTTTGATAAAAGTGAGGACGACGCCATGGCTCTGACCGCGTTAATGATTCTGGAAGACTTAG
GTGTGGACGCAGAGCTGTTGACGCTGATTGAGGCGGCTTTCGGCGAAATTTCATCAATACATTTGCCCACTAAA
ACTAAATTTAAATTCGGAGCCATGATGAAATCTGGAATGTTCCTCACACTGTTTGTGAACACAGTCATTAACAT
TGTAATCGCAAGCAGAGTGTTGAGAGAACGGCTAACCGGATCACCATGTGCAGCATTCATTGGAGATGACAATA

26 Feb 2026
2026201462

TCGTGAAAGGAGTCAAATCGGACAAATTAATGGCAGACAGGTGCGCCACCTGGTTGAATATGGAAGTCAAGATT
ATAGATGCTGTGGTGGGCGAGAAAGCGCCTTATTTCTGTGGAGGGTTTATTTTGTGTGACTCCGTGACCGGCAC
AGCGTGCCGTGTGGCAGACCCCCTAAAAAGGCTGTTTAAGCTTGGCAAACCTCTGGCAGCAGACGATGAACATG
ATGATGACAGGAGAAGGGCATTGCATGAAGAGTCAACACGCTGGAACCGAGTGGGTATTCTTTCAGAGCTGTGC
AAGGCAGTAGAATCAAGGTATGAAACCGTAGGAACTTCCATCATAGTTATGGCCATGACTACTCTAGCTAGCAG
TGTTAAATCATTCAGCTACCTGAGAGGGGCCCCTATAACTCTCTACGGCTAACCTGAATGGACTACGACTATCA
CGCCCAAACATTTACAGCCGCGGTGTCAAAAACCGCGTGGACGTGGTTAACATCCCTGCTGGGAGGATCAGCCG
TAATTATTATAATTGGCTTGGTGCTGGCTACTATTGTGGCCATGTACGTGCTGACCAACCAGAAACATAATTGA
ATACAGCAGCAATTGGCAAGCTGCTTACATAGAACTCGCGGCGATTGGCATGCCGCCTTAAAATTTTTATTTTA
TTTTTCTTTTCTTTTCCGAATCGGATTTTGTTTTTAATATTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

VEE Production Vector (SEQ ID NO:8); VEE genome with nucleotides 7544-11175 deleted, plus 5’ T7-promoter, plus 3’ restriction sites

TAATACGACTCACTATAGGATGggcggcgcatgagagaagcccagaccaattacctacccaaaATGGagaaagt
tcacgttgacatcgaggaagacagcccattcctcagagctttgcagcggagcttcccgcagtttgaggtagaag
ccaagcaggtcactgataatgaccatgctaatgccagagcgttttcgcatctggcttcaaaactgatcgaaacg
gaggtggacccatccgacacgatccttgacattggaagtgcgcccgcccgcagaatgtattctaagcacaagta
tcattgtatctgtccgatgagatgtgcggaagatccggacagattgtataagtatgcaactaagctgaagaaaa
actgtaaggaaataactgataaggaattggacaagaaaatgaaggagctcgccgccgtcatgagcgaccctgac
ctggaaactgagactatgtgcctccacgacgacgagtcgtgtcgctacgaagggcaagtcgctgtttaccagga
tgtatacgcggttgacggaccgacaagtctctatcaccaagccaataagggagttagagtcgcctactggatag
gctttgacaccacccctttatgtttaagaacttggctggagcatatccatcatactctaccaactgggccgac
gaaaccgtgttaacggctcgtaacataggcctatgcagctctgacgttatggagcggtcacgtagagggatgtc
cattcttagaaagaagtatttgaaaccatccaacaatgttctattctctgttggctcgaccatctaccacgaga
agagggacttactgaggagctggcacctgccgtctgtatttcacttacgtggcaagcaaaattacacatgtcgg
tgtgagactatagttagttgcgacgggtacgtcgttaaaagaatagctatcagtccaggcctgtatgggaagcc
ttcaggctatgctgctacgatgcaccgcgagggattcttgtgctgcaaagtgacagacacattgaacggggaga
gggtctcttttcccgtgtgcacgtatgtgccagctacattgtgtgaccaaatgactggcatactggcaacagat
gtcagtgcggacgacgcgcaaaaactgctggttgggctcaaccagcgtatagtcgtcaacggtcgcacccagag
aaacaccaataccatgaaaaattacctttgcccgtagtggcccaggcatttgctaggtgggcaaaggaatata
aggaagatcaagaagatgaaaggccactaggactacgagatagacagttagtcatggggtgttgttgggctttt
agaaggcacaagataacatctatttataagcgcccggatacccaaaccatcatcaaagtgaacagcgatttcca
ctcattcgtgctgcccaggataggcagtaacacattggagatcgggctgagaacaagaatcaggaaaatgttag
aggagcacaaggagccgtcacctctcattaccgccgaggacgtacaagaagctaagtgcgcagccgatgaggct
aaggaggtgcgtgaagccgaggagttgcgcgcagctctaccacctttggcagctgatgttgaggagcccactct
ggaagccgatgtcgacttgatgttacaagaggctggggccggctcagtggagacacctcgtggcttgataaagg
ttaccagctacgctggcgaggacaagatcggctcttacgctgtgctttctccgcaggctgtactcaagagtgaa
aaattatcttgcatccaccctctcgctgaacaagtcatagtgataacacactctggccgaaaagggcgttatgc
cgtggaaccataccatggtaaagtagtggtgccagagggacatgcaatacccgtccaggactttcaagctctga
gtgaaagtgccaccattgtgtacaacgaacgtgagttcgtaaacaggtacctgcaccatattgccacacatgga
ggagcgctgaacactgatgaagaatattacaaaactgtcaagcccagcgagcacgacggcgaatacctgtacga
catcgacaggaaacagtgcgtcaagaaagaactagtcactgggctagggctcacaggcgagctggtggatcctc
ccttccatgaattcgcctacgagagtctgagaacacgaccagccgctccttaccaagtaccaaccataggggtg
tatggcgtgccaggatcaggcaagtctggcatcattaaaagcgcagtcaccaaaaaagatctagtggtgagcgc
caagaaagaaaactgtgcagaaattataagggacgtcaagaaaatgaaaggctggacgtcaatgccagaactg
tggactcagtgctcttgaatggatgcaaacaccccgtagagaccctgtatattgacgaagcttttgcttgtcat
gcaggtactctcagagcgctcatagccattataagacctaaaaaggcagtgctctgcggggatcccaaacagtg
cggtttttttaacatgatgtgcctgaaagtgcattttaaccacgagatttgcacacaagtcttccacaaaagca
tctctcgccgttgcactaaatctgtgacttcggtcgtctcaaccttgttttacgacaaaaaaatgagaacgacg
aatccgaaagagactaagattgtgattgacactaccggcagtaccaaacctaagcaggacgatctcattctcac
ttgtttcagagggtgggtgaagcagttgcaaatagattacaaaggcaacgaaataatgacggcagctgcctctc
aagggctgacccgtaaaggtgtgtatgccgttcggtacaaggtgaatgaaaatcctctgtacgcacccacctca
gaacatgtgaacgtcctactgacccgcacggaggaccgcatcgtgtggaaaacactagccggcgacccatggat
aaaaacactgactgccaagtaccctgggaatttcactgccacgatagaggagtggcaagcagagcatgatgcca
tcatgaggcacatcttggagagaccggaccctaccgacgtcttccagaataaggcaaacgtgtgttgggccaag
gctttagtgccggtgctgaagaccgctggcatagacatgaccactgaacaatggaacactgtggattattttga
aacggacaaagctcactcagcagagatagtattgaaccaactatgcgtgaggttctttggactcgatctggact
ccggtctatttttctgcacccactgttccgttatccattaggaataatcactgggataactccccgtcgcctaac
atgtacgggctgaataaagaagtggtccgtcagctctctcgcaggtacccacaactgcctcgggcagttgccac

2026201462 26 Feb 2026

tggaagagtctatgacatgaacactggtacactgcgcaattatgatccgcgcataaacctagtacctgtaaaca
gaagactgcctcatgctttagtcctccaccataatgaacacccacagagtgacttttcttcattcgtcagcaaa
ttgaagggcagaactgtcctggtggtcggggaaaagttgtccgtcccaggcaaaatggttgactggttgtcaga
ccggcctgaggctaccttcagagctcggctggatttaggcatcccaggtgatgtgcccaaatatgacataatat
ttgttaatgtgaggaccccatataaataccatcactatcagcagtgtgaagaccatgccattaagcttagcatg
ttgaccaagaaagcttgtctgcatctgaatcccggcggaacctgtgtcagcataggttatggttacgctgacag
ggccagcgaaagcatcattggtgctatagcgcggcagttcaagttttcccgggtatgcaaaccgaaatcctcac
ttgaagagacggaagttctgtttgtattcattgggtacgatcgcaaggcccgtacgcacaatccttacaagctt
tcatcaaccttgaccaacatttatacaggttccagactccacgaagccggatgtgcaccctcatatcatgtggt
gcgaggggatattgccacggccaccgaaggagtgattataaatgctgctaacagcaaaggacaacctggcggag
gggtgtgcggagcgctgtataagaaattcccggaaagcttcgatttacagccgatcgaagtaggaaaagcgcga
ctggtcaaaggtgcagctaaacatatcattcatgccgtaggaccaaacttcaacaaagtttcggaggttgaagg
tgacaaacagttggcagaggcttatgagtccatcgctaagattgtcaacgataacaattacaagtcagtagcga
ttccactgttgtccaccggcatcttttccgggaacaaagatcgactaacccaatcattgaaccatttgctgaca
gctttagacaccactgatgcagatgtagccatatactgcagggacaagaaatgggaaatgactctcaaggaagc
agtggctaggagagaagcagtggaggagatatgcatatccgacgactcttcagtgacagaacctgatgcagagc
tggtgagggtgcatccgaagagttctttggctggaaggaagggctacagcacaagcgatggcaaaactttctca
tatttggaagggaccaagtttcaccaggcggccaaggatatagcagaaattaatgccatgtggcccgttgcaac
ggaggccaatgagcaggtatgcatgtatatcctcggagaaagcatgagcagtattaggtcgaaatgccccgtcg
aagagtcggaagcctccacaccacctagcacgctgccttgcttgtgcatccatgccatgactccagaaagagta
cagcgcctaaaagcctcacgtccagaacaaattactgtgtgctcatcctttccattgccgaagtatagaatcac
tggtgtgcagaagatccaatgctcccagcctatattgttctcaccgaaagtgcctgcgtatattcatccaagga
agtatctcgtggaaacaccaccggtagacgagactccggagccatcggcagagaaccaatccacagaggggaca
cctgaacaaccaccacttataaccgaggatgagaccaggactagaacgcctgagccgatcatcatcgaagagga
agaagaggatagcataagtttgctgtcagatggcccgacccaccaggtgctgcaagtcgaggcagacattcacg
ggccgccctctgtatctagctcatcctggtccattcctcatgcatccgactttgatgtggacagtttatccata
cttgacaccctggagggagctagcgtgaccagcggggcaacgtcagccgagactaactcttacttcgcaaagag
tatggagtttctggcgcgaccggtgcctgcgcctcgaacagtattcaggaaccctccacatcccgctccgcgca
caagaacaccgtcacttgcacccagcagggcctgctcgagaaccagcctagtttccaccccgccaggcgtgaat
agggtgatcactagagaggagctcgaggcgcttaccccgtcacgcactcctagcaggtcggtctcgagaaccag
cctggtctccaacccgccaggcgtaaatagggtgattacaagagaggagtttgaggcgttcgtagcacaacaac
aatgacggtttgatgcgggtgcatacatcttttcctccgacaccggtcaagggcatttacaacaaaaatcagta
aggcaaacggtgctatccgaagtggtgttggagaggaccgaattggagatttcgtatgccccgcgcctcgacca
agaaaaagaagaattactacgcaagaaattacagttaaatcccacacctgctaacagaagcagataccagtcca
ggaaggtggagaacatgaaagccataacagctagacgtattctgcaaggcctagggcattatttgaaggcagaa
ggaaaagtggagtgctaccgaaccctgcatcctgttcctttgtattcatctagtgtgaaccgtgccttttcaag
ccccaaggtcgcagtggaagcctgtaacgccatgttgaaagagaactttccgactgtggcttcttactgtatta
ttccagagtacgatgcctatttggacatggttgacggagcttcatgctgcttagacactgccagtttttgccct
gcaaagctgcgcagctttccaaagaaacactcctatttggaacccacaatacgatcggcagtgccttcagcgat
ccagaacacgctccagaacgtcctggcagctgccacaaaaagaaattgcaatgtcacgcaaatgagagaattgc
ccgtattggattcggcggcctttaatgtggaatgcttcaagaaatatgcgtgtaataatgaatattgggaaacg
tttaaagaaaaccccatcaggcttactgaagaaaacgtggtaaattacattaccaaattaaaaggaccaaaagc
tgctgctctttttgcgaagacacataatttgaatatgttgcaggacataccaatggacaggtttgtaatggact
taaagagagacgtgaaagtgactccaggaacaaaacatactgaagaacggcccaaggtacaggtgatccaggct
gccgatccgctagcaacagcgtatctgtgcggaatccaccgagagctggttaggagattaaatgcggtcctgct
tccgaacattcatacactgtttgatatgtcggctgaagactttgacgctattatagccgagcacttccagcctg
gggattgtgttctggaaactgacatcgcgtcgtttgataaaagtgaggacgacgccatggctctgaccgcgtta
atgattctggaagacttaggtgtggacgcagagctgttgacgctgattgaggcggctttcggcgaaatttcatc
aatacatttgcccactaaaactaaatttaaattcggagccatgatgaaatctggaatgttcctcacactgtttg
tgaacacagtcattaacattgtaatcgcaagcagagtgttgagagaacggctaaccggatcaccatgtgcagca
ttcattggagatgacaatatcgtgaaaggagtcaaatcggacaaattaatggcagacaggtgcgccacctggtt
gaatatggaagtcaagattatagatgctgtggtgggcgagaaagcgccttatttctgtggagggtttatttgt
gtgactccgtgaccggcacagcgtgccgtgtggcagacccccctaaaaaggctgtttaagcttggcaaacctctg
gcagcagacgatgaacatgatgatgacaggagaagggcattgcatgaagagtcaacacgctggaaccgagtggg
tattctttcagagctgtgcaaggcagtagaatcaaggtatgaaaccgtaggaacttccatcatagttatggcca
tgactactctagctagcagtgttaaatcattcagctacctgagaggggcccctataactctctacggcTAAcct
gaatggactacgactatcacgcccaaacatttacagccgcggtgtcaaaaaccgcgtggacgtggttaacatcc
ctgctgggaggatcagccgtaattattataattggcttggtgctggctactattgtggccatgtacgtgctgac
caaccagaaacataattgaatacagcagcaattggcaagctgcttacatagaactcgcggcgattggcatgccg
ccttaaaatttttatttattttttctttttctttttccgaatcggattttgtttttaatatttcAAAAAAAAAAA

2026201462 26 Feb 2026

AAAA

2026201462 26 Feb 2026

GCGAGGGGATATTGCCACGGCCACCGAAGGAGTGATTATAAATGCTGCTAACAGCAAAGGACAACCTGGCGGAG
GGGTGTGCGGAGCGCTGTATAAGAAATTCCCGGAAAGCTTCGATTTACAGCCGATCGAAGTAGGAAAAGCGCGA
CTGGTCAAAGGTGCAGCTAAACATATCATTCATGCCGTAGGACCAAACTTCAACAAAGTTTCGGAGGTTGAAGG
TGACAAACAGTTGGCAGAGGCTTATGAGTCCATCGCTAAGATTGTCAACGATAACAATTACAAGTCAGTAGCGA
TTCCACTGTTGTCCACCGGCATCTTTTCCGGGAACAAAGATCGACTAACCCAATCATTGAACCATTTGCTGACA
GCTTTAGACACCACTGATGCAGATGTAGCCATATACTGCAGGGACAAGAAATGGGAAATGACTCTCAAGGAAGC
AGTGGCTAGGAGAGAAGCAGTGGAGGAGATATGCATATCCGACGACTCTTCAGTGACAGAACCTGATGCAGAGC
TGGTGAGGGTGCATCCGAAGAGTTCTTTGGCTGGAAGGAAGGGCTACAGCACAAGCGATGGCAAAACTTTCTCA
TATTTGGAAGGGACCAAGTTTCACCAGGCGGCCAAGGATATAGCAGAAATTAATGCCATGTGGCCCGTTGCAAC
GGAGGCCAATGAGCAGGTATGCATGTATATCCTCGGAGAAAGCATGAGCAGTATTAGGTCGAAATGCCCCGTCG
AAGAGTCGGAAGCCTCCACACCACCTAGCACGCTGCCTTGCTTGTGCATCCATGCCATGACTCCAGAAAGAGTA
CAGCGCCTAAAAGCCTCACGTCCAGAACAAATTACTGTGTGCTCATCCTTTCCATTGCCGAAGTATAGAATCAC
TGGTGTGCAGAAGATCCAATGCTCCCAGCCTATATTGTTCTCACCGAAAGTGCCTGCGTATATTCATCCAAGGA
AGTATCTCGTGGAAACACCACCGGTAGACGAGACTCCGGAGCCATCGGCAGAGAACCAATCCACAGAGGGGACA
CCTGAACAACCACCACTTATAACCGAGGATGAGACCAGGACTAGAACGCCTGAGCCGATCATCATCGAAGAGGA
AGAAGAGGATAGCATAAGTTTGCTGTCAGATGGCCCGACCCACCAGGTGCTGCAAGTCGAGGCAGACATTCACG
GGCCGCCCTCTGTATCTAGCTCATCCTGGTCCATTCCTCATGCATCCGACTTTGATGTGGACAGTTTATCCATA
CTTGACACCCTGGAGGGAGCTAGCGTGACCAGCGGGGCAACGTCAGCCGAGACTAACTCTTACTTCGCAAAGAG
TATGGAGTTTCTGGCGCGACCGGTGCCTGCGCCTCGAACAGTATTCAGGAACCCTCCACATCCCGCTCCGCGCA
CAAGAACACCGTCACTTGCACCCAGCAGGGCCTGCTCGAGAACCAGCCTAGTTTCCACCCCGCCAGGCGTGAAT
AGGGTGATCACTAGAGAGGAGCTCGAGGCGCTTACCCCGTCACGCACTCCTAGCAGGTCGGTCTCGAGAACCAG
CCTGGTCTCCAACCCGCCAGGCGTAAATAGGGTGATTACAAGAGAGGAGTTTGAGGCGTTCGTAGCACAACAAC
AATGACGGTTTGATGCGGGTGCATACATCTTTTCCTCCGACACCGGTCAAGGGCATTTACAACAAAAATCAGTA
AGGCAAACGGTGCTATCCGAAGTGGTGTTGGAGAGGACCGAATTGGAGATTTCGTATGCCCCGCGCCTCGACCA
AGAAAAAGAAGAATTACTACGCAAGAAATTACAGTTAAATCCCACACCTGCTAACAGAAGCAGATACCAGTCCA
GGAAGGTGGAGAACATGAAAGCCATAACAGCTAGACGTATTCTGCAAGGCCTAGGGCATTATTTGAAGGCAGAA
GGAAAAGTGGAGTGCTACCGAACCCTGCATCCTGTTCCTTTGTATTCATCTAGTGTGAACCGTGCCTTTTCAAG
CCCCAAGGTCGCAGTGGAAGCCTGTAACGCCATGTTGAAAGAGAACTTTCCGACTGTGGCTTCTTACTGTATTA
TTCCAGAGTACGATGCCTATTTGGACATGGTTGACGGAGCTTCATGCTGCTTAGACACTGCCAGTTTTTGCCCT
GCAAAGCTGCGCAGCTTTCCAAAGAAACACTCCTATTTGGAACCCACAATACGATCGGCAGTGCCTTCAGCGAT
CCAGAACACGCTCCAGAACGTCCTGGCAGCTGCCACAAAAAGAAATTGCAATGTCACGCAAATGAGAGAATTGC
CCGTATTGGATTCGGCGGCCTTTAATGTGGAATGCTTCAAGAAATATGCGTGTAATAATGAATATTGGGAAACG
TTTAAAGAAAACCCCATCAGGCTTACTGAAGAAAACGTGGTAAATTACATTACCAAATTAAAAGGACCAAAAGC
TGCTGCTCTTTTTGCGAAGACACATAATTTGAATATGTTGCAGGACATACCAATGGACAGGTTTGTAATGGACT
TAAAGAGAGACGTGAAAGTGACTCCAGGAACAAAACATACTGAAGAACGGCCCAAGGTACAGGTGATCCAGGCT
GCCGATCCGCTAGCAACAGCGTATCTGTGCGGAATCCACCGAGAGCTGGTTAGGAGATTAAATGCGGTCCTGCT
TCCGAACATTCATACACTGTTTGATATGTCGGCTGAAGACTTTGACGCTATTATAGCCGAGCACTTCCAGCCTG
GGGATTGTGTTCTGGAAACTGACATCGCGTCGTTTGATAAAAGTGAGGACGACGCCATGGCTCTGACCGCGTTA
ATGATTCTGGAAGACTTAGGTGTGGACGCAGAGCTGTTGACGCTGATTGAGGCGGCTTTCGGCGAAATTTCATC
AATACATTTGCCCACTAAAACTAAATTTAAATTCGGAGCCATGATGAAATCTGGAATGTTCCTCACACTGTTTG
TGAACACAGTCATTAACATTGTAATCGCAAGCAGAGTGTTGAGAGAACGGCTAACCGGATCACCATGTGCAGCA
TTCATTGGAGATGACAATATCGTGAAAGGAGTCAAATCGGACAAATTAATGGCAGACAGGTGCGCCACCTGGTT
GAATATGGAAGTCAAGATTATAGATGCTGTGGTGGGCGAGAAAGCGCCTTATTTCTGTGGAGGGTTTATTTTGT
GTGACTCCGTGACCGGCACAGCGTGCCGTGTGGCAGACCCCCTAAAAAGGCTGTTTAAGCTTGGCAAACCTCTG
GCAGCAGACGATGAACATGATGATGACAGGAGAAGGGCATTGCATGAAGAGTCAACACGCTGGAACCGAGTGGG
TATTCTTTCAGAGCTGTGCAAGGCAGTAGAATCAAGGTATGAAACCGTAGGAACTTCCATCATAGTTATGGCCA
TGACTACTCTAGCTAGCAGTGTTAAATCATTCAGCTACCTGAGAGGGGCCCCTATAACTCTCTACGGCTAACCT
GAATGGACTACGACTATCACGCCCAAACATTTACAGCCGCGGTGTCAAAAACCGCGTGGACGTGGTTAACATCC
CTGCTGGGAGGATCAGCCGTAATTATTATAATTGGCTTGGTGCTGGCTACTATTGTGGCCATGTACGTGCTGAC
CAACCAGAAACATAATTGAATACAGCAGCAATTGGCAAGCTGCTTACATAGAACTCGCGGCGATTGGCATGCCG
CCTTAAAATTTTTATTTTATTTTTCTTTTCTTTTCCGAATCGGATTTTGTTTTTAATATTTCAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAtacgta
gtttaaac

VEE-UbAAY (SEQ ID NO:14); VEE delivery vector with MHC class I mouse tumor epitopes SIINFEKL and AH1-A5 inserted

ATGggcggcgcatgagagaagcccagaccaattacctacccaaaatggagaaagttcacgttgacatc
gaggaagacagcccattcctcagagctttgcagcggagcttcccgcagtttgaggtagaagccaagcaggtcac
tgataatgaccatgctaatgccagagcgttttcgcatctggcttcaaaactgatcgaaacggaggtggacccat
ccgacacgatccttgacattggaagtgcgcccgcccgcagaatgtattctaagcacaagtatcattgtatctgt
ccgatgagatgtgcggaagatccggacagattgtataagtatgcaactaagctgaagaaaaactgtaaggaaat

2026201462 26 Feb 2026

aactgataaggaattggacaagaaaatgaaggagctcgccgccgtcatgagcgaccctgacctggaaactgaga
ctatgtgcctccacgacgacgagtcgtgtcgctacgaagggcaagtcgctgtttaccaggatgtatacgcggtt
gacggaccgacaagtctctatcaccaagccaataagggagttagagtcgcctactggataggctttgacaccac
ccctttttatgtttaagaacttggctggagcatatccatcatactctaccaactgggccgacgaaaccgtgttaa
cggctcgtaacataggcctatgcagctctgacgttatggagcggtcacgtagagggatgtccattcttagaaag
aagtatttgaaaccatccaacaatgttctattctctgttggctcgaccatctaccacgagaagagggacttact
gaggagctggcacctgccgtctgtatttcacttacgtggcaagcaaaattacacatgtcggtgtgagactatag
ttagttgcgacgggtacgtcgttaaaagaatagctatcagtccaggcctgtatgggaagccttcaggctatgct
gctacgatgcaccgcgagggattcttgtgctgcaaagtgacagacacattgaacggggagagggtctcttttcc
cgtgtgcacgtatgtgccagctacattgtgtgaccaaatgactggcatactggcaacagatgtcagtgcggacg
acgcgcaaaaactgctggttgggctcaaccagcgtatagtcgtcaacggtcgcacccagagaaacaccaatacc
atgaaaaattacctttgcccgtagtggcccaggcatttgctaggtgggcaaaggaatataaggaagatcaaga
agatgaaaggccactaggactacgagatagacagttagtcatggggtgttgttgggcttttagaaggcacaaga
taacatctatttataagcgcccggatacccaaaccatcatcaaagtgaacagcgatttccactcattcgtgctg
cccaggataggcagtaacacattggagatcgggctgagaacaagaatcaggaaaatgttagaggagcacaagga
gccgtcacctctcattaccgccgaggacgtacaagaagctaagtgcgcagccgatgaggctaaggaggtgcgtg
aagccgaggagttgcgcgcagctctaccacctttggcagctgatgttgaggagcccactctggaagccgatgtc
gacttgatgttacaagaggctggggccggctcagtggagacacctcgtggcttgataaaggttaccagctacgc
tggcgaggacaagatcggctcttacgctgtgctttctccgcaggctgtactcaagagtgaaaaattatcttgca
tccaccctctcgctgaacaagtcatagtgataacacactctggccgaaaagggcgttatgccgtggaaccatac
catggtaaagtagtggtgccagagggacatgcaatacccgtccaggactttcaagctctgagtgaaagtgccac
cattgtgtacaacgaacgtgagttcgtaaacaggtacctgcaccatattgccacacatggaggagcgctgaaca
ctgatgaagaatattacaaaactgtcaagcccagcgagcacgacggcgaatacctgtacgacatcgacaggaaa
cagtgcgtcaagaaagaactagtcactgggctagggctcacaggcgagctggtggatcctcccttccatgaatt
cgcctacgagagtctgagaacacgaccagccgctccttaccaagtaccaaccataggggtgtatggcgtgccag
gatcaggcaagtctggcatcattaaaagcgcagtcaccaaaaaagatctagtggtgagcgccaagaaagaaaac
tgtgcagaaattataagggacgtcaagaaaatgaaagggctggacgtcaatgccagaactgtggactcagtgct
cttgaatggatgcaaacaccccgtagagaccctgtatattgacgaagcttttgcttgtcatgcaggtactctca
gagcgctcatagccattataagacctaaaaaggcagtgctctgcggggatcccaaacagtgcggtttttttaac
atgatgtgcctgaaagtgcattttaaccacgagatttgcacacaagtcttccacaaaagcatctctcgccgttg
cactaaatctgtgacttcggtcgtctcaaccttgttttacgacaaaaaaatgagaacgacgaatccgaaagaga
ctaagattgtgattgacactaccggcagtaccaaacctaagcaggacgatctcattctcacttgtttcagaggg
tgggtgaagcagttgcaaatagattacaaaggcaacgaaataatgacggcagctgcctctcaagggctgacccg
taaaggtgtgtatgccgttcggtacaaggtgaatgaaaatcctctgtacgcacccacctcagaacatgtgaacg
tcctactgacccgcacggaggaccgcatcgtgtggaaaacactagccggcgacccatggataaaaacactgact
gccaagtaccctgggaatttcactgccacgatagaggagtggcaagcagagcatgatgccatcatgaggcacat
cttggagagaccggaccctaccgacgtcttccagaataaggcaaacgtgtgttgggccaaggctttagtgccgg
tgctgaagaccgctggcatagacatgaccactgaacaatggaacactgtggattattttgaaacggacaaagct
cactcagcagagatagtattgaaccaactatgcgtgaggttctttggactcgatctggactccggtctattttc
tgcacccactgttccgttatccattaggaataatcactgggataactccccgtcgcctaacatgtacgggctga
ataaagaagtggtccgtcagctctctcgcaggtacccacaactgcctcgggcagttgccactggaagagtctat
gacatgaacactggtacactgcgcaattatgatccgcgcataaacctagtacctgtaaacagaagactgcctca
tgctttagtcctccaccataatgaacacccacagagtgacttttcttcattcgtcagcaaattgaagggcagaa
ctgtcctggtggtcggggaaaagttgtccgtcccaggcaaaatggttgactggttgtcagaccggcctgaggct
accttcagagctcggctggatttaggcatcccaggtgatgtgcccaaatatgacataatatttgttaatgtgag
gaccccatataaataccatcactatcagcagtgtgaagaccatgccattaagcttagcatgttgaccaagaaag
cttgtctgcatctgaatcccggcggaacctgtgtcagcataggttatggttacgctgacagggccagcgaaagc
atcattggtgctatagcgcggcagttcaagttttcccgggtatgcaaaccgaaatcctcacttgaagagacgga
agttctgtttgtattcattgggtacgatcgcaaggcccgtacgcacaatccttacaagctttcatcaaccttga
ccaacatttatacaggttccagactccacgaagccggatgtgcaccctcatatcatgtggtgcgaggggatatt
gccacggccaccgaaggagtgattataaatgctgctaacagcaaaggacaacctggcggaggggtgtgcggagc
gctgtataagaaattcccggaaagcttcgatttacagccgatcgaagtaggaaaagcgcgactggtcaaaggtg
cagctaaacatatcattcatgccgtaggaccaaacttcaacaaagtttcggaggttgaaggtgacaaacagttg
gcagaggcttatgagtccatcgctaagattgtcaacgataacaattacaagtcagtagcgattccactgttgtc
caccggcatcttttccgggaacaaagatcgactaacccaatcattgaaccatttgctgacagctttagacacca
ctgatgcagatgtagccatatactgcagggacaagaaatgggaaatgactctcaaggaagcagtggctaggaga
gaagcagtggaggagatatgcatatccgacgactcttcagtgacagaacctgatgcagagctggtgagggtgca
tccgaagagttctttggctggaaggaagggctacagcacaagcgatggcaaaactttctcatatttggaaggga
ccaagtttcaccaggcggccaaggatatagcagaaattaatgccatgtggcccgttgcaacggaggccaatgag
caggtatgcatgtatatcctcggagaaagcatgagcagtattaggtcgaaatgccccgtcgaagagtcggaagc

ctccacaccacctagcacgctgccttgcttgtgcatccatgccatgactccagaaagagtacagcgcctaaaag
cctcacgtccagaacaaattactgtgtgctcatcctttccattgccgaagtatagaatcactggtgtgcagaag
atccaatgctcccagcctatattgttctcaccgaaagtgcctgcgtatattcatccaaggaagtatctcgtgga
aacaccaccggtagacgagactccggagccatcggcagagaaccaatccacagaggggacacctgaacaaccac
cacttataaccgaggatgagaccaggactagaacgcctgagccgatcatcatcgaagaggaagaagaggatagc
ataagtttgctgtcagatggcccgacccaccaggtgctgcaagtcgaggcagacattcacgggccgccctctgt
atctagctcatcctggtccattcctcatgcatccgactttgatgtggacagtttatccatacttgacaccctgg
agggagctagcgtgaccagcggggcaacgtcagccgagactaactcttacttcgcaaagagtatggagtttctg
gcgcgaccggtgcctgcgcctcgaacagtattcaggaaccctccacatcccgctccgcgcacaagaacaccgtc
acttgcacccagcagggcctgctcgagaaccagcctagtttccaccccgccaggcgtgaatagggtgatcacta
gagaggagctcgaggcgcttaccccgtcacgcactcctagcaggtcggtctcgagaaccagcctggtctccaac
ccgccaggcgtaaatagggtgattacaagagaggagtttgaggcgttcgtagcacaacaacaatgacggtttga
tgcgggtgcatacatcttttcctccgacaccggtcaagggcatttacaacaaaaatcagtaaggcaaacggtgc
tatccgaagtggtgttggagaggaccgaattggagatttcgtatgccccgcgcctcgaccaagaaaaagaagaa
ttactacgcaagaaattacagttaaatcccacacctgctaacagaagcagataccagtccaggaaggtggagaa
catgaaagccataacagctagacgtattctgcaaggcctagggcattatttgaaggcagaaggaaaagtggagt
gctaccgaaccctgcatcctgttcctttgtattcatctagtgtgaaccgtgccttttcaagccccaaggtcgca
gtggaagcctgtaacgccatgttgaaagagaactttccgactgtggcttcttactgtattattccagagtacga
tgcctatttggacatggttgacggagcttcatgctgcttagacactgccagtttttgccctgcaaagctgcgca
gctttccaaagaaacactcctatttggaacccacaatacgatcggcagtgccttcagcgatccagaacacgctc
cagaacgtcctggcagctgccacaaaaagaaattgcaatgtcacgcaaatgagagaattgcccgtattggattc
ggcggcctttaatgtggaatgcttcaagaaatatgcgtgtaataatgaatattgggaaacgtttaaagaaaacc
ccatcaggcttactgaagaaaacgtggtaaattacattaccaaattaaaaggaccaaaagctgctgctcttttt
gcgaagacacataatttgaatatgttgcaggacataccaatggacaggtttgtaatggacttaaagagagacgt
gaaagtgactccaggaacaaaacatactgaagaacggcccaaggtacaggtgatccaggctgccgatccgctag
caacagcgtatctgtgcggaatccaccgagagctggttaggagattaaatgcggtcctgcttccgaacattcat
acactgtttgatatgtcggctgaagactttgacgctattatagccgagcacttccagcctggggattgtgttct
ggaaactgacatcgcgtcgtttgataaaagtgaggacgacgccatggctctgaccgcgttaatgattctggaag
acttaggtgtggacgcagagctgttgacgctgattgaggcggctttcggcgaaatttcatcaatacatttgccc
actaaaactaaatttaaattcggagccatgatgaaatctggaatgttcctcacactgtttgtgaacacagtcat
taacattgtaatcgcaagcagagtgttgagagaacggctaaccggatcaccatgtgcagcattcattggagatg
acaatatcgtgaaaggagtcaaatcggacaaattaatggcagacaggtgcgccacctggttgaatatggaagtc
aagattatagatgctgtggtgggcgagaaagcgccttatttctgtggagggtttattttgtgtgactccgtgac
cggcacagcgtgccgtgtggcagacccccctaaaaaggctgtttaagcttggcaaacctctggcagcagacgatg
aacatgatgatgacaggagaagggcattgcatgaagagtcaacacgctggaaccgagtgggtattctttcagag
ctgtgcaaggcagtagaatcaaggtatgaaaccgtaggaacttccatcatagttatggccatgactactctagc
tagcagtgttaaatcattcagctacctgagaggggcccctataactctctacggctaacctgaatggactacga
ctctagaatagtctttaattaaagtccgccatatgaggccaccatgCAGATCTTCGTGAAGACCCTGACCGGCA
AGACCATCACCCTAGAGGTGGAGCCCAGTGACACCATCGAGAACGTGAAGGCCAAGATCCAGGATAAAGAGGGC
ATCCCCCCTGACCAGCAGAGGCTGATCTTTGCCGGCAAGCAGCTGGAAGATGGCCGCACCCTCTCTGATTACAA
CATCCAGAAGGAGTCAACCCTGCACCTGGTCCTTCGCCTGAGAGGTGGCGCTGCTTACAGTATAATCAACTTTG
AAAAACTGGCTGCTTACGGCATCCTGGGCTTTGTGTTTACACTGGCTGCCTACCTGCTGTTTGGCTATCCTGTG
TACGTGGCCGCTTATGGACTGTGTACCCTGGTGGCCATGCTGGCTGCTTACAATCTGGTGCCTATGGTGGCCAC
AGTGGCCGCCTATTGTCTTGGCGGACTGCTGACAATGGTGGCAGCCTACAgcccgagctatgcgtatcatcagt
ttGCAGCCTACGGCCCAGGACCAGGCgCTAAATTTGTGGCTGCCTGGACACTGAAAGCCGCCGCTGGACCAGGT
CCTGGACAGTACATCAAGGCCAACAGCAAGTTCATCGGCATCACCGAACTCGGCCCAGGACCAGGCTATCCCTA
CGATGTGCCTGATTACGCCTGATagTGATGATTCGAACGGCCGtatcacgcccaaacatttacagccgcggtgt
caaaaaccgcgtggacgtggttaacatccctgctgggaggatcagccgtaattattataattggcttggtgctg
gctactattgtggccatgtacgtgctgaccaaccagaaacataattgaatacagcagcaattggcaagctgctt
acatagaactcgcggcgattggcatgccgccttaaaatttttattttattttttctttttctttccgaatcgga
ttttgtttttaatatttcAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA

VEE-Luciferase (SEQ ID NO:15); VEE delivery vector with luciferase gene inserted at 7545

ATGggcggcgcatgagagaagcccagaccaattacctacccaaaATGGagaaagttcacgttgacatcgaggaa
gacagcccattcctcagagctttgcagcggagcttcccgcagtttgaggtagaagccaagcaggtcactgataa
tgaccatgctaatgccagagcgttttcgcatctggcttcaaaactgatcgaaacggaggtggacccatccgaca
cgatccttgacattggaagtgcgcccgcccgcagaatgtattctaagcacaagtatcattgtatctgtccgatg

2026201462 26 Feb 2026

agatgtgcggaagatccggacagattgtataagtatgcaactaagctgaagaaaaactgtaaggaaataactga
taaggaattggacaagaaaatgaaggagctcgccgccgtcatgagcgaccctgacctggaaactgagactatgt
gcctccacgacgacgagtcgtgtcgctacgaagggcaagtcgctgtttaccaggatgtatacgcggttgacgga
ccgacaagtctctatcaccaagccaataagggagttagagtcgcctactggataggctttgacaccacccctttt
tatgtttaagaacttggctggagcatatccatcatactctaccaactgggccgacgaaaccgtgttaacggctc
gtaacataggcctatgcagctctgacgttatggagcggtcacgtagagggatgtccattcttagaaagaagtat
ttgaaaccatccaacaatgttctattctctgttggctcgaccatctaccacgagaagagggacttactgaggag
ctggcacctgccgtctgtatttcacttacgtggcaagcaaaattacacatgtcggtgtgagactatagttagtt
gcgacgggtacgtcgttaaaagaatagctatcagtccaggcctgtatgggaagccttcaggctatgctgctacg
atgcaccgcgagggattcttgtgctgcaaagtgacagacacattgaacggggagagggtctcttttcccgtgtg
cacgtatgtgccagctacattgtgtgaccaaatgactggcatactggcaacagatgtcagtgcggacgacgcgc
aaaaactgctggttgggctcaaccagcgtatagtcgtcaacggtcgcacccagagaaacaccaataccatgaaa
aattacctttgcccgtagtggcccaggcatttgctaggtgggcaaaggaatataaggaagatcaagaagatga
aaggccactaggactacgagatagacagttagtcatggggtgttgttgggcttttagaaggcacaagataacat
ctatttataagcgcccggatacccaaaccatcatcaaagtgaacagcgatttccactcattcgtgctgcccagg
ataggcagtaacacattggagatcgggctgagaacaagaatcaggaaaatgttagaggagcacaaggagccgtc
acctctcattaccgccgaggacgtacaagaagctaagtgcgcagccgatgaggctaaggaggtgcgtgaagccg
aggagttgcgcgcagctctaccacctttggcagctgatgttgaggagcccactctggaagccgatgtcgacttg
atgttacaagaggctggggccggctcagtggagacacctcgtggcttgataaaggttaccagctacgctggcga
ggacaagatcggctcttacgctgtgctttctccgcaggctgtactcaagagtgaaaaattatcttgcatccacc
ctctcgctgaacaagtcatagtgataacacactctggccgaaaagggcgttatgccgtggaaccataccatggt
aaagtagtggtgccagagggacatgcaatacccgtccaggactttcaagctctgagtgaaagtgccaccattgt
gtacaacgaacgtgagttcgtaaacaggtacctgcaccatattgccacacatggaggagcgctgaacactgatg
aagaatattacaaaactgtcaagcccagcgagcacgacggcgaatacctgtacgacatcgacaggaaacagtgc
gtcaagaaagaactagtcactgggctagggctcacaggcgagctggtggatcctcccttccatgaattcgccta
cgagagtctgagaacacgaccagccgctccttaccaagtaccaaccataggggtgtatggcgtgccaggatcag
gcaagtctggcatcattaaaagcgcagtcaccaaaaaagatctagtggtgagcgccaagaaagaaaactgtgca
gaaattataagggacgtcaagaaaatgaaagggctggacgtcaatgccagaactgtggactcagtgctcttgaa
tggatgcaaacaccccgtagagaccctgtatattgacgaagcttttgcttgtcatgcaggtactctcagagcgc
tcatagccattataagacctaaaaaggcagtgctctgcggggatcccaaacagtgcggtttttttaacatgatg
tgcctgaaagtgcattttaaccacgagatttgcacacaagtcttccacaaaagcatctctcgccgttgcactaa
atctgtgacttcggtcgtctcaaccttgttttacgacaaaaaaatgagaacgacgaatccgaaagagactaaga
ttgtgattgacactaccggcagtaccaaacctaagcaggacgatctcattctcacttgtttcagagggtgggtg
aagcagttgcaaatagattacaaaggcaacgaaataatgacggcagctgcctctcaagggctgacccgtaaagg
tgtgtatgccgttcggtacaaggtgaatgaaaatcctctgtacgcacccacctcagaacatgtgaacgtcctac
tgacccgcacggaggaccgcatcgtgtggaaaacactagccggcgacccatggataaaaacactgactgccaag
taccctgggaatttcactgccacgatagaggagtggcaagcagagcatgatgccatcatgaggcacatcttgga
gagaccggaccctaccgacgtcttccagaataaggcaaacgtgtgttgggccaaggctttagtgccggtgctga
agaccgctggcatagacatgaccactgaacaatggaacactgtggattattttgaaacggacaaagctcactca
gcagagatagtattgaaccaactatgcgtgaggttctttggactcgatctggactccggtctatttttctgcacc
cactgttccgttatccattaggaataatcactgggataactccccgtcgcctaacatgtacgggctgaataaag
aagtggtccgtcagctctctcgcaggtacccacaactgcctcgggcagttgccactggaagagtctatgacatg
aacactggtacactgcgcaattatgatccgcgcataaacctagtacctgtaaacagaagactgcctcatgcttt
agtcctccaccataatgaacacccacagagtgacttttcttcattcgtcagcaaattgaagggcagaactgtcc
tggtggtcggggaaaagttgtccgtcccaggcaaaatggttgactggttgtcagaccggcctgaggctaccttc
agagctcggctggatttaggcatcccaggtgatgtgcccaaatatgacataatatttgttaatgtgaggacccc
atataaataccatcactatcagcagtgtgaagaccatgccattaagcttagcatgttgaccaagaaagcttgtc
tgcatctgaatcccggcggaacctgtgtcagcataggttatggttacgctgacagggccagcgaaagcatcatt
ggtgctatagcgcggcagttcaagttttcccgggtatgcaaaccgaaatcctcacttgaagagacggaagttct
gtttgtattcattgggtacgatcgcaaggcccgtacgcacaatccttacaagctttcatcaaccttgaccaaca
tttatacaggttccagactccacgaagccggatgtgcaccctcatatcatgtggtgcgaggggatattgccacg
gccaccgaaggagtgattataaatgctgctaacagcaaaggacaacctggcggaggggtgtgcggagcgctgta
taagaaattcccggaaagcttcgatttacagccgatcgaagtaggaaaagcgcgactggtcaaaggtgcagcta
aacatatcattcatgccgtaggaccaaacttcaacaaagtttcggaggttgaaggtgacaaacagttggcagag
gcttatgagtccatcgctaagattgtcaacgataacaattacaagtcagtagcgattccactgttgtccaccgg
catcttttccgggaacaaagatcgactaacccaatcattgaaccatttgctgacagctttagacaccactgatg
cagatgtagccatatactgcagggacaagaaatgggaaatgactctcaaggaagcagtggctaggagagaagca
gtggaggagatatgcatatccgacgactcttcagtgacagaacctgatgcagagctggtgagggtgcatccgaa
gagttctttggctggaaggaagggctacagcacaagcgatggcaaaactttctcatatttggaagggaccaagt
ttcaccaggcggccaaggatatagcagaaattaatgccatgtggcccgttgcaacggaggccaatgagcaggta

2026201462 26 Feb 2026

tgcatgtatatcctcggagaaagcatgagcagtattaggtcgaaatgccccgtcgaagagtcggaagcctccac
accacctagcacgctgccttgcttgtgcatccatgccatgactccagaaagagtacagcgcctaaaagcctcac
gtccagaacaaattactgtgtgctcatcctttccattgccgaagtatagaatcactggtgtgcagaagatccaa
tgctcccagcctatattgttctcaccgaaagtgcctgcgtatattcatccaaggaagtatctcgtggaaacacc
accggtagacgagactccggagccatcggcagagaaccaatccacagaggggacacctgaacaaccaccactta
taaccgaggatgagaccaggactagaacgcctgagccgatcatcatcgaagaggaagaagaggatagcataagt
ttgctgtcagatggcccgacccaccaggtgctgcaagtcgaggcagacattcacgggccgccctctgtatctag
ctcatcctggtccattcctcatgcatccgactttgatgtggacagtttatccatacttgacaccctggagggag
ctagcgtgaccagcggggcaacgtcagccgagactaactcttacttcgcaaagagtatggagtttctggcgcga
ccggtgcctgcgcctcgaacagtattcaggaaccctccacatcccgctccgcgcacaagaacaccgtcacttgc
acccagcagggcctgctcgagaaccagcctagtttccaccccgccaggcgtgaatagggtgatcactagagagg
agctcgaggcgcttaccccgtcacgcactcctagcaggtcggtctcgagaaccagcctggtctccaacccgcca
ggcgtaaatagggtgattacaagagaggagtttgaggcgttcgtagcacaacaacaatgacggtttgatgcggg
tgcatacatcttttcctccgacaccggtcaagggcatttacaacaaaaatcagtaaggcaaacggtgctatccg
aagtggtgttggagaggaccgaattggagatttcgtatgccccgcgcctcgaccaagaaaaagaagaattacta
cgcaagaaattacagttaaatcccacacctgctaacagaagcagataccagtccaggaaggtggagaacatgaa
agccataacagctagacgtattctgcaaggcctagggcattatttgaaggcagaaggaaaagtggagtgctacc
gaaccctgcatcctgttcctttgtattcatctagtgtgaaccgtgccttttcaagccccaaggtcgcagtggaa
gcctgtaacgccatgttgaaagagaactttccgactgtggcttcttactgtattattccagagtacgatgccta
tttggacatggttgacggagcttcatgctgcttagacactgccagtttttgccctgcaaagctgcgcagctttc
caaagaaacactcctatttggaacccacaatacgatcggcagtgccttcagcgatccagaacacgctccagaac
gtcctggcagctgccacaaaaagaaattgcaatgtcacgcaaatgagagaattgcccgtattggattcggcggc
ctttaatgtggaatgcttcaagaaatatgcgtgtaataatgaatattgggaaacgtttaaagaaaaccccatca
ggcttactgaagaaaacgtggtaaattacattaccaaattaaaaggaccaaaagctgctgctctttttgcgaag
acacataatttgaatatgttgcaggacataccaatggacaggtttgtaatggacttaaagagagacgtgaaagt
gactccaggaacaaaacatactgaagaacggcccaaggtacaggtgatccaggctgccgatccgctagcaacag
cgtatctgtgcggaatccaccgagagctggttaggagattaaatgcggtcctgcttccgaacattcatacactg
tttgatatgtcggctgaagactttgacgctattatagccgagcacttccagcctggggattgtgttctggaaac
tgacatcgcgtcgtttgataaaagtgaggacgacgccatggctctgaccgcgttaatgattctggaagacttag
gtgtggacgcagagctgttgacgctgattgaggcggctttcggcgaaatttcatcaatacatttgcccactaaa
actaaatttaaattcggagccatgatgaaatctggaatgttcctcacactgtttgtgaacacagtcattaacat
tgtaatcgcaagcagagtgttgagagaacggctaaccggatcaccatgtgcagcattcattggagatgacaata
tcgtgaaaggagtcaaatcggacaaattaatggcagacaggtgcgccacctggttgaatatggaagtcaagatt
atagatgctgtggtgggcgagaaagcgccttatttctgtggagggtttattttgtgtgactccgtgaccggcac
agcgtgccgtgtggcagacccccctaaaaaggctgtttaagcttggcaaacctctggcagcagacgatgaacatg
atgatgacaggagaagggcattgcatgaagagtcaacacgctggaaccgagtgggtattctttcagagctgtgc
aaggcagtagaatcaaggtatgaaaccgtaggaacttccatcatagttatggccatgactactctagctagcag
tgttaaatcattcagctacctgagaggggcccctataactctctacggcTAAcctgaatggactacgactctag
aatagtctttaattaaagtccgccatatgagatggaagatgccaaaaacattaagaagggcccagcgccattct
acccactcgaagacgggaccgccggcgagcagctgcacaaagccatgaagcgctacgccctggtgcccggcacc
atcgcctttaccgacgcacatatcgaggtggacattacctacgccgagtacttcgagatgagcgttcggctggc
agaagctatgaagcgctatgggctgaatacaaaccatcggatcgtggtgtgcagcgagaatagcttgcagttct
tcatgcccgtgttgggtgccctgttcatcggtgtggctgtggccccagctaacgacatctacaacgagcgcgag
ctgctgaacagcatgggcatcagccagcccaccgtcgtattcgtgagcaagaaagggctgcaaaagatcctcaa
cgtgcaaaagaagctaccgatcatacaaaagatcatcatcatggatagcaagaccgactaccagggcttccaaa
gcatgtacaccttcgtgacttcccatttgccacccggcttcaacgagtacgacttcgtgcccgagagcttcgac
cgggacaaaaccatcgccctgatcatgaacagtagtggcagtaccggattgcccaagggcgtagccctaccgca
ccgcaccgcttgtgtccgattcagtcatgcccgcgaccccatcttcggcaaccagatcatccccgacaccgcta
tcctcagcgtggtgccatttcaccacggcttcggcatgttcaccacgctgggctacttgatctgcggctttcgg
gtcgtgctcatgtaccgcttcgaggaggagctattcttgcgcagcttgcaagactataagattcaatctgccct
gctggtgcccacactatttagcttcttcgctaagagcactctcatcgacaagtacgacctaagcaacttgcacg
agatcgccagcggcggggcgccgctcagcaaggaggtaggtgaggccgtggccaaacgcttccacctaccaggc
atccgccagggctacggcctgacagaaacaaccagcgccattctgatcacccccgaaggggacgacaagcctgg
cgcagtaggcaaggtggtgcccttcttcgaggctaaggtggtggacttggacaccggtaagacactgggtgtga
accagcgcggcgagctgtgcgtccgtggccccatgatcatgagcggctacgttaacaaccccgaggctacaaac
gctctcatcgacaaggacggctggctgcacagcggcgacatcgcctactgggacgaggacgagcacttcttcat
cgtggaccggctgaagagcctgatcaaatacaagggctaccaggtagccccagccgaactggagagcatcctgc
tgcaacaccccaacatcttcgacgccggggtcgccggcctgcccgacgacgatgccggcgagctgcccgccgca
gtcgtcgtgctggaacacggtaaaaccatgaccgagaaggagatcgtggactatgtggccagccaggttacaac
cgccaagaagctgcgcggtggtgttgtgttcgtggacgaggtgcctaaaggactgaccggcaagttggacgccc

2026201462 26 Feb 2026

gcaagatccgcgagattctcattaaggccaagaagggcggcaagatcgccgtgtaaTTCGAACGGCCGtatcac
gcccaaacatttacagccgcggtgtcaaaaaccgcgtggacgtggttaacatccctgctgggaggatcagccgt
aattattataattggcttggtgctggctactattgtggccatgtacgtgctgaccaaccagaaacataattgaa
tacagcagcaattggcaagctgcttacatagaactcgcggcgattggcatgccgccttaaaatttttatttttat
ttttttcttttctttttccgaatcggattttgtttttaatatttcAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

ubiquitin (SEQ ID NO:38)
>UbG76 0-228
ATGCAGATCTTCGTGAAGACCCTGACCGGCAAGACCATCACCCTAGAGGTGGAGCCCAGTGACACCATCG
AGAACGTGAAGGCCAAGATCCAGGATAAAGAGGGCATCCCCCCTGACCAGCAGAGGCTGATCTTTGCCGGCAAGCA
GCTGGAAGATGGCCGCACCCTCTCTGATTACAACATCCAGAAGGAGTCAACCCTGCACCTGGTCCTTCGCCTGAGA
GGTGGC

Ubiquitin A76 (SEQ ID NO:39)
>UbA76 0-228
ATGCAGATCTTCGTGAAGACCCTGACCGGCAAGACCATCACCCTAGAGGTGGAGCCCAGTGACACCATCG
AGAACGTGAAGGCCAAGATCCAGGATAAAGAGGGCATCCCCCCTGACCAGCAGAGGCTGATCTTTGCCGGCAAGCA
GCTGGAAGATGGCCGCACCCTCTCTGATTACAACATCCAGAAGGAGTCAACCCTGCACCTGGTCCTTCGCCTGAGA
GGTGCC

HLA-A2 (MHC class I) signal peptide (SEQ ID NO:40)
>MHC SignalPep 0-78
atggccgtcatggcgccccgaaccctcgtcctgctactctcgggggctctggccctgacccagacctggg
cgggctct

HLA-A2 (MHC class I) Trans Membrane domain (SEQ ID NO:41)
>HLA A2 TM Domain 0-201
CCGtcttcccagcccaccatccCCATCGTGGGCAtcattgctggcctggttctctttggagctgtgatca
ctggagctgtggtcgctgctgtgatgtggaggaggaagagctcagatagaaaaggagggagctactctcaggctgc
aagcagtgacagtgcccagggctctgatgtgtctctcacagcttgtaaagtgtga

IgK Leader Seq (SEQ ID NO:42)
>IgK Leader Seq 0-60
atggagaccgatacactgctgctgtgggtgctgctcctgtgggtgccaggaagcacaggc

Human DC-Lamp (SEQ ID NO:43)
>HumanDCLAMP 0-3178
ggcaccgattcggggcctgcccggacttcgccgcacgctgcagaacctcgcccagcgcccaccatgcccc
ggcagctcagcgcggcggccgcgctcttcgcgtccctggccgtaattttgcacgatggcagtcaaatgagagcaaa
agcatttccagaaaccagagattattctcaacctactgcagcagcaacagtacaggacataaaaaaacctgtccag
caaccagctaagcaagcacctcaccaaactttagcagcaagattcatggatggtcatatcacctttcaaacagcgg
ccacagtaaaaattccaacaactaccccagcaactacaaaaaacactgcaaccaccagcccaattacctacaccct
ggtcacaacccaggccacacccaacaactcacacacagctcctccagttactgaagttacagtcggccctagctta
gcccctattcactgccacccaccatcaccccaccagctcatacagctggaaccagttcatcaaccgtcagccaca
caactgggaacaccactcaacccagtaaccagaccacccttccagcaactttatcgatagcactgcacaaaagcac
aaccggtcagaagcctgatcaacccacccatgccccaggaacaacggcagctgcccacaataccacccgcacagct
gcacctgcctccacggttcctgggcccacccttgcacctcagccatcgtcagtcaagactggaatttatcaggttc
taaacggaagcagactctgtataaaagcagagatggggatacagctgattgttcaagacaaggagtcggttttttc
acctcggagatacttcaacatcgaccccaacgcaacgcaagcctctgggaactgtggcacccgaaaatccaaccctt
ctgttgaattttcagggcggatttgtgaatctcacatttaccaaggatgaagaatcatattatatcagtgaagtgg
gagcctatttgaccgtctcagatccagagacagtttaccaaggaatcaaacatgcggtggtgatgttccagacagc
agtcgggcattccttcaagtgcgtgagtgaacagagcctccagttgtcagcccacctgcaggtgaaaacaaccgat
gtccaacttcaagcctttgattttgaagatgaccactttggaaatgtggatgagtgctcgtctgactacacaattg
tgcttcctgtgattggggccatcgtggttggtctctgccttatgggtatgggtgtctataaaatccgcctaaggtg
tcaatcatctggataccagagaatctaattgttgcccgggggggaatgaaaataatggaatttagagaactctttca
tcccttccaggatggatgttgggaaattccctcagagtgtgggtccttcaaacaatgtaaaccaccatcttctatt
caaatgaagtgagtcatgtgtgatttaagttcaggcagcacatcaatttctaaatacttttgtttatttttatgaa
agatatagtgagctgtttattttctagtttcctttagaatattttagccactcaaagtcaacatttgagatatgtt
gaattaacataatatatgtaaagtagaataagccttcaaattataaaccaagggtcaattgtaactaatactactg

2026201462 26 Feb 2026

tgtgtgcattgaagattttatttaccttgatcttaacaaagcctttgctttgttatcaaatggactttcagtgc
ttttactatctgtgttttatggtttcatgtaacatacatattcctggtgtagcacttaactccttttccactttaa
atttgtttttgtttttttgagacggagtttcactcttgtcacccaggctggagtacagtggcacgatctcggcttat
ggcaacctccgcctcccgggttcaagtgattctcctgcttcagcttcccgagtagctgggattacaggcacacact
accacgcctggctaatttttgtatttttattatagacgggtttcaccatgttggccagactggtcttgaactcttg
acctcaggtgatccacccacctcagcctcccaaagtgctgggattacaggcatgagccattgcgcccggccttaaa
tgtttttttttaatcatcaaaaagaacaacatatctcaggttgtctaagtgtttttatgtaaaaccaacaaaaagaa
caaatcagcttatatttttttatcttgatgactcctgctccagaattgctagactaagaattaggtggctacagatg
gtagaactaaacaataagcaagagacaataataatggcccttaattattaacaaagtgccagagtctaggctaagc
actttatctatatctcatttcattctcacaacttataagtgaatgagtaaactgagacttaagggaactgaatcac
ttaaatgtcacctggctaactgatggcagagccagagcttgaattcatgttggtctgacatcaaggtctttggtct
tctccctacaccaagttacctacaagaacaatgacaccacactctgcctgaaggctcacacctcataccagcatac
gctcaccttacagggaaatgggtttatccaggatcatgagacattagggtagatgaaaggagagctttgcagataa
caaaatagcctatccttaataaatcctccactctctggaaggagactgaggggctttgtaaaacattagtcagttg
ctcatttttatgggattgcttagctgggctgtaaagatgaaggcatcaaataaactcaaagtatttttaaatttt
ttgataatagagaaacttcgctaaccaactgttctttcttgagtgtatagccccatcttgtggtaacttgctgctt
ctgcacttcatatccatatttcctattgttcactttattctgtagagcagcctgccaagaattttatttctgctgt
ttttttgctgctaaagaaaggaactaagtcaggatgttaacagaaaagtccacataaccctagaattcttagtca
aggaataattcaagtcagcctagagaccatgttgactttcctcatgtgtttccttatgactcagtaagttggcaag
gtcctgactttagtcttaataaaacattgaattgtagtaaaggtttttgcaataaaaacttactttgg

Mouse LAMP1 (SEQ ID NO:44)
>MouseLamp1 0-1858
attccggaggtgaaaaacaatggcacaacgtgtataatggccagcttctctgcctcctttctgaccacct
acgagactgcgaatggttctcagatcgtgaacatttccctgccagcctctgcagaagtactgaaaaatggcagttc
ttgtggtaaagaaaatgtttctgaccccagcctcacaattacttttggaagaggatatttactgacactcaacttc
acaaaaaatacaacacgttacagtgtccagcatatgtattttacatataacttgtcagatacagaacattttccca
atgccatcagcaaagagatctacaccatggattccacaactgacatcaaggcagacatcaacaaagcataccggtg
tgtcagtgatatccgggtctacatgaagaatgtgaccgttgtgctccgggatgccactatccaggcctacctgtcg
agtggcaacttcagcaaggaagagacacactgcacacaggatggaccttccccaaccactgggccacccagcccct
caccaccacttgtgcccacaaaccccactgtatccaagtacaatgttactggtaacaacggaacctgcctgctggc
ctctatggcactgcaactgaatatcacctacctgaaaaaggacaacaagacggtgaccagagcgttcaacatcagc
ccaaatgacacatctagtgggagttgcggtatcaacttggtgaccctgaaagtggagaacaagaacagagccctgg
aattgcagtttgggatgaatgccagctctagcctgtttttcttgcaaggagtgcgcttgaatatgactcttcctga
tgccctagtgcccacattcagcatctccaaccattcactgaaagctcttcaggccactgtgggaaactcatacaag
tgcaacactgaggaacacatctttgtcagcaagatgctctccctcaatgtcttcagtgtgcaggtccaggctttca
aggtggacagtgacaggtttgggtctgtggaagagtgtgttcaggatggtaacaacatgttgatccccattgctgt
gggcggtgccctggcagggctgatcctcatcgtcctcattgcctacctcattggcaggaagaggagtcacgccggc
tatcagaccatctagcctggtgggcaggtgcaccagagatgcacaggggcctgttctcacatccccaagcttagat
aggtgtggaagggaggcacactttctggcaaactgttttaaaatctgctttatcaaatgtgaagttcatcttgcaa
catttactatgcacaaaggaataactattgaaatgacggtgttaattttgctaactgggttaaatattgatgagaa
ggctccactgatttgacttttaagacttggtgtttggttcttcattcttttactcagatttaagcctatcaaaggg
atactctggtccagaccttggcctggcaagggtggctgatggttaggctgcacacacttaagaagcaacgggagca
gggaaggcttgcacacaggcacgcacagggtcaacctctggacacttggcttgggctacctggccttgggggggct
gaactctggcatctggctgggtacacacccccccaatttctgtgctctgccacccgtgagctgccactttcctaaa
tagaaaatggcattatttttatttacttttttgtaaagtgatttccagtcttgtgttggcgttcagggtggccctg
tctctgcactgtgtacaataatagattcacactgctgacgtgtcttgcagcgtaggtgggttgtacactgggcatc
agctcacgtaatgcattgcctgtaacgatgctaataaaaa

Human Lamp1 cDNA (SEQ ID NO:45)
>Human Lamp1 0-2339
ggcccaaccgccgcccgcgcccccgctctccgcaccgtacccggccgcctcgcgccatggcggcccccgg
cagcgcccggcgacccctgctgctgctactgctgttgctgctgctcggcctcatgcattgtgcgtcagcagcaatg
tttatggtgaaaaatggcaacgggaccgcgtgcataatggccaacttctctgctgccttctcagtgaactacgaca
ccaagagtggccctaagaacatgacctttgacctgccatcagatgccacagtggtgctcaaccgcagctcctgtgg
aaaagagaacacttctgaccccagtctcgtgattgcttttggaagaggacatacactcactctcaatttcacgaga
aatgcaacacgttacagcgtccagctcatgagttttgtttataacttgtcagacacacacctttccccaatgcga
gctccaaagaaatcaagactgtggaatctataactgacatcagggcagatatagataaaaaatacagatgtgttag
tggcacccaggtccacatgaacaacgtgaccgtaacgctccatgatgccaccatccaggcgtacctttccaacagc
agcttcagcaggggagagacacgctgtgaacaagacaggccttccccaaccacagcgccccctgcgccacccagcc

2026201462 26 Feb 2026

cctcgccctcacccgtgcccaagagcccctctgtggacaagtacaacgtgagcggcaccaacgggacctgcctgct
ggccagcatggggctgcagctgaacctcacctatgagaggaaggacaacacgacggtgacaaggcttctcaacatc
aaccccaacaagacctcggccagcgggagctgcggcgcccacctggtgactctggagctgcacagcgagggcacca
ccgtcctgctcttccagttcgggatgaatgcaagttctagccggtttttcctacaaggaatccagttgaatacaat
tcttcctgacgccagagaccctgcctttaaagctgccaacggctccctgcgagcgctgcaggccacagtcggcaat
tcctacaagtgcaacgcggaggagcacgtccgtgtcacgaaggcgttttcagtcaatatattcaaagtgtgggtcc
aggctttcaaggtggaaggtggccagtttggctctgtggaggagtgtctgctggacgagaacagcatgctgatccc
catcgctgtgggtggtgccctggcggggctggtcctcatcgtcctcatcgcctacctcgtcggcaggaagaggagt
cacgcaggctaccagactatctagcctggtgcacgcaggcacagcagctgcaggggcctctgttcctttctctggg
cttagggtcctgtcgaaggggaggcacactttctggcaaacgtttctcaaatctgcttcatccaatgtgaagttca
tcttgcagcatttactatgcacaacagagtaactatcgaaatgacggtgttaattttgctaactgggttaaatatt
ttgctaactggttaaacattaatatttaccaaagtaggattttgagggtgggggtgctctctctgaggggggtgggg
gtgccgctgtctctgaggggtgggggtgccgctgtctctgaggggtgggggtgccgctctctctgaggggggtgggg
gtgccgctttctctgaggggggtgggggtgccgctctctctgaggggggtgggggtgctgctctctccgaggggtgga
atgccgctgtctctgaggggtgggggtgccgctctaaattggctccatatcatttgagtttagggttctggtgttt
ggtttcttcattctttactgcactcagatttaagccttacaaagggaaagcctctggccgtcacacgtaggacgca
tgaaggtcactcgtggtgaggctgacatgctcacacattacaacagtagagagggaaaatcctaagacagaggaac
tccagagatgagtgtctggagcgcttcagttcagctttaaaggccaggacgggccacacgtggctggcggcctcgt
tccagtggcggcacgtccttgggcgtctctaatgtctgcagctcaagggctggcacttttttaaatataaaaatgg
gtgttatttttatttttttttgtaaagtgatttttggtcttctgttgacattcggggtgatcctgttctgcgctgt
gtacaatgtgagatcggtgcgttctcctgatgttttgccgtggcttggggattgtacacgggaccagctcacgtaa
tgcattgcctgtaacaatgtaataaaaagcctctttcttttaaaaaaaaaaaaaaaaaaaaaaa

Tetanus toxoid nulceic acid sequence (SEQ ID NO:46)
CAGTACATCAAGGCCAACAGCAAGTTCATCGGCATCACCGAACTC

Tetanus toxoid amino acid sequence (SEQ ID NO:47)
QYIKANSKFIGITEL

PADRE nulceotide sequence (SEQ ID NO:48)
GCTAAATTTGTGGCTGCCTGGACACTGAAAGCCGCCGCT

PADRE amino acid sequence (SEQ ID NO:49)
AKFVAAWTLKAAA

WPRE (SEQ ID NO:50)
>WPRE 0-593
aatcaacctctggattacaaaatttgtgaaagattgactggtattcttaactatgttgctccttttacgc
tatgtggatacgctgctttaatgcctttgtatcatgctattgcttcccgtatggctttcattttctcctccttgta
taaatcctggttgctgtctctttatgaggagttgtggcccgttgtcaggcaacgtggcgtggtgtgcactgtgttt
gctgacgcaacccccactggttggggcattgccaccacctgtcagctcctttccgggactttcgctttcccctcc
ctattgccacggcggaactcatcgccgcctgccttgcccgctgctggacaggggctcggctgttgggcactgacaa
ttccgtggtgttgtcggggaagctgacgtcctttccatggctgctcgcctgtgttgccacctggattctgcgcggg
acgtccttctgctacgtcccttcggccctcaatccagcggaccttccttcccgcggcctgctgccggctctgcggc
ctcttccgcgtcttcgccttcgccctcagacgagtcggatctccctttgggccgcctccccgcctgt

IRES (SEQ ID NO:51)
>eGFP_IRES_SEAP_Insert 1746-2335
tctccccccccccctctcccctcccccccccctaacgttactggccgaagccgcttggaataaggccggt
gtgcgtttgtctatatgttattttccaccatattgccgtcttttggcaatgtgagggcccggaaacctggccctgt
cttcttgacgagcattcctaggggtctttcccctctcgccaaaggaatgcaaggtctgttgaatgtcgtgaaggaa
gcagttcctctggaagcttcttgaagacaaacaacgtctgtagcgacccctttgcaggcagcggaacccccccacctg
gcgacaggtgcctctgcggccaaaagccacgtgtataagatacacctgcaaaggcggcacaaccccagtgccacgt
tgtgagttggatagttgtggaaagagtcaaatggctctcctcaagcgtattcaacaaggggctgaaggatgcccag
aaggtaccccattgtatgggatctgatctggggcctcggtgcacatgctttacatgtgtttagtcgaggttaaaaa
aacgtctaggccccccgaaccacggggacgtggttttcctttgaaaaacacgatgataatatg

GFP (SEQ ID NO:52)
atggtgagcaagggcgaggagctgttcaccggggtggtgcccatcctggtcgagctggacggcgacgtaa
acggccacaagttcagcgtgtccggcgagggcgagggcgatgccacctacggcaagctgaccctgaagttcatctg

2026201462 26 Feb 2026

caccaccggcaagctgcccgtgccctggcccaccctcgtgaccaccctgacctacggcgtgcagtgcttcagccgc
taccccgaccacatgaagcagcacgacttcttcaagtccgccatgcccgaaggctacgtccaggagcgcaccatct
tcttcaaggacgacggcaactacaagacccgcgccgaggtgaagttcgagggcgacaccctggtgaaccgcatcga
gctgaagggcatcgacttcaaggaggacggcaacatcctggggcacaagctggagtacaactacaacagccacaac
gtctatatcatggccgacaagcagaagaacggcatcaaggtgaacttcaagatccgccacaacatcgaggacggca
gcgtgcagctcgccgaccactaccagcagaacaccccatcggcgacggccccgtgctgctgcccgacaaccacta
cctgagcacccagtccgccctgagcaaagaccccaacgagaagcgcgatcacatggtcctgctggagttcgtgacc
gccgccgggatcactctcggcatggacgagctgtacaagtag

SEAP (SEQ ID NO:53)

atgctgctgctgctgctgctgctgggcctgaggctacagctctccctgggcatcatcccagttgaggagg
agaacccggacttctggaaccgcgaggcagccgaggccctgggtgccgccaagaagctgcagcctgcacagacagc
cgccaagaacctcatcatcttcctgggcgatgggatgggggtgtctacggtgacagctgccaggatcctaaaaggg
cagaagaaggacaaactggggcctgagataccctggccatggaccgcttcccatatgtggctctgtccaagacat
acaatgtagacaaacatgtgccagacagtggagccacagccacggcctacctgtgcggggtcaagggcaacttcca
gaccattggcttgagtgcagccgcccgctttaaccagtgcaacacgacacgcggcaacgaggtcatctccgtgatg
aatcgggccaagaaagcagggaagtcagtgggagtggtaaccaccacacgagtgcagcacgcctcgccagccggca
cctacgcccacacggtgaaccgcaactggtactcggacgccgacgtgcctgcctcggcccgccaggaggggtgcca
ggacatcgctacgcagctcatctccaacatggacattgacgtgatcctaggtggaggccgaaagtacatgtttcgc
atgggaaccccagaccctgagtacccagatgactacagccaaggtgggaccaggctggacgggaagaatctggtgc
aggaatggctggcgaagcgccagggtgcccggtatgtgtggaaccgcactgagctcatgcaggcttccctggaccc
gtctgtgacccatctcatgggtctctttgagcctggagacatgaaatacgagatccaccgagactccacactggac
ccctccctgatggagatgacagaggctgccctgcgcctgctgagcaggaacccccgcggcttcttcctcttcgtgg
agggtggtcgcatcgaccatggtcatcatgaaagcagggcttaccgggcactgactgagacgatcatgttcgacga
cgccattgagagggcgggccagctcaccagcgaggaggacacgctgagcctcgtcactgccgaccactcccacgtc
ttctccttcggaggctacccccctgcgagggagctccatcttcgggctggcccctggcaaggcccgggacaggaagg
cctacacggtcctcctatacggaaacggtccaggctatgtgctcaaggacggcgcccggccggatgttaccgagag
cgagagcgggagccccgagtatcggcagcagtcagcagtgcccctggacgaagagacccacgcaggcgaggacgtg
gcggtgttcgcgcgcggcccgcaggcgcacctggttcacggcgtgcaggagcagaccttcatagcgcacgtcatgg
ccttcgccgcctgcctggagccctacaccgcctgcgacctggcgccccccgccggcaccaccgacgccgcgcaccc
gggttactctagagtcggggcggccggccgcttcgagcagacatgataa

Firefly Luciferase (SEQ ID NO:54)

atggaagatgccaaaaacattaagaagggcccagcgccattctacccactcgaagacgggaccgccggcg
agcagctgcacaaagccatgaagcgctacgccctggtgcccggcaccatcgcctttaccgacgcacatatcgaggt
ggacattacctacgccgagtacttcgagatgagcgttcggctggcagaagctatgaagcgctatgggctgaataca
aaccatcggatcgtggtgtgcagcgagaatagcttgcagttcttcatgcccgtgttgggtgccctgttcatcggtg
tggctgtggccccagctaacgacatctacaacgagcgcgagctgctgaacagcatgggcatcagccagcccaccgt
cgtattcgtgagcaagaaagggctgcaaaagatcctcaacgtgcaaaagaagctaccgatcatacaaaagatcatc
atcatggatagcaagaccgactaccagggcttccaaagcatgtacaccttcgtgacttcccatttgccacccggct
tcaacgagtacgacttcgtgcccgagagcttcgaccgggacaaaaccatcgccctgatcatgaacagtagtggcag
taccggattgcccaagggcgtagccctaccgcaccgcaccgcttgtgtccgattcagtcatgcccgcgaccccatc
ttcggcaaccagatcatccccgacaccgctatcctcagcgtggtgccatttcaccacggcttcggcatgttcacca
cgctgggctacttgatctgcggctttcgggtcgtgctcatgtaccgcttcgaggaggagctattcttgcgcagctt
gcaagactataagattcaatctgccctgctggtgcccacactatttagcttcttcgctaagagcactctcatcgac
aagtacgacctaagcaacttgcacgagatcgccagcggcggggcgccgctcagcaaggaggtaggtgaggccgtgg
ccaaacgcttccacctaccaggcatccgccagggctacggcctgacagaaacaaccagcgccattctgatcacccc
cgaaggggacgacaagcctggcgcagtaggcaaggtggtgcccttcttcgaggctaaggtggtggacttggacacc
ggtaagacactgggtgtgaaccagcgcggcgagctgtgcgtccgtggccccatgatcatgagcggctacgttaaca
accccgaggctacaaacgctctcatcgacaaggacggctggctgcacagcggcgacatcgcctactgggacgagga
cgagcacttcttcatcgtggaccggctgaagagcctgatcaaatacaagggctaccaggtagccccagccgaactg
gagagcatcctgctgcaacaccccaacatcttcgacgccggggtcgccggcctgcccgacgacgatgccggcgagc
tgcccgccgcagtcgtcgtgctggaacacggtaaaaccatgaccgagaaggagatcgtggactatgtggccagcca
ggttacaaccgccaagaagctgcgcggtggtgttgtgttcgtggacgaggtgcctaaaggactgaccggcaagttg
gacgcccgcaagatccgcgagattctcattaaggccaagaagggcggcaagatcgccgtgtaa

FMDV 2A (SEQ ID NO:55)

GTAAAGCAAACACTGAACTTTGACCTTCTCAAGTTGGCTGGAGACGTTGAGTCCAATCCTGGGCCC

2026201462 26 Feb 2026

2026201462 26 Feb 2026

References

1. Desrichard, A., Snyder, A. & Chan, T. A. Cancer Neoantigens and Applications for Immunotherapy. *Clin. Cancer Res. Off. J. Am. Assoc. Cancer Res.* (2015). doi:10.1158/1078-0432.CCR-14-3175

2. Schumacher, T. N. & Schreiber, R. D. Neoantigens in cancer immunotherapy. *Science* **348,** 69–74 (2015).

3. Gubin, M. M., Artyomov, M. N., Mardis, E. R. & Schreiber, R. D. Tumor neoantigens: building a framework for personalized cancer immunotherapy. *J. Clin. Invest.* **125,** 3413–3421 (2015).

4. Rizvi, N. A. *et al.* Cancer immunology. Mutational landscape determines sensitivity to PD-1 blockade in non-small cell lung cancer. *Science* **348,** 124–128 (2015).

5. Snyder, A. *et al.* Genetic basis for clinical response to CTLA-4 blockade in melanoma. *N. Engl. J. Med.* **371,** 2189–2199 (2014).

6. Carreno, B. M. *et al.* Cancer immunotherapy. A dendritic cell vaccine increases the breadth and diversity of melanoma neoantigen-specific T cells. *Science* **348,** 803–808 (2015).

7. Tran, E. *et al.* Cancer immunotherapy based on mutation-specific CD4+ T cells in a patient with epithelial cancer. *Science* **344,** 641–645 (2014).

8. Hacohen, N. & Wu, C. J.-Y. United States Patent Application: 0110293637 - COMPOSITIONS AND METHODS OF IDENTIFYING TUMOR SPECIFIC NEOANTIGENS. (A1). at <http://appft1.uspto.gov/netacgi/nph-Parser?Sect1=PTO1&Sect2=HITOFF&d=PG01&p=1&u=/netahtml/PTO/srchnum.html&r=1&f=G&l=50&s1=20110293637.PGNR.>

9. Lundegaard, C., Hoof, I., Lund, O. & Nielsen, M. State of the art and challenges in sequence based T-cell epitope prediction. *Immunome Res.* **6 Suppl 2,** S3 (2010).

10. Yadav, M. *et al.* Predicting immunogenic tumour mutations by combining mass spectrometry and exome sequencing. *Nature* **515,** 572–576 (2014).

11. Bassani-Sternberg, M., Pletscher-Frankild, S., Jensen, L. J. & Mann, M. Mass spectrometry of human leukocyte antigen class I peptidomes reveals strong effects of protein abundance and turnover on antigen presentation. *Mol. Cell. Proteomics MCP* **14,** 658–673 (2015).

12. Van Allen, E. M. *et al.* Genomic correlates of response to CTLA-4 blockade in metastatic melanoma. *Science* **350,** 207–211 (2015).

13. Yoshida, K. & Ogawa, S. Splicing factor mutations and cancer. *Wiley Interdiscip. Rev. RNA* **5,** 445–459 (2014).

14. Cancer Genome Atlas Research Network. Comprehensive molecular profiling of lung adenocarcinoma. *Nature* **511,** 543–550 (2014).

15. Rajasagi, M. *et al.* Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. *Blood* **124,** 453–462 (2014).

16. Downing, S. R. *et al.* United States Patent Application: 0120208706 - OPTIMIZATION OF MULTIGENE ANALYSIS OF TUMOR SAMPLES. (A1). at <http://appft1.uspto.gov/netacgi/nph-Parser?Sect1=PTO1&Sect2=HITOFF&d=PG01&p=1&u=/netahtml/PTO/srchnum.html&r=1&f=G&l=50&s1=20120208706.PGNR.>

17. Target Capture for NextGen Sequencing - IDT. at <http://www.idtdna.com/pages/products/nextgen/target-capture>

18. Shukla, S. A. *et al.* Comprehensive analysis of cancer-associated somatic mutations in class I HLA genes. *Nat. Biotechnol.* **33,** 1152–1158 (2015).

2026201462 26 Feb 2026

19. Cieslik, M. *et al.* The use of exome capture RNA-seq for highly degraded RNA with application to clinical cancer sequencing. *Genome Res.* **25,** 1372–1381 (2015).

20. Bodini, M. *et al.* The hidden genomic landscape of acute myeloid leukemia: subclonal structure revealed by undetected mutations. *Blood* **125,** 600–605 (2015).

21. Saunders, C. T. *et al.* Strelka: accurate somatic small-variant calling from sequenced tumor-normal sample pairs. *Bioinforma. Oxf. Engl.* **28,** 1811–1817 (2012).

22. Cibulskis, K. *et al.* Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. *Nat. Biotechnol.* **31,** 213–219 (2013).

23. Wilkerson, M. D. *et al.* Integrated RNA and DNA sequencing improves mutation detection in low purity tumors. *Nucleic Acids Res.* **42,** e107 (2014).

24. Mose, L. E., Wilkerson, M. D., Hayes, D. N., Perou, C. M. & Parker, J. S. ABRA: improved coding indel detection via assembly-based realignment. *Bioinforma. Oxf. Engl.* **30,** 2813–2815 (2014).

25. Ye, K., Schulz, M. H., Long, Q., Apweiler, R. & Ning, Z. Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. *Bioinforma. Oxf. Engl.* **25,** 2865–2871 (2009).

26. Lam, H. Y. K. *et al.* Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. *Nat. Biotechnol.* **28,** 47–55 (2010).

27. Frampton, G. M. *et al.* Development and validation of a clinical cancer genomic profiling test based on massively parallel DNA sequencing. *Nat. Biotechnol.* **31,** 1023–1031 (2013).

28. Boegel, S. *et al.* HLA typing from RNA-Seq sequence reads. *Genome Med.* **4,** 102 (2012).

29. Liu, C. *et al.* ATHLATES: accurate typing of human leukocyte antigen through exome sequencing. *Nucleic Acids Res.* **41,** e142 (2013).

30. Mayor, N. P. *et al.* HLA Typing for the Next Generation. *PloS One* **10,** e0127153 (2015).

31. Roy, C. K., Olson, S., Graveley, B. R., Zamore, P. D. & Moore, M. J. Assessing long-distance RNA sequence connectivity via RNA-templated DNA-DNA ligation. *eLife* **4,** (2015).

32. Song, L. & Florea, L. CLASS: constrained transcript assembly of RNA-seq reads. *BMC Bioinformatics* **14 Suppl 5,** S14 (2013).

33. Maretty, L., Sibbesen, J. A. & Krogh, A. Bayesian transcriptome assembly. *Genome Biol.* **15,** 501 (2014).

34. Pertea, M. *et al.* StringTie enables improved reconstruction of a transcriptome from RNA-seq reads. *Nat. Biotechnol.* **33,** 290–295 (2015).

35. Roberts, A., Pimentel, H., Trapnell, C. & Pachter, L. Identification of novel transcripts in annotated genomes using RNA-Seq. *Bioinforma. Oxf. Engl.* (2011). doi:10.1093/bioinformatics/btr355

36. Vitting-Seerup, K., Porse, B. T., Sandelin, A. & Waage, J. spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. *BMC Bioinformatics* **15,** 81 (2014).

37. Rivas, M. A. *et al.* Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. *Science* **348,** 666–669 (2015).

38. Skelly, D. A., Johansson, M., Madeoy, J., Wakefield, J. & Akey, J. M. A powerful and flexible statistical framework for testing hypotheses of allele-specific gene expression from RNA-seq data. *Genome Res.* **21,** 1728–1737 (2011).

39. Anders, S., Pyl, P. T. & Huber, W. HTSeq--a Python framework to work with high-throughput sequencing data. *Bioinforma. Oxf. Engl.* **31,** 166–169 (2015).

20262014462 26 Feb 2026

40. Furney, S. J. *et al.* SF3B1 mutations are associated with alternative splicing in uveal melanoma. *Cancer Discov.* (2013). doi:10.1158/2159-8290.CD-13-0330

41. Zhou, Q. *et al.* A chemical genetics approach for the functional assessment of novel cancer genes. *Cancer Res.* (2015). doi:10.1158/0008-5472.CAN-14-2930

42. Maguire, S. L. *et al.* SF3B1 mutations constitute a novel therapeutic target in breast cancer. *J. Pathol.* **235,** 571–580 (2015).

43. Carithers, L. J. *et al.* A Novel Approach to High-Quality Postmortem Tissue Procurement: The GTEx Project. *Biopreservation Biobanking* **13,** 311–319 (2015).

44. Xu, G. *et al.* RNA CoMPASS: a dual approach for pathogen and host transcriptome analysis of RNA-seq datasets. *PloS One* **9,** e89445 (2014).

45. Andreatta, M. & Nielsen, M. Gapped sequence alignment using artificial neural networks: application to the MHC class I system. *Bioinforma. Oxf. Engl.* (2015). doi:10.1093/bioinformatics/btv639

46. Jørgensen, K. W., Rasmussen, M., Buus, S. & Nielsen, M. NetMHCstab - predicting stability of peptide-MHC-I complexes; impacts for cytotoxic T lymphocyte epitope discovery. *Immunology* **141,** 18–26 (2014).

47. Larsen, M. V. *et al.* An integrative approach to CTL epitope prediction: a combined algorithm integrating MHC class I binding, TAP transport efficiency, and proteasomal cleavage predictions. *Eur. J. Immunol.* **35,** 2295–2303 (2005).

48. Nielsen, M., Lundegaard, C., Lund, O. & Keşmir, C. The role of the proteasome in generating cytotoxic T-cell epitopes: insights obtained from improved predictions of proteasomal cleavage. *Immunogenetics* **57,** 33–41 (2005).

49. Boisvert, F.-M. *et al.* A Quantitative Spatial Proteomics Analysis of Proteome Turnover in Human Cells. *Mol. Cell. Proteomics* **11,** M111.011429–M111.011429 (2012).

50. Duan, F. *et al.* Genomic and bioinformatic profiling of mutational neoepitopes reveals new rules to predict anticancer immunogenicity. *J. Exp. Med.* **211,** 2231–2248 (2014).

51. Janeway's Immunobiology: 9780815345312: Medicine & Health Science Books @ Amazon.com. at <http://www.amazon.com/Janeways-Immunobiology-Kenneth-Murphy/dp/0815345313>

52. Calis, J. J. A. *et al.* Properties of MHC Class I Presented Peptides That Enhance Immunogenicity. *PLoS Comput. Biol.* **9,** e1003266 (2013).

53. Zhang, J. *et al.* Intratumor heterogeneity in localized lung adenocarcinomas delineated by multiregion sequencing. *Science* **346,** 256–259 (2014)

54. Walter, M. J. *et al.* Clonal architecture of secondary acute myeloid leukemia. *N. Engl. J. Med.* 366, 1090–1098 (2012).

55. Hunt DF, Henderson RA, Shabanowitz J, Sakaguchi K, Michel H, Sevilir N, Cox AL, Appella E, Engelhard VH. Characterization of peptides bound to the class I MHC molecule HLA-A2.1 by mass spectrometry. Science 1992. 255: 1261-1263.

56. Zarling AL, Polefrone JM, Evans AM, Mikesh LM, Shabanowitz J, Lewis ST, Engelhard VH, Hunt DF. Identification of class I MHC-associated phosphopeptides as targets for cancer immunotherapy. Proc Natl Acad Sci U S A. 2006 Oct 3;103(40):14889-94.

57. Bassani-Sternberg M, Pletscher-Frankild S, Jensen LJ, Mann M. Mass spectrometry of human leukocyte antigen class I peptidomes reveals strong effects of protein abundance and turnover on antigen presentation. Mol Cell Proteomics. 2015 Mar;14(3):658-73. doi: 10.1074/mcp.M114.042812.

58. Abelin JG, Trantham PD, Penny SA, Patterson AM, Ward ST, Hildebrand WH, Cobbold M, Bai DL, Shabanowitz J, Hunt DF. Complementary IMAC enrichment methods for HLA-associated phosphopeptide identification by mass spectrometry. Nat Protoc. 2015 Sep;10(9):1308-18. doi: 10.1038/nprot.2015.086. Epub 2015 Aug 6

2026201462 26 Feb 2026

59. Barnstable CJ, Bodmer WF, Brown G, Galfre G, Milstein C, Williams AF, Ziegler A. Production of monoclonal antibodies to group A erythrocytes, HLA and other human cell surface antigens-new tools for genetic analysis. Cell. 1978 May;14(1):9-20.

60. Goldman JM, Hibbin J, Kearney L, Orchard K, Th'ng KH. HLA-DR monoclonal antibodies inhibit the proliferation of normal and chronic granulocytic leukaemia myeloid progenitor cells. Br J Haematol. 1982 Nov;52(3):411-20.

61. Eng JK, Jahan TA, Hoopmann MR. Comet: an open-source MS/MS sequence database search tool. Proteomics. 2013 Jan;13(1):22-4. doi: 10.1002/pmic.201200439. Epub 2012 Dec 4.

62. Eng JK, Hoopmann MR, Jahan TA, Egertson JD, Noble WS, MacCoss MJ. A deeper look into Comet--implementation and features. J Am Soc Mass Spectrom. 2015 Nov;26(11):1865-74. doi: 10.1007/s13361-015-1179-x. Epub 2015 Jun 27.

63. Lukas Käll, Jesse Canterbury, Jason Weston, William Stafford Noble and Michael J. MacCoss. Semi-supervised learning for peptide identification from shotgun proteomics datasets. Nature Methods 4:923 – 925, November 2007

64. Lukas Käll, John D. Storey, Michael J. MacCoss and William Stafford Noble. Assigning confidence measures to peptides identified by tandem mass spectrometry. Journal of Proteome Research, 7(1):29-34, January 2008

65. Lukas Käll, John D. Storey and William Stafford Noble. Nonparametric estimation of posterior error probabilities associated with peptides identified by tandem mass spectrometry. Bioinformatics, 24(16):i42-i48, August 2008

66. Kinney RM, BJ Johnson , VL Brown , DW Trent. Nucleotide Sequence of the 26 S mRNA of the Virulent Trinidad Donkey Strain of Venezuelan Equine Encephalitis Virus and Deduced Sequence of the Encoded Structural Proteins. Virology 152 (2), 400-413. 1986 Jul 30.

67. Jill E Slansky, Frédérique M Rattis, Lisa F Boyd, Tarek Fahmy, Elizabeth M Jaffee, Jonathan P Schneck, David H Margulies, Drew M Pardoll. Enhanced Antigen-Specific Antitumor Immunity with Altered Peptide Ligands that Stabilize the MHC-Peptide-TCR Complex. Immunity, Volume 13, Issue 4, 1 October 2000, Pages 529-538.

68. A Y Huang, P H Gulden, A S Woods, M C Thomas, C D Tong, W Wang, V H Engelhard, G Pasternack, R Cotter, D Hunt, D M Pardoll, and E M Jaffee. The immunodominant major histocompatibility complex class I-restricted antigen of a murine colon tumor derives from an endogenous retroviral gene product. Proc Natl Acad Sci U S A.; 93(18): 9730–9735, 1996 Sep 3.

69. JOHNSON, BARBARA J. B., RICHARD M. KINNEY, CRYSTLE L. KOST AND DENNIS W. TRENT. Molecular Determinants of Alphavirus Neurovirulence: Nucleotide and Deduced Protein Sequence Changes during Attenuation of Venezuelan Equine Encephalitis Virus. J Gen Virol 67:1951-1960, 1986.

70. Aarnoudse, C.A., Krüse, M., Konopitzky, R., Brouwenstijn, N., and Schrier, P.I. (2002). TCR reconstitution in Jurkat reporter cells facilitates the identification of novel tumor antigens by cDNA expression cloning. Int J Cancer 99, 7–13.

71. Alexander, J., Sidney, J., Southwood, S., Ruppert, J., Oseroff, C., Maewal, A., Snoke, K., Serra, H.M., Kubo, R.T., and Sette, A. (1994). Development of high potency universal DR-restricted helper epitopes by modification of high affinity DR-blocking peptides. Immunity 1, 751–761.

72. Banu, N., Chia, A., Ho, Z.Z., Garcia, A.T., Paravasivam, K., Grotenbreg, G.M., Bertoletti, A., and Gehring, A.J. (2014). Building and optimizing a virus-specific T cell receptor library for targeted immunotherapy in viral infections. Scientific Reports 4, 4166.

73. Cornet, S., Miconnet, I., Menez, J., Lemonnier, F., and Kosmatopoulos, K. (2006). Optimal organization of a polypeptide-based candidate cancer vaccine composed of cryptic

2026201462 26 Feb 2026

tumor peptides with enhanced immunogenicity. Vaccine 24, 2102–2109.

74. Depla, E., van der Aa, A., Livingston, B.D., Crimi, C., Allosery, K., de Brabandere, V., Krakover, J., Murthy, S., Huang, M., Power, S., et al. (2008). Rational design of a multiepitope vaccine encoding T-lymphocyte epitopes for treatment of chronic hepatitis B virus infections. Journal of Virology 82, 435–450.

75. Ishioka, G.Y., Fikes, J., Hermanson, G., Livingston, B., Crimi, C., Qin, M., del Guercio, M.F., Oseroff, C., Dahlberg, C., Alexander, J., et al. (1999). Utilization of MHC class I transgenic mice for development of minigene DNA vaccines encoding multiple HLA-restricted CTL epitopes. J Immunol 162, 3915–3925.

76. Janetzki, S., Price, L., Schroeder, H., Britten, C.M., Welters, M.J.P., and Hoos, A. (2015). Guidelines for the automated evaluation of Elispot assays. Nat Protoc 10, 1098–1115.

77. Lyons, G.E., Moore, T., Brasic, N., Li, M., Roszkowski, J.J., and Nishimura, M.I. (2006). Influence of human CD8 on antigen recognition by T-cell receptor-transduced cells. Cancer Res 66, 11455–11461.

78. Nagai, K., Ochi, T., Fujiwara, H., An, J., Shirakata, T., Mineno, J., Kuzushima, K., Shiku, H., Melenhorst, J.J., Gostick, E., et al. (2012). Aurora kinase A-specific T-cell receptor gene transfer redirects T lymphocytes to display effective antileukemia reactivity. Blood 119, 368–376.

79. Panina-Bordignon, P., Tan, A., Termijtelen, A., Demotz, S., Corradin, G., and Lanzavecchia, A. (1989). Universally immunogenic T cell epitopes: promiscuous binding to human MHC class II and promiscuous recognition by T cells. Eur J Immunol 19, 2237–2242.

80. Vitiello, A., Marchesini, D., Furze, J., Sherman, L.A., and Chesnut, R.W. (1991). Analysis of the HLA-restricted influenza-specific cytotoxic T lymphocyte response in transgenic mice carrying a chimeric human-mouse class I major histocompatibility complex. J Exp Med 173, 1007–1015.

81. Yachi, P.P., Ampudia, J., Zal, T., and Gascoigne, N.R.J. (2006). Altered peptide ligands induce delayed CD8-T cell receptor interaction--a role for CD8 in distinguishing antigen quality. Immunity 25, 203–211.

82. Pushko P, Parker M, Ludwig GV, Davis NL, Johnston RE, Smith JF. Replicon-helper systems from attenuated Venezuelan equine encephalitis virus: expression of heterologous genes in vitro and immunization against heterologous pathogens in vivo. Virology. 1997 Dec 22;239(2):389-401.

83. Strauss, JH and E G Strauss. The alphaviruses: gene expression, replication, and evolution. Microbiol Rev. 1994 Sep; 58(3): 491–562.

84. Rhême C, Ehrengruber MU, Grandgirard D. Alphaviral cytotoxicity and its implication in vector development. Exp Physiol. 2005 Jan;90(1):45-52. Epub 2004 Nov 12.

85. Riley, Michael K. II, and Wilfred Vermerris. Recent Advances in Nanomaterials for Gene Delivery—A Review. Nanomaterials 2017, 7(5), 94.

86. Frolov I, Hardy R, Rice CM. Cis-acting RNA elements at the 5' end of Sindbis virus genome RNA regulate minus- and plus-strand RNA synthesis. RNA. 2001 Nov;7(11):1638-51.

87. Jose J, Snyder JE, Kuhn RJ. A structural and functional perspective of alphavirus replication and assembly. Future Microbiol. 2009 Sep;4(7):837-56.

88. Bo Li and C. olin N. Dewey. RSEM: accurate transcript quantification from RNA-Seq data with or without a referenfe genome. BMC Bioinformatics, 12:323, August 2011

89. Hillary Pearson, Tariq Daouda, Diana Paola Granados, Chantal Durette, Eric Bonneil, Mathieu Courcelles, Anja Rodenbrock, Jean-Philippe Laverdure, Caroline Côté, Sylvie Mader, Sébastien Lemieux, Pierre Thibault, and Claude Perreault. MHC class I-associated peptides derive from selective regions of the human genome. The Journal of Clinical Investigation, 2016,

20262014622 26 Feb 2026

90. Juliane Liepe, Fabio Marino, John Sidney, Anita Jeko, Daniel E. Bunting, Alessandro Sette, Peter M. Kloetzel, Michael P. H. Stumpf, Albert J. R. Heck, Michele Mishto. A large fraction of HLA class I ligands are proteasome-generated spliced peptides. Science, 21, October 2016.

91. Mommen GP., Marino, F., Meiring HD., Poelen, MC., van Gaans-van den Brink, JA., Mohammed S., Heck AJ., and van Els CA. Sampling From the Proteome to the Human Leukocyte Antigen-DR (HLA-DR) Ligandome Proceeds Via High Specificity. Mol Cell Proteomics 15(4): 1412-1423, April 2016.

92. Sebastian Kreiter, Mathias Vormehr, Niels van de Roemer, Mustafa Diken, Martin Löwer, Jan Diekmann, Sebastian Boegel, Barbara Schrörs, Fulvia Vascotto, John C. Castle, Arbel D. Tadmor, Stephen P. Schoenberger, Christoph Huber, Özlem Türeci, and Ugur Sahin. Mutant MHC class II epitopes drive therapeutic immune responses to caner. Nature 520, 692-696, April 2015.

93. Tran E., Turcotte S., Gros A., Robbins P.F., Lu Y.C., Dudley M.E., Wunderlich J.R., Somerville R.P., Hogan K., Hinrichs C.S., Parkhurst M.R., Yang J.C., Rosenberg S.A. Cancer immunotherapy based on mutation-specific CD4+ T cells in a patient with epithelial cancer. Science 344(6184) 641-645, May 2014.

94. Andreatta M., Karosiene E., Rasmussen M., Stryhn A., Buus S., Nielsen M. Accurate pan-specific prediction of peptide-MHC class II binding affinity with improved binding core identification. Immunogenetics 67(11-12) 641-650, November 2015.

95. Nielsen, M., Lund, O. NN-align. An artificial neural network-based alignment algorithm for MHC class II peptide binding prediction. BMC Bioinformatics 10:296, September 2009.

96. Nielsen, M., Lundegaard, C., Lund, O. Prediction of MHC class II binding affinity using SMM-align, a novel stabilization matrix alignment method. BMC Bioinformatics 8:238, July 2007.

97. Zhang, J., et al. PEAKS DB: de novo sequencing assisted database search for sensitive and accurate peptide identification. Molecular & Cellular Proteomics. 11(4):1-8. 1/2/2012.

98. Jensen, Kamilla Kjaergaard, et al. “Improved Methods for Prediting Peptide Binding Affinity to MHC Class II Molecules.” Immunology, 2018, doi:10.1111/imm.12889.

99. Carter, S.L., Cibulskis, K., Helman, E., McKenna, A., Shen, H., Zack, T., Laird, P.W., Onofrio, R.C., Winckler, W., Weir, B.A., et al. (2012). Absolute quantification of somatic DNA alterations in human cancer. Nat. Biotechnol. 30, 413–421

100. McGranahan, N., Rosenthal, R., Hiley, C.T., Rowan, A.J., Watkins, T.B.K., Wilson, G.A., Birkbak, N.J., Veeriah, S., Van Loo, P., Herrero, J., et al. (2017). Allele-Specific HLA Loss and Immune Escape in Lung Cancer Evolution. Cell 171, 1259–1271.e11.

101. Shukla, S.A., Rooney, M.S., Rajasagi, M., Tiao, G., Dixon, P.M., Lawrence, M.S., Stevens, J., Lane, W.J., Dellagatta, J.L., Steelman, S., et al. (2015). Comprehensive analysis of cancer-associated somatic mutations in class I HLA genes. Nat. Biotechnol. 33, 1152–1158.

102. Van Loo, P., Nordgard, S.H., Lingjærde, O.C., Russnes, H.G., Rye, I.H., Sun, W., Weigman, V.J., Marynen, P., Zetterberg, A., Naume, B., et al. (2010). Allele-specific copy number analysis of tumors. Proc. Natl. Acad. Sci. U. S. A. 107, 16910–16915.

103. Van Loo, P., Nordgard, S.H., Lingjærde, O.C., Russnes, H.G., Rye, I.H., Sun, W., Weigman, V.J., Marynen, P., Zetterberg, A., Naume, B., et al. (2010). Allele-specific copy number analysis of tumors. Proc. Natl. Acad. Sci. U. S. A. 107, 16910–16915.

2026201462 26 Feb 2026

VARIOUS EMBODIMENTS

1. Disclosed herein is a viral vector comprising a neoantigen or plurality of neoantigens. In certain embodiments, a neoantigen is identified using a method dislcosed herein, e.g., below. In certain embodiments, a neoantigen has at least one characteristic or property as disclosed herein, e.g., below.

2. Disclosed herein is a method for identifying one or more neoantigens from a tumor cell of a subject that are likely to be presented on the tumor cell surface, comprising the steps of:

   obtaining at least one of exome, transcriptome or whole genome tumor nucleotide sequencing data from the tumor cell of the subject, wherein the tumor nucleotide sequencing data is used to obtain data representing peptide sequences of each of a set of neoantigens, and wherein the peptide sequence of each neoantigen comprises at least one alteration that makes it distinct from the corresponding wild-type, parental peptide sequence;

   inputting the peptide sequence of each neoantigen into one or more presentation models to generate a set of numerical likelihoods that each of the neoantigens is presented by one or more MHC alleles on the tumor cell surface of the tumor cell of the subject, the set of numerical likelihoods having been identified at least based on received mass spectrometry data; and

   selecting a subset of the set of neoantigens based on the set of numerical likelihoods to generate a set of selected neoantigens.

3. In certain embodiments, a number of the set of selected neoantigens is 20.

4. In certain embodiments, the presentation model represents dependence between:

   presence of a pair of a particular one of the MHC alleles and a particular amino acid at a particular position of a peptide sequence; and

   likelihood of presentation on the tumor cell surface, by the particular one of the MHC alleles of the pair, of such a peptide sequence comprising the particular amino acid at the particular position.

5. In certain embodiments, inputting the peptide sequence comprises:

   applying the one or more presentation models to the peptide sequence of the corresponding neoantigen to generate a dependency score for each of the one or more MHC alleles

2026201462 26 Feb 2026

indicating whether the MHC allele will present the corresponding neoantigen based on at least positions of amino acids of the peptide sequence of the corresponding neoantigen.

6. In certain embodiments, the method further comprises:

transforming the dependency scores to generate a corresponding per-allele likelihood for each MHC allele indicating a likelihood that the corresponding MHC allele will present the corresponding neoantigen; and

combining the per-allele likelihoods to generate the numerical likelihood.

7. In certain embodiments, the transforming the dependency scores model the presentation of the peptide sequence of the corresponding neoantigen as mutually exclusive.

8. In certain embodiments, the method further comprises:

transforming a combination of the dependency scores to generate the numerical likelihood.

9. In certain embodiments, the transforming the combination of the dependency scores models the presentation of the peptide sequence of the corresponding neoantigen as interfering between MHC alleles.

10. In certain embodiments, the set of numerical likelihoods are further identified by at least an allele noninteracting feature, and further comprising:

applying an allele noninteracting one of the one or more presentation models to the allele noninteracting features to generate a dependency score for the allele noninteracting features indicating whether the peptide sequence of the corresponding neoantigen will be presented based on the allele noninteracting features.

11. In certain embodiments, the method further comprises:

combining the dependency score for each MHC allele in the one or more MHC alleles with the dependency score for the allele noninteracting feature;

transforming the combined dependency scores for each MHC allele to generate a corresponding per-allele likelihood for the MHC allele indicating a likelihood that the corresponding MHC allele will present the corresponding neoantigen; and

combining the per-allele likelihoods to generate the numerical likelihood.

2026201462 26 Feb 2026

12. In certain embodiments, the method further comprises:

transforming a combination of the dependency scores for each of the MHC alleles and the dependency score for the allele noninteracting features to generate the numerical likelihood.

13. In certain embodiments, a set of numerical parameters for the presentation model is trained based on a training data set including at least a set of training peptide sequences identified as present in a plurality of samples and one or more MHC alleles associated with each training peptide sequence, wherein the training peptide sequences are identified through mass spectrometry on isolated peptides eluted from MHC alleles derived from the plurality of samples.

14. In certain embodiments, the training data set further includes data on mRNA expression levels of the tumor cell.

15. In certain embodiments, the samples comprise cell lines engineered to express a single MHC class I or class II allele.

16. In certain embodiments, the samples comprise cell lines engineered to express a plurality of MHC class I or class II alleles.

17. In certain embodiments, the samples comprise human cell lines obtained or derived from a plurality of patients.

18. In certain embodiments, the samples comprise fresh or frozen tumor samples obtained from a plurality of patients.

19. In certain embodiments, the samples comprise fresh or frozen tissue samples obtained from a plurality of patients.

20. In certain embodiments, the samples comprise peptides identified using T-cell assays.

21. In certain embodiments, the training data set further comprises data associated with:

peptide abundance of the set of training peptides present in the samples;

peptide length of the set of training peptides in the samples.

22. In certain embodiments, the training data set is generated by comparing the set of training peptide sequences via alignment to a database comprising a set of known protein sequences, wherein the set of training protein sequences are longer than and include the

2026201462 26 Feb 2026

training peptide sequences.

23. In certain embodiments, the training data set is generated based on performing or having performed mass spectrometry on a cell line to obtain at least one of exome, transcriptome, or whole genome peptide sequencing data from the cell line, the peptide sequencing data including at least one protein sequence including an alteration.

24. In certain embodiments, the trainnig data set is generated based on obtaining at least one of exome, transcriptome, and whole genome normal nucleotide sequencing data from normal tissue samples.

25. In certain embodiments, the training data set further comprises data associated with proteome sequences associated with the samples.

26. In certain embodiments, the training data set further comprises data associated with MHC peptidome sequences associated with the samples.

27. In certain embodiments, the training data set further comprises data associated with peptide-MHC binding affinity measurements for at least one of the isolated peptides.

28. In certain embodiments, the training data set further comprises data associated with peptide-MHC binding stability measurements for at least one of the isolated peptides.

29. In certain embodiments, the training data set further comprises data associated with transcriptomes associated with the samples.

30. In certain embodiments, the training data set further comprises data associated with genomes associated with the samples.

31. In certain embodiments, the training peptide sequences are of lengths within a range of k-mers where k is between 8-15, inclusive.

32. In certain embodiments, the method further comprises encoding the peptide sequence using a one-hot encoding scheme.

33. In certain embodiments, the method further comprises encoding the training peptide sequences using a left-padded one-hot encoding scheme.

34. Also disclosed herein is a method of treating a subject having a tumor, comprising performing any of the steps of the methods disclosed herein, and further comprising obtaining a tumor vaccine comprising the set of selected neoantigens, and administering the

2026201462 26 Feb 2026

tumor vaccine to the subject.

35. Also disclosed herein is a method of manufacturing a tumor vaccine, comprising performing any of the steps a method disclosed herein, and further comprising producing or having produced a tumor vaccine comprising the set of selected neoantigens.

36. Also disclosed herien is a tumor vaccine comprising a set of selected neoantigens, selected by performing a method disclosed herein.

37. In certain embodiments, the tumor vaccine comprises one or more of a nucleotide sequence, a polypeptide sequence, RNA, DNA, a cell, a plasmid, or a vector.

38. In certain embodiments, the tumor vaccine comprises one or more neoantigens presented on the tumor cell surface.

39. In certain embodiments, the tumor vaccine comprises one or more neoantigens that is immunogenic in the subject.

40. In certain embodiments, the tumor vaccine does not comprise one or more neoantigens that induce an autoimmune response against normal tissue in the subject.

41. In certain embodiments, the tumor vaccine further comprises an adjuvant.

42. In certain embodiments, the tumor vaccine further comprises an excipient.

43. In certain embodiments, selecting the set of selected neoantigens comprises selecting neoantigens that have an increased likelihood of being presented on the tumor cell surface relative to unselected neoantigens based on the presentation model.

44. In certain embodiments, selecting the set of selected neoantigens comprises selecting neoantigens that have an increased likelihood of being capable of inducing a tumor-specific immune response in the subject relative to unselected neoantigens based on the presentation model.

45. In certain embodiments, selecting the set of selected neoantigens comprises selecting neoantigens that have an increased likelihood of being capable of being presented to naïve T cells by professional antigen presenting cells (APCs) relative to unselected neoantigens based on the presentation model, optionally wherein the APC is a dendritic cell (DC).

46. In certain embodiments, selecting the set of selected neoantigens comprises selecting neoantigens that have a decreased likelihood of being subject to inhibition via central or

2026201462 26 Feb 2026

peripheral tolerance relative to unselected neoantigens based on the presentation model.

47. In certain embodiments, selecting the set of selected neoantigens comprises selecting neoantigens that have a decreased likelihood of being capable of inducing an autoimmune response to normal tissue in the subject relative to unselected neoantigens based on the presentation model.

48. In certain embodiments, exome or transcriptome nucleotide sequencing data is obtained by performing sequencing on the tumor tissue.

49. In certain embodiments, sequencing is next generation sequencing (NGS) or any massively parallel sequencing approach.

50. In certain embodiments, the set of numerical likelihoods are further identified by at least MHC-allele interacting features comprising at least one of:

    a. The predicted affinity with which the MHC allele and the neoantigen encoded peptide bind.

    b. The predicted stability of the neoantigen encoded peptide-MHC complex.

    c. The sequence and length of the neoantigen encoded peptide.

    d. The probability of presentation of neoantigen encoded peptides with similar sequence in cells from other individuals expressing the particular MHC allele as assessed by mass-spectrometry proteomics or other means.

    e. The expression levels of the particular MHC allele in the subject in question (e.g. as measured by RNA-seq or mass spectrometry).

    f. The overall neoantigen encoded peptide-sequence-independent probability of presentation by the particular MHC allele in other distinct subjects who express the particular MHC allele.

    g. The overall neoantigen encoded peptide-sequence-independent probability of presentation by MHC alleles in the same family of molecules (e.g., HLA-A, HLA-B, HLA-C, HLA-DQ, HLA-DR, HLA-DP) in other distinct subjects.

51. In certain embodiments, the set of numerical likelihoods are further identified by at least MHC-allele noninteracting features comprising at least one of:

2026201462 26 Feb 2026

a. The C- and N-terminal sequences flanking the neoantigen encoded peptide within its source protein sequence.
b. The presence of protease cleavage motifs in the neoantigen encoded peptide, optionally weighted according to the expression of corresponding proteases in the tumor cells (as measured by RNA-seq or mass spectrometry).
c. The turnover rate of the source protein as measured in the appropriate cell type.
d. The length of the source protein, optionally considering the specific splice variants ("isoforms") most highly expressed in the tumor cells as measured by RNA-seq or proteome mass spectrometry, or as predicted from the annotation of germline or somatic splicing mutations detected in DNA or RNA sequence data.
e. The level of expression of the proteasome, immunoproteasome, thymoproteasome, or other proteases in the tumor cells (which may be measured by RNA-seq, proteome mass spectrometry, or immunohistochemistry).
f. The expression of the source gene of the neoantigen encoded peptide (e.g., as measured by RNA-seq or mass spectrometry).
g. The typical tissue-specific expression of the source gene of the neoantigen encoded peptide during various stages of the cell cycle.
h. A comprehensive catalog of features of the source protein and/or its domains as can be found in e.g. uniProt or PDB http://www.rcsb.org/pdb/home/home.do.
i. Features describing the properties of the domain of the source protein containing the peptide, for example: secondary or tertiary structure (e.g., alpha helix vs beta sheet); Alternative splicing.
j. The probability of presentation of peptides from the source protein of the neoantigen encoded peptide in question in other distinct subjects.
k. The probability that the peptide will not be detected or over-represented by mass spectrometry due to technical biases.
l. The expression of various gene modules/pathways as measured by RNASeq (which need not contain the source protein of the peptide) that are informative about the state of the tumor cells, stroma, or tumor-infiltrating lymphocytes (TILs).
m. The copy number of the source gene of the neoantigen encoded peptide in the tumor cells.
n. The probability that the peptide binds to the TAP or the measured or predicted binding affinity of the peptide to the TAP.

2026201462 26 Feb 2026

o. The expression level of TAP in the tumor cells (which may be measured by RNA-seq, proteome mass spectrometry, immunohistochemistry).

p. Presence or absence of tumor mutations, including, but not limited to:

i. Driver mutations in known cancer driver genes such as EGFR, KRAS, ALK, RET, ROS1, TP53, CDKN2A, CDKN2B, NTRK1, NTRK2, NTRK3

ii. In genes encoding the proteins involved in the antigen presentation machinery (e.g., B2M, HLA-A, HLA-B, HLA-C, TAP-1, TAP-2, TAPBP, CALR, CNX, ERP57, HLA-DM, HLA-DMA, HLA-DMB, HLA-DO, HLA-DOA, HLA-DOB, HLA-DP, HLA-DPA1, HLA-DPB1, HLA-DQ, HLA-DQA1, HLA-DQA2, HLA-DQB1, HLA-DQB2, HLA-DR, HLA-DRA, HLA-DRB1, HLA-DRB3, HLA-DRB4, HLA-DRB5 or any of the genes coding for components of the proteasome or immunoproteasome). Peptides whose presentation relies on a component of the antigen-presentation machinery that is subject to loss-of-function mutation in the tumor have reduced probability of presentation.

q. Presence or absence of functional germline polymorphisms, including, but not limited to:

i. In genes encoding the proteins involved in the antigen presentation machinery (e.g., B2M, HLA-A, HLA-B, HLA-C, TAP-1, TAP-2, TAPBP, CALR, CNX, ERP57, HLA-DM, HLA-DMA, HLA-DMB, HLA-DO, HLA-DOA, HLA-DOB, HLA-DP, HLA-DPA1, HLA-DPB1, HLA-DQ, HLA-DQA1, HLA-DQA2, HLA-DQB1, HLA-DQB2, HLA-DR, HLA-DRA, HLA-DRB1, HLA-DRB3, HLA-DRB4, HLA-DRB5 or any of the genes coding for components of the proteasome or immunoproteasome)

r. Tumor type (e.g., NSCLC, melanoma).

s. Clinical tumor subtype (e.g., squamous lung cancer vs. non-squamous).

t. Smoking history.

u. The typical expression of the source gene of the peptide in the relevant tumor type or clinical subtype, optionally stratified by driver mutation.

52. In certain embodiments, the at least one mutation is a frameshift or nonframeshift indel, missense or nonsense substitution, splice site alteration, genomic rearrangement or gene fusion, or any genomic or expression alteration giving rise to a neoORF.

2026201462 26 Feb 2026

53. In certain embodiments, the tumor cell is selected from the group consisting of: lung cancer, melanoma, breast cancer, ovarian cancer, prostate cancer, kidney cancer, gastric cancer, colon cancer, testicular cancer, head and neck cancer, pancreatic cancer, brain cancer, B-cell lymphoma, acute myelogenous leukemia, chronic myelogenous leukemia, chronic lymphocytic leukemia, and T cell lymphocytic leukemia, non-small cell lung cancer, and small cell lung cancer.

54. In certain embodiments, the method further comprises obtaining a tumor vaccine comprising the set of selected neoantigens or a subset thereof, optionally further comprising administering the tumor vaccine to the subject.

55. In certain embodiments, at least one of neoantigens in the set of selected neoantigens, when in polypeptide form, comprises at least one of: a binding affinity with MHC with an IC50 value of less than 1000nM, for MHC Class 1 polypeptides a length of 8-15, 8, 9, 10, 11, 12, 13, 14, or 15 amino acids, presence of sequence motifs within or near the polypeptide in the parent protein sequence promoting proteasome cleavage, and presence of sequence motifs promoting TAP transport.

56. Also disclosed herein is a method for generating a model for identifying one or more neoantigens that are likely to be presented on a tumor cell surface of a tumor cell, comprising executing the steps of:

receiving mass spectrometry data comprising data associated with a plurality of isolated peptides eluted from major histocompatibility complex (MHC) derived from a plurality of samples;

obtaining a training data set by at least identifying a set of training peptide sequences present in the samples and one or more MHCs associated with each training peptide sequence;

training a set of numerical parameters of a presentation model using the training data set comprising the training peptide sequences, the presentation model providing a plurality of numerical likelihoods that peptide sequences from the tumor cell are presented by one or more MHC alleles on the tumor cell surface.

57. In certain embodiments, the presentation model represents dependence between:

presence of a particular amino acid at a particular position of a peptide sequence; and

2026201462 26 Feb 2026

likelihood of presentation, by one of the MHC alleles on the tumor cell, of the peptide sequence containing the particular amino acid at the particular position.

58. In certain embodiments, the samples comprise cell lines engineered to express a single MHC class I or class II allele.

59. In certain embodiments, the samples comprise cell lines engineered to express a plurality of MHC class I or class II alleles.

60. In certain embodiments, the samples comprise human cell lines obtained or derived from a plurality of patients.

61. In certain embodiments, the samples comprise fresh or frozen tumor samples obtained from a plurality of patients.

62. In certain embodiments, the samples comprise peptides identified using T-cell assays.

63. In certain embodiments, the training data set further comprises data associated with:

peptide abundance of the set of training peptides present in the samples;

peptide length of the set of training peptides in the samples.

64. In certain embodiments, obtaining the training data set comprises:

obtaining a set of training protein sequences based on the training peptide sequences by comparing the set of training peptide sequences via alignment to a database comprising a set of known protein sequences, wherein the set of training protein sequences are longer than and include the training peptide sequences.

65. In certain embodiments, obtaining the training data set comprises:

performing or having performed mass spectrometry on a cell line to obtain at least one of exome, transcriptome, or whole genome nucleotide sequencing data from the cell line, the nucelotide sequencing data including at least one protein sequence including a mutation.

66. In certain embodiments, training the set of parameters of the presetation model comprises:

encoding the training peptide sequences using a one-hot encoding scheme.

67. In certain embodiments, the method further comprises:

2026201462 26 Feb 2026

obtaining at least one of exome, transcriptome, and whole genome normal nucleotide sequencing data from normal tissue samples; and

training the set of parameters of the presentation model using the normal nucleotide sequencing data.

68. In certain embodiments, the training data set further comprises data associated with proteome sequences associated with the samples.

69. In certain embodiments, the training data set further comprises data associated with MHC peptidome sequences associated with the samples.

70. In certain embodiments, the training data set further comprises data associated with peptide-MHC binding affinity measurements for at least one of the isolated peptides.

71. In certain embodiments, the training data set further comprises data associated with peptide-MHC binding stability measurements for at least one of the isolated peptides.

72. In certain embodiments, the training data set further comprises data associated with transcriptomes associated with the samples.

73. In certain embodiments, the training data set further comprises data associated with genomes associated with the samples.

74. In certain embodiments, training the set of numerical parameters further comprises:

logistically regressing the set of parameters.

75. In certain embodiments, the training peptide sequences are of lengths within a range of k-mers where k is between 8-15, inclusive.

76. In certain embodiments, training the set of numerical parameters of the presetation model comprises:

encoding the training peptide sequences using a left-padded one-hot encoding scheme.

77. In certain embodiments, training the set of numerical parameters further comprises:

determining values for the set of parameters using a deep learning algorithm.

78. Also disclosed herein is a method for generating a model for identifying one or more neoantigens that are likely to be presented on a tumor cell surface of a tumor cell, comprising executing the steps of:

2026201462 26 Feb 2026

receiving mass spectrometry data comprising data associated with a plurality of isolated peptides eluted from major histocompatibility complex (MHC) derived from a plurality of fresh or frozen tumor samples;

obtaining a training data set by at least identifying a set of training peptide sequences present in the tumor samples and presented on one or more MHC alleles associated with each training peptide sequence;

obtaining a set of training protein sequences based on the training peptide sequences; and

training a set of numerical parameters of a presentation model using the training protein sequences and the training peptide sequences, the presentation model providing a plurality of numerical likelihoods that peptide sequences from the tumor cell are presented by one or more MHC alleles on the tumor cell surface.

79. In certain embodiments, the presentation model represents dependence between:

presence of a pair of a particular one of the MHC alleles and a particular amino acid at a particular position of a peptide sequence; and

likelihood of presentation on the tumor cell surface, by the particular one of the MHC alleles of the pair, of such a peptide sequence comprising the particular amino acid at the particular position.

2026201462 26 Feb 2026

CLAIMS

What is claimed is:

1. A composition for delivery of a neoantigen expression system, comprising:

the neoantigen expression system,

wherein the neoantigen expression system comprises one or more vectors,

the one or more vectors comprising:

(a) an RNA alphavirus backbone, wherein the RNA alphavirus backbone comprises:

(i) at least one promoter nucleotide sequence, and

(ii) at least one polyadenylation (poly(A)) sequence; and

(b) a neoantigen cassette, wherein the neoantigen cassette comprises:

(i) at least one neoantigen-encoding nucleic acid sequence derived from a tumor present within a subject, comprising:

(I) at least one tumor-specific and subject-specific MHC class I neoantigen-encoding nucleic acid sequence derived from the tumor, and comprising:

(A) a MHC class I epitope encoding nucleic acid sequence with at least one alteration that makes the encoded peptide sequence distinct from the corresponding peptide sequence encoded by a wild-type nucleic acid sequence, and

(B) optionally, a 5’ linker sequence, and

(C) optionally, a 3’ linker sequence;

(ii) optionally, a second promoter nucleotide sequence operably linked to the neoantigen-encoding nucleic acid sequence; and

(iii) optionally, at least one MHC class II antigen-encoding nucleic acid sequence;

(iv) optionally, at least one nucleic acid sequence encoding a GPGPG amino acid linker sequence (SEQ ID NO:56); and

(v) optionally, at least one second poly(A) sequence, wherein the second poly(A) sequence is a native poly(A) sequence or an exogenous poly(A) sequence to the alphavirus.

2026201462 26 Feb 2026

2. A composition for delivery of a neoantigen expression system, comprising:

the neoantigen expression system,

wherein the neoantigen expression system comprises one or more vectors,

the one or more vectors comprising:

(a) an RNA alphavirus backbone, wherein the RNA alphavirus backbone comprises the nucleic acid sequence set forth in SEQ ID NO:6, wherein the RNA alphavirus backbone sequence comprises a 26S promoter nucleotide sequence and a poly(A) sequence, wherein the 26S promoter sequence is endogenous to the RNA alphavirus backbone, and wherein the poly(A) sequence is endogenous to the RNA alphavirus backbone; and

(b) a neoantigen cassette integrated between the 26S promoter nucleotide sequence and the poly(A) sequence , wherein the neoantigen cassette comprises:

(i) at least one neoantigen-encoding nucleic acid sequence derived from a tumor present within a subject, comprising:

(I) at least 10 tumor-specific and subject-specific MHC class I neoantigen-encoding nucleic acid sequences linearly linked to each other and each comprising:

(A) a MHC class I epitope encoding nucleic acid sequence with at least one alteration that makes the encoded peptide sequence distinct from the corresponding peptide sequence encoded by a wild-type nucleic acid sequence, wherein the MHC I epitope encoding nucleic acid sequence encodes a MHC class I epitope 7-15 amino acids in length,

(B) a 5’ linker sequence, wherein the 5’ linker sequence encodes a native N-terminal amino acid sequence of the MHC I epitope, and wherein the 5’ linker sequence encodes a peptide that is at least 3 amino acids in length,

(C) a 3’ linker sequence, wherein the 3’ linker sequence encodes a native N-terminal acid sequence of the MHC I epitope, and wherein the 3’ linker sequence encodes a peptide that is at least 3 amino acids in length, and

2026201462 26 Feb 2026

wherein the neoantigen cassette is operably linked to the 26S promoter nucleotide sequence, wherein each of the MHC class I neoantigen-encoding nucleic acid sequences encodes a polypeptide that is between 13 and 25 amino acids in length, and wherein each 3' end of each MHC class I neoantigen-encoding nucleic acid sequence is linked to the 5' end of the following MHC class I neoantigen-encoding nucleic acid sequence with the exception of the final MHC class I neoantigen-encoding nucleic acid sequence in the neoantigen cassette; and

(ii) at least two MHC class II antigen-encoding nucleic acid sequences comprising:

(I) a PADRE MHC class II sequence (SEQ ID NO:48),

(II) a Tetanus toxoid MHC class II sequence (SEQ ID NO:46),

(III) a first nucleic acid sequence encoding a GPGPG amino acid linker sequence linking the PADRE MHC class II sequence and the Tetanus toxoid MHC class II sequence,

(IV) a second nucleic acid sequence encoding a GPGPG amino acid linker sequence linking the 5' end of the at least two MHC class II antigen-encoding nucleic acid sequences to the at least 20 tumor-specific and subject-specific MHC class I neoantigen-encoding nucleic acid sequences,

(V) optionally, a third nucleic acid sequence encoding a GPGPG amino acid linker sequence at the 3' end of the at least two MHC class II antigen-encoding nucleic acid sequences.

2026201462 26 Feb 2026

3. The composition of claim 1, wherein an ordered sequence of each element of the neoantigen cassette is described in the formula, from 5' to 3', comprising:

$$P_a\text{-}(L5_b\text{-}N_c\text{-}L3_d)_X\text{-}(G5_e\text{-}U_f)_Y\text{-}G3_g$$

wherein P comprises the second promoter nucleotide sequence, where a = 0 or 1,

N comprises one of the MHC class I epitope encoding nucleic acid sequences, where c = 1,

L5 comprises the 5' linker sequence, where b = 0 or 1,

L3 comprises the 3' linker sequence, where d = 0 or 1,

G5 comprises one of the at least one nucleic acid sequences encoding a GPGPG amino acid linker, where e = 0 or 1,

G3 comprises one of the at least one nucleic acid sequences encoding a GPGPG amino acid linker, where g = 0 or 1,

U comprises one of the at least one MHC class II antigen-encoding nucleic acid sequence, where f = 1,

X = 1 to 400, where for each X the corresponding N_c is a epitope encoding nucleic acid sequence, and

Y = 0, 1, or 2, where for each Y the corresponding U_f is an antigen-encoding nucleic acid sequence.

4. The composition of claim 3, wherein for each X the corresponding N_c is a distinct MHC class I epitope encoding nucleic acid sequence.

5. The composition of claim 3 or 4, wherein for each Y the corresponding U_f is a distinct MHC class II antigen-encoding nucleic acid sequence.

2026201462 26 Feb 2026

6. The composition of any one of claims 3-5 , wherein

a = 0, b = 1, d = 1, e = 1, g = 1, h = 1, X = 20, Y = 2,

the at least one promoter nucleotide sequence is a single 26S promoter nucleotide sequence provided by the RNA alphavirus backbone,

the at least one polyadenylation poly(A) sequence is a poly(A) sequence of at least 100 consecutive A nucleotides provided by the RNA alphavirus backbone,

each N encodes a MHC class I epitope 7-15 amino acids in length,

L5 is a native 5' linker sequence that encodes a native N-terminal amino acid sequence of the MHC I epitope, and wherein the 5' linker sequence encodes a peptide that is at least 3 amino acids in length,

L3 is a native 3' linker sequence that encodes a native nucleic-terminal acid sequence of the MHC I epitope, and wherein the 3' linker sequence encodes a peptide that is at least 3 amino acids in length,

U is each of a PADRE class II sequence and a Tetanus toxoid MHC class II sequence,

the RNA alphavirus backbone is the sequence set forth in SEQ ID NO:6, and
each of the MHC class I neoantigen-encoding nucleic acid sequences encodes a polypeptide that is between 13 and 25 amino acids in length.

7. The composition of any of the above claims, the composition further comprising a nanoparticulate delivery vehicle.

8. The composition of claim 7, wherein the nanoparticulate delivery vehicle is a lipid nanoparticle (LNP).

9. The composition of claim 8, wherein the LNP comprises ionizable amino lipids.

10. The composition of claim 9, wherein the ionizable amino lipids comprise MC3-like (dilinoleylmethyl-4-dimethylaminobutyrate) molecules.

11. The composition of any of claims claim 7-10, wherein the nanoparticulate delivery vehicle encapsulates the neoantigen expression system.

12. The composition of claim 8, further comprising a plurality of LNPs, wherein the LNPs comprise:

the neoantigen expression system;

a cationic lipid;

2026201462 26 Feb 2026

a non-cationic lipid; and

a conjugated lipid that inhibits aggregation of the LNPs, wherein at least about 95% of the LNPs in the plurality of LNPs either:

(a) have a non-lamellar morphology; or

(b) are electron-dense.

13. The composition of claim 12, wherein the non-cationic lipid is a mixture of (1) a phospholipid and (2) cholesterol or a cholesterol derivative.

14. The composition of claim 12 or 13, wherein the conjugated lipid that inhibits aggregation of the LNPs is a polyethyleneglycol (PEG)-lipid conjugate.

15. The composition of claim 14, wherein the PEG-lipid conjugate is selected from the group consisting of: a PEG-diacylglycerol (PEG-DAG) conjugate, a PEG dialkyloxypropyl (PEG-DAA) conjugate, a PEG-phospholipid conjugate, a PEG-ceramide (PEG-Cer) conjugate, and a mixture thereof.

16. The composition of claim 15, wherein the PEG-DAA conjugate is a member selected from the group consisting of: a PEG-didecyloxypropyl (C_{10}) conjugate, a PEG-dilauryloxypropyl (C_{12}) conjugate, a PEG-dimyristyloxypropyl (C_{14}) conjugate, a PEG-dipalmityloxypropyl (C_{16}) conjugate, a PEG-distearyloxypropyl (C_{18}) conjugate, and a mixture thereof.

17. The composition of any one of claims 12-16, wherein the non-lamellar morphology of the LNPs comprises an inverse hexagonal (H_{II}) or cubic phase structure.

18. The composition of claim 12-17, wherein the cationic lipid comprises from about 10 mol % to about 50 mol % of the total lipid present in the LNPs.

19. The composition of any one of claims 12-17, wherein the cationic lipid comprises from about 20 mol % to about 50 mol % of the total lipid present in the LNPs.

20. The composition of any one of claims 12-17, wherein the cationic lipid comprises from about 20 mol % to about 40 mol % of the total lipid present in the LNPs.

21. The composition of any one of claims 12-20, wherein the non-cationic lipid comprises from about 10 mol % to about 60 mol % of the total lipid present in the LNPs.

22. The composition of any one of claims 12-20, wherein the non-cationic lipid comprises from about 20 mol % to about 55 mol % of the total lipid present in the LNPs.

23. The composition of any one of claims 12-20, wherein the non-cationic lipid comprises from about 25 mol % to about 50 mol % of the total lipid present in the LNPs.

2026201462 26 Feb 2026

24. The composition of any one of claims 12-23, wherein the conjugated lipid comprises from about 0.5 mol % to about 20 mol % of the total lipid present in the LNPs.
25. The composition of any one of claims 12-23, wherein the conjugated lipid comprises from about 2 mol % to about 20 mol % of the total lipid present in the LNPs.
26. The composition of any one of claims 12-23, wherein the conjugated lipid comprises from about 1.5 mol % to about 18 mol % of the total lipid present in the LNPs.
27. The composition of any one of claims 12-26, wherein greater than 95% of the LNPs have a non-lamellar morphology.
28. The composition of any one of claims 12-27, wherein greater than 95% of the LNPs are electron dense.
29. The composition of any one of claims 8-28, further comprising a plurality of LNPs, wherein the LNPs comprise:

a cationic lipid comprising from 50 mol % to 65 mol % of the total lipid present in the LNPs;

a conjugated lipid that inhibits aggregation of LNPs comprising from 0.5 mol % to 2 mol % of the total lipid present in the LNPs; and

a non-cationic lipid comprising either:

(a) a mixture of a phospholipid and cholesterol or a derivative thereof, wherein the phospholipid comprises from 4 mol % to 10 mol % of the total lipid present in the LNPs and the cholesterol or derivative thereof comprises from 30 mol % to 40 mol % of the total lipid present in the LNPs;

(b) a mixture of a phospholipid and cholesterol or a derivative thereof, wherein the phospholipid comprises from 3 mol % to 15 mol % of the total lipid present in the LNPs and the cholesterol or derivative thereof comprises from 30 mol % to 40 mol % of the total lipid present in the LNPs; or

(c) up to 49.5 mol % of the total lipid present in the LNPs and comprising a mixture of a phospholipid and cholesterol or a derivative thereof, wherein the cholesterol or derivative thereof comprises from 30 mol % to 40 mol % of the total lipid present in the LNPs.

2026201462 26 Feb 2026

30. The composition of any one of claims 8-28, further comprising a plurality of LNPs, wherein the LNPs comprise:

a cationic lipid comprising from 50 mol % to 85 mol % of the total lipid present in the LNPs;

a conjugated lipid that inhibits aggregation of LNPs comprising from 0.5 mol % to 2 mol % of the total lipid present in the LNPs; and

a non-cationic lipid comprising from 13 mol % to 49.5 mol % of the total lipid present in the LNPs.

31. The composition of claim 29, wherein the phospholipid comprises dipalmitoylphosphatidylcholine (DPPC), distearoylphosphatidylcholine (DSPC), or a mixture thereof.

32. The composition of claim 29 or 30, wherein the conjugated lipid comprises a polyethyleneglycol (PEG)-lipid conjugate.

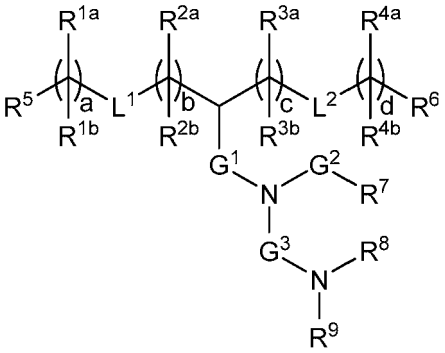
33. The composition of claim 32, wherein the PEG-lipid conjugate comprises a PEG-diacylglycerol (PEG-DAG) conjugate, a PEG-dialkyloxypropyl (PEG-DAA) conjugate, or a mixture thereof.

34. The composition of claim 33, wherein the PEG-DAA conjugate comprises a PEG-dimyristyloxypropyl (PEG-DMA) conjugate, a PEG-distearyloxypropyl (PEG-DSA) conjugate, or a mixture thereof.

35. The composition of any one of claims 32-34, wherein the PEG portion of the conjugate has an average molecular weight of about 2,000 daltons.

36. The composition of any one of claims 29-35, wherein the conjugated lipid comprises from 1 mol % to 2 mol % of the total lipid present in the LNPs.

37. The composition of any one of claims 8-36, wherein the LNP comprises a compound having a structure of Formula I:



2026201462 26 Feb 2026

I

or a pharmaceutically acceptable salt, tautomer, prodrug or stereoisomer thereof, wherein:

L^1 and L^2 are each independently -0(C=0)-, -(C=0)0-, -C(=0)-, -0-, -$S(0)_x$-, -S-S-, -C(=0)S-, -SC(=0)-, - R^aC(=0)-, -C(=0) R^a-, - R^aC(=0) R^a-, -OC(=0) R^a-, - R^aC(=0)0- or a direct bond;

G^1 is Ci-C_2 alkylene, - (C=0)-, -0(C=0)-, -SC(=0)-, - R^aC(=0)- or a direct bond:

-C(=0)-, -(C=0)0-, -C(=0)S-, -C(=0) R^a- or a direct bond;

G is Ci-C_6 alkylene;

R^a is H or C1-C12 alkyl;

R^{la} and R^{lb} are, at each occurrence, independently either: (a) H or C_1-C_{12} alkyl; or (b) R^{la} is H or C_1-C_{12} alkyl, and R^{lb} together with the carbon atom to which it is bound is taken together with an adjacent R^{lb} and the carbon atom to which it is bound to form a carbon-carbon double bond;

R^{2a} and R^{2b} are, at each occurrence, independently either: (a) H or C_1-C_{12} alkyl; or (b) R^{2a} is H or C_1-C_{12} alkyl, and R^{2b} together with the carbon atom to which it is bound is taken together with an adjacent R^{2b} and the carbon atom to which it is bound to form a carbon-carbon double bond;

R^{3a} and R^{3b} are, at each occurrence, independently either (a): H or C_1-C_{12} alkyl; or (b) R^{3a} is H or C_1-C_{12} alkyl, and R^{3b} together with the carbon atom to which it is bound is taken together with an adjacent R and the carbon atom to which it is bound to form a carbon-carbon double bond;

R^{4a} and R^{4b} are, at each occurrence, independently either: (a) H or C1-C12 alkyl; or (b) R^{4a} is H or C1-C12 alkyl, and R^{4b} together with the carbon atom to which it is bound is taken together with an adjacent R^{4b} and the carbon atom to which it is bound to form a carbon-carbon double bond;

R^5 and R^6 are each independently H or methyl;

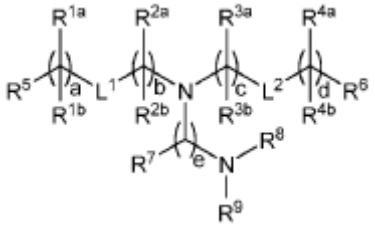
R^7 is C4-C20 alkyl;

R^8 and R^9 are each independently C1-C12 alkyl; or R^8 and R^9, together with the nitrogen atom to which they are attached, form a 5, 6 or 7-membered heterocyclic ring;

2026201462 26 Feb 2026

a, b, c and d are each independently an integer from 1 to 24; and x is 0, 1 or 2.

38. The composition of any one of claims 8-36, wherein the LNP comprises a compound having a structure of Formula II:



II

or a pharmaceutically acceptable salt, tautomer, prodrug or stereoisomer thereof, wherein:

L^1 and L^2 are each independently -0(C=0)-, -(C=0)0- or a carbon-carbon double bond;

R^{la} and R^{lb} are, at each occurrence, independently either (a) H or C_1-C_{12} alkyl, or (b) R^{la} is H or C_1-C_{12} alkyl, and R^{lb} together with the carbon atom to which it is bound is taken together with an adjacent R^{lb} and the carbon atom to which it is bound to form a carbon-carbon double bond;

R^{2a} and R^{2b} are, at each occurrence, independently either (a) H or C_1-C_{12} alkyl, or (b) R^{2a} is H or C_1-C_{12} alkyl, and R^{2b} together with the carbon atom to which it is bound is taken together with an adjacent R^{2b} and the carbon atom to which it is bound to form a carbon-carbon double bond;

R^{3a} and R^{3b} are, at each occurrence, independently either (a) H or C_1-C_{12} alkyl, or (b) R^{3a} is H or C_1-C_{12} alkyl, and R^{3b} together with the carbon atom to which it is bound is taken together with an adjacent R^{3b} and the carbon atom to which it is bound to form a carbon-carbon double bond;

R^{4a} and R^{4b} are, at each occurrence, independently either (a) H or C_1-C_{12} alkyl, or (b) R^{4a} is H or C_1-C_{12} alkyl, and R^{4b} together with the carbon atom to which it is bound is taken together with an adjacent R^{4b} and the carbon atom to which it is bound to form a carbon-carbon double bond;

R^5 and R^6 are each independently methyl or cycloalkyl;

R^7 is, at each occurrence, independently H or C_1-C_{12} alkyl;

2026201462 26 Feb 2026

R^8 and R^9 are each independently unsubstituted C1-C12 alkyl; or R^8 and R^9, together with the nitrogen atom to which they are attached, form a 5, 6 or 7-membered heterocyclic ring comprising one nitrogen atom;

a and d are each independently an integer from 0 to 24; b and c are each independently an integer from 1 to 24; and e is 1 or 2,

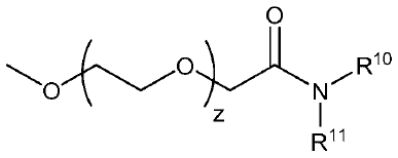
provided that:

at least one of R^{1a}, R^{2a}, R^{3a} or R^{4a} is C1-C12 alkyl, or at least one of L^1 or L^2 is -0(C=0)- or -(C=0)0-; and

R^{1a} and R^{1b} are not isopropyl when a is 6 or n-butyl when a is 8.

39. The composition of claims 37 or 39, further comprising one or more excipients comprising a neutral lipid, a steroid, and a polymer conjugated lipid.
40. The composition of claim 39, wherein the neutral lipid comprises at least one of l,2-Distearoyl-*sn*-glycero-3-phosphocholine (DSPC), l,2-Dipalmitoyl-*sn*-glycero-3-phosphocholine (DPPC), l,2-Dimyristoyl-*sn*-glycero-3-phosphocholine (DMPC), 1-Palmitoyl-2-oleoyl-*sn*-glycero-3-phosphocholine (POPC), 1,2-dioleoyl-*sn*-glycero-3-phosphocholine (DOPC), and l,2-Dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE).
41. The composition of claim 40, wherein the neutral lipid is DSPC.
42. The composition of any one of claim 39-41, wherein the molar ratio of the compound to the neutral lipid ranges from about 2:1 to about 8:1.
43. The composition of any one of claims 39-42, wherein the steroid is cholesterol.
44. The composition of claim 43, wherein the molar ratio of the compound to cholesterol ranges from about 2:1 to 1:1.
45. The composition of any one of claims 39-44, wherein the polymer conjugated lipid is a pegylated lipid.
46. The composition of claim 45, wherein the molar ratio of the compound to the pegylated lipid ranges from about 100:1 to about 25:1.
47. The composition of claims 45 or 46, wherein the pegylated lipid is PEG-DAG, a PEG polyethylene (PEG-PE), a PEG-succinoyl-diacylglycerol (PEG-S-DAG), PEG-cer or a PEG dialkyoxypropylcarbamate.
48. The composition of claims 45 or 46, wherein the pegylated lipid has the following structure III:

2026201462 26 Feb 2026



III

or a pharmaceutically acceptable salt, tautomer or stereoisomer thereof, wherein:

R^{10} and R^{11} are each independently a straight or branched, saturated or unsaturated alkyl chain containing from 10 to 30 carbon atoms, wherein the alkyl chain is optionally interrupted by one or more ester bonds; and

z has a mean value ranging from 30 to 60.

49. The composition of claim 48, wherein R^{10} and R^{11} are each independently straight, saturated alkyl chains having 12 to 16 carbon atoms.
50. The composition of any one of claims 48 or 49, wherein the average z is about 45.
51. The composition of any one of claims 8-50, wherein the LNP self-assembles into non-bilayer structures when mixed with polyanionic nucleic acid.
52. The composition of claim 51, wherein the non-bilayer structures have a diameter between 60nm and 120nm.
53. The composition of claim 51, wherein the non-bilayer structures have a diameter of about 70nm, about 80nm, about 90nm, or about 100nm.
54. The composition of any one of claims 7-53, wherein the nanoparticulate delivery vehicle has a diameter of about 100nm.
55. The composition of any one of claims 1, 3-5, or 7-54, wherein the neoantigen cassette is integrated between the at least one promoter nucleotide sequence and the at least one poly(A) sequence.
56. The composition of any one of claims 1, 3-5, or 7-55, wherein the at least one promoter nucleotide sequence is operably linked to the neoantigen-encoding nucleic acid sequence.
57. The composition of any one of claims 1, 3-5, or 7-56, wherein the one or more vectors comprise one or more +-stranded RNA vectors.
58. The composition of claim 57 wherein the one or more +-stranded RNA vectors comprise a 5’ 7-methylguanosine (m7g) cap.

2026201462 26 Feb 2026

59. The composition of claim 57 or 58, wherein the one or more +-stranded RNA vectors are produced by *in vitro* transcription.

60. The composition of any one of claims 1, 3-5, or 7-59, wherein the one or more vectors are self-replicating within a mammalian cell.

61. The composition of any one of claims 1, 3-5, or 7-60, wherein the RNA alphavirus backbone comprises at least one nucleotide sequence of an Aura virus, a Fort Morgan virus, a Venezuelan equine encephalitis virus, a Ross River virus, a Semliki Forest virus, a Sindbis virus, or a Mayaro virus.

62. The composition of any one of claims 1, 3-5, or 7-60, wherein the RNA alphavirus backbone comprises at least one nucleotide sequence of a Venezuelan equine encephalitis virus.

63. The composition of claim 61 or 62, wherein the RNA alphavirus backbone comprises at least sequences for nonstructural protein-mediated amplification, a 26S promoter sequence, a poly(A) sequence, a nonstructural protein 1 (nsP1) gene, a nsP2 gene, a nsP3 gene, and a nsP4 gene encoded by the nucleotide sequence of the Aura virus, the Fort Morgan virus, the Venezuelan equine encephalitis virus, the Ross River virus, the Semliki Forest virus, the Sindbis virus, or the Mayaro virus.

64. The composition of claim 61 or 62, wherein the RNA alphavirus backbone comprises at least sequences for nonstructural protein-mediated amplification, a 26S promoter sequence, and a poly(A) sequence encoded by the nucleotide sequence of the Aura virus, the Fort Morgan virus, the Venezuelan equine encephalitis virus, the Ross River virus, the Semliki Forest virus, the Sindbis virus, or the Mayaro virus.

65. The composition of claim 63 or 64, wherein sequences for nonstructural protein-mediated amplification are selected from the group consisting of: an alphavirus 5’ UTR, a 51-nt CSE, a 24-nt CSE, a 26S subgenomic promoter sequence, a 19-nt CSE, an alphavirus 3’ UTR, or combinations thereof.

66. The composition of any one of claims 63-65, wherein the RNA alphavirus backbone does not encode structural virion proteins capsid, E2 and E1.

67. The composition of claim 66, wherein the neoantigen cassette is inserted in place of structural virion proteins within the nucleotide sequence of the Aura virus, the Fort Morgan virus, the Venezuelan equine encephalitis virus, the Ross River virus, the Semliki Forest virus, the Sindbis virus, or the Mayaro virus.

2026201462 26 Feb 2026

68. The composition of claim 61 or 62, wherein the Venezuelan equine encephalitis virus comprises the sequence of SEQ ID NO:3 or SEQ ID NO:5.
69. The composition of claim 61 or 62, wherein the Venezuelan equine encephalitis virus comprises the sequence of SEQ ID NO:3 or SEQ ID NO:5 further comprising a deletion between base pair 7544 and 11175.
70. The composition of claim 69, wherein the RNA alphavirus backbone comprises the sequence set forth in SEQ ID NO:6 or SEQ ID NO:7.
71. The composition of claim 69 or 70, wherein the neoantigen cassette is inserted at position 7544 to replace the deletion between base pairs 7544 and 11175 as set forth in the sequence of SEQ ID NO:3 or SEQ ID NO:5.
72. The composition of claim 67-71, wherein the insertion of the neoantigen cassette provides for transcription of a polycistronic RNA comprising the nsP1-4 genes and the at least one antigen-encoding nucleic acid sequence, wherein the nsP1-4 genes and the at least one antigen-encoding nucleic acid sequence are in separate open reading frames.
73. The composition of any one of claims 1, 3-5, or 7-72, wherein the at least one promoter nucleotide sequence is the native 26S promoter nucleotide sequence encoded by the RNA alphavirus backbone.
74. The composition of any one of claims 1, 3-5, or 7-72, wherein the at least one promoter nucleotide sequence is an exogenous RNA promoter.
75. The composition of any one of claims 1, 3-5, or 7-74, wherein the second promoter nucleotide sequence is a 26S promoter nucleotide sequence.
76. The composition of any one of claims 1, 3-5, or 7-74, wherein the second promoter nucleotide sequence comprises multiple 26S promoter nucleotide sequences, wherein each 26S promoter nucleotide sequence provides for transcription of one or more of the separate open reading frames.
77. The composition of any one of the above claims, wherein the one or more vectors are each at least 300nt in size.
78. The composition of any one of the above claims, wherein the one or more vectors are each at least 1kb in size.
79. The composition of any one of the above claims, wherein the one or more vectors are each 2kb in size.

2026201462 26 Feb 2026

80. The composition of any one of the above claims, wherein the one or more vectors are each less than 5kb in size.

81. The composition of any one of the above claims, wherein at least one of the at least one neoantigen-encoding nucleic acid sequences encodes a polypeptide sequence or portion thereof that is presented by MHC class I on the tumor cell.

82. The composition of any one of claims 1, 3-5, or 7-81, wherein each antigen-encoding nucleic acid sequence is linked directly to one another.

83. The composition of any one of claims 1, 3-5, or 7-82, wherein at least one of the at least one antigen-encoding nucleic acid sequences is linked to a distinct antigen-encoding nucleic acid sequence with a nucleic acid sequence encoding a linker.

84. The composition of claim 83, wherein the linker links two MHC class I sequences or an MHC class I sequence to an MHC class II sequence.

85. The composition of claim 84, wherein the linker is selected from the group consisting of: (1) consecutive glycine residues, at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 residues in length; (2) consecutive alanine residues, at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 residues in length; (3) two arginine residues (RR); (4) alanine, alanine, tyrosine (AAY); (5) a consensus sequence at least 2, 3, 4, 5, 6, 7, 8 , 9, or 10 amino acid residues in length that is processed efficiently by a mammalian proteasome; and (6) one or more native sequences flanking the antigen derived from the cognate protein of origin and that is at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 2-20 amino acid residues in length.

86. The composition of claim 83, wherein the linker links two MHC class II sequences or an MHC class II sequence to an MHC class I sequence.

87. The composition of claim 86, wherein the linker comprises the sequence GPGPG.

88. The composition of any one of claims 1, 3-5, or 7-87, wherein at least one sequence of the at least one antigen-encoding nucleic acid sequences is linked, operably or directly, to a separate or contiguous sequence that enhances the expression, stability, cell trafficking, processing and presentation, and/or immunogenicity of the at least one antigen-encoding nucleic acid sequences.

89. The composition of claim 88, wherein the separate or contiguous sequence comprises at least one of: a ubiquitin sequence, a ubiquitin sequence modified to increase proteasome targeting (e.g., the ubiquitin sequence contains a Gly to Ala substitution at position 76), an immunoglobulin signal sequence (e.g., IgK), a major histocompatibility

2026201462 26 Feb 2026

class I sequence, lysosomal-associated membrane protein (LAMP)-1, human dendritic cell lysosomal-associated membrane protein, and a major histocompatibility class II sequence; optionally wherein the ubiquitin sequence modified to increase proteasome targeting is A76.

90. The composition of any of the above claims, wherein at least one of the at least one neoantigen-encoding nucleic acid sequences encodes a polypeptide sequence or portion thereof that has increased binding affinity to its corresponding MHC allele relative to the translated, corresponding wild-type nucleic acid sequence.

91. The composition of any of the above claims, wherein at least one of the at least one neoantigen-encoding nucleic acid sequences encodes a polypeptide sequence or portion thereof that has increased binding stability to its corresponding MHC allele relative to the translated, corresponding wild-type nucleic acid sequence.

92. The composition of any of the above claims, wherein at least one of the at least one neoantigen-encoding nucleic acid sequences encodes a polypeptide sequence or portion thereof that has an increased likelihood of presentation on its corresponding MHC allele relative to the translated, corresponding wild-type nucleic acid sequence.

93. The composition of any of the above claims, wherein the at least one alteration comprises a point mutation, a frameshift mutation, a non-frameshift mutation, a deletion mutation, an insertion mutation, a splice variant, a genomic rearrangement, or a proteasome-generated spliced antigen.

94. The composition of any of the above claims, wherein the tumor is selected from the group consisting of: lung cancer, melanoma, breast cancer, ovarian cancer, prostate cancer, kidney cancer, gastric cancer, colon cancer, testicular cancer, head and neck cancer, pancreatic cancer, bladder cancer, brain cancer, B-cell lymphoma, acute myelogenous leukemia, adult acute lymphoblastic leukemia, chronic myelogenous leukemia, chronic lymphocytic leukemia, T cell lymphocytic leukemia, non-small cell lung cancer, and small cell lung cancer.

95. The composition of any one of claims 1, 3-5, or 7-94, wherein the at least one neoantigen-encoding nucleic acid sequence comprises at least 2-10, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleic acid sequences.

96. The composition of any one of claims 1, 3-5, or 7-94, wherein the at least one neoantigen-encoding nucleic acid sequence comprises at least 11-20, 15-20, 11-100, 11-

2026201462 26 Feb 2026

200, 11-300, 11-400, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or up to 400 nucleic acid sequences.

97. The composition of any one of claims 1, 3-5, or 7-94, wherein the at least one neoantigen-encoding nucleic acid sequence comprises at least 2-400 nucleic acid sequences and wherein at least two of the neoantigen-encoding nucleic acid sequences encode polypeptide sequences or portions thereof that are presented by MHC class I on the tumor cell surface.

98. The composition of claim 2 or 6, wherein at least two of the neoantigen-encoding nucleic acid sequences encode polypeptide sequences or portions thereof that are presented by MHC class I on the tumor cell surface.

99. The composition of any of the above claims, wherein when administered to the subject and translated, at least one of the neoantigens enocoded by the at least one neoantigen-encoding nucleic acid sequence are presented on antigen presenting cells resulting in an immune response targeting at least one of the neoantigens on the tumor cell surface.

100. The composition of any of the above claims, wherein the at least one neoantigen-encoding nucleic acid sequences when administered to the subject and translated, at least one of the MHC class I or class II neoantigens are presented on antigen presenting cells resulting in an immune response targeting at least one of the neoantigens on the tumor cell surface, and optionally wherein the expression of each of the at least one neoantigen-encoding nucleic acid sequences is driven by the at least one promoter nucleotide sequence.

101. The composition of any one of claims 1, 3-5, or 7-100, wherein each MHC class I neoantigen-encoding nucleic acid sequence encodes a polypeptide sequence between 8 and 35 amino acids in length, optionally 9-17, 9-25, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34 or 35 amino acids in length.

102. The composition of any one of claims 1, 3-5, or 7-101, wherein the at least one MHC class II antigen-encoding nucleic acid sequence is present.

103. The composition of any one of claims 1, 3-5, or 7-101, wherein the at least one MHC class II antigen-encoding nucleic acid sequence is present and comprises at least one MHC class II neoantigen-encoding nucleic acid sequence that comprises at least one alteration that makes the encoded peptide sequence distinct from the corresponding peptide sequence encoded by a wild-type nucleic acid sequence.

2026201462 26 Feb 2026

104. The composition of any one of claims 1, 3-5, or 7-103, wherein the at least one MHC class II antigen-encoding nucleic acid sequence is 12-20, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 20-40 amino acids in length.

105. The composition of any one of claims 1, 3-5, or 7-104, wherein the at least one MHC class II antigen-encoding nucleic acid sequence is present and comprises at least one universal MHC class II antigen-encoding nucleic acid sequence, optionally wherein the at least one universal sequence comprises at least one of Tetanus toxoid and PADRE.

106. The composition of any one of claims 1, 3-5, or 7-105, wherein the at least one promoter nucleotide sequence or the second promoter nucleotide sequence is inducible.

107. The composition of any one of claims 1, 3-5, or 7-105, wherein the at least one promoter nucleotide sequence or the second promoter nucleotide sequence is non-inducible.

108. The composition of any one of claims 1, 3-5, or 7-107, wherein the at least one poly(A) sequence comprises a poly(A) sequence native to the alphavirus.

109. The composition of any one of claims 1, 3-5, or 7-107, wherein the at least one poly(A) sequence comprises a poly(A) sequence exogenous to the alphavirus.

110. The composition of any one of claims 1, 3-5, or 7-109, wherein the at least one poly(A) sequence is operably linked to at least one of the at least one antigen-encoding nucleic acid sequences.

111. The composition of any one of claims 1, 3-5, or 7-110, wherein the at least one poly(A) sequence is at least 20 , at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, or at least 90 consecutive A nucleotides.

112. The composition of any one of claims 1, 3-5, or 7-110, wherein the at least one poly(A) sequence is at least 100 consecutive A nucleotides.

113. The composition of any of the above claims, wherein the neoantigen cassette further comprises at least one of: an intron sequence, a woodchuck hepatitis virus posttranscriptional regulatory element (WPRE) sequence, an internal ribosome entry sequence (IRES) sequence, a nucleotide sequence encoding a 2A self cleaving peptide sequence, a nucleotide sequence encoding a Furin cleavage site, or a sequence in the 5’ or 3’ non-coding region known to enhance the nuclear export, stability, or translation efficiency of mRNA that is operably linked to at least one of the at least one antigen-encoding nucleic acid sequences.

2026201462 26 Feb 2026

114. The composition of any of the above claims, wherein the neoantigen cassette further comprises a reporter gene, including but not limited to, green fluorescent protein (GFP), a GFP variant, secreted alkaline phosphatase, luciferase, a luciferase variant, or a detectable peptide or epitope.

115. The composition of claim 114, wherein the detectable peptide or epitope is selected from the group consisting of an HA tag, a Flag tag, a His-tag, or a V5 tag.

116. The composition of any of the above claims, wherein the one or more vectors further comprises one or more nucleic acid sequences encoding at least one immune modulator.

117. The composition of claim 116, wherein the immune modulator is an anti-CTLA4 antibody or an antigen-binding fragment thereof, an anti-PD-1 antibody or an antigen-binding fragment thereof, an anti-PD-L1 antibody or an antigen-binding fragment thereof, an anti-4-1BB antibody or an antigen-binding fragment thereof, or an anti-OX-40 antibody or an antigen-binding fragment thereof.

118. The composition of claim 117, wherein the antibody or antigen-binding fragment thereof is a Fab fragment, a Fab' fragment, a single chain Fv (scFv), a single domain antibody (sdAb) either as single specific or multiple specificities linked together (e.g., camelid antibody domains), or full-length single-chain antibody (e.g., full-length IgG with heavy and light chains linked by a flexible linker).

119. The composition of claim 117 or 118, wherein the heavy and light chain sequences of the antibody are a contiguous sequence separated by either a self-cleaving sequence such as 2A or IRES; or the heavy and light chain sequences of the antibody are linked by a flexible linker such as consecutive glycine residues.

120. The composition of claim 116, wherein the immune modulator is a cytokine.

121. The composition of claim 120, wherein the cytokine is at least one of IL-2, IL-7, IL-12, IL-15, or IL-21 or variants thereof of each.

122. The composition of any one of claims 1, 3-5, or 7-121, wherein the at least one MHC class I neoantigen-encoding nucleic acid sequence is selected by performing the steps of:

(a) obtaining at least one of exome, transcriptome, or whole genome tumor nucleotide sequencing data from the tumor, wherein the tumor nucleotide sequencing data is used to obtain data representing peptide sequences of each of a set of neoantigens;

2026201462 26 Feb 2026

(b) inputting the peptide sequence of each neoantigen into a presentation model to generate a set of numerical likelihoods that each of the neoantigens is presented by one or more of the MHC alleles on the tumor cell surface of the tumor, the set of numerical likelihoods having been identified at least based on received mass spectrometry data; and

(c) selecting a subset of the set of neoantigens based on the set of numerical likelihoods to generate a set of selected neoantigens which are used to generate the at least one MHC class I neoantigen-encoding nucleic acid sequence.

123. The composition of claim 2 or 6, wherein each of the MHC class I epitope encoding nucleic acid sequences is selected by performing the steps of:

(a) obtaining at least one of exome, transcriptome, or whole genome tumor nucleotide sequencing data from the tumor, wherein the tumor nucleotide sequencing data is used to obtain data representing peptide sequences of each of a set of neoantigens;

(b) inputting the peptide sequence of each neoantigen into a presentation model to generate a set of numerical likelihoods that each of the neoantigens is presented by one or more of the MHC alleles on the tumor cell surface of the tumor, the set of numerical likelihoods having been identified at least based on received mass spectrometry data; and

(c) selecting a subset of the set of neoantigens based on the set of numerical likelihoods to generate a set of selected neoantigens which are used to generate the at least 20 MHC class I neoantigen-encoding nucleic acid sequences.

124. The composition of claim 122, wherein a number of the set of selected neoantigens is 2-20.

125. The composition of claim 122-124, wherein the presentation model represents dependence between:

(a) presence of a pair of a particular one of the MHC alleles and a particular amino acid at a particular position of a peptide sequence; and

(b) likelihood of presentation on the tumor cell surface, by the particular one of the MHC alleles of the pair, of such a peptide sequence comprising the particular amino acid at the particular position.

2026201462 26 Feb 2026

126. The composition of claim 122-125, wherein selecting the set of selected neoantigens comprises selecting neoantigens that have an increased likelihood of being presented on the tumor cell surface relative to unselected neoantigens based on the presentation model.

127. The composition of claim 122-126, wherein selecting the set of selected neoantigens comprises selecting neoantigens that have an increased likelihood of being capable of inducing a tumor-specific immune response in the subject relative to unselected neoantigens based on the presentation model.

128. The composition of claim 122-127, wherein selecting the set of selected neoantigens comprises selecting neoantigens that have an increased likelihood of being capable of being presented to naïve T cells by professional antigen presenting cells (APCs) relative to unselected neoantigens based on the presentation model, optionally wherein the APC is a dendritic cell (DC).

129. The composition of claim 122-128, wherein selecting the set of selected neoantigens comprises selecting neoantigens that have a decreased likelihood of being subject to inhibition via central or peripheral tolerance relative to unselected neoantigens based on the presentation model.

130. The composition of claim 122-129, wherein selecting the set of selected neoantigens comprises selecting neoantigens that have a decreased likelihood of being capable of inducing an autoimmune response to normal tissue in the subject relative to unselected neoantigens based on the presentation model.

131. The composition of claim 122-130, wherein exome or transcriptome nucleotide sequencing data is obtained by performing sequencing on the tumor tissue.

132. The composition of claim131, wherein the sequencing is next generation sequencing (NGS) or any massively parallel sequencing approach.

133. The composition of any of the above claims, wherein the neoantigen cassette comprises junctional epitope sequences formed by adjacent sequences in the neoantigen cassette.

134. The composition of claim 133, wherein at least one or each junctional epitope sequence has an affinity of greater than 500 nM for MHC.

135. The composition of claims 133 or 134, wherein each junctional epitope sequence is non-self.

136. The composition of any of the above claims, wherein the neoantigen cassette does not encode a non-therapeutic MHC class I or class II epitope nucleic acid sequence

2026201462 26 Feb 2026

comprising a translated, wild-type nucleic acid sequence, wherein the non-therapeutic epitope is predicted to be displayed on an MHC allele of the subject.

137. The composition of claim 136, wherein the non-therapeutic predicted MHC class I or class II epitope sequence is a junctional epitope sequence formed by adjacent sequences in the neoantigen cassette.

138. The composition of claims 133-137, wherein the prediction is based on presentation likelihoods generated by inputting sequences of the non-therapeutic epitopes into a presentation model.

139. The composition of any one of claims 133-138, wherein an order of the at least one antigen-encoding nucleic acid sequences in the neoantigen cassette is determined by a series of steps comprising:

(a) generating a set of candidate neoantigen cassette sequences corresponding to different orders of the at least one antigen-encoding nucleic acid sequences;

(b) determining, for each candidate neoantigen cassette sequence, a presentation score based on presentation of non-therapeutic epitopes in the candidate neoantigen cassette sequence; and

(c) selecting a candidate cassette sequence associated with a presentation score below a predetermined threshold as the neoantigen cassette sequence for a neoantigen vaccine.

140. A pharmaceutical composition comprising the composition of any of the above claims and a pharmaceutically acceptable carrier.

141. The composition of claim 140, wherein the composition further comprises an adjuvant.

142. The pharmaceutical composition of claim 140 or 141, wherein the composition further comprises an immune modulator.

143. The pharmaceutical composition of claim 142, wherein the immune modulator is an anti-CTLA4 antibody or an antigen-binding fragment thereof, an anti-PD-1 antibody or an antigen-binding fragment thereof, an anti-PD-L1 antibody or an antigen-binding fragment thereof, an anti-4-1BB antibody or an antigen-binding fragment thereof, or an anti-OX-40 antibody or an antigen-binding fragment thereof.

144. An isolated nucleotide sequence or set of isolated nucleotide sequences comprising the neoantigen cassette of any of the above composition claims and one or more elements obtained from the sequence of SEQ ID NO:3 or SEQ ID NO:5,optionally wherein the one or more elements are selected from the group consisting of the sequences necessary for nonstructural protein-mediated amplification, the 26S promoter nucleotide

2026201462 26 Feb 2026

sequence, the poly(A) sequence, and the nsP1-4 genes of the sequence set forth in SEQ ID NO:3 or SEQ ID NO:5,and optionally wherein the nucleotide sequence is cDNA.

145. The isolated nucleotide sequence of claim 144, wherein the sequence or set of isolated nucleotide sequences comprises the neoantigen cassette of any of the above composition claims inserted at position 7544 of the sequence set forth in SEQ ID NO:6 or SEQ ID NO:7.

146. The isolated nucleotide sequence of claim 144 or 145, further comprising:

a T7 or SP6 RNA polymerase promoter nucleotide sequence 5' of the one or more elements obtained from the sequence of SEQ ID NO:3 or SEQ ID NO:5; and

optionally, one or more restriction sites 3' of the poly(A) sequence.

147. The isolated nucleotide sequence of claim 144, wherein the neoantigen cassette of any of the above composition claims is inserted at position 7563 of SEQ ID NO:8 or SEQ ID NO:9.

148. A vector or set of vectors comprising the nucleotide sequence of claims 144-147.

149. An isolated cell comprising the nucleotide sequence or set of isolated nucleotide sequences of claims 144-148, optionally wherein the cell is a BHK-21, CHO, HEK293 or variants thereof, 911, HeLa, A549, LP-293, PER.C6, or AE1-2a cell.

150. A kit comprising the composition of any of the above composition claims and instructions for use.

151. A method for treating a subject with cancer, the method comprising administering to the subject the composition of any of the above composition claims or the pharmaceutical composition of any of claims 140-143..

152. The method of claim 151, wherein the at least one MHC class I neoantigen-encoding nucleic acid sequence derived from a tumor are derived from the tumor of the subject with cancer.

153. The method of claim 151, wherein the at least one MHC class I neoantigen-encoding nucleic acid sequence are not derived from the tumor of the subject with cancer.

154. A method for inducing an immune response in a subject, the method comprising administering to the subject the composition of any of the above composition claims or the pharmaceutical composition of any of claims 140-143.

155. The method of claims 151-154, wherein the composition is administered intramuscularly (IM), intradermally (ID), subcutaneously (SC), or intravenously (IV).

2026201462 26 Feb 2026

156. The method of claims 151-154, wherein the composition is administered intramuscularly.

157. The method of any of claims 151-156, the method further comprising administration of one or more immune modulators, optionally wherein the immune modulator is administered before, concurrently with, or after administration of the composition or pharmaceutical composition.

158. The method of claim 157, wherein the one or more immune modulators are selected from the group consisting of: an anti-CTLA4 antibody or an antigen-binding fragment thereof, an anti-PD-1 antibody or an antigen-binding fragment thereof, an anti-PD-L1 antibody or an antigen-binding fragment thereof, an anti-4-1BB antibody or an antigen-binding fragment thereof, or an anti-OX-40 antibody or an antigen-binding fragment thereof.

159. The method of claim 157 or 158, wherein the immune modulator is administered intravenously (IV), intramuscularly (IM), intradermally (ID), or subcutaneously (SC).

160. The method of claim 159, wherein the subcutaneous administration is near the site of the composition or pharmaceutical composition administration or in close proximity to one or more vector or composition draining lymph nodes.

161. The method of any one of claims 151-160, further comprising administering to the subject a second vaccine composition.

162. The method of claim 161, wherein the second vaccine composition is administered prior to the administration of the composition or the pharmaceutical composition of any one of claims 151-160.

163. The method of claim 161, wherein the second vaccine composition is administered subsequent to the administration of the composition or the pharmaceutical composition of any one of claims 151-160.

164. The method of claim 162 or 163, wherein the second vaccine composition is the same as the composition or the pharmaceutical composition of any one of claims 151-160.

165. The method of claim 162 or 163, wherein the second vaccine composition is different from the composition or the pharmaceutical composition of any one of claims 151-160.

166. The method of claim 165, wherein the second vaccine composition comprises a chimpanzee adenovirus vector encoding at least one antigen-encoding nucleic acid sequence.

2026201462 26 Feb 2026

167. The method of claim 166, wherein the at least one antigen-encoding nucleic acid sequence encoded by the chimpanzee adenovirus vector is the same as the at least one antigen-encoding nucleic acid sequence of any of the above composition claims.

168. A method of manufacturing the one or more vectors of any of the above composition claims, the method comprising:

(a) obtaining a linearized DNA sequence comprising the RNA alphavirus backbone and the neoantigen cassette;

(b) in vitro transcribing the linearized DNA sequence by addition of the linearized DNA sequence to a in vitro transcription reaction containing all the necessary components to trancribe the linearized DNA sequence into RNA, optionally further comprising in vitro addition of the m7g cap to the resulting RNA; and

(c) isolating the one or more vectors from the in vitro transcription reaction.

169. The method of manufacturing of claim 168, wherein the linearized DNA sequence is generated by linearizing a DNA plasmid sequence or by amplification using PCR.

170. The method of manufacturing of claim 169, wherein the DNA plasmid sequence is generated using one of bacterial recombination or full genome DNA synthesis or full genome DNA synthesis with amplification of synthesized DNA in bacterial cells.

171. The method of manufacturing of claim 168, wherein isolating the one or more vectors from the *in vitro* transcription reaction involves one or more of phenol chloroform extraction, silica column based purification, or similar RNA purification methods.

172. A method of manufacturing the composition of any of the above composition claims for delivery of the neoantigen expression system, the method comprising:

(a) providing components for the nanoparticulate delivery vehicle;

(b) providing the neoantigen expression system; and

(c) providing conditions sufficient for the nanoparticulate delivery vehicle and the neoantigen expression system to produce the composition for delivery of the neoantigen expression system.

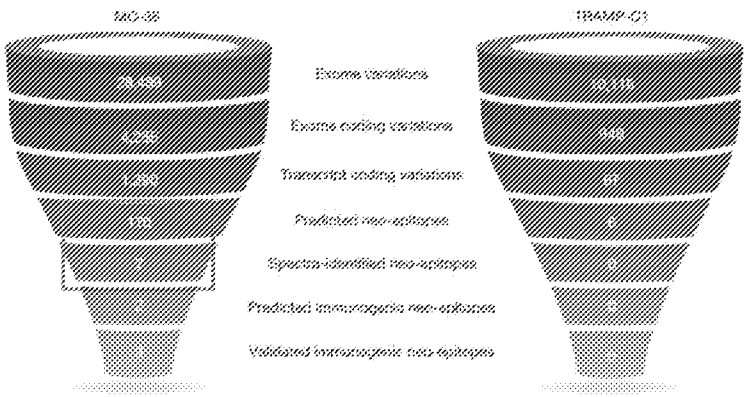
173. The method of manufacturing of claim 172, wherein the conditions are provided by microfluidic mixing.

2026201462 26 Feb 2026

FIG 1A

This data, for application number 2018266705, is current as of 2023-04-19 21:00 AEST

Most recent literature suggests <5% of predicted bound peptides can be found presented on tumor cells



- **Only 7/170 (4%)** predicted neo-epitopes were eluted and detected by mass-spec
- Possibly due to sensitivity limits of particular mass-spec detection approach

Yadav, Nature Vol 515 17 November 2014

NetMHCcon IC50≤500nM		MS-based identification	
		HLAp	Not detected
Prediction	Binders	1,579	47,777
	Non-binders	153	1,140,967

3%

NetMHCcon IC50≤50nM		MS-based identification	
		HLAp	Not detected
Prediction	Binders	1,133	14,059
	Non-binders	599	1,174,685

Bassani-Sternberg M, Mol Cell Proteomics. 2015;14(3):658-73

FIG 1B

26 Feb 2026
2026201462

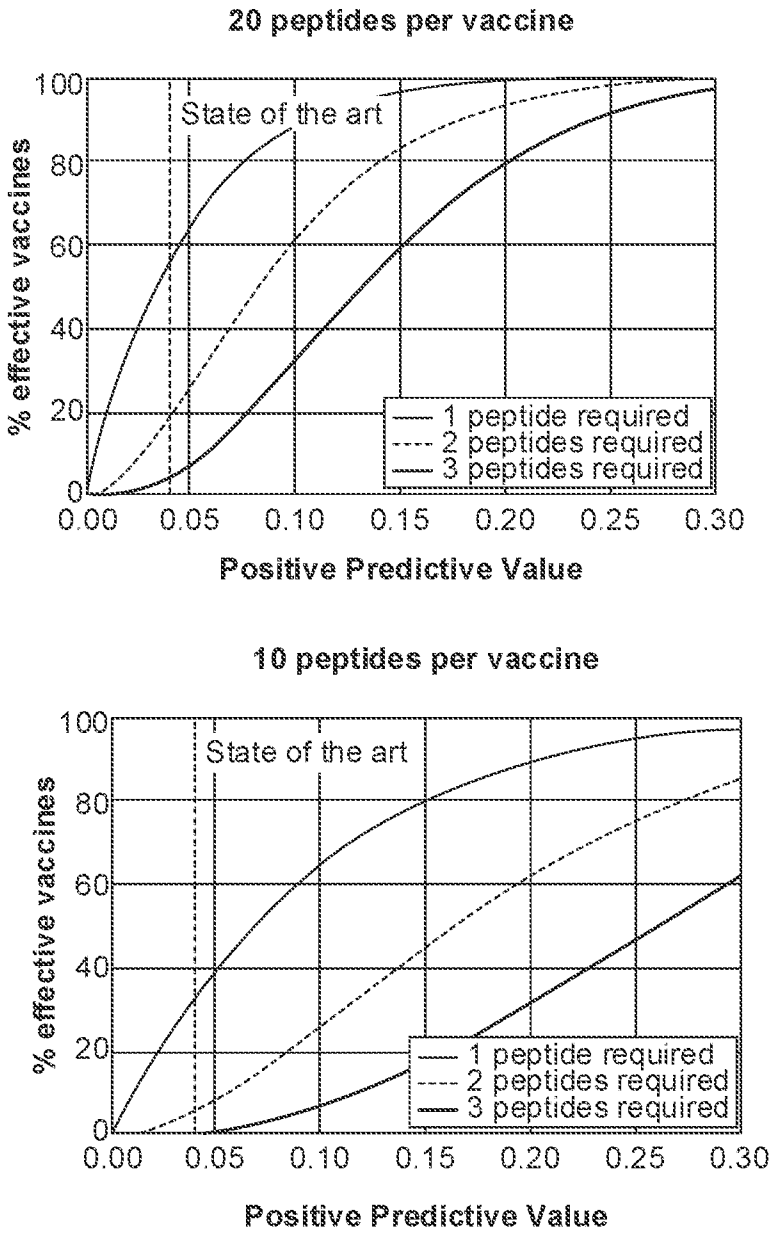
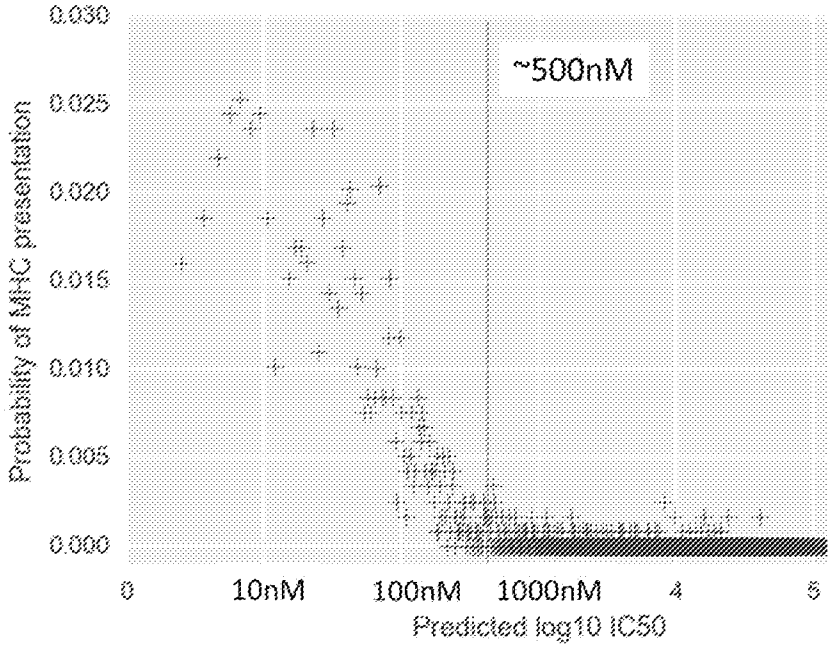


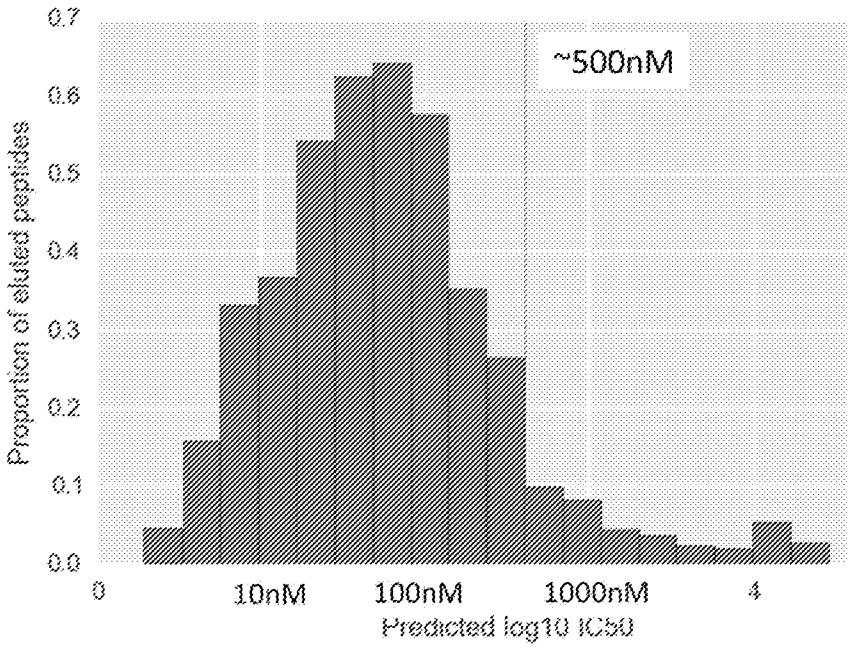
FIG 1C

Binding prediction necessary but not sufficient

Binding affinity prediction vs. mass-spec peptide detection in JY (EBV)-immortalized LCL



Max of affinity predictions for HLA-A-0201 and HLA-B-0702, restricted to genes in whole proteome



Data from Bassani-Sternberg M, Mol Cell Proteomics. 2015; Gritstone analysis

FIG 1D

2026201462 26 Feb 2026

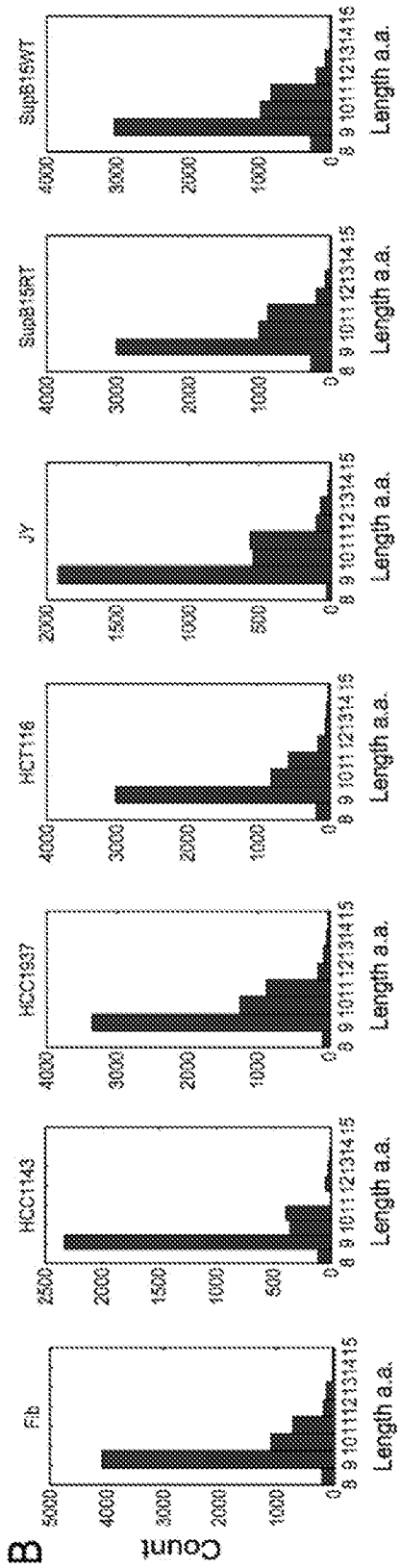


FIG 1E

26 Feb 2026
2026201462

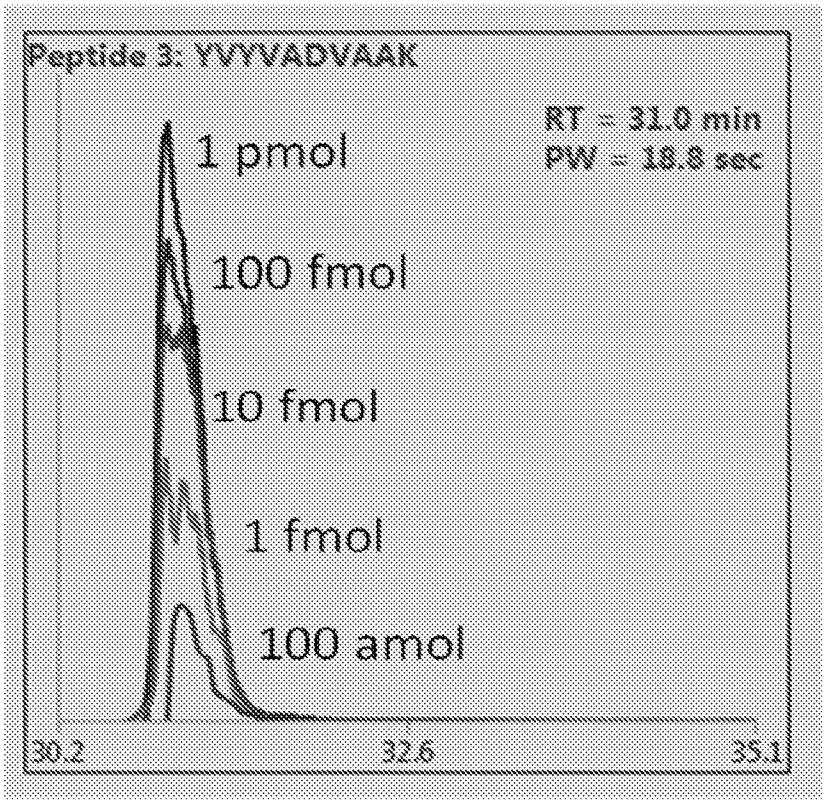


FIG 1F

2026201462 26 Feb 2026

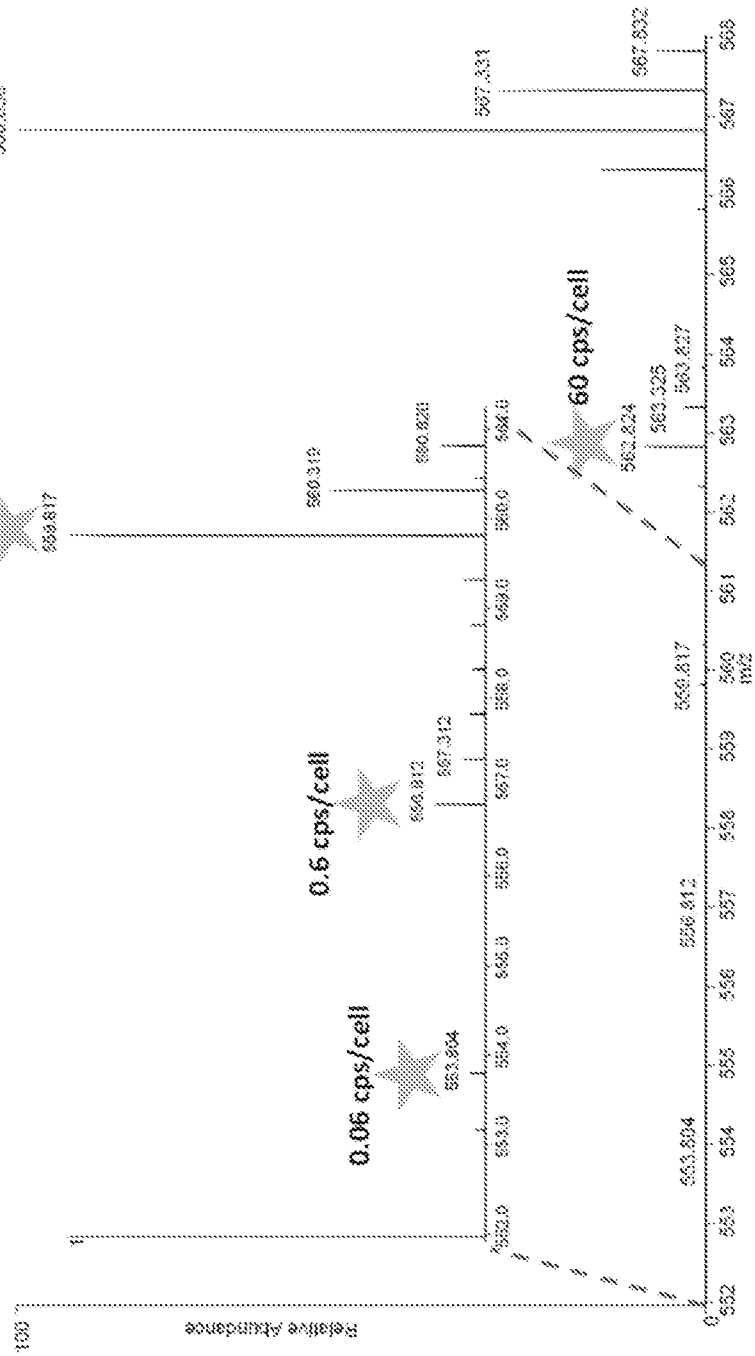


FIG 1F (Cont)

2026201462 26 Feb 2026

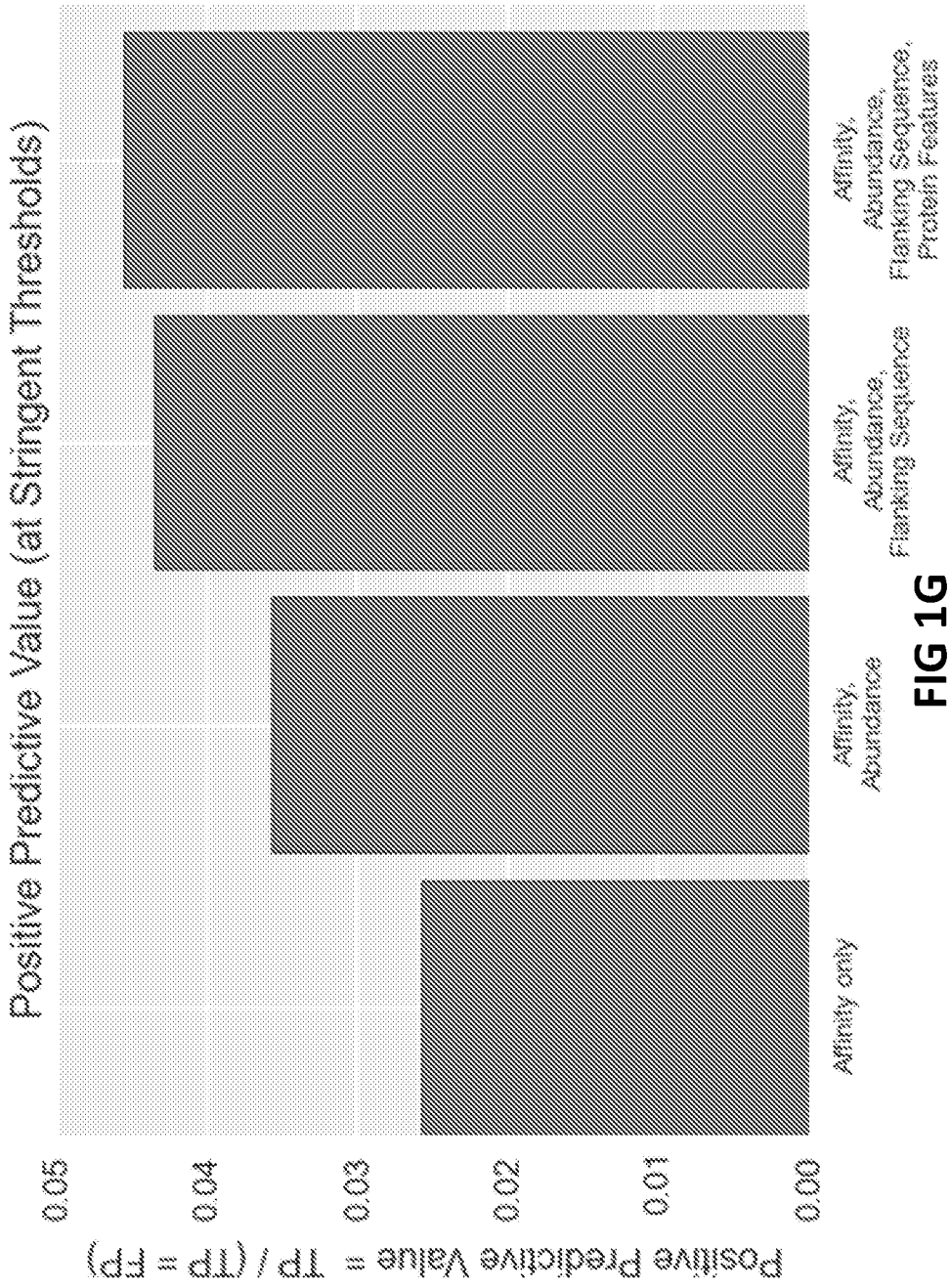


FIG 1G

2026201462 26 Feb 2026

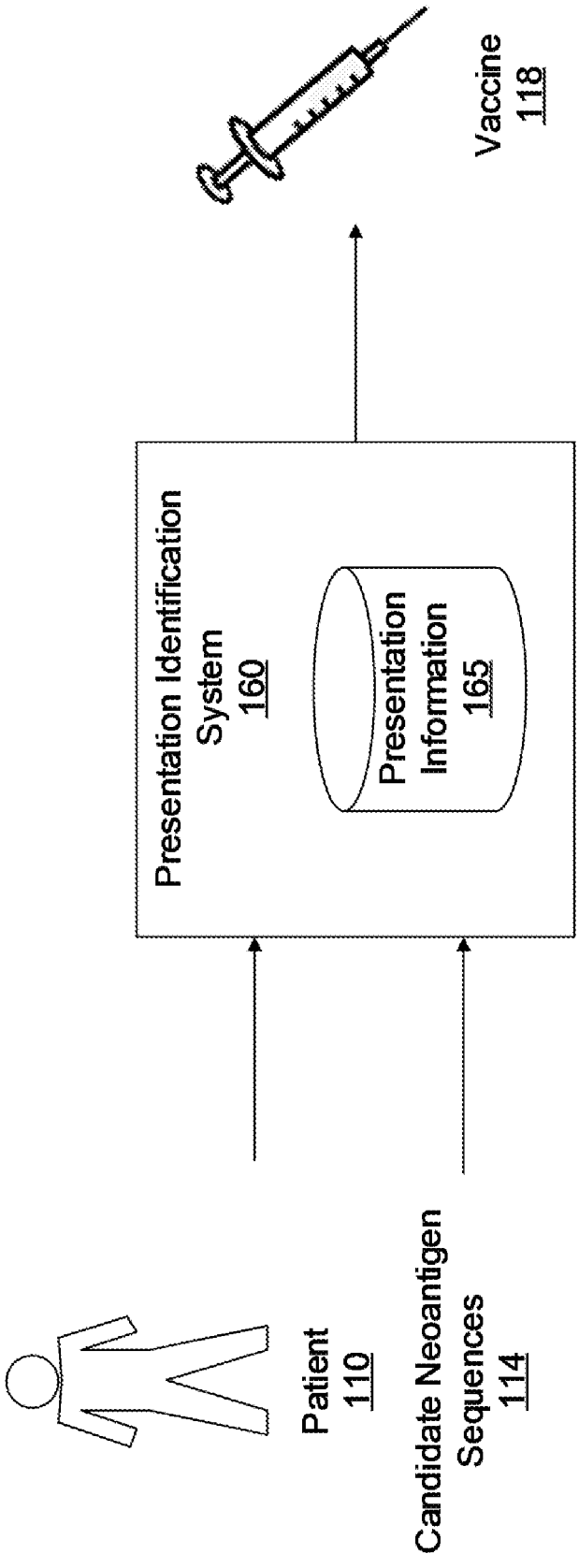


FIG 2A

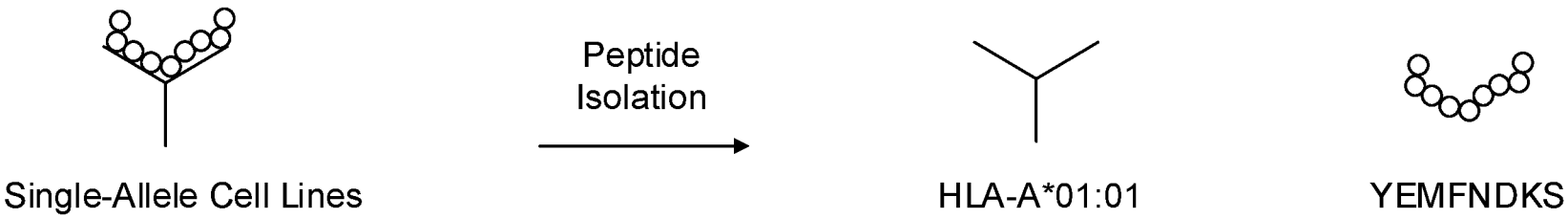

Peptide
Isolation
Single-Allele Cell Lines
HLA-A*01:01
YEMFNDKSF

FIG 2B

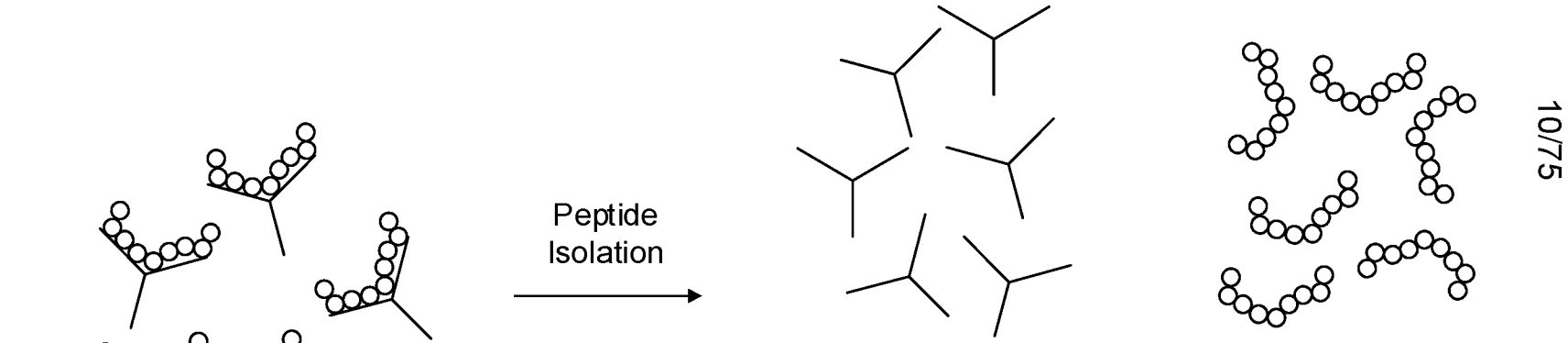

Peptide
Isolation
Multiple-Allele Cell Lines
HLA-A*01:01
HLA-A*02:01
HLA-B*07:02
HLA-B*08:01
HLA-C*01:03
HLA-C*01:04
YEMFNDKSF
HROEIFSHDFJ
FJIEJFOESS
NEIOREIREI
JFKSIFEMMSJDSSU
KNFLENFIESOFI

FIG 2C


Peptide
Isolation
Single-Allele Cell Lines
HLA-DRB1*12:01
YEMFNDKSFQRAPDDKMF

FIG. 2D

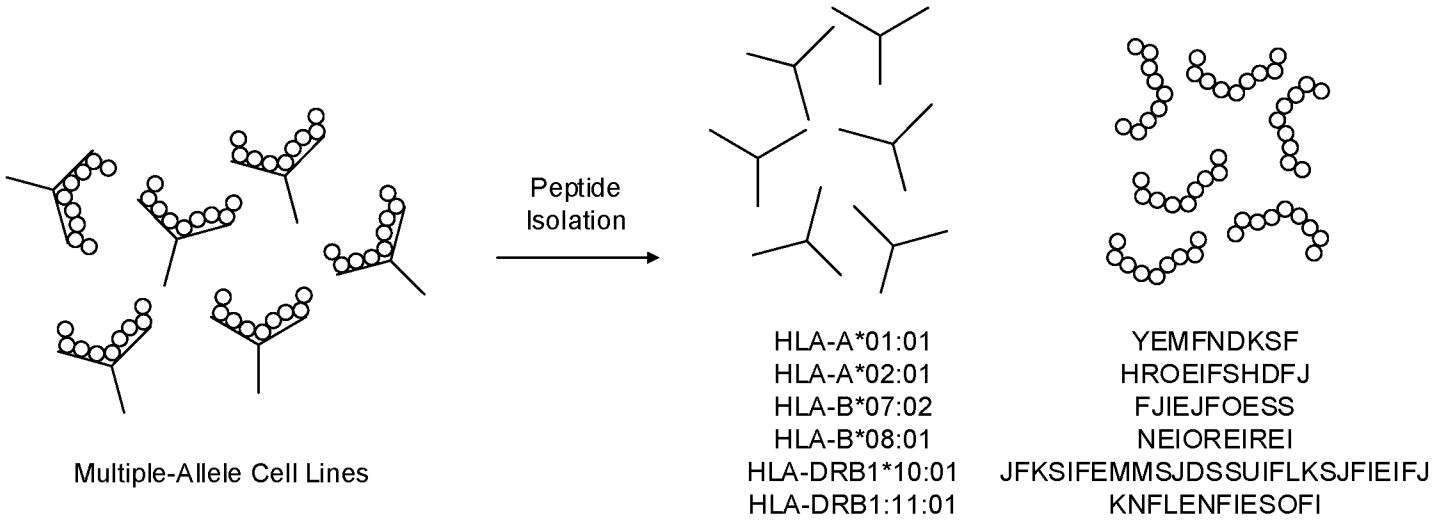

Peptide
Isolation
Multiple-Allele Cell Lines
HLA-A*01:01
HLA-A*02:01
HLA-B*07:02
HLA-B*08:01
HLA-DRB1*10:01
HLA-DRB1:11:01
YEMFNDKSF
HROEIFSHDFJ
FJIEJFOESS
NEIOREIREI
JFKSIFEMMSJDSSUIFLKSJFIEIFJ
KNFLENFIESOFI

FIG. 2E

2026201462 26 Feb 2026

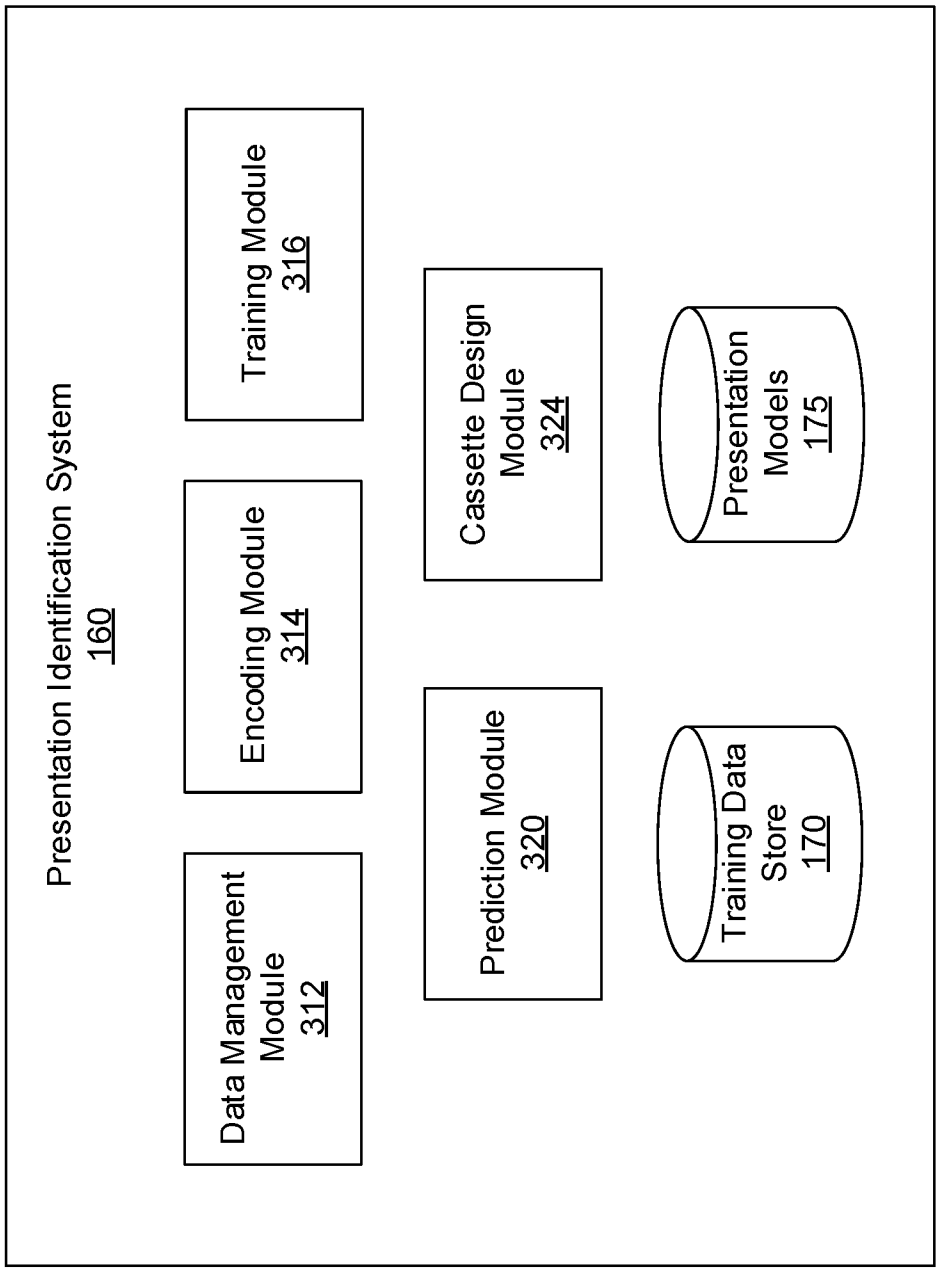


FIG 3

Training Data
170A

Allele-Dependent (x^i) | Allele-Independent (w^i)

Peptide Sequence (p^i)	Affinity (b^i-nM)	Stability (s^i-h)	Allele (a^i)	C-Flanking Sequence (c^i)	mRNA Q. (m^i-*FPKM*)	Label (y^i)
QCEIOWARE	1000	1	HLA-C*01:03	FJELFISBOSJFIE	10^2	Not Presented
FIEUHFWI	1500	15	HLA-C*01:03	FEGRKUOOI	10^{-3}	Presented
FEWRHRJTRUJR	650	20	HLA-C*01:03	PJFIOEJOIJGEIO	10^1	Presented
QIEJOEIJE	500	1	HLA-B*07:02	PJFIOEJOIJGEIO	1	Presented
	600	14	HLA-C*01:03			
	1200	7	HLA-A*01:01			

FIG 4A

Training Data
170A

Allele-Dependent (x^i)

Peptide Sequence (p^i)	Affinity (b^i-nM)	Stability (s^i-h)	Allele (a^i)
QCEIOWAREFLKEIGJ	1000	1	HLA-DRB3:01:01

FIG 4B

2026201462 26 Feb 2026

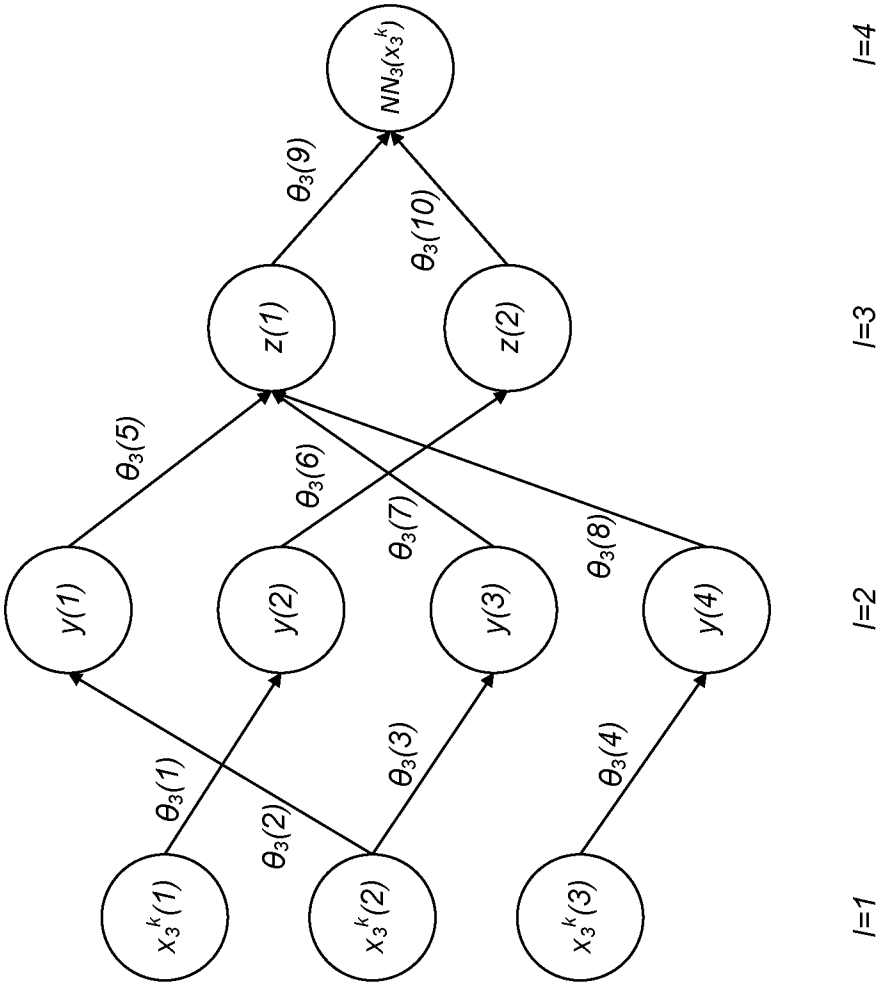


FIG 5

2026201462 26 Feb 2026

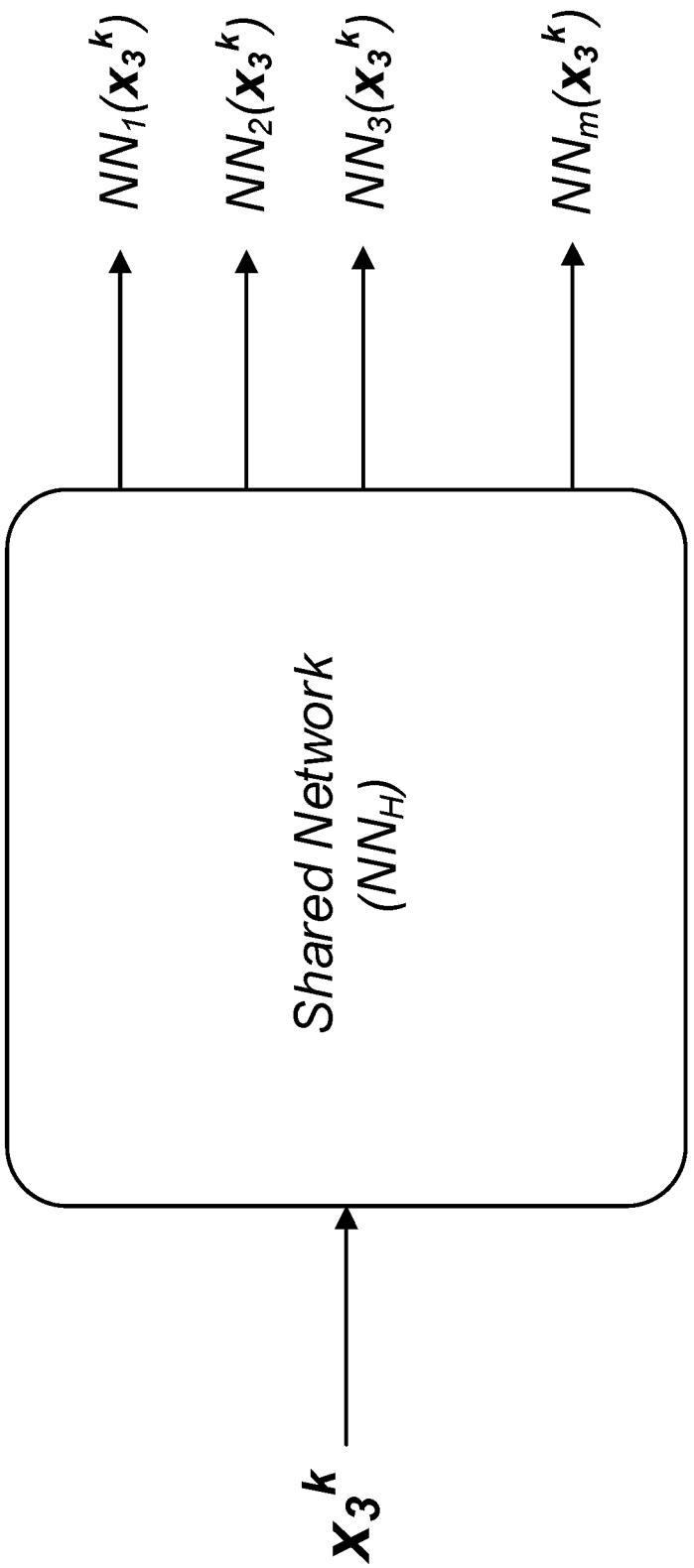


FIG 6A

2026201462 26 Feb 2026

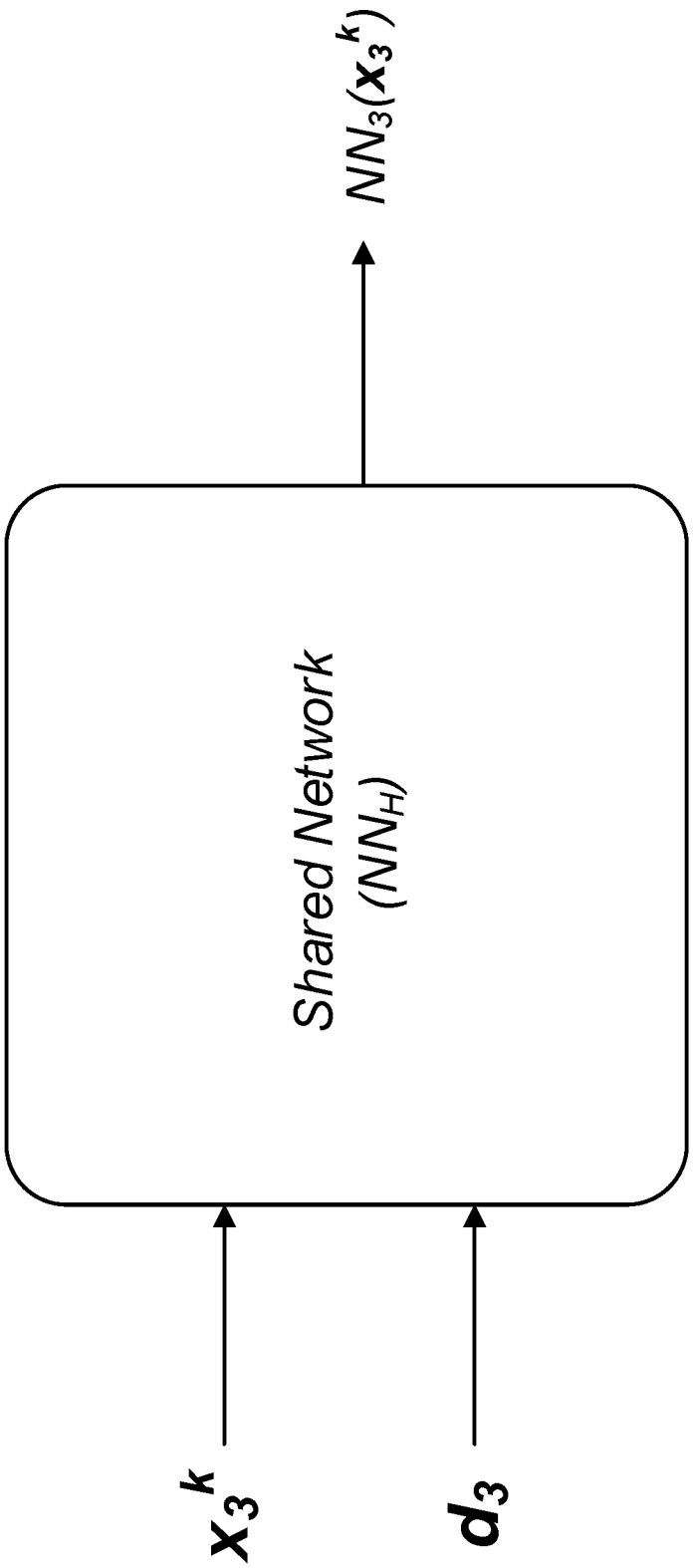


FIG 6B

2026201462 26 Feb 2026

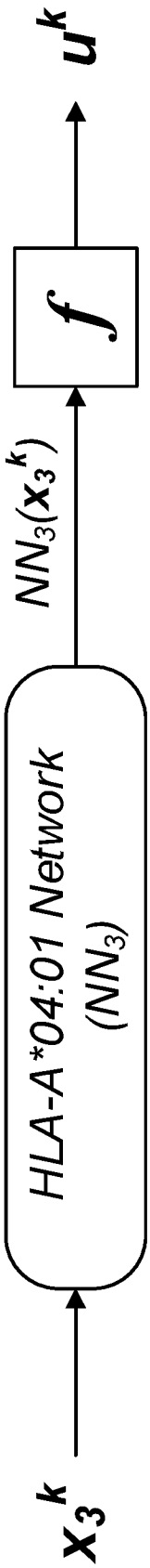


FIG 7

2026201462 26 Feb 2026

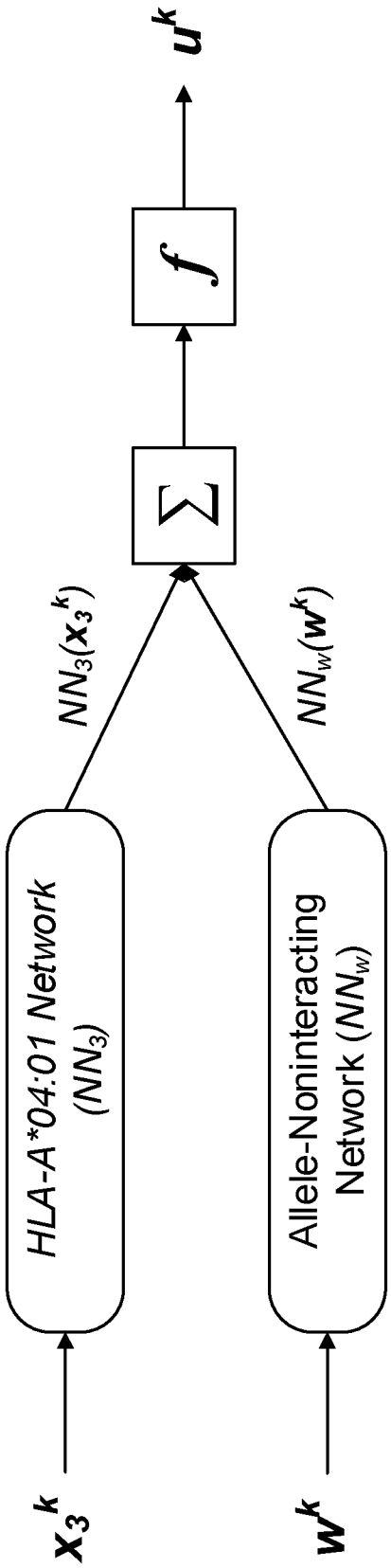


FIG 8

2026201462 26 Feb 2026

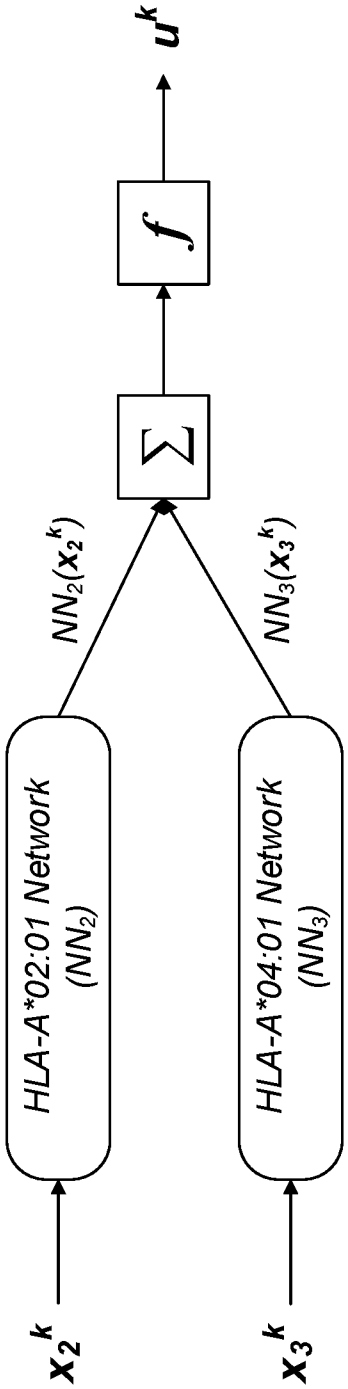


FIG 9

2026201462 26 Feb 2026

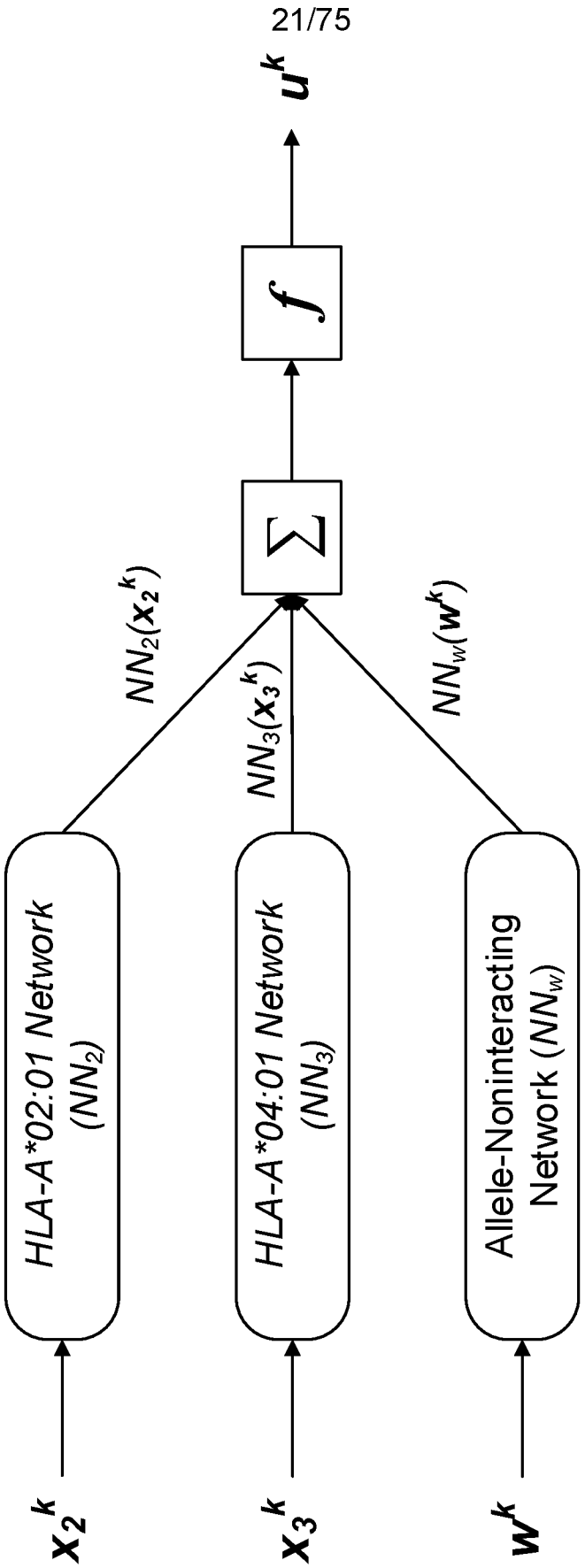


FIG 10

2026201462 26 Feb 2026

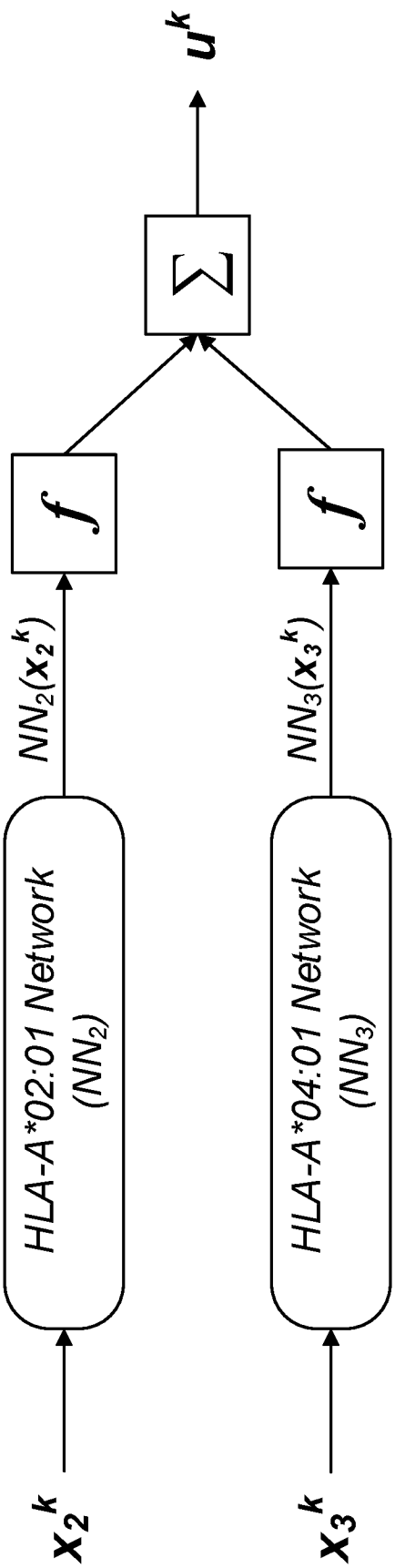


FIG 11

2026201462 26 Feb 2026

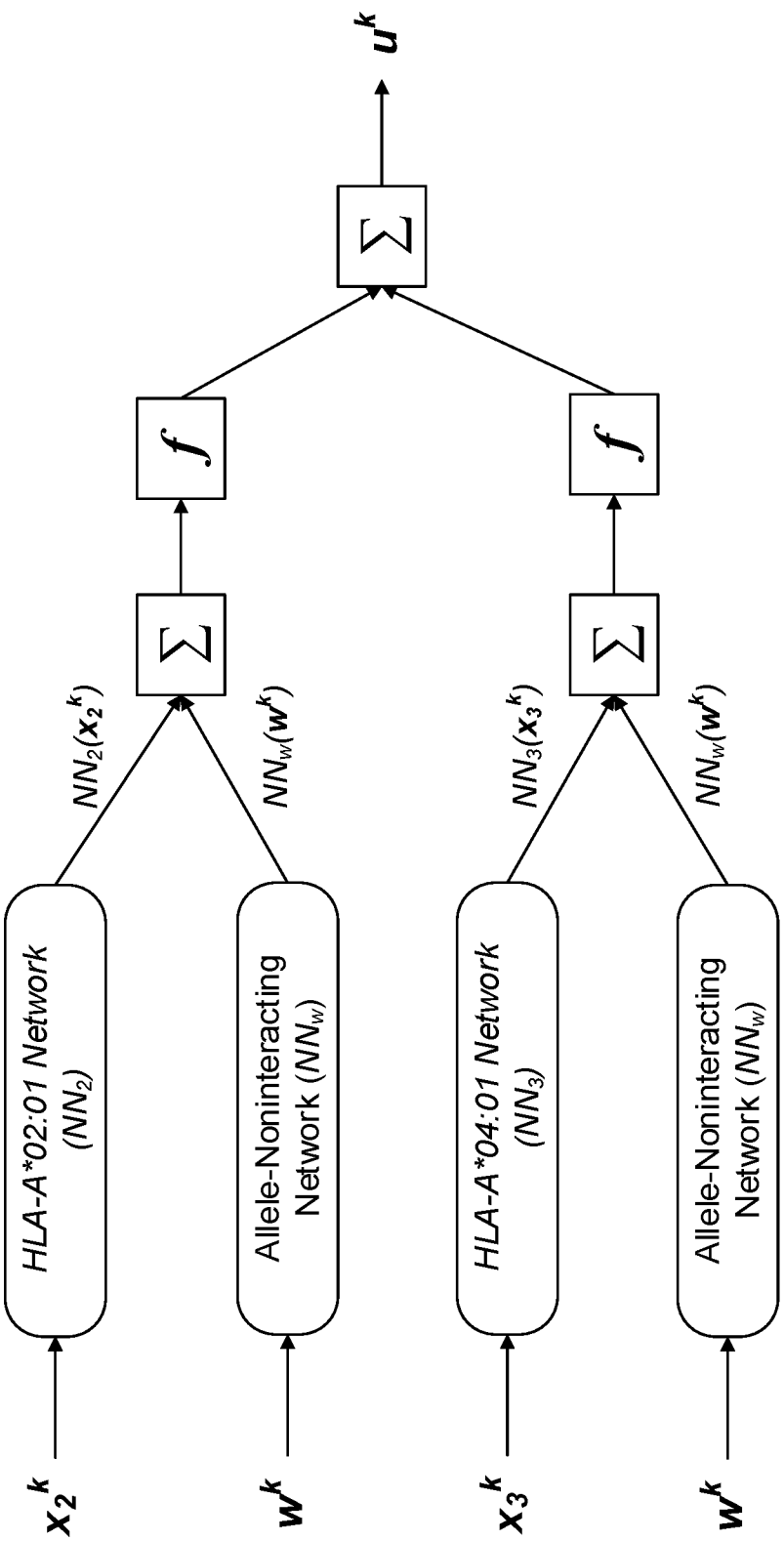


FIG 12

2026201462 26 Feb 2026

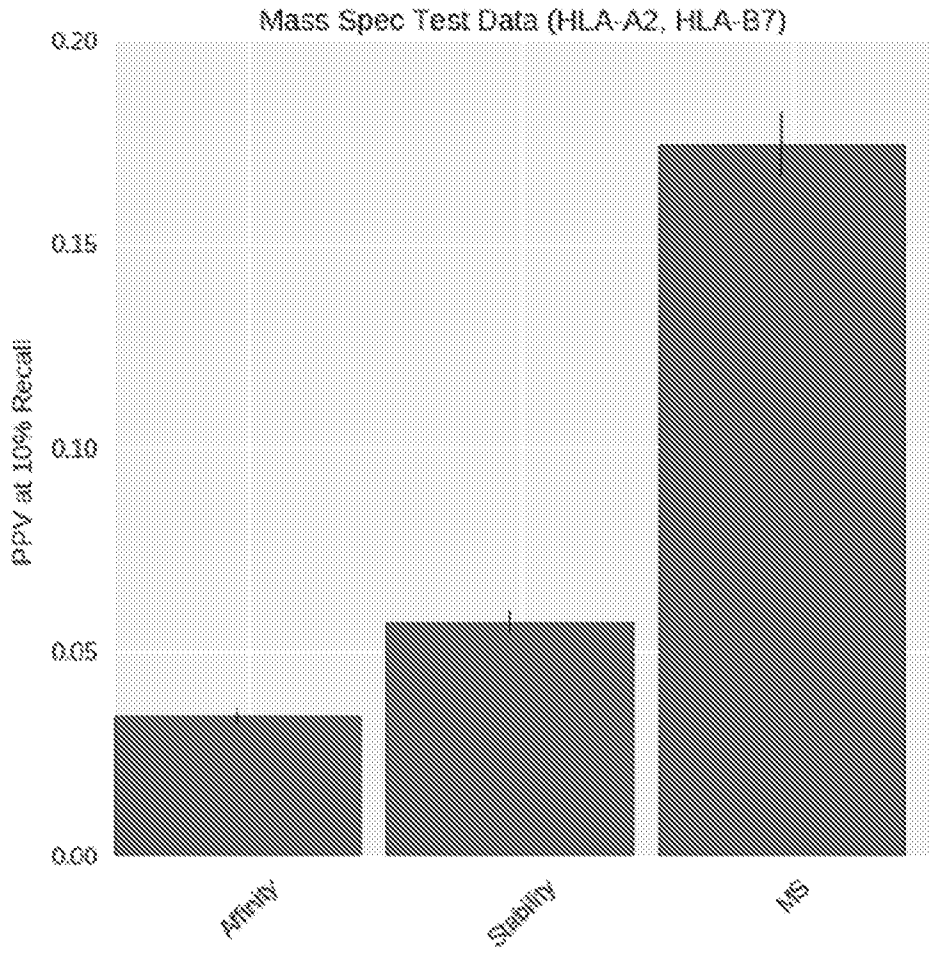


FIG 13A

2026201462 26 Feb 2026

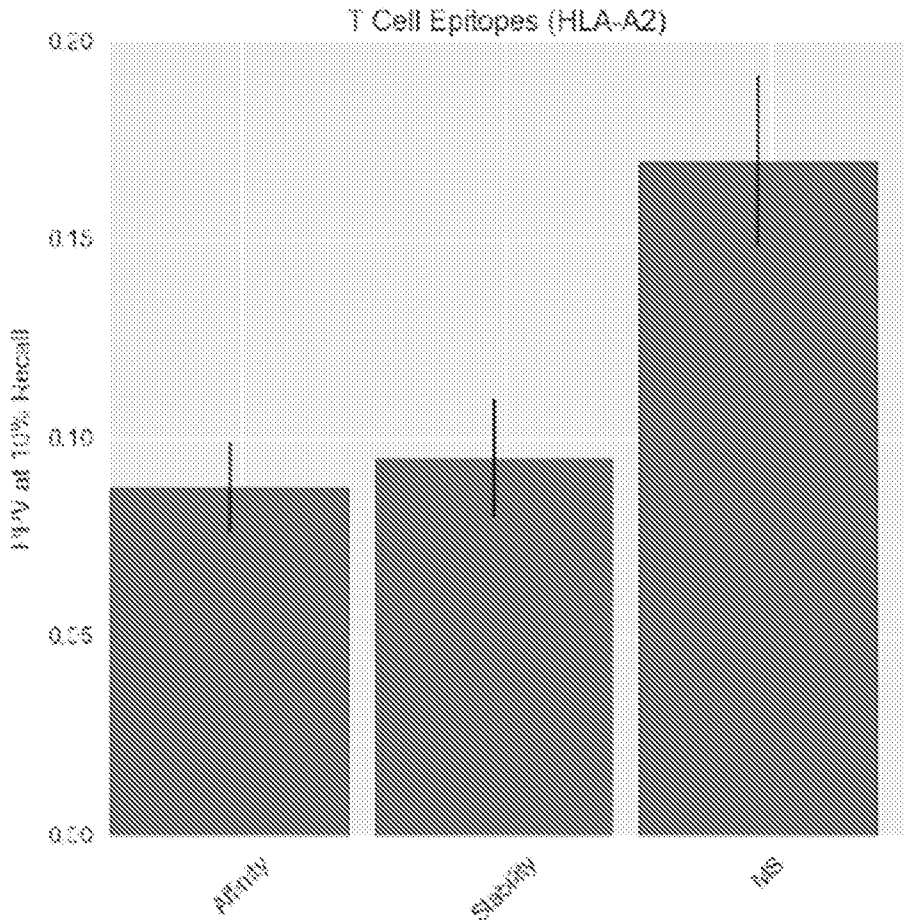


FIG 13B

Model	AUC	Log Loss	PPV at 10% Recall
Sigmoid-of-Sums	0.9278	$12.2 \cdot 10^{-4}$	0.114
Sum-of-Sigmoids	0.9723	$5.78 \cdot 10^{-4}$	0.152
Hyperbolic Tangent	**0.9734**	$\mathbf{5.72 \cdot 10^{-4}}$	0.156
Second Order	0.9727	$5.74 \cdot 10^{-4}$	**0.160**

FIG 13C

Model	AUC	Log Loss	PPV at 10% Recall
With A2/B7 Single-Allele Data	**0.9818**	$5.40 \cdot 10^{-4}$	**0.215**
Without A2/B7 Single-Allele Data	0.9803	$\mathbf{5.31 \cdot 10^{-4}}$	0.211

FIG 13D

Setup	Correlation
A2 model predicting B7	0.004
A2 model predicting A2	0.294
B7 model predicting B7	0.366
B7 model predicting A2	0.002

FIG 13E

Allele	P2	P9
A2	L 80%	V 58%
	M 5%	L 32%
B7	P 98%	L 76 %
		V 8%

FIG 13F

Model	AUC	Log Loss	PPV at 10% Recall
Allele-interacting	0.9723	$5.78 \cdot 10^{-4}$	0.152
Allele-noninteracting	**0.9732**	$5.53 \cdot 10^{-4}$	**0.188**

FIG 13G

2026201462 26 Feb 2026

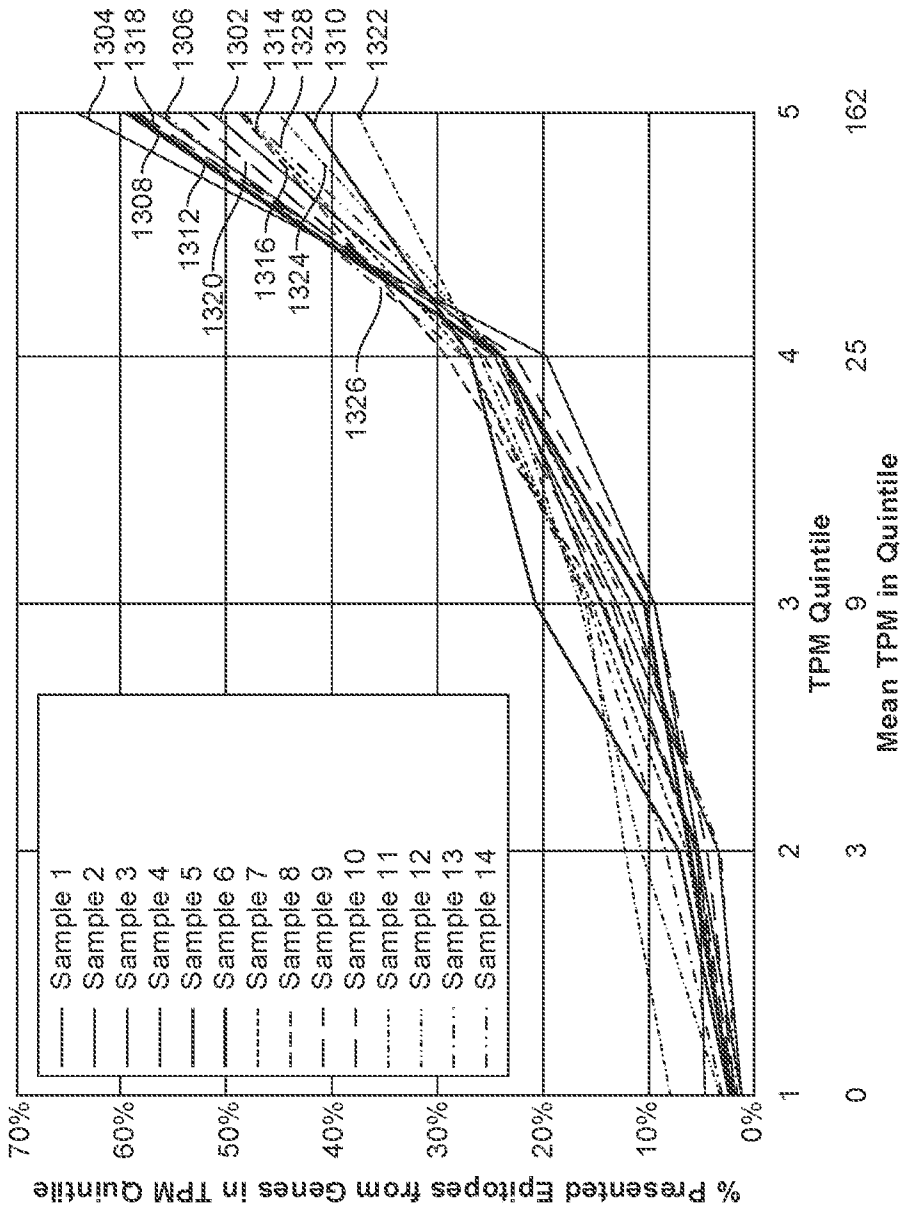


FIG 13H

26 Feb 2026
2026201462

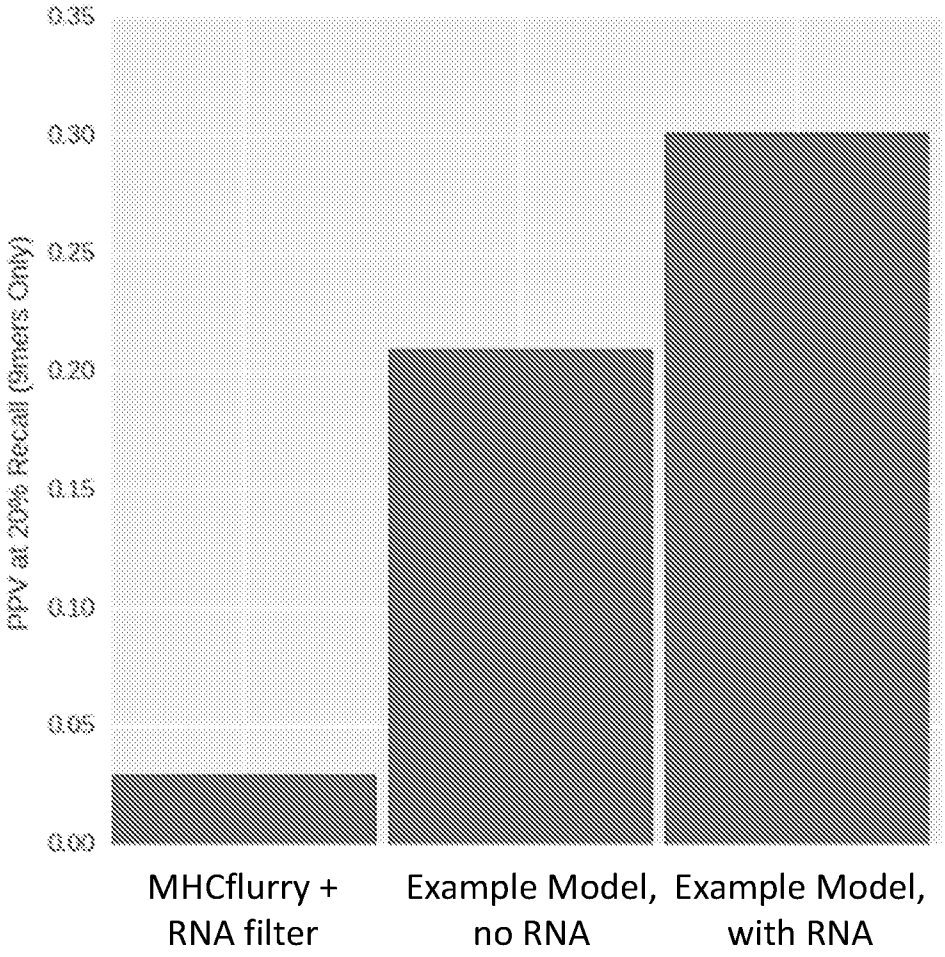


FIG 13I

26 Feb 2026

2026201462

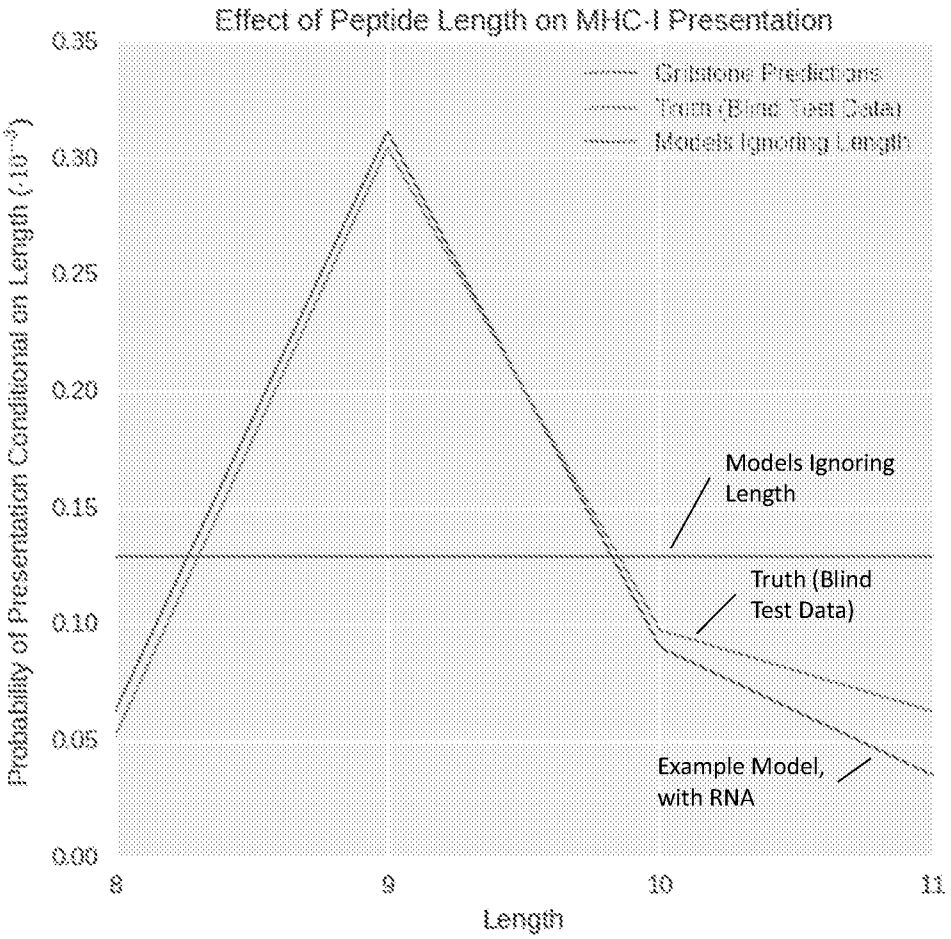


FIG 13J

26 Feb 2026 2026201462

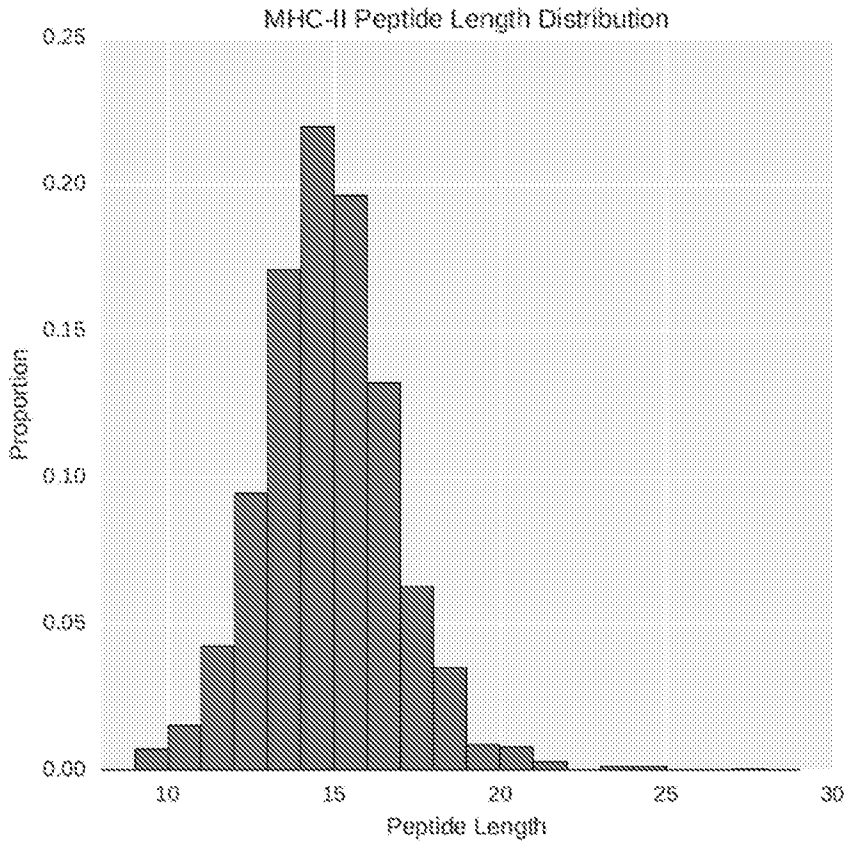


FIG 13K

26 Feb 2026
2026201462

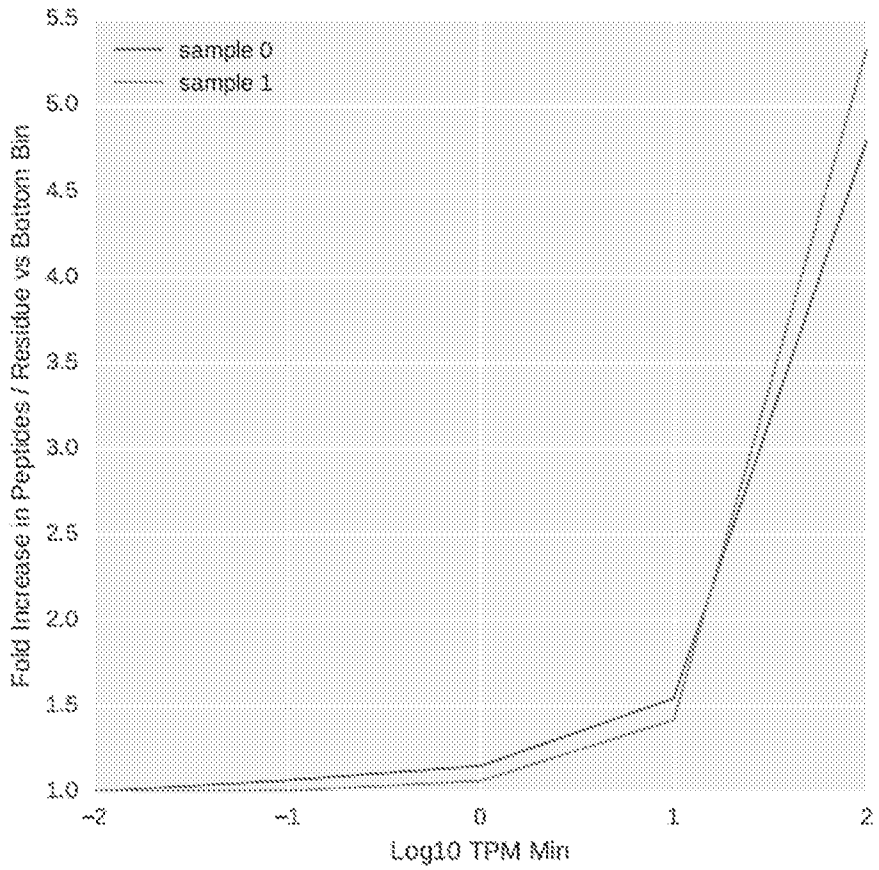


FIG 13L

26 Feb 2026
2026201462

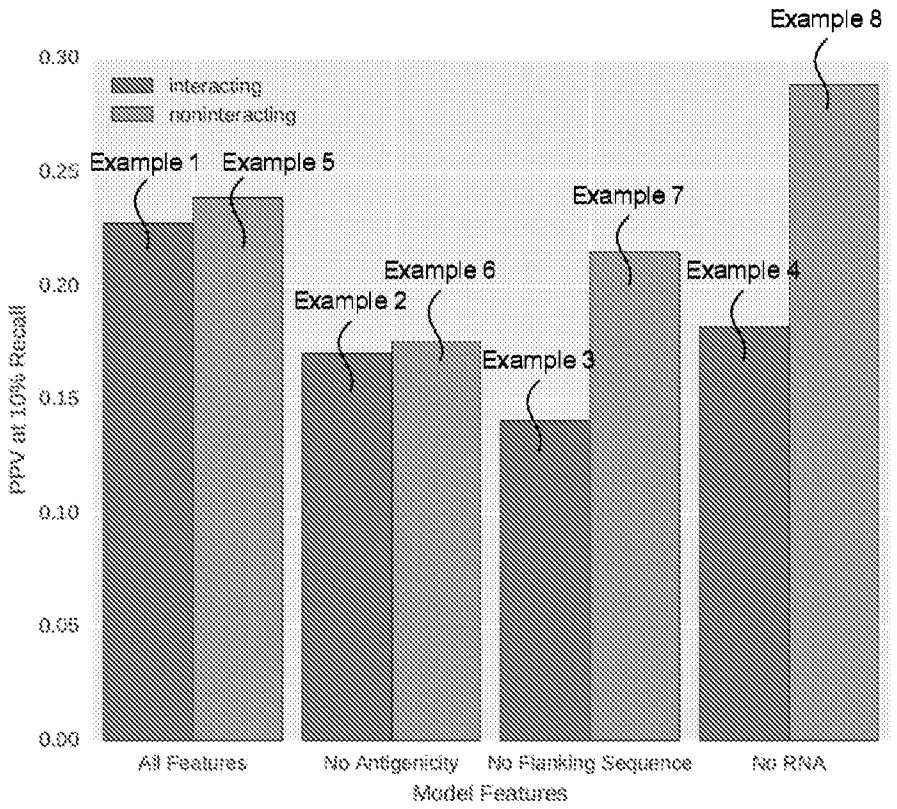


FIG 13M

26 Feb 2026
2026201462

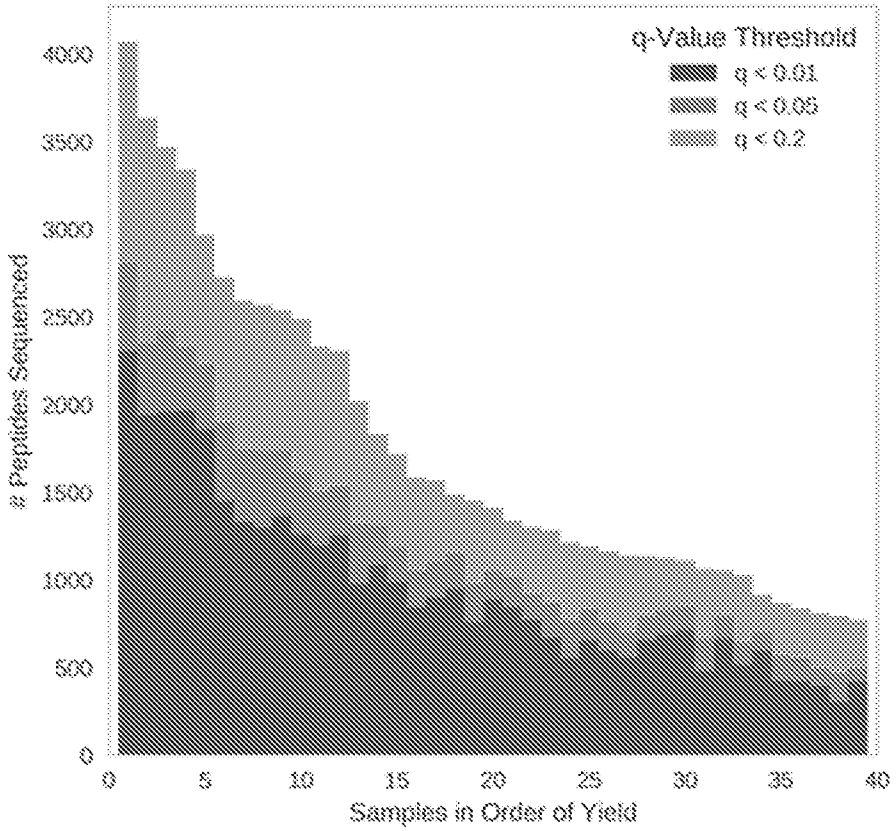


FIG 13N

2026201462 26 Feb 2026

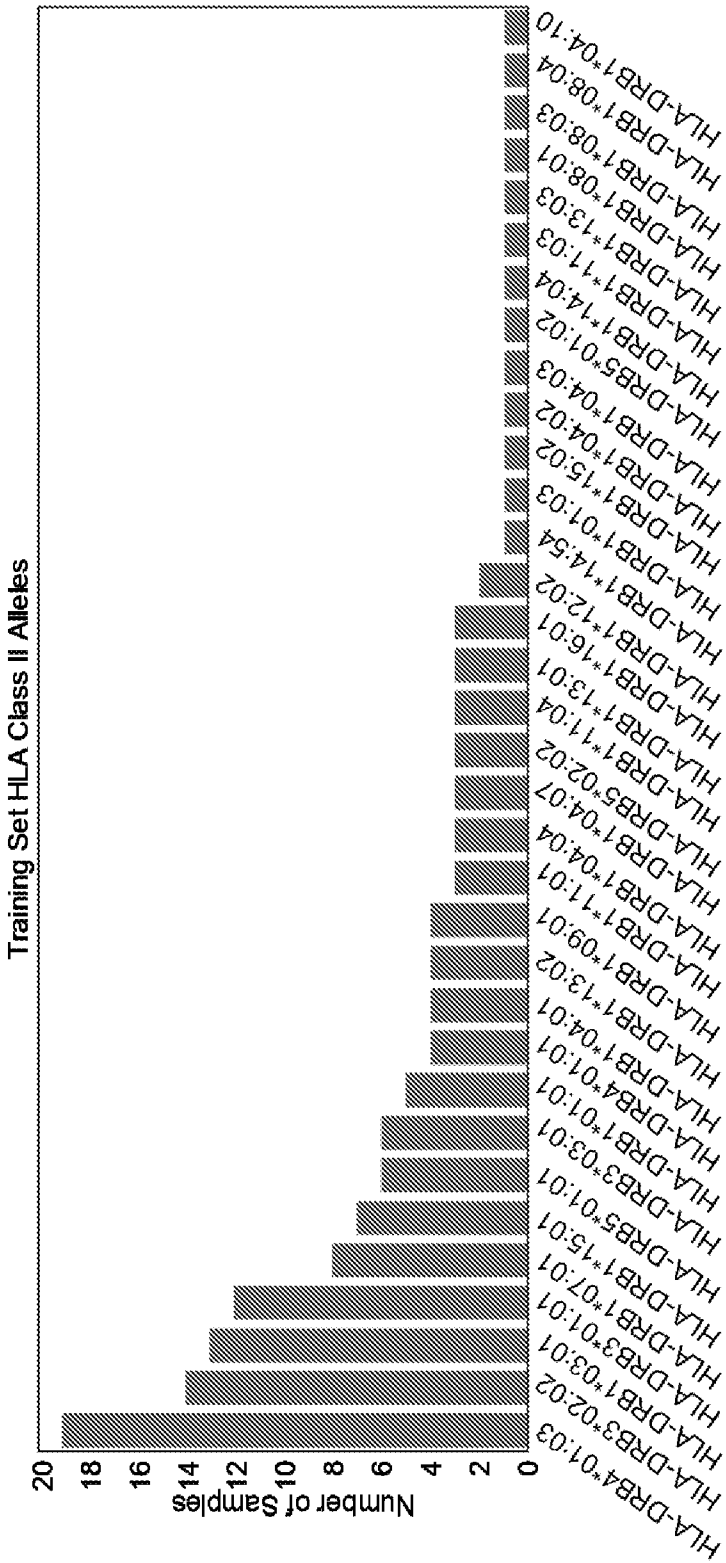


FIG 13-O

2026201462 26 Feb 2026

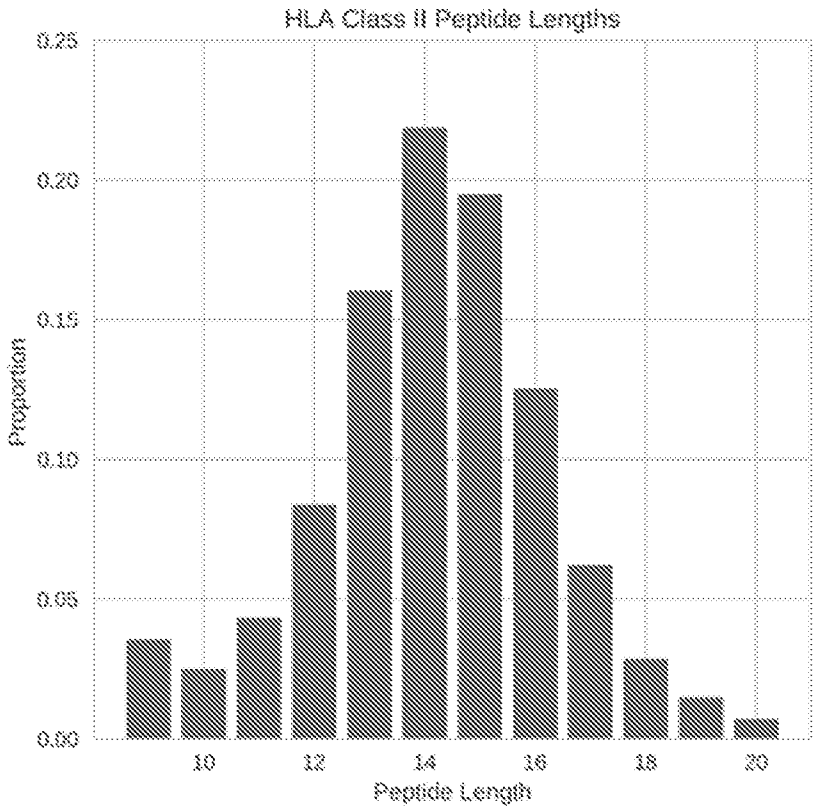


FIG 13P

2026201462 26 Feb 2026

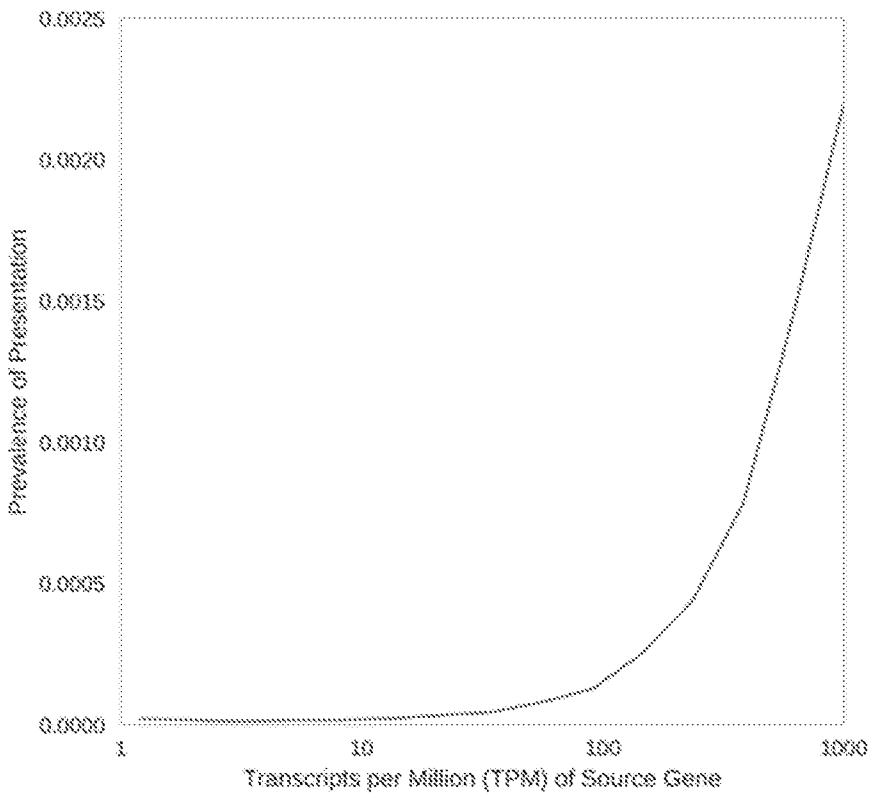


FIG 13Q

26 Feb 2026
2026201462

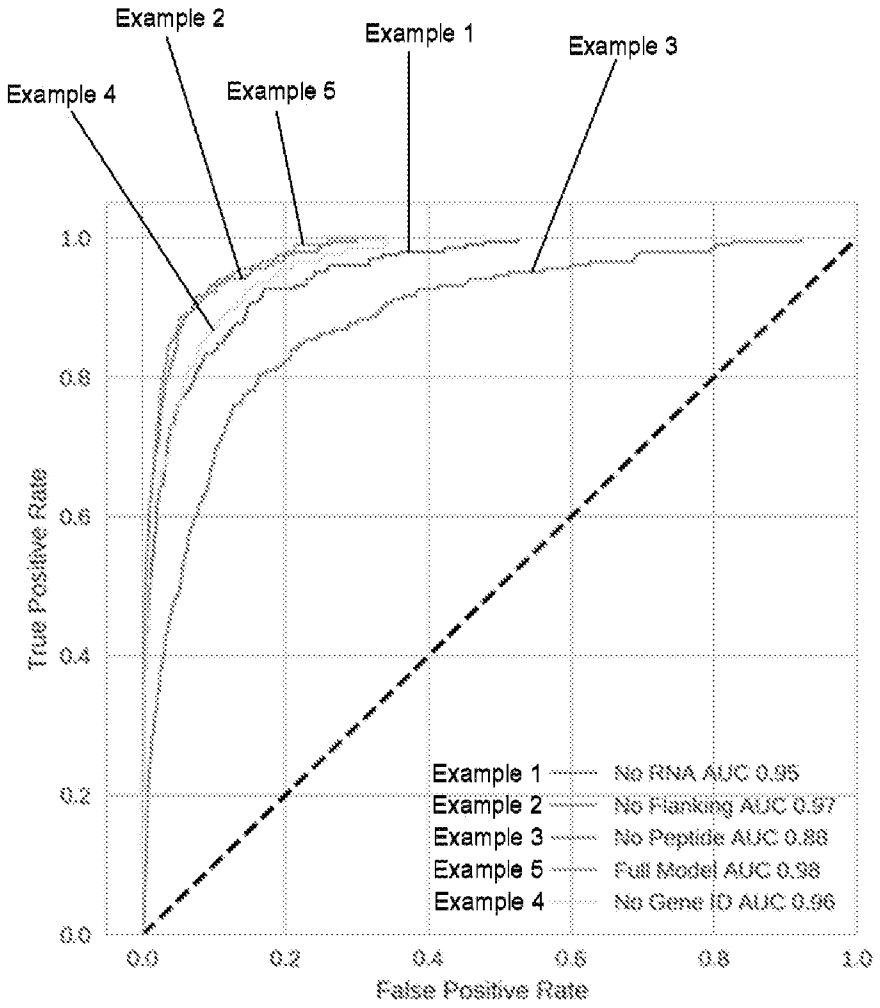


FIG 13H

2026201462 26 Feb 2026

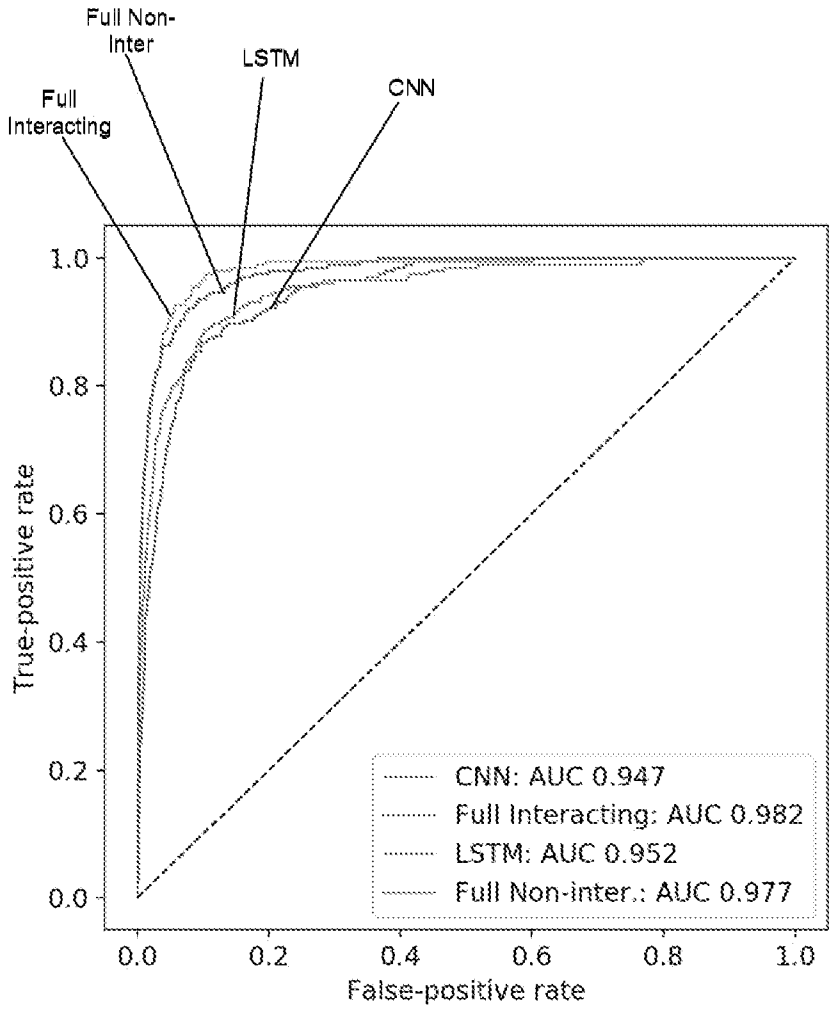


FIG 13S

2026201462 26 Feb 2026

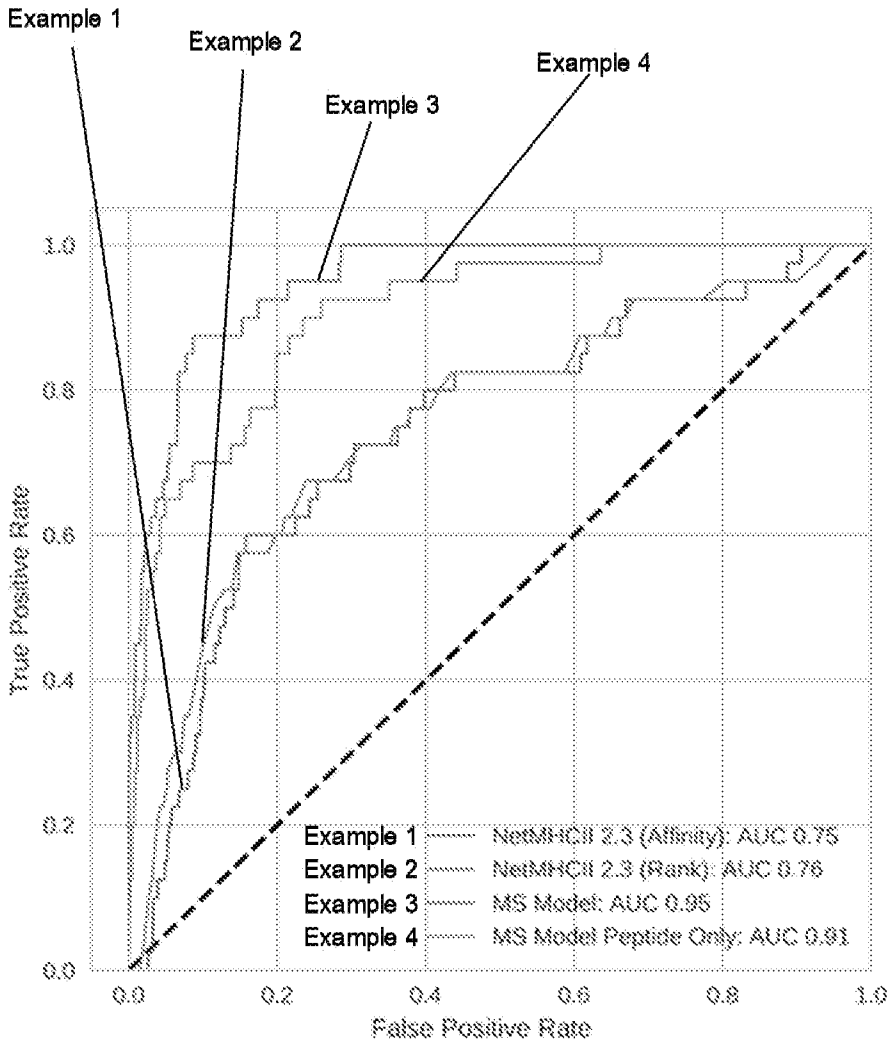


FIG 13T

26 Feb 2026
2026201462

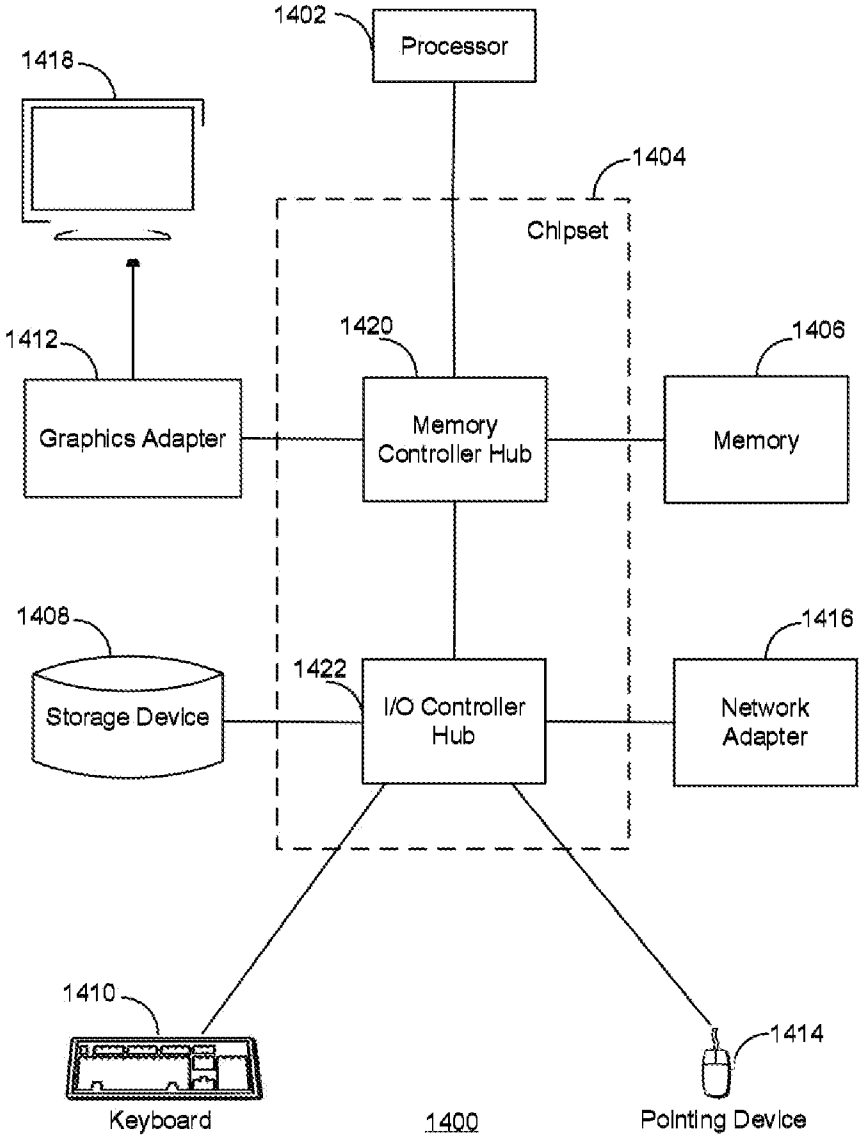


FIG 14

2026201462 26 Feb 2026

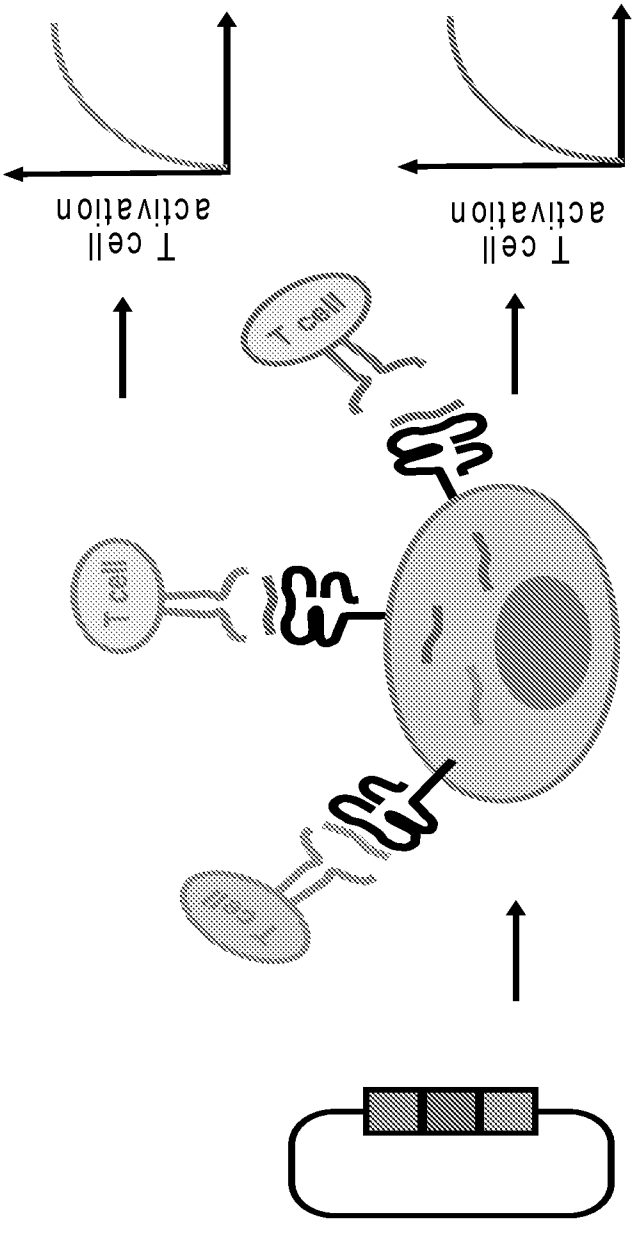


FIG 15

FIG 16A

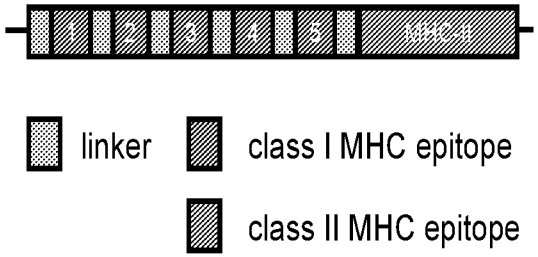


FIG 16B

#	HLA	Sequence	Origin
1	A*0201	NLVPMVATV	HCMV pp65 (495– 503)
2	A*0201	CLGGLLTMV	EBV LMP2A(426-434)
3	A*0201	GLCTLVAML	EBV BMLF1 (280–288)
4	A*0201	LLFGYPVYV	HTLV-1 Tax (11-19)
5	A*0201	GILGFVFTL	Influenza A Matrix 1 (58– 66)
	MHC-II	AKFVAAWTLKAAA	PADRE (artificial seq)
	MHC-II	QYIKANSKFIGITE	Tetanus toxoid (830–844)

2026201462 26 Feb 2026

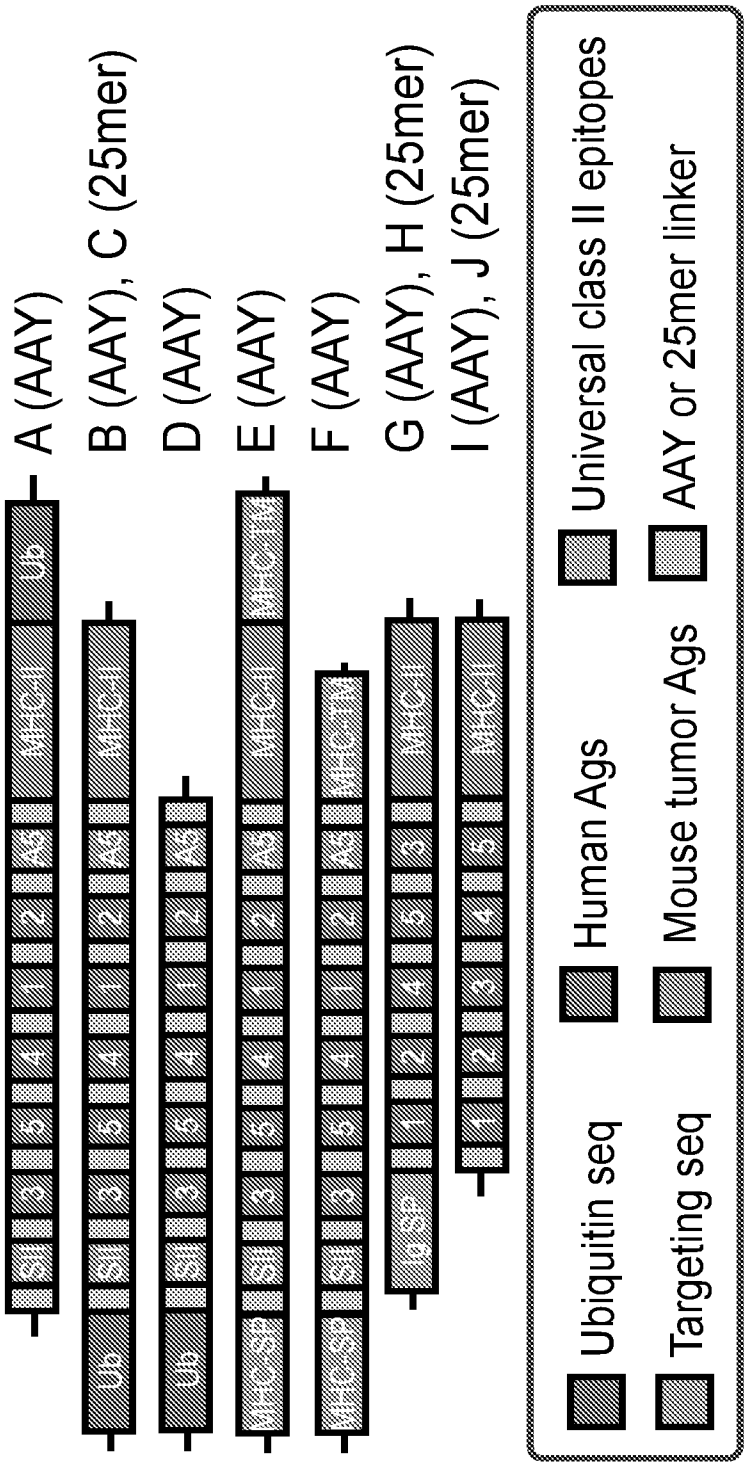


FIG 17

2026201462 26 Feb 2026

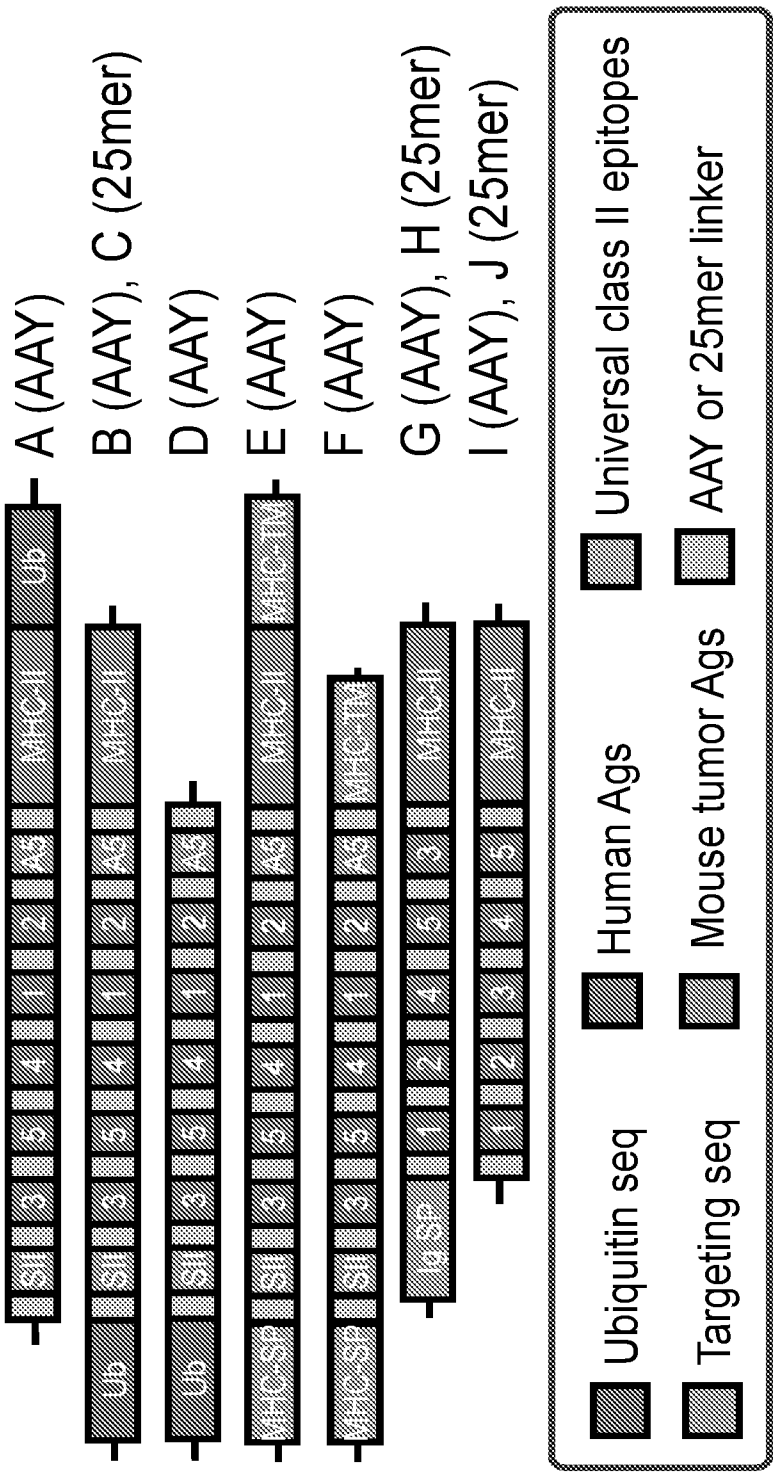


FIG 18

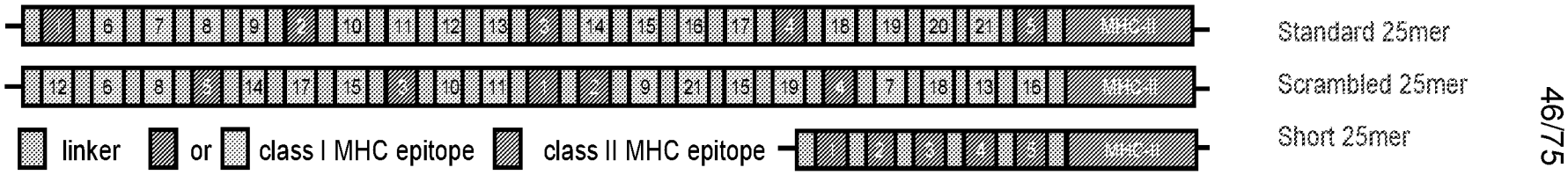

Standard 25mer
Scrambled 25mer
Short 25mer
MHC-II
linker
or
class I MHC epitope
class II MHC epitope

FIG 19A

26 Feb 2026 2026201462

#	HLA	Sequence	Origin
1	A*02:01	NLVPMVATV	HCMV pp65 495-504
2	A*02:01	CLGGLLTMV	EBV LMP-2 426-434
3	A*02:01	GLCTLVAML	EBV BMLF-1 259-267
4	A*02:01	LLFGYPVYV	HTLV1 Tax 11-19
5	A*02:01	GILGFVFTL	Influenza A MP 58-66
6	A*02:01	DLMGYIPAV	HCV core 132-140
7	A*02:01	FLPSDFFPSV	HBV core antigen 18-27
8	A*02:01	FLLTRILTI	HBV envelope 183-191
9	A*02:01	WLSLLVPFV	HBV surface antigen 172-181
10	A*02:01	FLLSLGIHL	HBV polymerase 573-581
11	A*02:01	ILKEPVHGV	HIV-1 RT 476-484
12	A*02:01	YMLDLQPETT	HPV 16 E7 11-20
13	A*02:01	CINGVCWTV	HCV NS3 1073-1081
14	A*02:01	YLLPRRGPRL	HCV core 35-44
15	A*02:01	FLYALALLL	EBV LMP-2 356-364
16	A*02:01	AAGIGILTV	MELAN-A/MART-1 (27-35)
17	A*02:01	SLLMWITQV	NY-ESO-1(157-165) C9V
18	A*03:01	KLGGALQAK	CVM-IE1
19	A*03:01	RLRAEAQVK	EBV-EBNA-3a
20	B*44:05	EENLLDFVRF	EBV EBNASC (281-290)
21	B*44:05	EEYLQAFTY	Self ABCD3 protein

FIG 19B

2026201462 26 Feb 2026



FIG 20A

NHP Epitopes

	MHC	Sequence
1	Mamu*01	CTPYDINQM
4	Mamu*01	TTPESANL
7	Mamu*01	CAPPGYALL
10	Mamu*01	SGPKTNIIV
14	Mamu*01	LSPRTLNAW
18	Mamu*01	TVPWPNASL

Human Epitopes

	HLA	Sequence
3	A*02:01	GILGFVFTL
6	A*02:01	LLFGYPVYV
9	A*02:01	GLCTLVAML
12	A*02:01	NLVPMVATV
16	A*02:01	CLGGLLTMV

Murine MHC-I Epitopes

	MHC	Sequence
2	H-2Kb	SIINFEKL
5	H-2Ld	SPSYAYHQF
8	H-2Db	EGPRNQDWL
11	H-2Kb	DWENVSPEL
13	H-2Kb	SIIVFNLL
15	H-2Db	ASMTNMELM
17	H-2Db	AQLANDVVL
19	H-2Kb	SVYDFFVWL
20	H-2Ld	MNKYAYHML

Universal MHC-II Epitopes

	HLA	Sequence
1	MHC-II	AKFVAAWTLKAAA
2	MHC-II	QYIKANSKFIGITEL

FIG 20B

2026201462 26 Feb 2026

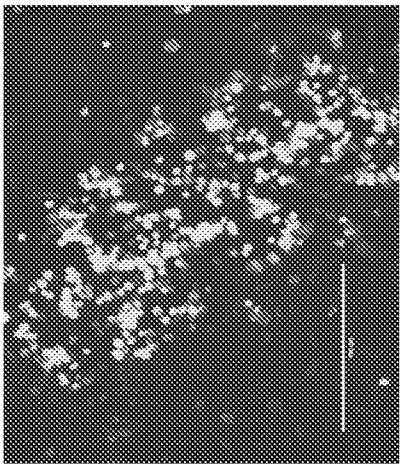


FIG 21C

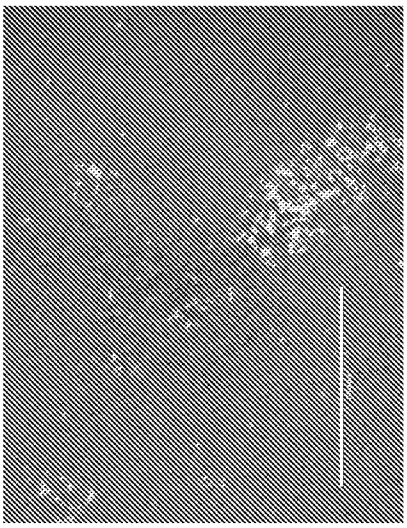


FIG 21B

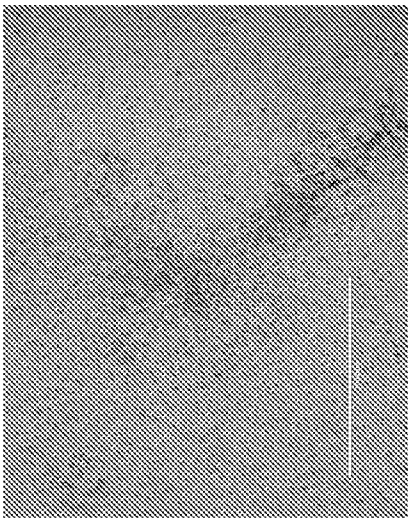


FIG 21A

2026201462 26 Feb 2026

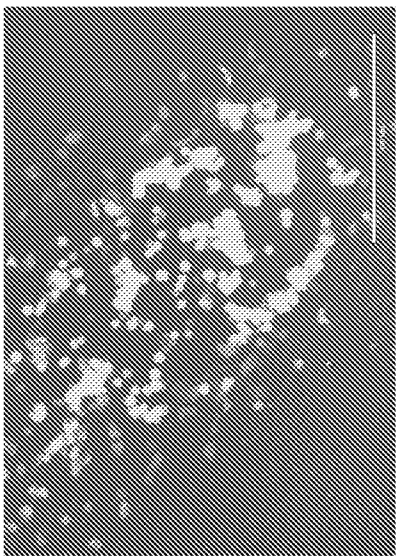


FIG 22C

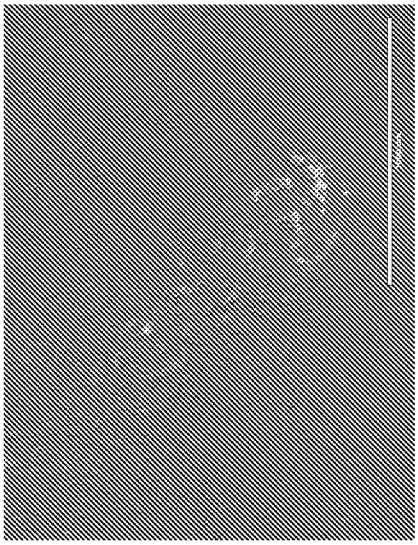


FIG 22B

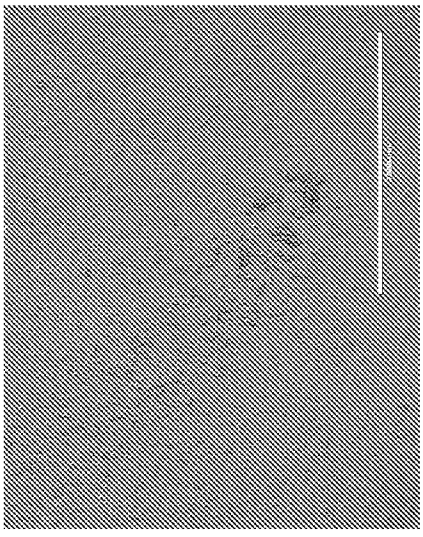


FIG 22A

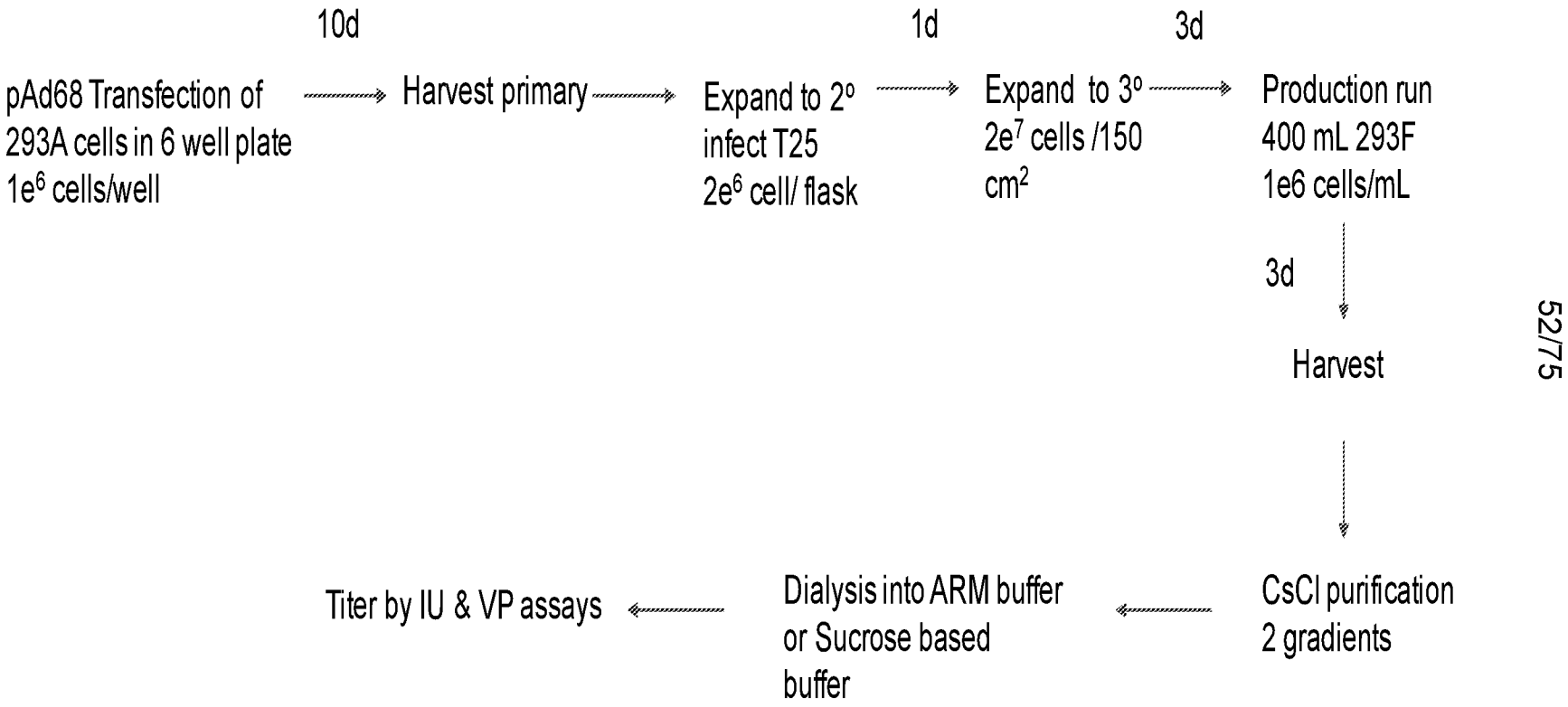

10d
1d
3d
pAd68 Transfection of 293A cells in 6 well plate 1e6 cells/well
Harvest primary
Expand to 2° infect T25 2e6 cell/ flask
Expand to 3° 2e7 cells /150 cm2
Production run 400 mL 293F 1e6 cells/mL
3d
Harvest
CsCl purification 2 gradients
Dialysis into ARM buffer or Sucrose based buffer
Titer by IU & VP assays

FIG 23

2026201462 26 Feb 2026

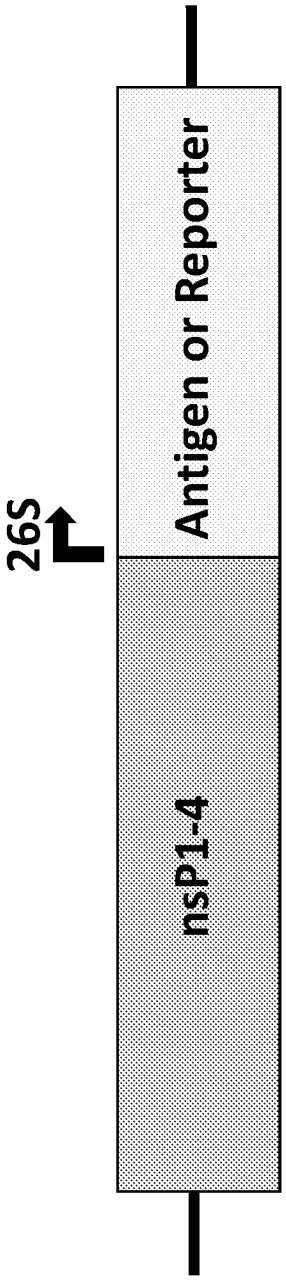


FIG 24

2026201462 26 Feb 2026

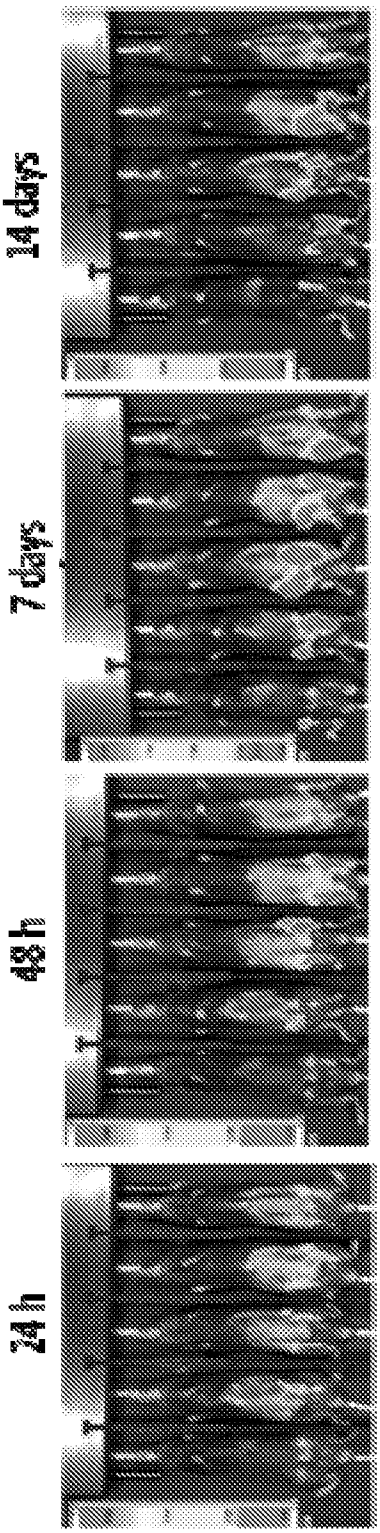


FIG 25

2026201462 26 Feb 2026

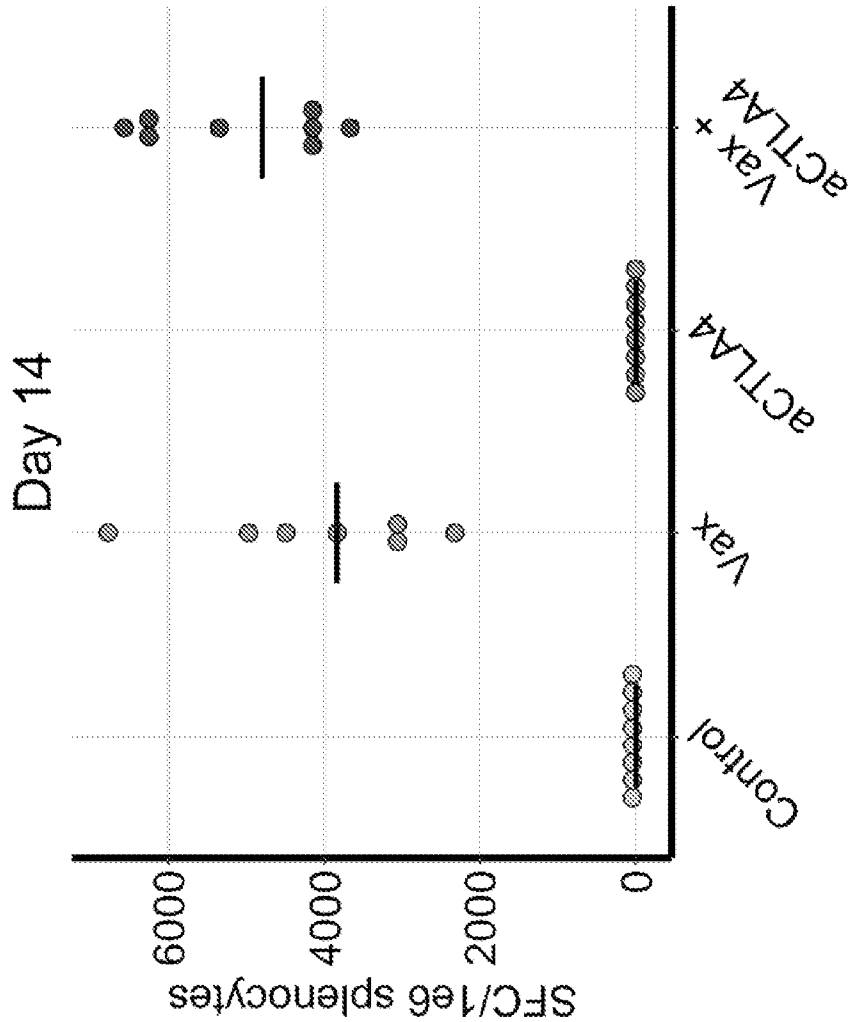


FIG 26A

2026201462 26 Feb 2026

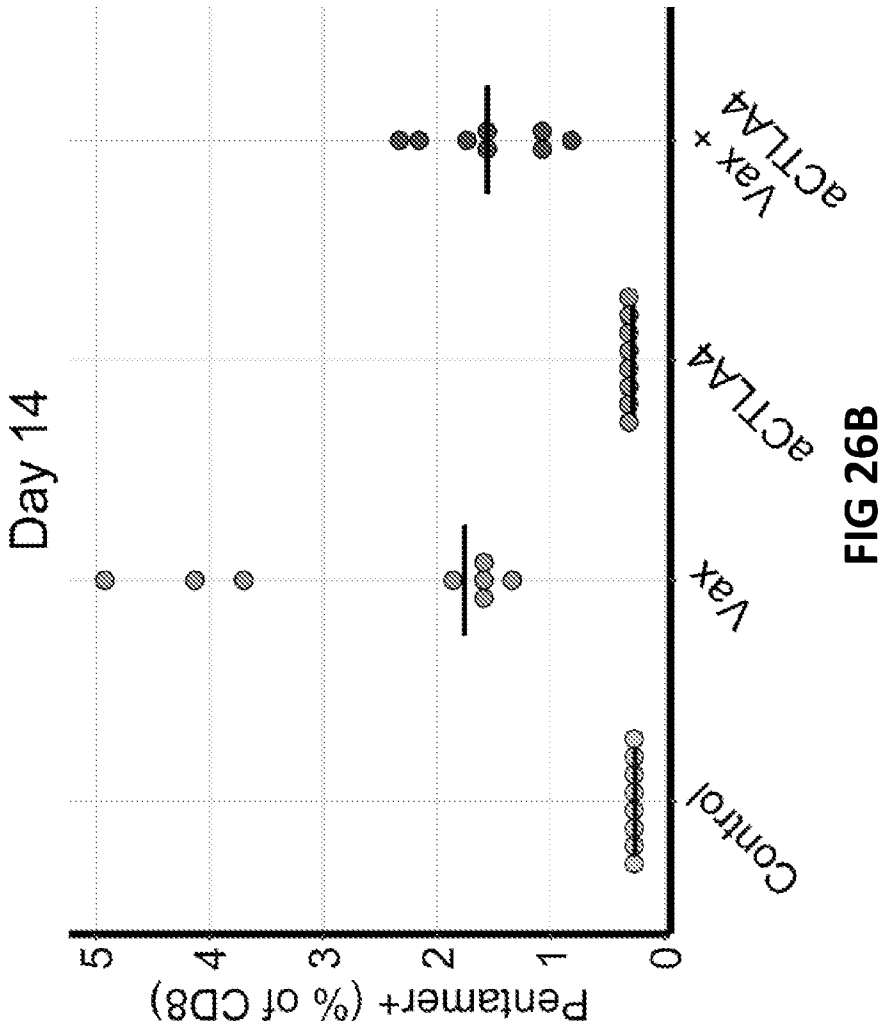


FIG 26B

2026201462 26 Feb 2026

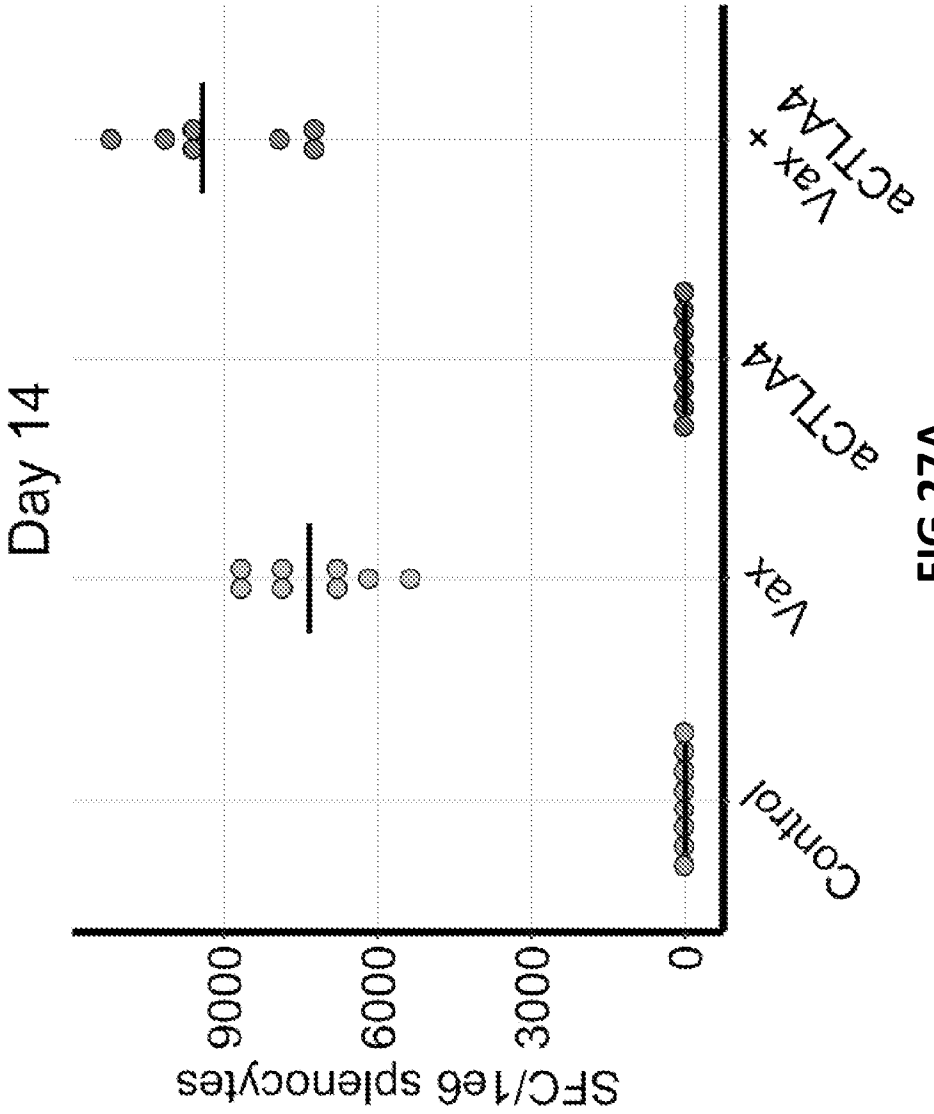


FIG 27A

2026201462 26 Feb 2026

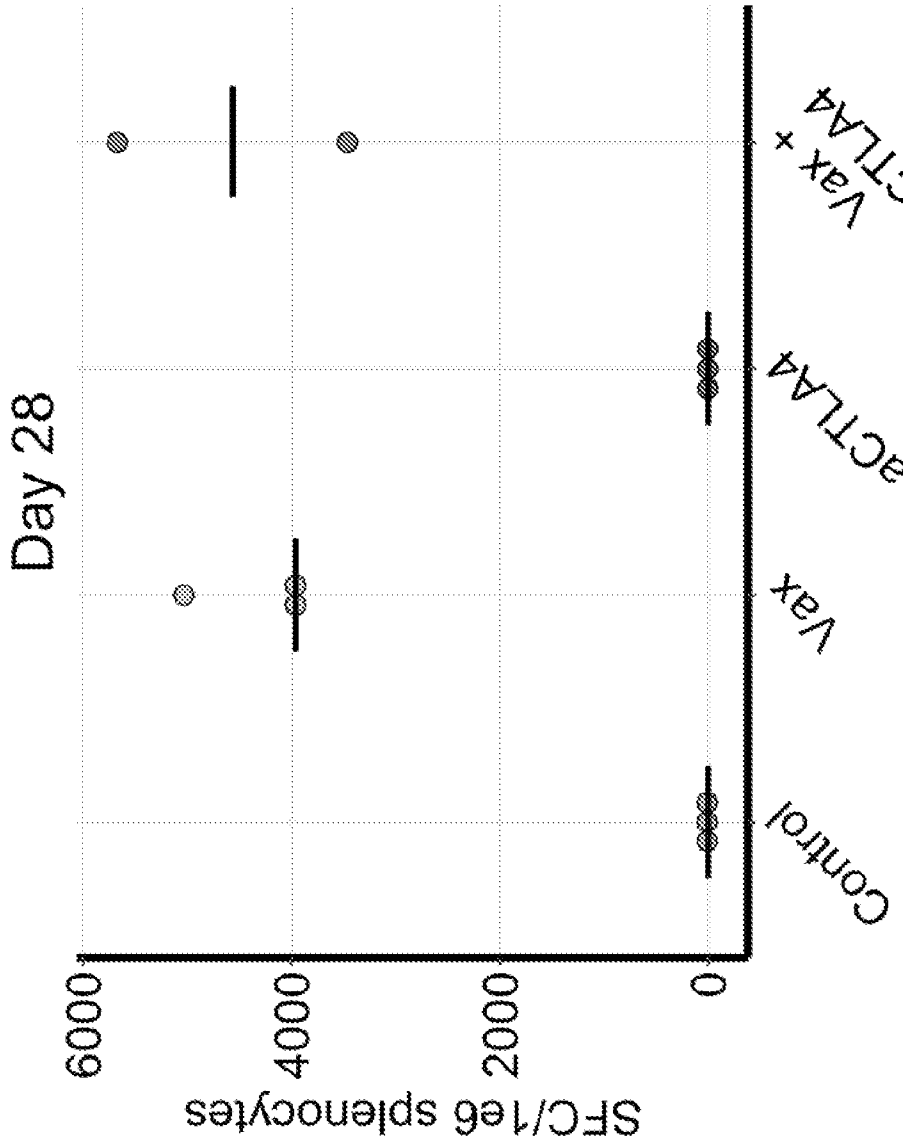


FIG 27B

2026201462 26 Feb 2026

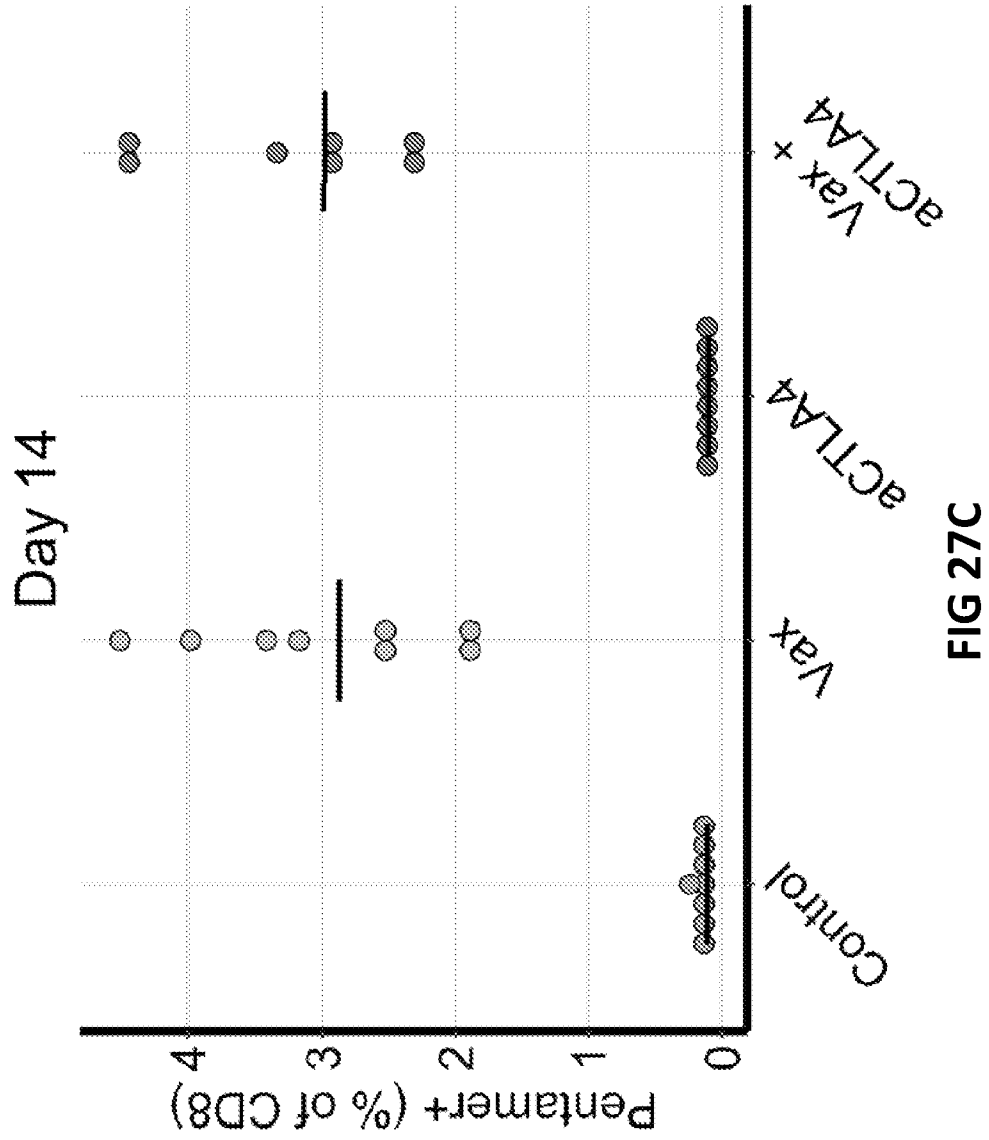


FIG 27C

2026201462 26 Feb 2026

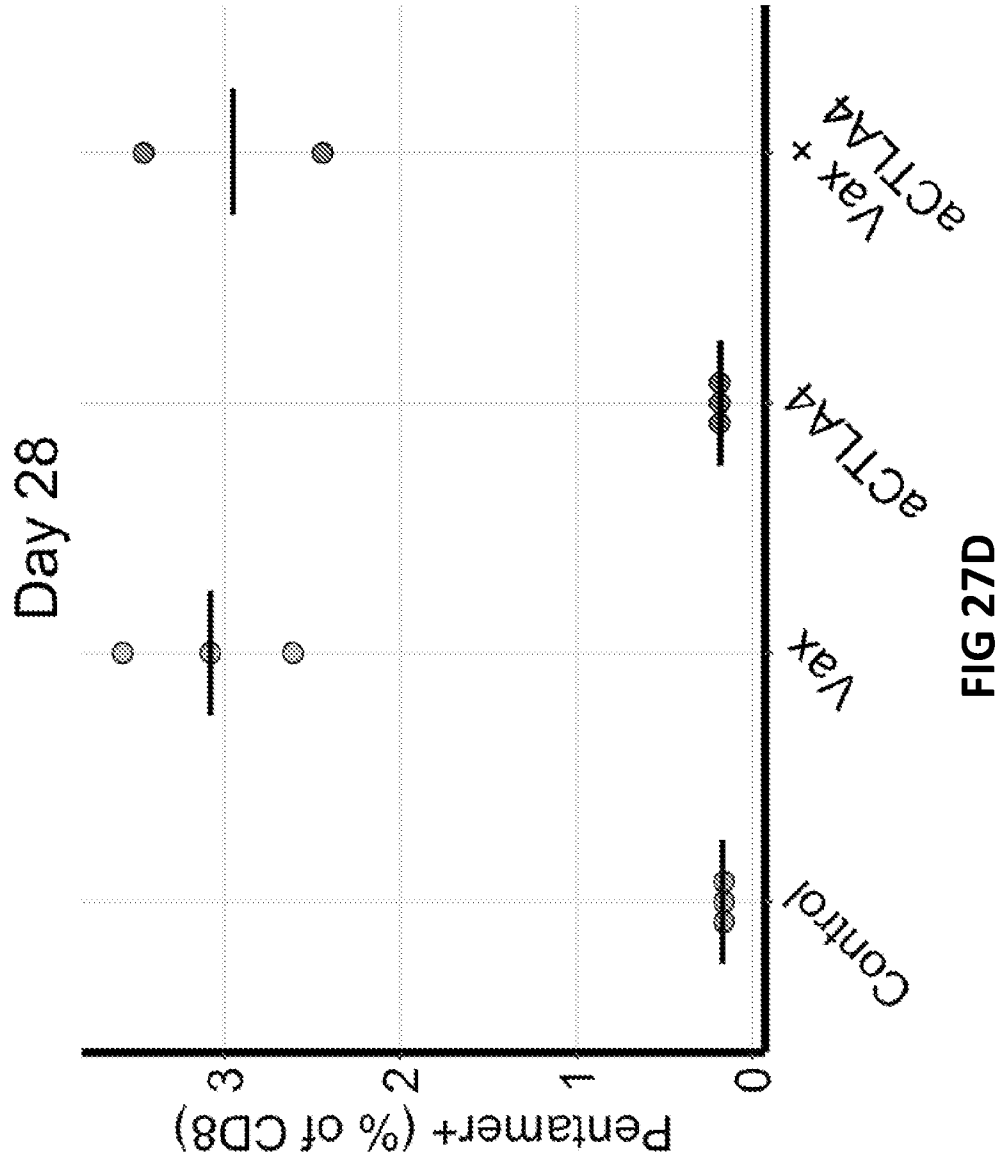


FIG 27D

2026201462 26 Feb 2026

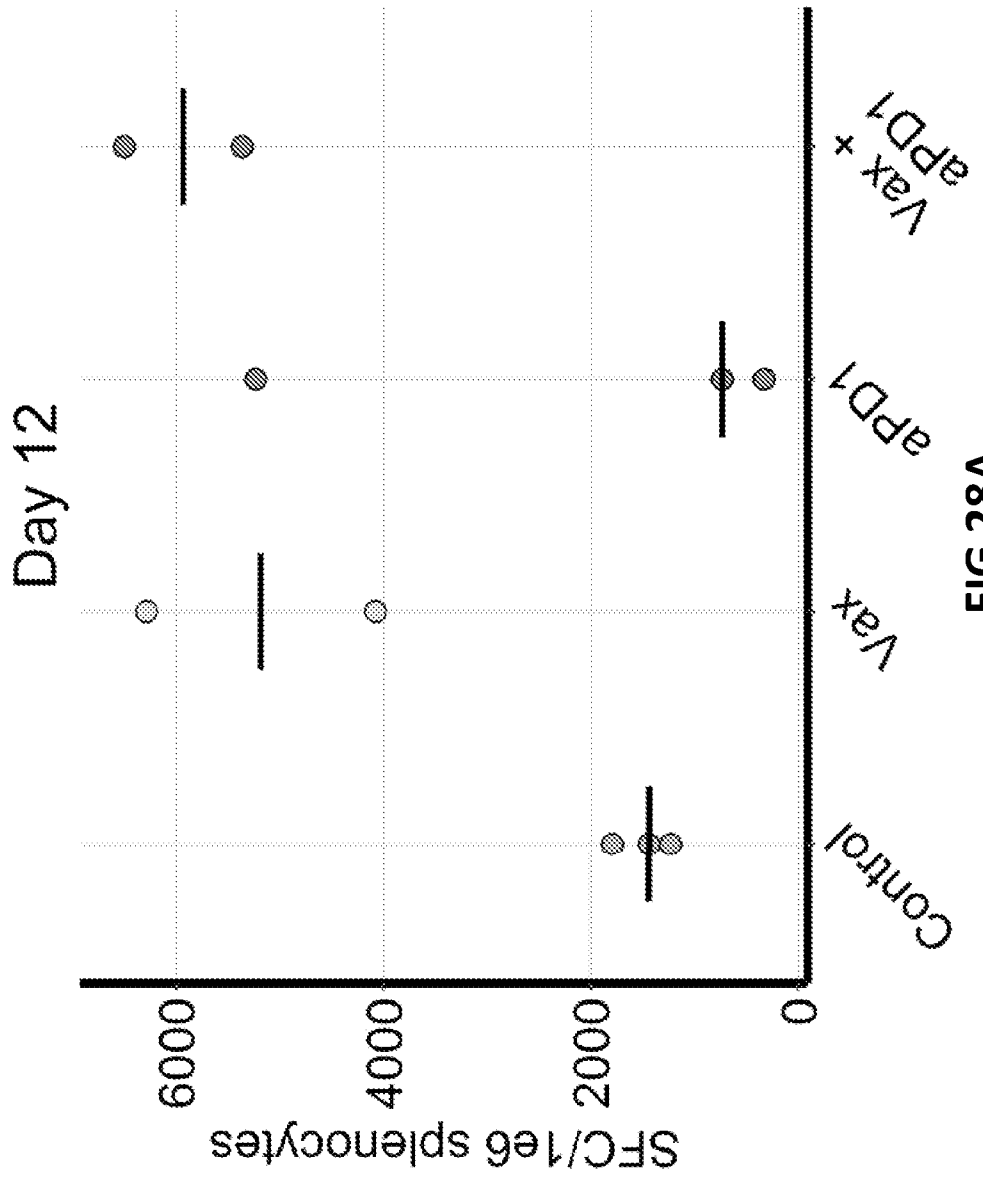


FIG 28A

2026201462 26 Feb 2026

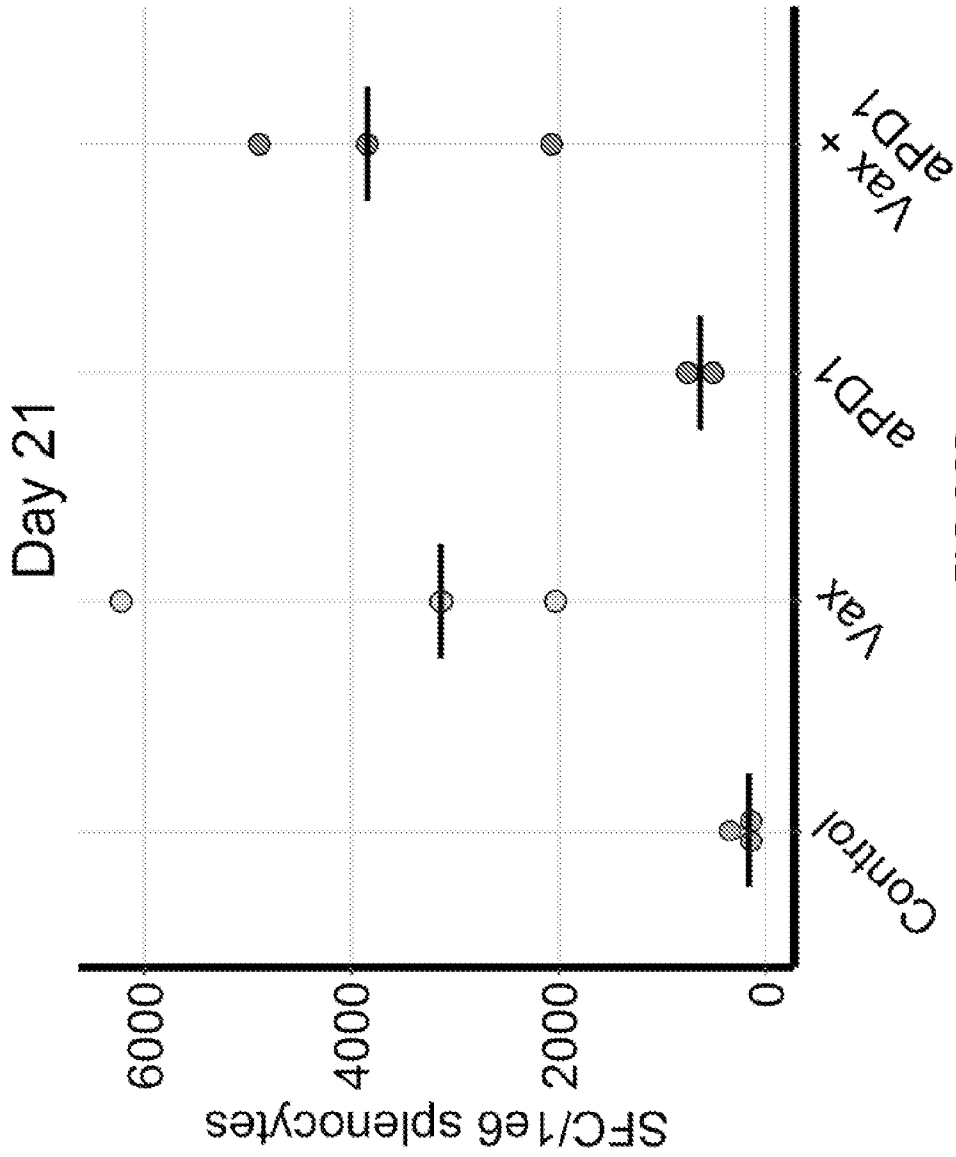


FIG 28B

26 Feb 2026
2026201462

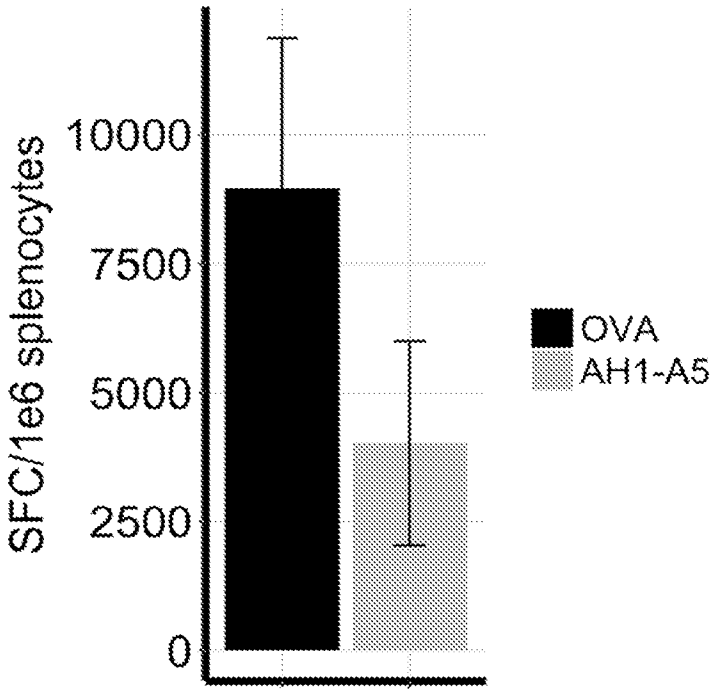


FIG 29

2026201462 26 Feb 2026

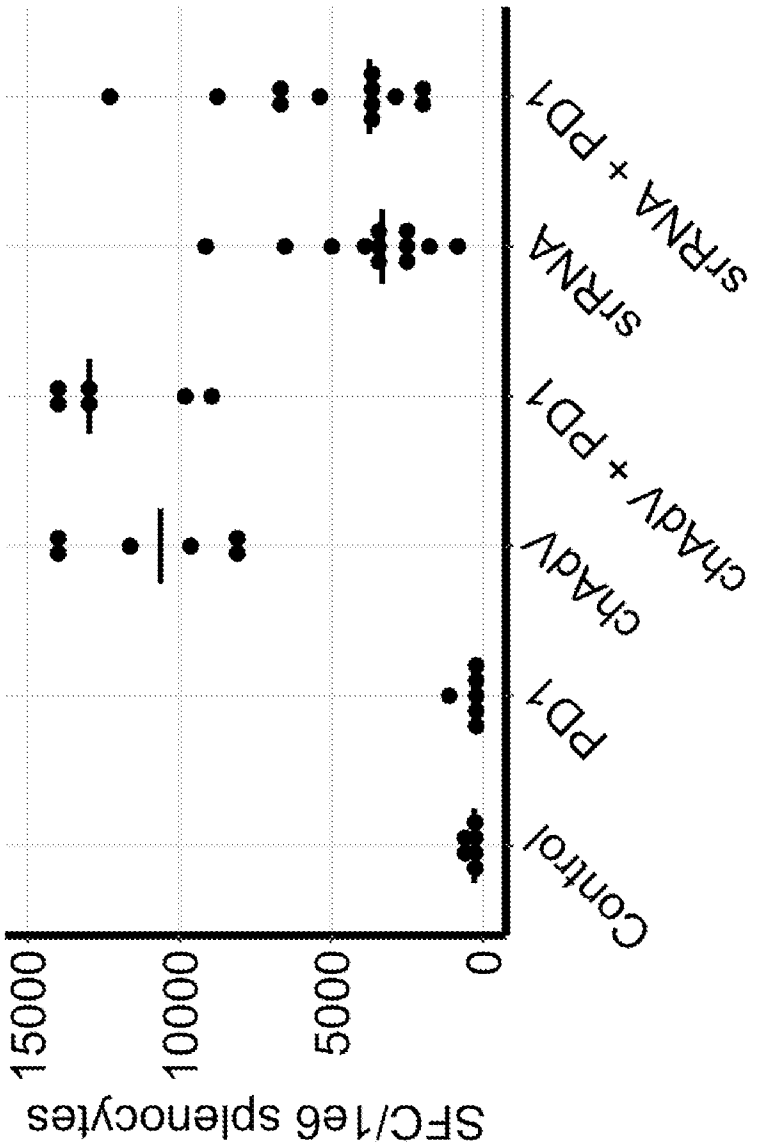


FIG 30

2026201462 26 Feb 2026

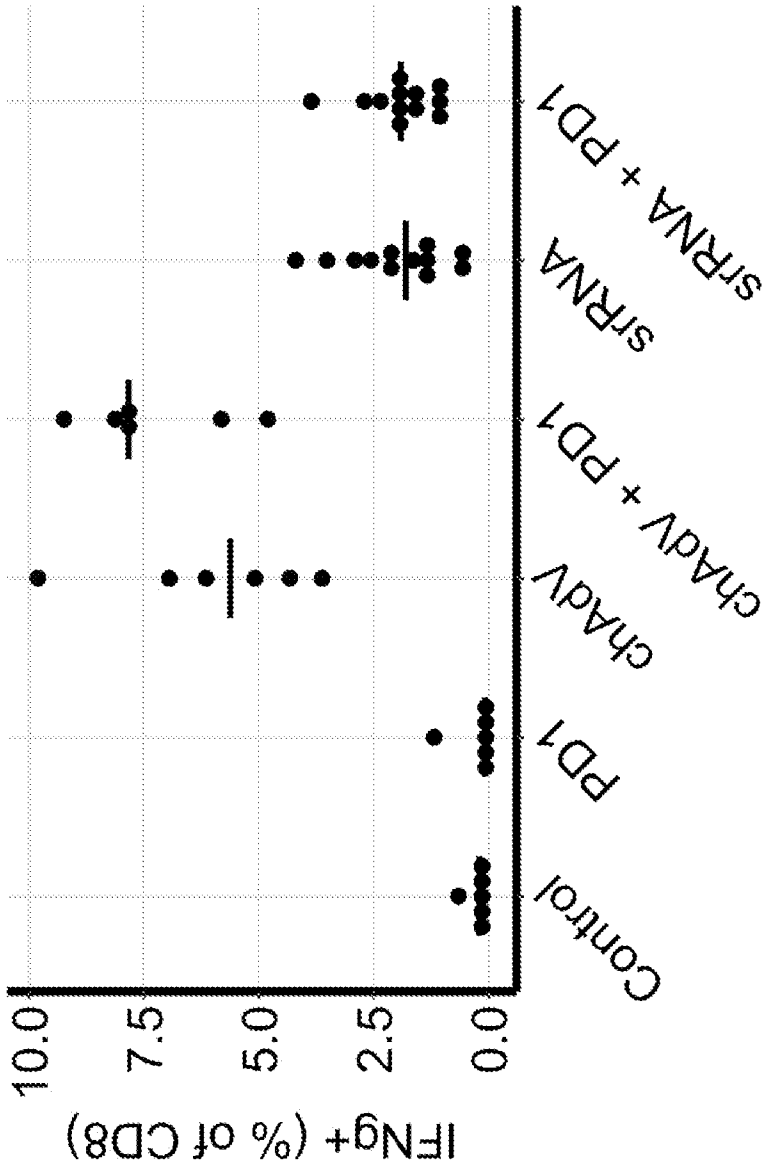


FIG 31

2026201462 26 Feb 2026

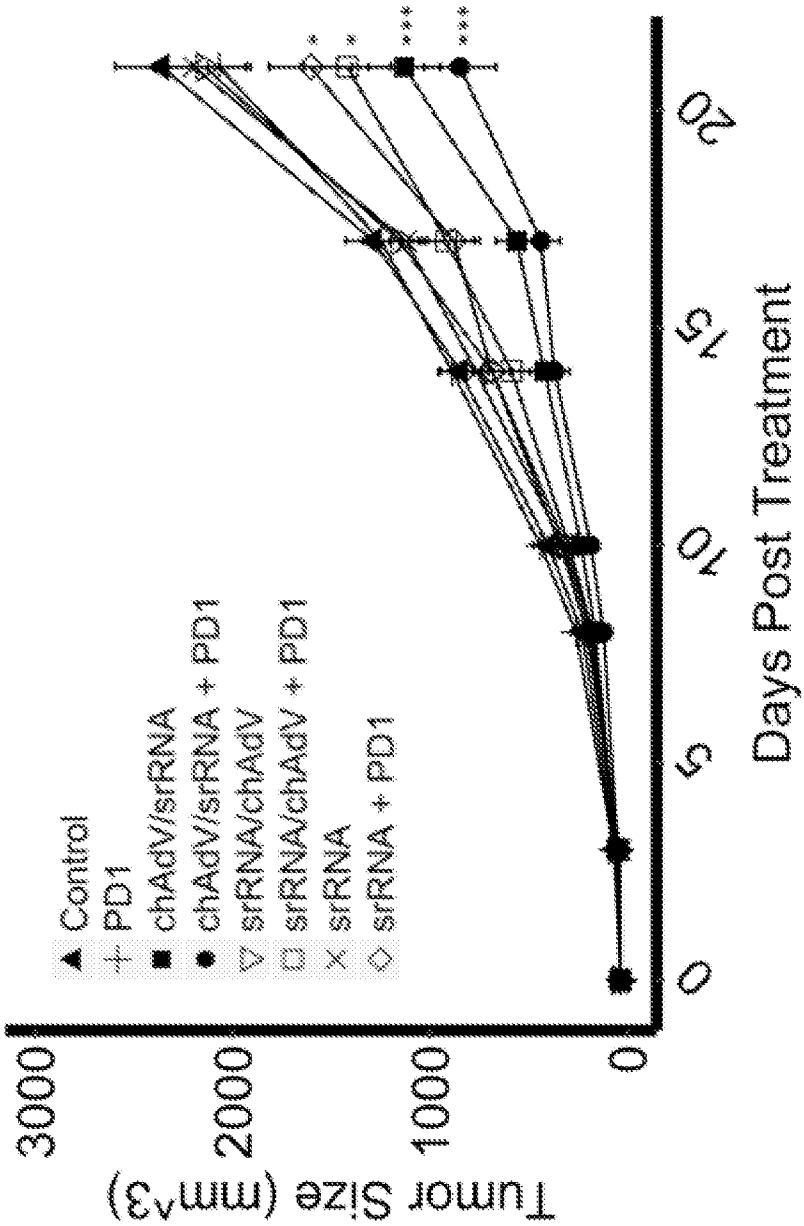


FIG 32

2026201462 26 Feb 2026

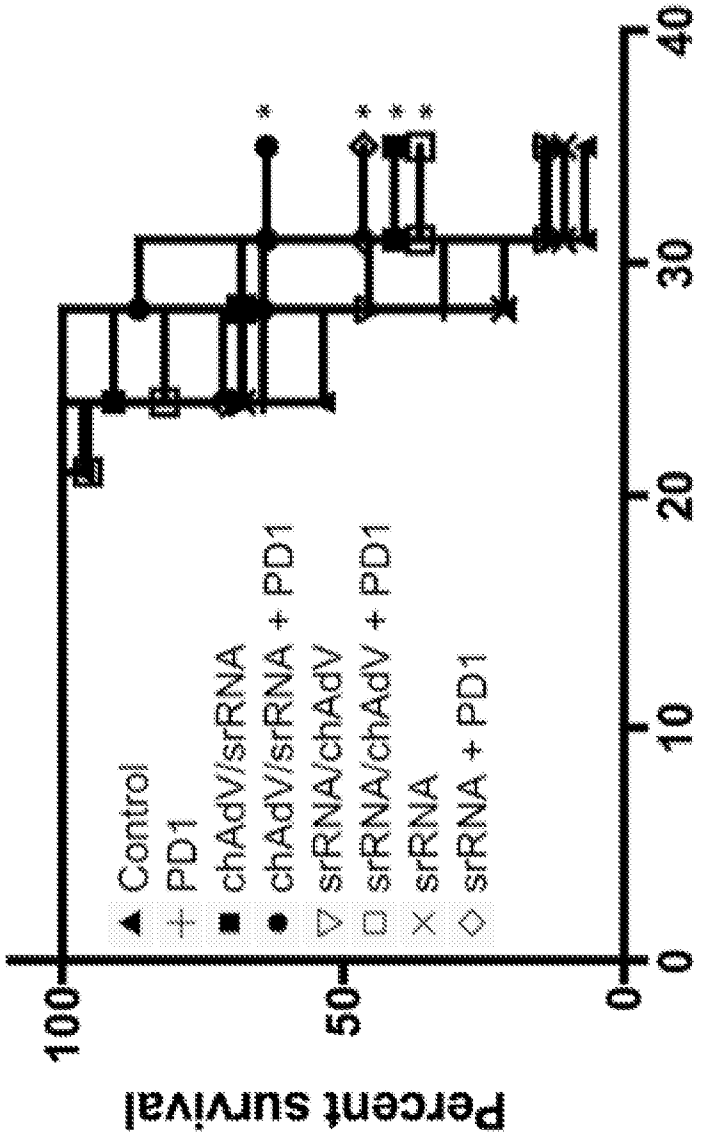


FIG 33

2026201462 26 Feb 2026

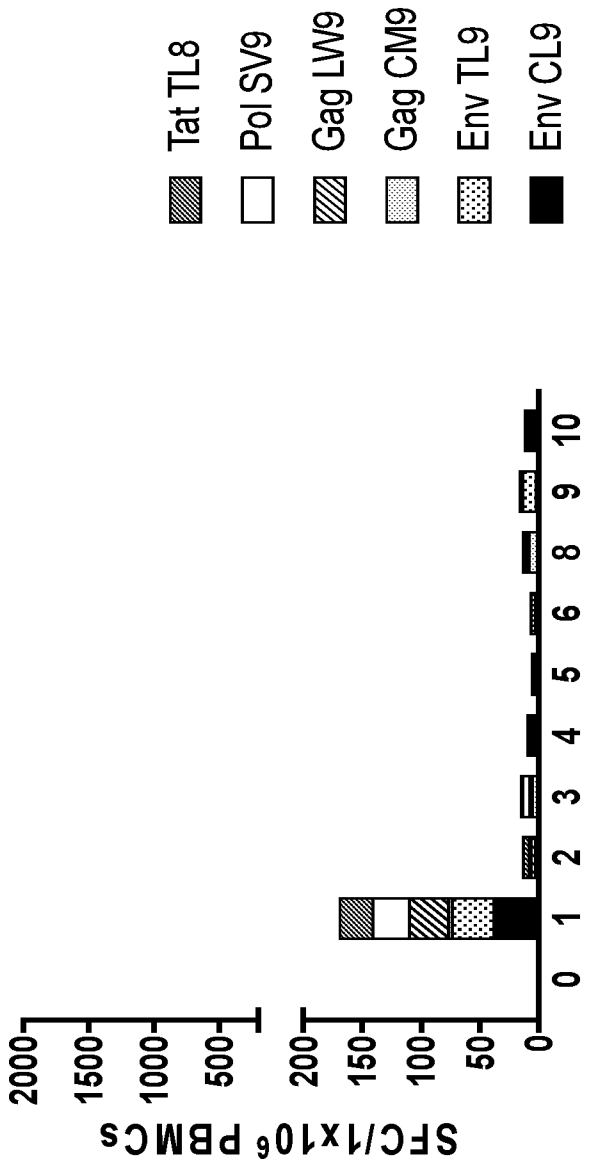


FIG 34A

2026201462 26 Feb 2026

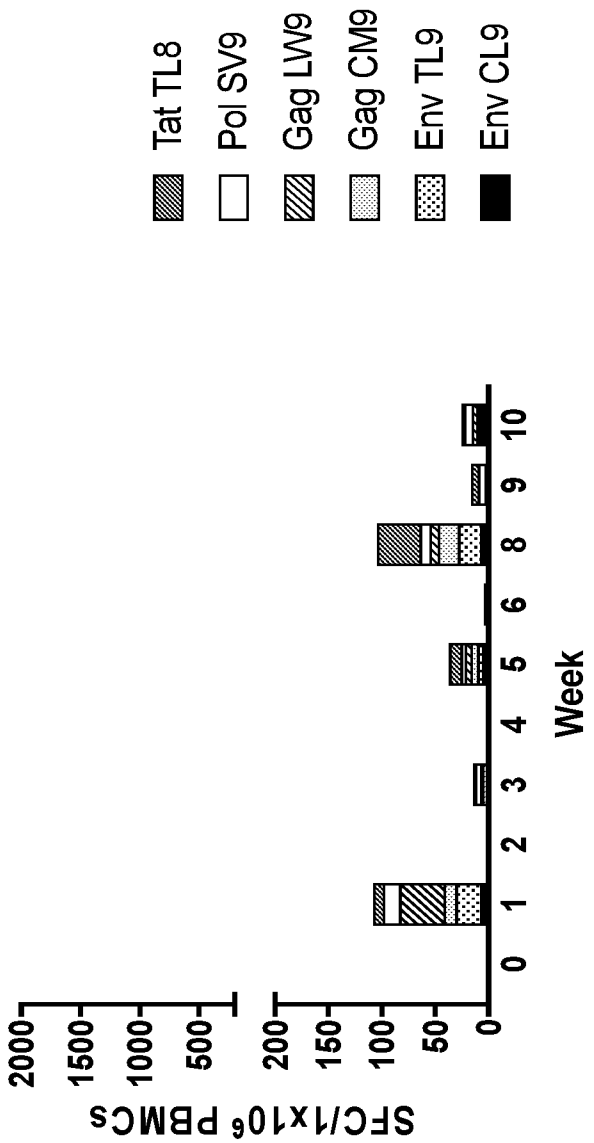


FIG 34B

2026201462 26 Feb 2026

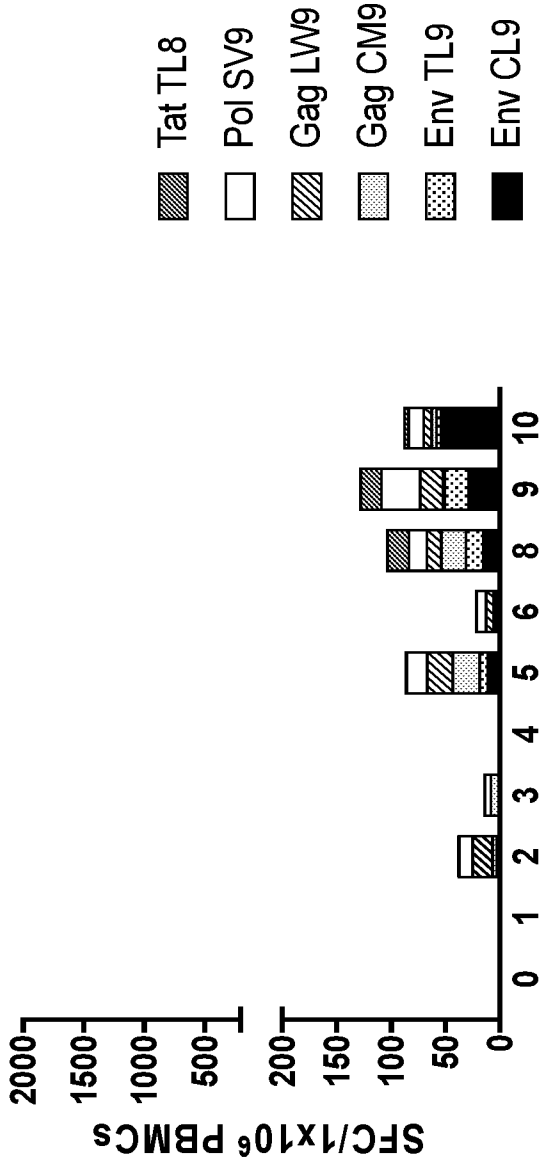


FIG 34C

2026201462 26 Feb 2026

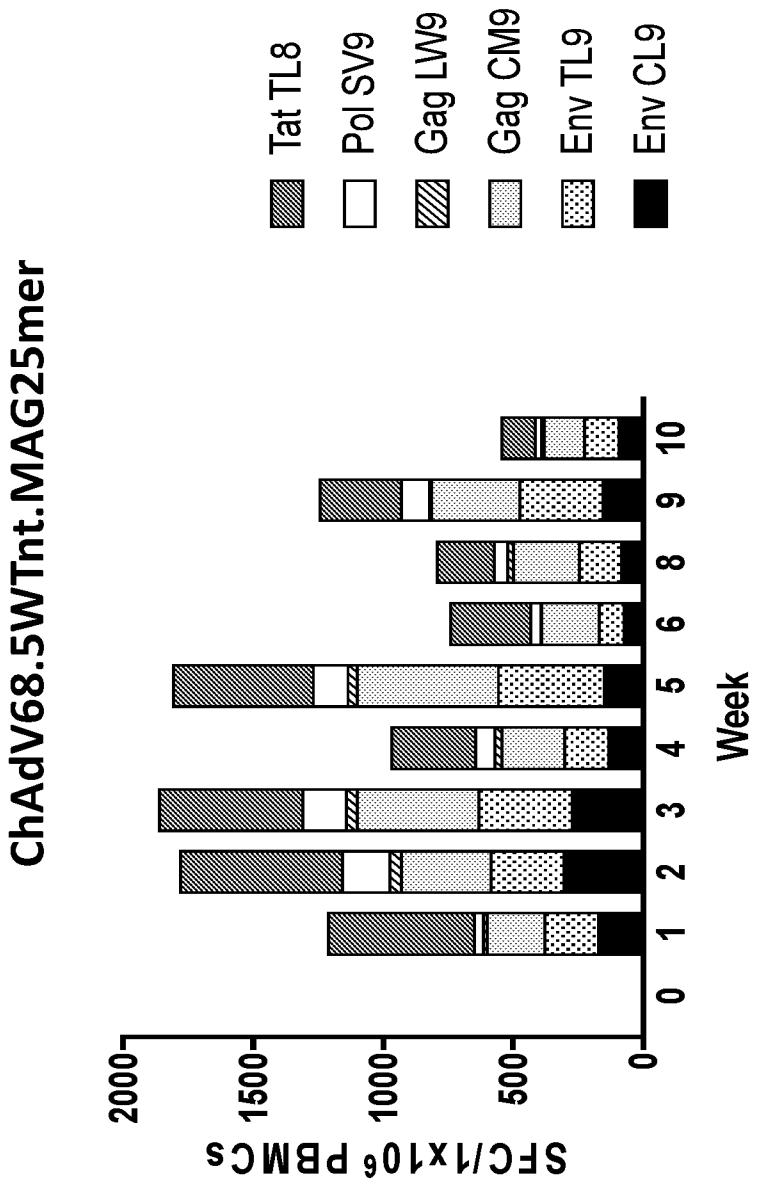


FIG 34D

2026201462 26 Feb 2026

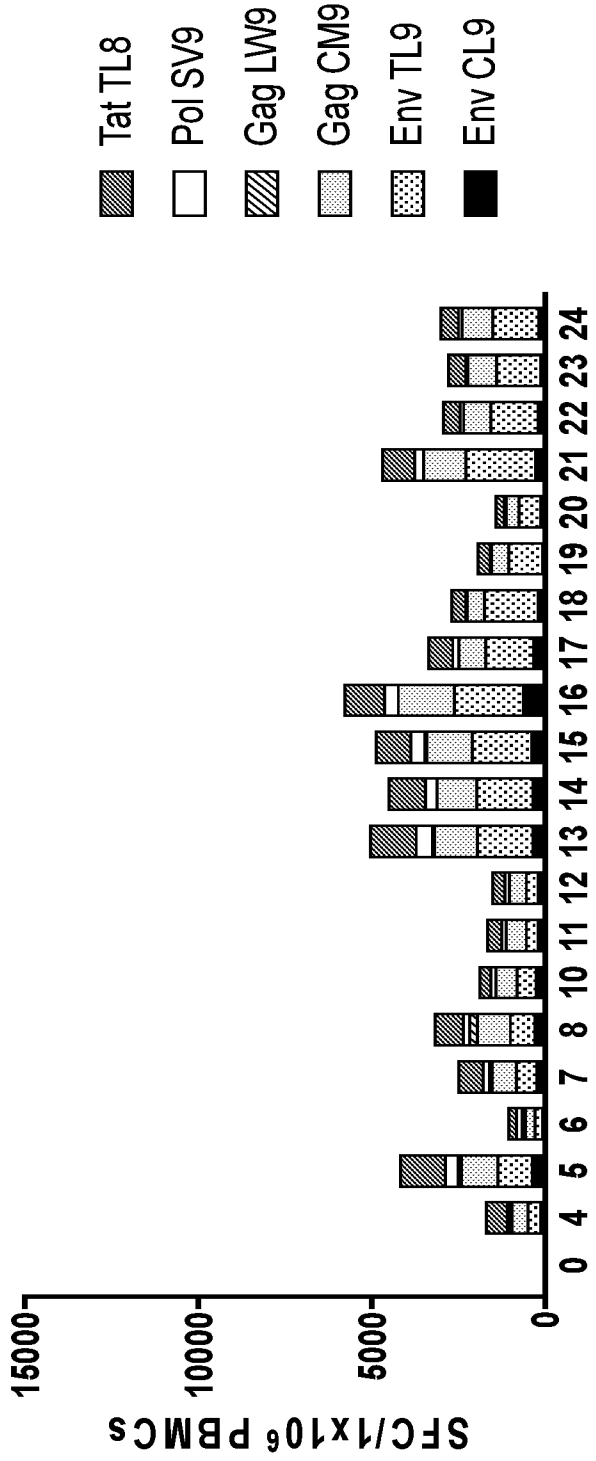


FIG 35

2026201462 26 Feb 2026



FIG 36

2026201462 26 Feb 2026

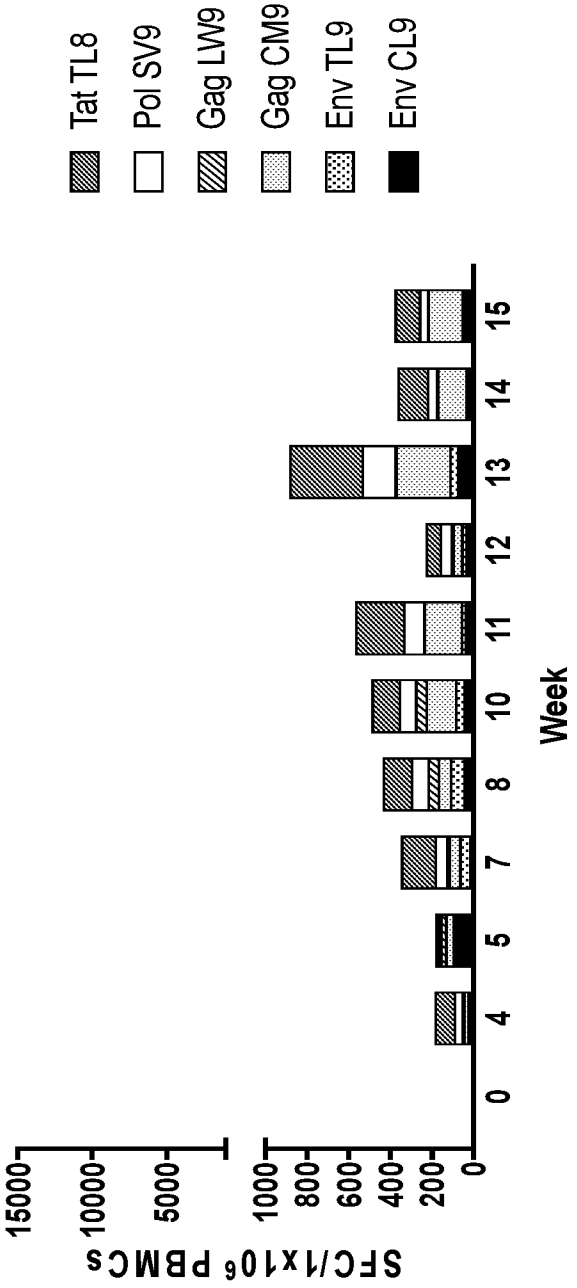


FIG 37

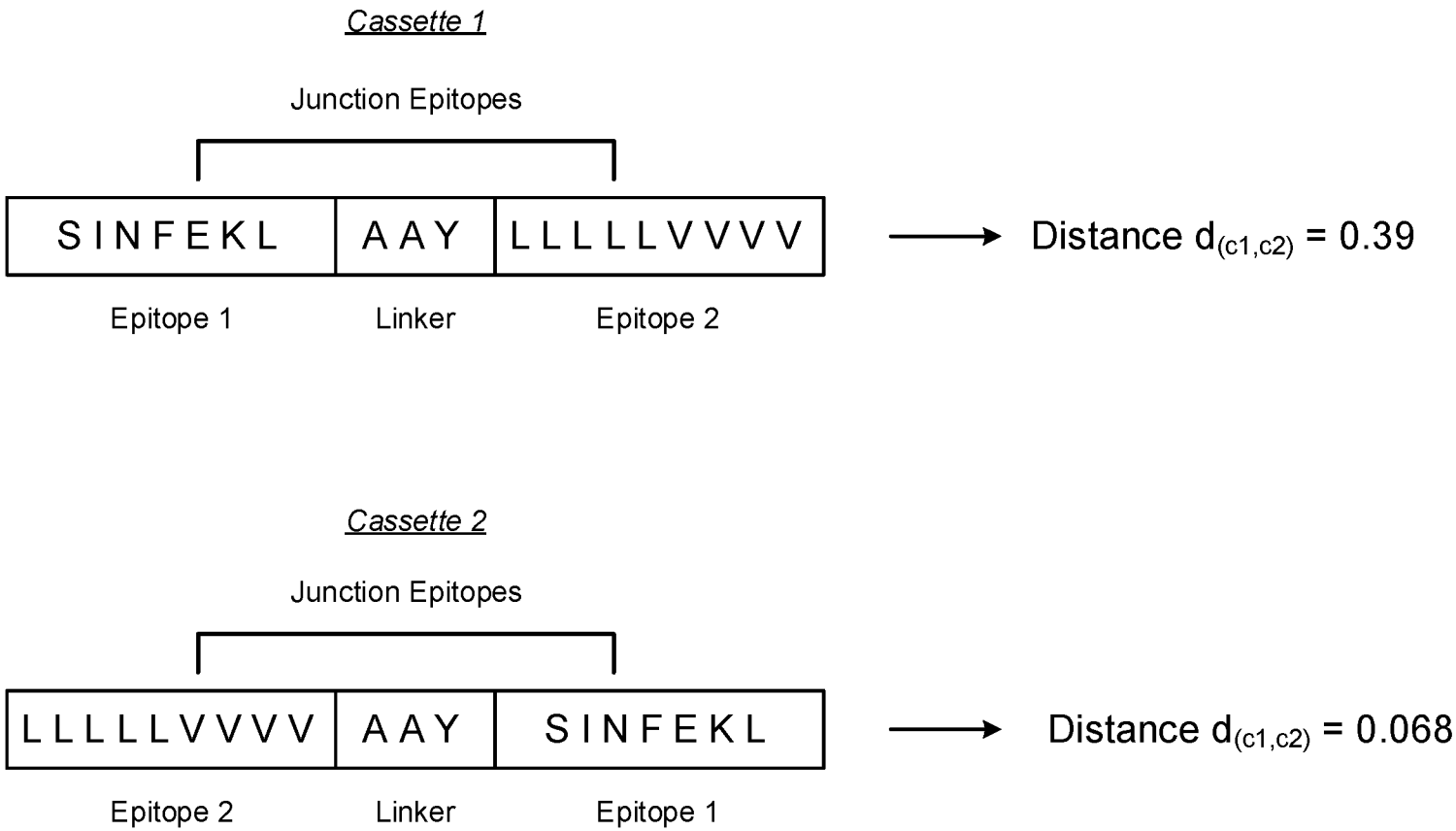

Cassette 1
Junction Epitopes
S I N F E K L
A A Y
L L L L L V V V V
Epitope 1
Linker
Epitope 2
Distance d(c1,c2) = 0.39
Cassette 2
Junction Epitopes
L L L L L V V V V
A A Y
S I N F E K L
Epitope 2
Linker
Epitope 1
Distance d(c1,c2) = 0.068

FIG 38

2026201462 26 Feb 2026

Sequence Listing

1	**Sequence Listing Information**	
1-1	File Name	189162AU01.xml
1-2	DTD Version	V1_3
1-3	Software Name	WIPO Sequence
1-4	Software Version	2.2.0
1-5	Production Date	2023-04-18
1-6	Original free text language code	
1-7	Non English free text language code	
2	**General Information**	
2-1	Current application: IP Office	AU
2-2	Current application: Application number	
2-3	Current application: Filing date	2018-05-08
2-4	Current application: Applicant file reference	189162AU01
2-5	Earliest priority application: IP Office	US
2-6	Earliest priority application: Application number	62/503,283
2-7	Earliest priority application: Filing date	2017-05-08
2-8en	Applicant name	GRITSTONE ONCOLOGY, INC.
2-8	Applicant name: Name Latin	
2-9en	Inventor name	
2-9	Inventor name: Name Latin	
2-10en	Invention title	ALPHAVIRUS NEOANTIGEN VECTORS
2-11	Sequence Total Quantity	193

2026201462 26 Feb 2026

3-1	**Sequences**	
3-1-1	Sequence Number [ID]	1
3-1-2	Molecule Type	DNA
3-1-3	Length	36519
3-1-4	Features	**misc_feature 1..36519**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..36519
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-1-5	Residues	ccatcttcaa taatatacct caaacttttt gtgcgcgtta atatgcaaat gaggcgtttg 60 aatttgggga ggaagggcgg tgattggtcg agggatgagc gaccgttagg ggcggggcga 120 gtgacgtttt gatgacgtgg ttgcgaggag gagccagttt gcaagttctc gtgggaaaag 180 tgacgtcaaa cgaggtgtgg tttgaacacg gaaatactca attttcccgc gctctctgac 240 aggaaatgag gtgtttctgg gcggatgcaa gtgaaaacgg gccattttcg cgcgaaaact 300 gaatgaggaa gtgaaaatct gagtaatttc gcgtttatgg cagggaggag tatttgccga 360 gggccgagta gactttgacc gattacgtgg gggtttcgat taccgtgttt ttcacctaaa 420 tttccgcgta cggtgtcaaa gtccggtgtt tttacgtagg tgtcagctga tcgccagggt 480 atttaaacct gcgctctcca gtcaagaggc cactcttgag tgccagcgag aagagtttc 540 tcctccgcgc cgcgagtcag atctacactt tgaaagatga ggcacctgag agacctgccc 600 gatgagaaaa tcatcatcgc ttccgggaac gagattctgg aactggtggt aaatgccatg 660 atgggcgacg accctccgga gccccccacc ccatttgaga caccttcgct gcacgatttg 720 tatgatctgg aggtggatgt gcccgaggac gatcccaatg aggaggcggt aaatgatttt 780 tttagcgatg ccgcgctgct agctgccgag gaggcttcga gctctagctc agacagcgac 840 tcttcactgc ataccctag acccggcaga ggtgagaaaa agatccccga gcttaaaggg 900 gaagagatgg acttgcgctg ctatgaggaa tgcttgcccc cgagcgatga tgaggacgag 960 caggcgatcc agaacgcagc gagccaggga gtgcaagccg ccagcgagag ctttgcgctg 1020 gactgcccgc ctctgcccgg acacggctgt aagtcttgtg aatttcatcg catgaatact 1080 ggagataaag ctgtgttgtg tgcactttgc tatatgagag cttacaacca ttgtgtttac 1140 agtaagtgtg attaagttga actttagagg gaggcagaga gcagggtgac tgggcgatga 1200 ctggtttatt tatgtatata tgttctttat ataggtcccg tctctgacgc agatgatgag 1260 acccccacta caaagtccac ttcgtcaccc ccagaaattg gcacatctcc acctgagaat 1320 attgttagac cagttcctgt tagagccact gggaggagag cagctgtgga atgtttggat 1380 gacttgctac agggtggggt tgaacctttg gacttgtgta cccggaaacg ccccaggcac 1440 taagtgccac acatgtgtgt ttacttgagg tgatgtcagt atttataggg tgtggagtgc 1500 aataaaaaat gtgttgactt taagtgcgtg gtttatgact caggggtggg gactgtgagt 1560 atataagcag gtgcagacct gtgtggttag ctcagagcgg catggagatt tggacggtct 1620 tggaagactt tcacaagact agacagctgc tagagaacgc ctcgaacgga gtctcttacc 1680 tgtggagatt ctgcttcggt ggcgacctag ctaggctagt ctacagggcc aaacaggatt 1740 atagtgaaca atttgaggtt attttgagag agtgttctgg tctttttgac gctcttaact 1800 tgggccatca gtctcacttt aaccagagga tttcgagagc ccttgatttt actactcctg 1860 gcagaaccac tgcagcagta gccttttttg cttttattct tgacaaatgg agtcaagaaa 1920 cccatttcag cagggattac cagctggatt tcttagcagt agctttgtgg agaacatgga 1980 agtgccagcg cctgaatgca atctccggct acttgccggt acagccgcta gacactctga 2040 ggatcctgaa tctccaggag agtcccaggg cacgccaacg tcgccagcag cagcagcagg 2100 aggaggatca agaagagaac ccgagagccg gcctggaccc tccggcggag gaggaggagt 2160 agctgacctg tttcctgaac tgcgccgggt gctgactagg tcttcgagtg gtcgggagag 2220 ggggattaag cgggagaggc atgatgagac taatcacaga actgaactga ctgtgggtct 2280 gatgagtcgc aagcgcccag aaacagtgtg gtggcatgag gtgcagtcga ctggcacaga 2340 tgaggtgtcg gtgatgcatg agaggttttc tctagaacaa gtcaagactt gttggttaga 2400 gcctgaggat gattgggagg tagccatcag gaattatgcc aagctggctc tgaggccaga 2460 caagaagtac aagattacta agctgataaa tatcagaaat gcctgctaca tctcagggaa 2520 tggggctgaa gtggagatct gtctccagga aagggtggct ttcagatgct gcatgatgaa 2580 tatgtacccg ggagtggtgg gcatggatgg ggttaccttt atgaacatga ggttcagggg 2640 agatgggtat aatggcacgg tctttatggc caataccaag ctgacagtcc atggctgctc 2700 cttctttggg tttaataaca cctgcatcga ggcctggggt caggtcggtg tgaggggctg 2760 cagtttttca gccaactgga tgggggtcgt gggcaggacc aagagtatgc tgtccgtgaa 2820 gaaatgcttg tttgagaggt gccacctggg ggtgatgagc gagggcgaag ccagaatccg 2880 ccactgcgcc tctaccgaga cgggctgctt tgtgctgtgc aagggcaatg ctaagatcaa 2940 gcataatatg atctgtggag cctcggacga gcgcggctac cagatgctga cctgcgccgg 3000 cgggaacagc catatgctgg ccaccgtaca tgtggcttcc catgctcgca agccctggcc 3060 cgagttcgag cacaatgtca tgaccaggtg caatatgcat ctggggtccc gccgaggcat 3120 gttcatgccc taccagtgca acctgaatta tgtgaaggtg ctgctggagc ccgatgccat 3180 gtccagagtg agcctgacgg gggtgtttga catgaatgtg gaggtgtgga agattctgag 3240 atatgatgaa tccaagacca ggtgccgagc ctgcgagtgc ggagggaagc atgccaggtt 3300 ccagcccgtg tgtgtggatg tgacggagga cctgcgaccc gatcatttgg tgttgccctg 3360 caccgggacg gagttcggtt ccagcgggga agaatctgac tagagtgagt agtgttctgg 3420 ggcgggggag gacctgcatg agggccagaa taactgaaat ctgtgctttt ctgtgtgttg 3480 cagcagcatg agcggaagcg gctcctttga gggaggggta ttcagccctt atctgacggg 3540 gcgtctcccc tcctgggcgg gagtgcgtca gaatgtgatg ggatccacgg tggacggccg 3600 gcccgtgcag cccgcgaact cttcaaccct gacctatgca accctgagct cttcgtcgtt 3660 ggacgcagct gccgccgcag ctgctgcatc tgccgccagc gccgtgcgcg gaatggccat 3720 gggcgccggc tactacggca ctctggtggc caactcgagt tccaccaata atcccgccag 3780 cctgaacgag gagaagctgt tgctgctgat ggcccagctc gaggccttga cccagcgcct 3840 gggcgagctg acccagcagg tggctcagct gcaggagcag acgcgggccg cggttgccac 3900

20262014626 26 Feb 2026

ggtgaaatcc aaataaaaaa tgaatcaata aataaacgga gacggttgtt gattttaaca 3960
cagagtctga atctttattt gatttttcgc gcgcggtagg ccctggacca ccggtctcga 4020
tcattgagca cccggtggat cttttccagg acccggtaga ggtgggcttg gatgttgagg 4080
tacatgggca tgagcccgtc ccgggggtgg aggtagctcc attgcagggc ctcgtgctcg 4140
ggggtggtgt tgtaaatcac ccagtcatag caggggcgca gggcatggtg ttgcacaata 4200
tctttgagga ggagactgat ggccacgggc agccctttgg tgtaggtgtt tacaaatctg 4260
ttgagctggg agggatgcat gcggggggag atgaggtgca tcttggcctg gatcttgaga 4320
ttggcgatgt taccgcccag atcccgcctg gggttcatgt tgtgcaggac caccagcacg 4380
gtgtatccgg tgcacttggg gaatttatca tgcaacttgg aagggaaggc gtgaaagaat 4440
ttggcgacgc ctttgtgccc gcccaggttt tccatgcact catccatgat gatggcgatg 4500
ggcccgtggg cggcggcctg ggcaaagacg tttcgggggt cggacacatc atagttgtgg 4560
tcctgggtga ggtcatcata ggccatttta atgaatttgg ggcggagggt gccggactgg 4620
gggacaaagg taccctcgat cccgggggcg tagttcccct cacagatctg catctcccag 4680
gctttgagct cggaggggag gatcatgtcc acctgcgggg cgataaagaa cacggtttcc 4740
ggggcggggg agatgagctg ggccgaaagc aagttccgga gcagctggga cttgccgcag 4800
ccggtggggc cgtagatgac cccgatgacc ggctgcaggt ggtagttgag ggagagacag 4860
ctgccgtcct cccggaggag gggggccacc tcgttcatca tctcgcgcac gtgcatgttc 4920
tcgcgcacca gttccgccag gaggcgctct ccccccaggg ataggagctc ctggagcgag 4980
gcgaagtttt tcagcggctt gagtccgtcg gccatgggca ttttggagag ggtttgttgc 5040
aagagttcca ggcggtccca gagctcggtg atgtgctcta cggcatctcg atccagcaga 5100
cctcctcgtt tcgcgggttg ggacggctgc gggagtaggg caccagacga tgggcgtcca 5160
gcgcagccag ggtccggtcc ttccagggtc gcagcgtccg cgtcagggtg gtctccgtca 5220
cggtgaaggg gtgcgcgccg ggctgggcgc ttgcgagggt gcgcttcagg ctcatccggc 5280
tggtcgaaaa ccgctcccga tcggcgccct gcgcgtcggc caggtagcaa ttgaccatga 5340
gttcgtagtt gagcgcctcg gccgcgtggc ctttggcgcg gagcttacct ttggaagtct 5400
gcccgcaggc gggacagagg agggacttga gggcgtagag cttgggggcg aggaagacgg 5460
actcgggggc gtaggcgtcc gcgccgcagt gggcgcagac ggtctcgcac tccacgagcc 5520
aggtgaggtc gggctggtcg gggtcaaaaa ccagtttccc gccgttcttt ttgatgcgtt 5580
tcttaccttt ggtctccatg agctcgtgtc cccgctgggt gacaaagagg ctgtccgtgt 5640
ccccgtagac cgactttatg ggccggtcct cgagcggtgt gccgcggtcc tcctcgtaga 5700
ggaaccccgc ccactccgag acgaaagccc gggtccaggc cagcacgaag gaggccacgt 5760
gggacgggta gcggtcgttg tccaccagcg ggtccacctt ttccagggta tgcaaacaca 5820
tgtccccctc gtccacatcc aggaaggtga ttggcttgta agtgtaggcc acgtgaccgg 5880
gggtcccggc cgggggggta taaaagggtg cgggtccctg ctcgtcctca ctgtcttccg 5940
gatcgctgtc caggagcgcc agctgttggg gtaggtattc cctctcgaag gcgggcatga 6000
cctcggcact caggttgtca gtttctagaa acgaggagga tttgatattg acggtgccgg 6060
cggagatgcc tttcaagagc ccctcgtcca tctggtcaga aaagacgatc tttttgttgt 6120
cgagcttggt ggcgaaggag ccgtagaggg cgttggagag gagcttggcg atggagcgca 6180
tggtctggtt tttttccttg tcggcgcgct ccttggcggc gatgttgagc tgcacgtact 6240
cgcgcgccac gcacttccat tcggggaaga cggtggtcag ctcgtcgggc acgattctga 6300
cctgccagcc ccgattatgc agggtgatga ggtccacact ggtggccacc tcgccgcgca 6360
ggggctcatt agtccagcag aggcgtccgc ccttgcgcga gcagaagggg ggcagggggt 6420
ccagcatgac ctcgtcgggg gggtcggcat cgatggtgaa gatgccgggc aggaggtcgg 6480
ggtcaaagta gctgatggaa gtggccagat cgtccagggc agcttgccat tcgcgcacgg 6540
ccagcgcgcg ctcgtaggga ctgaggggcg tgccccaggg catgggatgg gtaagcgcgg 6600
aggcgtacat gccgcagatg tcgtagacgt agaggggctc ctcgaggatg ccgatgtagg 6660
tggggtagca gcgccccccg cggatgctgg cgcgcacgta gtcatacagc tcgtgcgagg 6720
gggcgaggag ccccgggccc aggttggtgc gactgggctt ttcggcgcgg tagacgatct 6780
ggcggaaaat ggcatgcgag ttggaggaga tggtgggcct ttggaagatg ttgaagtggg 6840
cgtggggcag tccgaccgag tcgcggatga agtgggcgta ggagtcttgc agcttggcga 6900
cgagctcggc ggtgactagg acgtccagag cgcagtagtc gagggtctcc tggatgatgt 6960
catacttgag ctgtcccttt tgtttccaca gctcgcggtt gagaaggaac tcttcgcggt 7020
ccttccagta ctcttcgagg gggaacccgt cctgatctgc acggtaagag cctagcatgt 7080
agaactggtt gacggccttg taggcgcagc agcccttctc cacggggagg gcgtaggcct 7140
gggcggcctt gcgcagggag gtgtgcgtga gggcgaaagt gtccctgacc atgaccttga 7200
ggaactggtg cttgaagtcg atatcgtcgc agccccccctg ctcccagagc tggaagtccg 7260
tgcgcttctt gtaggcgggg ttgggcaaag cgaaagtaac atcgttgaag aggatcttgc 7320
ccgcgcgggg cataaagttg cgagtgatgc ggaaaggttg gggcacctcg gcccggttgt 7380
tgatgacctg ggcggcgagc acgatctcgt cgaagccgtt gatgttgtgg cccacgatgt 7440
agagttccac gaatcgcgga cggcccttga cgtggggcag tttcttgagc tcctcgtagg 7500
tgagctcgtc ggggtcgctg agcccgtgct gctcgagcgc ccagtcggcg agatgggggt 7560
tggcgcggag gaaggaagtc cagagatcca cggccagggc ggtttgcaga cggtcccggt 7620
actgacggaa ctgctgcccg acggccattt tttcgggggt gacgcagtag aaggtgcggg 7680
ggtccccgtg ccagcgatcc catttgagct ggagggcgag atcgagggcg agctcgacga 7740
gccggtcgtc cccggagagt ttcatgacca gcatgaaggg gacgagctgc ttgccgaagg 7800
accccatcca ggtgtaggtt tccacatcgt aggtgaggaa gagcctttcg gtgcgaggat 7860
gcgagccgat ggggaagaac tggatctcct gccaccaatt ggaggaatgg ctgttgatgt 7920
gatggaagta gaaatgccga cggcgcgccg aacactcgtg cttgtgttta tacaagcggc 7980
cacagtgctc gcaacgctgc acgggatgca cgtgctgcac gagctgtacc tgagttcctt 8040
tgacgaggaa tttcagtggg aagtggagtc gtggcgcctg catctcgtgc tgtactacgt 8100
cgtggtggtc ggcctggccc tcttctgcct cgatggtggt catgctgacg agcccgcgcg 8160
ggaggcaggt ccagacctcg gcgcgagcgg gtcggagagc gaggacgagg gcgcgcaggc 8220
cggagctgtc cagggtcctg agacgctgcg gagtcaggtc agtgggcagc ggcggcgcgc 8280
ggttgacttg caggagtttt tccagggcgc gcgggaggtc cagatggtac ttgatctcca 8340
ccgcgccatt ggtggcgacg tcgatggctt gcagggtccc gtgcccctgg ggtgtgacca 8400
ccgtcccccg tttcttcttg ggcggctggg gcgacggggg cggtgcctct tccatggtta 8460

20262014626 26 Feb 2026

gaagcggcgg cgaggacgcg cgccgggcgg caggggcggc tcggggcccg gaggcagggg 8520
cggcaggggc acgtcggcgc cgcgcgcggg taggttctgg tactgcgccc ggagaagact 8580
ggcgtgagcg acgacgcgac ggttgacgtc ctggatctga cgcctctggg tgaaggccac 8640
gggacccgtg agtttgaacc tgaaagagag ttcgacagaa tcaatctcgg tatcgttgac 8700
ggcggcctgc cgcaggatct cttgcacgtc gcccgagttg tcctggtagg cgatctcggt 8760
catgaactgc tcgatctcct cctcttgaag gtctccgcgg ccggcgcgct ccacggtggc 8820
cgcgaggtcg ttggagatgc ggcccatgag ctgcgagaag gcgttcatgc ccgcctcgtt 8880
ccagacgcgg ctgtagacca cgacgccctc gggatcgcgg gcgcgcatga ccacctgggc 8940
gaggttgagc tccacgtggc gcgtgaagac cgcgtagttg cagaggcgct ggtagaggta 9000
gttgagcgtg gtggcgatgt gctcggtgac gaagaaatac atgatccagc ggcggagcgg 9060
catctcgctg acgtcgccca gcgcctccaa acgttccatg gcctcgtaaa agtccacggc 9120
gaagttgaaa aactgggagt tgcgcgccga gacggtcaac tcctcctcca gaagacggat 9180
gagctcggcg atggtggcgc gcacctcgcg ctcgaaggcc cccgggagtt cctccacttc 9240
ctcttcttcc tcctccacta acatctcttc tacttcctcc tcaggcggca gtggtggcgg 9300
gggaggggcc ctgcgtcgcc ggcggcgcac gggcagacgg tcgatgaagc gctcgatggt 9360
ctcgccgcgc cggcgtcgca tggtctcggt gacggcgcgc ccgtcctcgc ggggccgcag 9420
cgtgaagacg ccgccgcgca tctccaggtg gccgggggcg tccccgttgg gcagggagag 9480
ggcgctgacg atgcatctta tcaattgccc cgtagggact ccgcgcaagg acctgagcgt 9540
ctcgagatcc acgggatctg aaaaccgctg aacgaaggct tcgagccagt cgcagtcgca 9600
aggtaggctg agcacggttt cttctggcgg gtcatgttgg ttgggagcgg ggcgggcgat 9660
gctgctggtg atgaagttga aataggcggt tctgagacgg cggatggtgg cgaggagcac 9720
caggtctttg ggcccggctt gctggatgcg cagacggtcg gccatgcccc aggcgtggtc 9780
ctgacacctg gccaggtcct tgtagtagtc ctgcatgagc cgctccacgg gcacctcctc 9840
ctcgcccgcg cggccgtgca tgcgcgtgag cccgaagccg cgctggggct ggacgagcgc 9900
caggtcggcg acgacgcgct cggcgaggat ggcttgctgg atctgggtga gggtggtctg 9960
gaagtcatca aagtcgacga agcggtggta ggctccggtg ttgatggtgt aggagcagtt 10020
ggccatgacg gaccagttga cggtctggtg gcccggacgc acgagctcgt ggtacttgag 10080
gcgcgagtag gcgcgcgtgt cgaagatgta gtcgttgcag gtgcgcacca ggtactggta 10140
gccgatgagg aagtgcggcg gcggctggcg gtagagcggc catcgctcgg tggcgggggc 10200
gccgggcgcg aggtcctcga gcatggtgcg gtggtagccg tagatgtacc tggacatcca 10260
ggtgatgccg gcggcggtgg tggaggcgcg cgggaactcg cggacgcggt tccagatgtt 10320
gcgcagcggc aggaagtagt tcatggtggg cacggtctgg cccgtgaggc gcgcgcagtc 10380
gtggatgctc tatacgggca aaaacgaaag cggtcagcgg ctcgactccg tggcctggag 10440
gctaagcgaa cgggttgggc tgcgcgtgta ccccggttcg aatctcgaat caggctggag 10500
ccgcagctaa cgtggtattg gcactcccgt ctcgacccaa gcctgcacca accctccagg 10560
atacggaggc gggtcgtttt gcaacttttt tttggaggcc ggatgagact agtaagcgcg 10620
gaaagcggcc gaccgcgatg gctcgctgcc gtagtctgga gaagaatcgc cagggttgcg 10680
ttgcggtgtg ccccggttcg aggccggccg gattccgcgg ctaacgaggg cgtggctgcc 10740
ccgtcgtttc caagacccca tagccagccg acttctccag ttacggagcg agcccctctt 10800
ttgttttgtt tgtttttgcc agatgcatcc cgtactgcgg cagatgcgcc cccaccaccc 10860
tccaccgcaa caacagcccc ctccacagcc ggcgcttctg cccccgcccc agcagcaact 10920
tccagccacg accgccgcgg ccgccgtgag cggggctgga cagagttatg atcaccagct 10980
ggccttggaa gagggcgagg ggctggcgcg cctgggggcg tcgtcgccgg agcggcaccc 11040
gcgcgtgcag atgaaaaggg acgctcgcga ggcctacgtg cccaagcaga acctgttcag 11100
agacaggagc ggcgaggagc ccgaggagat gcgcgcggcc cggttccacg cggggcggga 11160
gctgcggcgc ggcctggacc gaaagagggt gctgagggac gaggatttcg aggcggacga 11220
gctgacgggg atcagccccg cgcgcgcgca cgtggccgcg gccaacctgg tcacggcgta 11280
cgagcagacc gtgaaggagg agagcaactt ccaaaaatcc ttcaacaacc acgtgcgcac 11340
cctgatcgcg cgcgaggagg tgaccctggg cctgatgcac ctgtgggacc tgctggaggc 11400
catcgtgcag aaccccacca gcaagccgct gacggcgcag ctgttcctgg tggtgcagca 11460
tagtcgggac aacgaagcgt tcagggaggc gctgctgaat atcaccgagc ccgagggccg 11520
ctggctcctg gacctggtga acattctgca gagcatcgtg gtgcaggagc gcgggctgcc 11580
gctgtccgag aagctggcgg ccatcaactt ctcggtgctg agtttgggca agtactacgc 11640
taggaagatc tacaagaccc cgtacgtgcc catagacaag gaggtgaaga tcgacgggtt 11700
ttacatgcgc atgaccctga aagtgctgac cctgagcgac gatctggggg tgtaccgcaa 11760
cgacaggatg caccgtgcgg tgagcgccag caggcggcgc gagctgagcg accaggagct 11820
gatgcatagt ctgcagcggg ccctgaccgg ggccgggacc gaggggggaga gctactttga 11880
catgggcgcg gacctgcact ggcagcccag ccgccgggcc ttggaggcgg cggcaggacc 11940
ctacgtagaa gaggtggacg atgaggtgga cgaggagggc gagtacctgg aagactgatg 12000
gcgcgaccgt atttttgcta gatgcaacaa caacagccac ctcctgatcc cgcgatgcgg 12060
gcggcgctgc agagccagcc gtccggcatt aactcctcgg acgattggac ccaggccatg 12120
caacgcatca tggcgctgac gacccgcaac cccgaagcct ttagacagca gccccaggcc 12180
aaccggctct cggccatcct ggaggccgtg gtgccctcgc gctccaaccc cacgcacgag 12240
aaggtcctgg ccatcgtgaa cgcgctggtg gagaacaagg ccatccgcgg cgacgaggcc 12300
ggcctggtgt acaacgcgct gctggagcgc gtggcccgct acaacagcac caacgtgcag 12360
accaacctgg accgcatggt gaccgacgtg cgcgaggccg tggcccagcg cgagcggttc 12420
caccgcgagt ccaacctggg atccatggtg gcgctgaacg ccttcctcag cacccagccc 12480
gccaacgtgc cccggggcca ggaggactac accaacttca tcagcgccct gcgcctgatg 12540
gtgaccgagg tgccccagag cgaggtgtac cagtccgggc cggactactt cttccagacc 12600
agtcgccagg gcttgcagac cgtgaacctg agccaggctt tcaagaactt gcagggcctg 12660
tggggcgtgc aggccccggt cggggaccgc gcgacggtgt cgagcctgct gacgccgaac 12720
tcgcgcctgc tgctgctgct ggtggccccc ttcacggaca gcggcagcat caaccgcaac 12780
tcgtacctgg gctacctgat taacctgtac cgcgaggcca tcggccaggc gcacgtggac 12840
gagcagacct accaggagat cacccacgtg agccgcgccc tgggccagga cgacccgggc 12900
aacctggaag ccaccctgaa ctttttgctg accaaccggt cgcagaagat cccgccccag 12960
tacgcgctca gcaccgagga ggagcgcatc ctgcgttacg tgcagcagag cgtgggcctg 13020

20262014626 26 Feb 2026

ttcctgatgc aggaggggc caccccagc gccgcgctcg acatgaccgc gcgcaacatg 13080
gagcccagca tgtacgccag caaccgcccg ttcatcaata aactgatgga ctacttgcat 13140
cgggcggccg ccatgaactc tgactatttc accaacgcca tcctgaatcc ccactggctc 13200
ccgccgccgg ggttctacac gggcgagtac gacatgcccg accccaatga cgggttcctg 13260
tgggacgatg tggacagcag cgtgttctcc ccccgaccgg gtgctaacga gcgccccttg 13320
tggaagaagg aaggcagcga ccgacgcccg tcctcggcgc tgtccggccg cgagggtgct 13380
gccgcggcgg tgcccgaggc cgccagtcct ttcccgagct tgcccttctc gctgaacagt 13440
atccgcagca gcgagctggg caggatcacg cgcccgcgct tgctgggcga agaggagtac 13500
ttgaatgact cgctgttgag acccgagcgg gagaagaact tccccaataa cgggatagaa 13560
agcctggtgg acaagatgag ccgctggaag acgtatgcgc aggagcacag ggacgatccc 13620
cgggcgtcgc agggggccac gagccggggc agcgccgccc gtaaacgccg gtggcacgac 13680
aggcagcggg gacagatgtg ggacgatgag gactccgccg acgacagcag cgtgttggac 13740
ttgggtggga gtggtaaccc gttcgctcac ctgcgccccc gtatcgggcg catgatgtaa 13800
gagaaaccga aaataaatga tactcaccaa ggccatggcg accagcgtgc gttcgtttct 13860
tctctgttgt tgttgtatct agtatgatga ggcgtgcgta cccggagggt cctcctccct 13920
cgtacgagag cgtgatgcag caggcgatgg cggcggcggc gatgcagccc ccgctggagg 13980
ctccttacgt gcccccgcgg tacctggcgc ctacggaggg gcggaacagc attcgttact 14040
cggagctggc acccttgtac gataccaccc ggttgtacct ggtggacaac aagtcggcgg 14100
acatcgcctc gctgaactac cagaacgacc acagcaactt cctgaccacc gtggtgcaga 14160
acaatgactt cacccccacg gaggccagca cccagaccat caactttgac gagcgctcgc 14220
ggtggggcgg ccagctgaaa accatcatgc acaccaacat gcccaacgtg aacgagttca 14280
tgtacagcaa caagttcaag gcgcgggtga tggtctcccg caagacccca aatggggtga 14340
cagtgacaga ggattatgat ggtagtcagg atgagctgaa gtatgaatgg gtggaatttg 14400
agctgcccga aggcaacttc tcggtgacca tgaccatcga cctgatgaac aacgccatca 14460
tcgacaatta cttggcggtg gggcggcaga acggggtgct ggagagcgac atcggcgtga 14520
agttcgacac taggaacttc aggctgggct gggaccccgt gaccgagctg gtcatgcccg 14580
gggtgtacac caacgaggct ttccatcccg atattgtctt gctgcccggc tgcggggtgg 14640
acttcaccga gagccgcctc agcaacctgc tgggcattcg caagaggcag cccttccagg 14700
aaggcttcca gatcatgtac gaggatctgg agggggcaa catccccgcg ctcctggatg 14760
tcgacgccta tgagaaaagc aaggaggatg cagcagctga agcaactgca gccgtagcta 14820
ccgcctctac cgaggtcagg ggcgataatt ttgcaagcgc cgcagcagtg gcagcggccg 14880
aggcggctga aaccgaaagt aagatagtca ttcagccggt ggagaaggat agcaagaaca 14940
ggagctacaa cgtactaccg gacaagataa acaccgccta ccgcagctgg tacctagcct 15000
acaactatgg cgaccccgag aagggcgtgc gctcctggac gctgctcacc acctcggacg 15060
tcacctgcgg cgtggagcaa gtctactggt cgctgcccga catgatgcaa gacccggtca 15120
ccttccgctc cacgcgtcaa gttagcaact acccggtggt gggcgccgag ctcctgcccg 15180
tctactccaa gagcttcttc aacgagcagg ccgtctactc gcagcagctg cgcgccttca 15240
cctcgcttac gcacgtcttc aaccgcttcc ccgagaacca gatcctcgtc cgcccgcccg 15300
cgcccaccat taccaccgtc agtgaaaacg ttcctgctct cacagatcac gggaccctgc 15360
cgctgcgcag cagtatccgg ggagtccagc gcgtgaccgt tactgacgcc agacgccgca 15420
cctgccccta cgtctacaag gccctgggca tagtcgcgcc gcgcgtcctc tcgagccgca 15480
ccttctaaat gtccattctc atctcgccca gtaataacac cggttggggc ctgcgcgcgc 15540
ccagcaagat gtacggaggc gctcgccaac gctccacgca acaccccgtg cgcgtgcgcg 15600
ggcacttccg cgctccctgg ggcgccctca agggccgcgt gcggtcgcgc accaccgtcg 15660
acgacgtgat cgaccaggtg gtggccgacg cgcgcaacta cacccccgcc gccgcgcccg 15720
tctccaccgt ggacgccgtc atcgacagcg tggtggccga cgcgcgccgg tacgcccgcg 15780
ccaagagccg gcggcggcgc atcgcccggc ggcaccggag cacccccgcc atgcgcgcgg 15840
cgcgagcctt gctgcgcagg gccaggcgca cgggacgcag ggccatgctc agggcggcca 15900
gacgcgcggc ttcaggcgcc agcgccggca ggacccggag acgcgcggcc acggcggcgg 15960
cagcggccat cgccagcatg tcccgcccgc ggcgagggaa cgtgtactgg gtgcgcgacg 16020
ccgccaccgg tgtgcgcgtg cccgtgcgca cccgcccccc tcgcacttga agatgttcac 16080
ttcgcgatgt tgatgtgtcc cagcggcgag gaggatgtcc aagcgcaaat tcaaggaaga 16140
gatgctccag gtcatcgcgc ctgagatcta cggccctgcg gtggtgaagg aggaaagaaa 16200
gccccgcaaa atcaagcggg tcaaaaagga caaaaaggaa gaagaaagtg atgtggacgg 16260
attggtggag tttgtgcgcg agttcgcccc ccggcggcgc gtgcagtggc gcgggcggaa 16320
ggtgcaaccg gtgctgagac ccggcaccac cgtggtcttc acgcccggcg agcgctccgg 16380
caccgcttcc aagcgctcct acgacgaggt gtacggggat gatgatattc tggagcaggc 16440
ggccgagcgc ctgggcgagt ttgcttacgg caagcgcagc cgttccgcac cgaaggaaga 16500
ggcggtgtcc atcccgctgg accacggcaa ccccacgccg agcctcaagc ccgtgacctt 16560
gcagcaggtg ctgccgaccg cggcgccgcg ccgggggttc aagcgcgagg gcgaggatct 16620
gtaccccacc atgcagctga tggtgcccaa gcgccagaag ctggaagacg tgctggagac 16680
catgaaggtg gacccggacg tgcagcccga ggtcaaggtg cggcccatca agcaggtggc 16740
cccgggcctg ggcgtgcaga ccgtggacat caagattccc acggagccca tggaaacgca 16800
gaccgagccc atgatcaagc ccagcaccag caccatggag gtgcagacgg atccctggat 16860
gccatcggct cctagtcgaa gaccccggcg caagtacggc gcggccagcc tgctgatgcc 16920
caactacgcg ctgcatcctt ccatcatccc cacgccgggc taccgcggca cgcgcttcta 16980
ccgcggtcat accagcagcc gccgccgcaa gaccaccact cgccgccgcc gtcgccgcac 17040
cgccgctgca accacccctg ccgccctggt gcggagagtg taccgccgcg gccgcgcacc 17100
tctgaccctg ccgcgcgcgc gctaccaccc gagcatcgcc atttaaactt tcgcctgctt 17160
tgcagatcaa tggccctcac atgccgcctt cgcgttccca ttacgggcta ccgaggaaga 17220
aaaccgcgcc gtagaaggct ggcggggaac gggatgcgtc gccaccacca ccggcggcgg 17280
cgcgccatca gcaagcggtt gggggggaggc ttcctgcccg cgctgatccc catcatcgcc 17340
gcggcgatcg gggcgatccc cggcattgct tccgtggcgg tgcaggcctc tcagcgccac 17400
tgagacacac ttggaaacat cttgtaataa accaatggac tctgacgctc ctggtcctgt 17460
gatgtgtttt cgtagacaga tggaagacat caatttttcg tccctggctc cgcgacacgg 17520
cacgcggccg ttcatgggca cctggagcga catcggcacc agccaactga acgggggcgc 17580

20262014622 26 Feb 2026

cttcaattgg agcagtctct ggagcgggct taagaatttc gggtccacgc ttaaaaccta 17640
tggcagcaag gcgtggaaca gcaccacagg gcaggcgctg agggataagc tgaaagagca 17700
gaacttccag cagaaggtgg tcgatgggct cgcctcgggc atcaacgggg tggtggacct 17760
ggccaaccag gccgtgcagc ggcagatcaa cagccgcctg gacccggtgc cgcccgccgg 17820
ctccgtggag atgccgcagg tggaggagga gctgcctccc ctggacaagc ggggcgagaa 17880
gcgaccccgc cccgatgcgg aggagacgct gctgacgcac acggacgagc cgccccccgta 17940
cgaggaggcg gtgaaactgg gtctgcccac cacgcggccc atcgcgcccc tggccaccgg 18000
ggtgctgaaa cccgaaaagc ccgcgaccct ggacttgcct cctccccagc cttcccgccc 18060
ctctacagtg gctaagcccc tgccgccggt ggccgtggcc cgcgcgcgac ccgggggcac 18120
cgcccgccct catgcgaact ggcagagcac tctgaacagc atcgtgggtc tgggagtgca 18180
gagtgtgaag cgccgccgct gctattaaac ctaccgtagc gcttaacttg cttgtctgtg 18240
tgtgtatgta ttatgtcgcc gccgccgctg tccaccagaa ggaggagtga agaggcgcgt 18300
cgccgagttg caagatggcc accccatcga tgctgcccca gtgggcgtac atgcacatcg 18360
ccggacagga cgcttcggag tacctgagtc cgggtctggt gcagtttgcc cgcgccacag 18420
acacctactt cagtctgggg aacaagttta ggaaccccac ggtggcgccc acgcacgatg 18480
tgaccaccga ccgcagccag cggctgacgc tgcgcttcgt gcccgtggac cgcgaggaca 18540
acacctactc gtacaaagtg cgctacacgc tggccgtggg cgacaaccgc gtgctggaca 18600
tggccagcac ctactttgac atccgcggcg tgctggatcg gggccctagc ttcaaaccct 18660
actccggcac cgcctacaac agtctggccc ccaagggagc acccaacact tgtcagtgga 18720
catataaagc cgatggtgaa actgccacag aaaaaaccta tacatatgga aatgcacccg 18780
tgcagggcat taacatcaca aaagatggta ttcaacttgg aactgacacc gatgatcagc 18840
caatctacgc agataaaacc tatcagcctg aacctcaagt gggtgatgct gaatggcatg 18900
acatcactgg tactgatgaa aagtatggag gcagagctct taagcctgat accaaaatga 18960
agccttgtta tggttctttt gccaagccta ctaataaaga aggaggtcag gcaaatgtga 19020
aaacaggaac aggcactact aaagaatatg acatagacat ggctttcttt gacaacagaa 19080
gtgcggctgc tgctggccta gctccagaaa ttgttttgta tactgaaaat gtggatttgg 19140
aaactccaga tacccatatt gtatacaaag caggcacaga tgacagcagc tcttctatta 19200
atttgggtca gcaagccatg cccaacagac ctaactacat tggtttcaga gacaacttta 19260
tcgggctcat gtactacaac agcactggca atatgggggt gctggccggt caggcttctc 19320
agctgaatgc tgtggttgac ttgcaagaca gaaacaccga gctgtcctac cagctcttgc 19380
ttgactctct gggtgacaga acccggtatt tcagtatgtg gaatcaggcg gtggacagct 19440
atgatcctga tgtgcgcatt attgaaaatc atggtgtgga ggatgaactt cccaactatt 19500
gtttccctct ggatgctgtt ggcagaacag atacttatca gggaattaag gctaatggaa 19560
ctgatcaaac cacatggacc aaagatgaca gtgtcaatga tgctaatgag ataggcaagg 19620
gtaatccatt cgccatggaa atcaacatcc aagccaacct gtggaggaac ttcctctacg 19680
ccaacgtggc cctgtacctg cccgactctt acaagtacac gccggccaat gttaccctgc 19740
ccaccaacac caacacctac gattacatga acggccgggt ggtggcgccc tcgctggtgg 19800
actcctacat caacatcggg gcgcgctggt cgctggatcc catggacaac gtgaacccct 19860
tcaaccacca ccgcaatgcg gggctgcgct accgctccat gctcctgggc aacgggcgct 19920
acgtgccctt ccacatccag gtgccccaga aatttttcgc catcaagagc ctcctgctcc 19980
tgcccgggtc ctacacctac gagtggaact tccgcaagga cgtcaacatg atcctgcaga 20040
gctccctcgg caacgacctg cgcacggacg gggcctccat ctccttcacc agcatcaacc 20100
tctacgccac cttcttcccc atggcgcaca acacggcctc cacgctcgag gccatgctgc 20160
gcaacgacac caacgaccag tccttcaacg actacctctc ggcggccaac atgctctacc 20220
ccatcccggc caacgccacc aacgtgccca tctccatccc ctcgcgcaac tgggccgcct 20280
tccgcggctg gtccttcacg cgtctcaaga ccaaggagac gccctcgctg ggctccgggt 20340
tcgacccctа cttcgtctac tcgggctcca tcccctacct cgacggcacc ttctacctca 20400
accacacctt caagaaggtc tccatcacct tcgactcctc cgtcagctgg cccggcaacg 20460
accggctcct gacgcccaac gagttcgaaa tcaagcgcac cgtcgacggc gagggctaca 20520
acgtggccca gtgcaacatg accaaggact ggttcctggt ccagatgctg gcccactaca 20580
acatcggcta ccagggcttc tacgtgcccg agggctacaa ggaccgcatg tactccttct 20640
tccgcaactt ccagcccatg agccgccagg tggtggacga ggtcaactac aaggactacc 20700
aggccgtcac cctggcctac cagcacaaca actcgggctt cgtcggctac ctcgcgccca 20760
ccatgcgcca gggccagccc taccccgcca actaccccta cccgctcatc ggcaagagcg 20820
ccgtcaccag cgtcacccag aaaaagttcc tctgcgacag ggtcatgtgg cgcatcccct 20880
tctccagcaa cttcatgtcc atgggcgcgc tcaccgacct cggccagaac atgctctatg 20940
ccaactccgc ccacgcgcta gacatgaatt tcgaagtcga ccccatggat gagtccaccc 21000
ttctctatgt tgtcttcgaa gtcttcgacg tcgtccgagt gcaccagccc caccgcggcg 21060
tcatcgaggc cgtctacctg cgcaccccct tctcggccgg taacgccacc acctaagctc 21120
ttgcttcttg caagccatgg ccgcgggctc cggcgagcag gagctcaggg ccatcatccg 21180
cgacctgggc tgcgggccct acttcctggg caccttcgat aagcgcttcc cgggattcat 21240
ggccccgcac aagctggcct gcgccatcgt caacacggcc ggccgcgaga ccgggggcga 21300
gcactggctg gccttcgcct ggaacccgcg ctcgaacacc tgctacctct tcgacccctt 21360
cgggttctcg gacgagcgcc tcaagcagat ctaccagttc gagtacgagg gcctgctgcg 21420
ccgcagcgcc ctggccaccg aggaccgctg cgtcaccctg gaaaagtcca cccagaccgt 21480
gcagggtccg cgctcggccg cctgcgggct cttctgctgc atgttcctgc acgccttcgt 21540
gcactggccc gaccgcccca tggacaagaa ccccaccatg aacttgctga cgggggtgcc 21600
caacggcatg ctccagtcgc cccaggtgga acccaccctg cgccgcaacc aggaggcgct 21660
ctaccgcttc ctcaactccc actccgccta ctttcgctcc caccgcgcgc gcatcgagaa 21720
ggccaccgcc ttcgaccgca tgaatcaaga catgtaaacc gtgtgtgtat gttaaatgtc 21780
tttaataaac agcactttca tgttacacat gcatctgaga tgatttattt agaaatcgaa 21840
agggttctgc cgggtctcgg catggcccgc gggcagggac acgttgcgga actggtactt 21900
ggccagccac ttgaactcgg ggatcagcag tttgggcagc ggggtgtcgg ggaaggagtc 21960
ggtccacagc ttccgcgtca gttgcagggc gcccagcagg tcgggcgcgg agatcttgaa 22020
atcgcagttg ggacccgcgt tctgcgcgcg ggagttgcgg tacacggggt tgcagcactg 22080
gaacaccatc agggccgggt gcttcacgct cgccagcacc gtcgcgtcgg tgatgctctc 22140

20262014626 26 Feb 2026

```
cacgtcgagg tcctcggcgt tggccatccc gaaggggtc atcttgcagg tctgccttcc 22200
catggtgggc acgcacccgg gcttgtggtt gcaatcgcag tgcaggggga tcagcatcat 22260
ctgggcctgg tcggcgttca tccccgggta catggccttc atgaaagcct ccaattgcct 22320
gaacgcctgc tgggccttgg ctccctcggt gaagaagacc ccgcaggact tgctagagaa 22380
ctggttggtg gcgcacccgg cgtcgtgcac gcagcagcgc gcgtcgttgt tggccagctg 22440
caccacgctg cgcccccagc ggttctgggt gatcttggcc cggtcggggt tctccttcag 22500
cgcgcgctgc ccgttctcgc tcgccacatc catctcgatc atgtgctcct tctggatcat 22560
ggtggtcccg tgcaggcacc gcagcttgcc ctcggcctcg gtgcacccgt gcagccacag 22620
cgcgcacccg gtgcactccc agttcttgtg ggcgatctgg gaatgcgcgt gcacgaagcc 22680
ctgcaggaag cggcccatca tggtggtcag ggtcttgttg ctagtgaagg tcagcggaat 22740
gccgcggtgc tcctcgttga tgtacaggtg gcagatgcgg cggtacacct cgccctgctc 22800
gggcatcagc tggaagttgg ctttcaggtc ggtctccacg cggtagcggt ccatcagcat 22860
agtcatgatt tccataccct tctcccaggc cgagacgatg ggcaggctca tagggttctt 22920
caccatcatc ttagcgctag cagccgcggc caggggtcg ctctcgtcca gggtctcaaa 22980
gctccgcttg ccgtccttct cggtgatccg caccgggggg tagctgaagc ccacggccgc 23040
cagctcctcc tcggcctgtc tttcgtcctc gctgtcctgg ctgacgtcct gcaggaccac 23100
atgcttggtc ttgcggggtt tcttcttggg cggcagcggc ggcggagatg ttggagatgg 23160
cgaggggag cgcgagttct cgctcaccac tactatctct tcctcttctt ggtccgaggc 23220
cacgcggcgg taggtatgtc tcttcggggg cagaggcgga ggcgacgggc tctcgccgcc 23280
gcgacttggc ggatggctgg cagagcccct tccgcgttcg ggggtgcgct cccggcggcg 23340
ctctgactga cttcctccgc ggccggccat tgtgttctcc tagggaggaa caacaagcat 23400
ggagactcag ccatcgccaa cctcgccatc tgcccccacc gccgacgaga agcagcagca 23460
gcagaatgaa agcttaaccg ccccgccgcc cagccccgcc acctccgacg cggccgtccc 23520
agacatgcaa gagatggagg aatccatcga gattgacctg ggctatgtga cgcccgcgga 23580
gcacgaggag gagctggcag tgcgcttttc acaagaagag atacaccaag aacagccaga 23640
gcaggaagca gagaatgagc agagtcaggc tgggctcgag catgacggcg actacctcca 23700
cctgagcggg ggggaggacg cgctcatcaa gcatctggcc cggcaggcca ccatcgtcaa 23760
ggatgcgctg ctcgaccgca ccgaggtgcc cctcagcgtg gaggagctca gccgcgccta 23820
cgagttgaac ctcttctcgc cgcgcgtgcc ccccaagcgc cagcccaatg gcacctgcga 23880
gcccaacccg cgcctcaact tctacccggt cttcgcggtg cccgaggccc tggccaccta 23940
ccacatcttt ttcaagaacc aaaagatccc cgtctcctgc cgcgccaacc gcacccgcgc 24000
cgacgccctt ttcaacctgg gtcccggcgc ccgcctacct gatatcgcct ccttggaaga 24060
ggttcccaag atcttcgagg gtctgggcag cgacgagact cgggccgcga acgctctgca 24120
aggagaagga ggagagcatg agcaccacag cgccctggtc gagttggaag gcgacaacgc 24180
gcggctggcg gtgctcaaac gcacggtcga gctgacccat ttcgcctacc cggctctgaa 24240
cctgcccccc aaagtcatga gcgcggtcat ggaccaggtg ctcatcaagc gcgcgtcgcc 24300
catctccgag gacgagggca tgcaagactc cgaggagggc aagcccgtgg tcagcgacga 24360
gcagctggcc cggtggctgg gtcctaatgc tagtccccag agtttggaag agcggcgcaa 24420
actcatgatg gccgtggtcc tggtgaccgt ggagctggag tgcctgcgcc gcttcttcgc 24480
cgacgcggag accctgcgca aggtcgagga gaacctgcac tacctcttca ggcacgggtt 24540
cgtgcgccag gcctgcaaga tctccaacgt ggagctgacc aacctggtct cctacatggg 24600
catcttgcac gagaaccgcc tggggcagaa cgtgctgcac accaccctgc gcggggaggc 24660
ccggcgcgac tacatccgcg actgcgtcta cctctacctc tgccacacct ggcagacggg 24720
catgggcgtg tggcagcagt gtctggagga gcagaacctg aaagagctct gcaagctcct 24780
gcagaagaac ctcaagggtc tgtggaccgg gttcgacgag cgcaccaccg cctcggacct 24840
ggccgacctc attttccccg agcgcctcag gctgacgctg cgcaacggcc tgcccgactt 24900
tatgagccaa agcatgttgc aaaactttcg ctctttcatc ctcgaacgct ccggaatcct 24960
gcccgccacc tgctccgcgc tgccctcgga cttcgtgccg ctgaccttcc gcgagtgccc 25020
cccgccgctg tggagccact gctacctgct gcgcctggcc aactacctgg cctaccactc 25080
ggacgtgatc gaggacgtca gcggcgaggg cctgctcgag tgccactgcc gctgcaacct 25140
ctgcacgccg caccgctccc tggcctgcaa cccccagctg ctgagcgaga cccagatcat 25200
cggcaccttc gagttgcaag ggcccagcga aggcgagggt tcagccgcca agggggtct 25260
gaaactcacc ccggggctgt ggacctcggc ctacttgcgc aagttcgtgc ccgaggacta 25320
ccatcccttc gagatcaggt tctacgagga ccaatcccat ccgcccaagg ccgagctgtc 25380
ggcctgcgtc atcacccagg gggcgatcct ggcccaattg caagccatcc agaaatcccg 25440
ccaagaattc ttgctgaaaa agggccgcgg ggtctacctc gacccccaga ccggtgagga 25500
gctcaacccc ggcttccccc aggatgcccc gaggaaacaa gaagctgaaa gtggagctgc 25560
cgcccgtgga ggatttggag gaagactggg agaacagcag tcaggcagag gaggaggaga 25620
tggaggaaga ctgggacagc actcaggcag aggaggacag cctgcaagac agtctggagg 25680
aagacgagga ggaggcagag gaggaggtgg aagaagcagc cgccgccaga ccgtcgtcct 25740
cggcgggga gaaagcaagc agcacggata ccatctccgc tccgggtcgg ggtcccgctc 25800
gaccacacag tagatgggac gagaccggac gattcccgaa ccccaccacc cagaccggta 25860
agaaggagcg gcagggatac aagtcctggc gggggcacaa aaacgccatc gtctcctgct 25920
tgcaggcctg cgggggcaac atctccttca cccggcgcta cctgctcttc caccgcgggg 25980
tgaactttcc ccgcaacatc ttgcattact accgtcacct ccacagcccc tactacttcc 26040
aagaagaggc agcagcagca gaaaaagacc agcagaaaac cagcagctag aaaatccaca 26100
gcggcggcag caggtggact gaggatcgcg gcgaacgagc cggcgcaaac ccgggagctg 26160
aggaaccgga tctttcccac cctctatgcc atcttccagc agagtcgggg gcaggagcag 26220
gaactgaaag tcaagaaccg ttctctgcgc tcgctcaccc gcagttgtct gtatcacaag 26280
agcgaagacc aacttcagcg cactctcgag gacgccgagg ctctcttcaa caagtactgc 26340
gcgctcactc ttaaagagta gcccgcgccc gcccagtcgc agaaaaaggc gggaattacg 26400
tcacctgtgc ccttcgccct agccgcctcc acccatcatc atgagcaaag agattcccac 26460
gccttacatg tggagctacc agccccagat gggcctggcc gccggtgccg cccaggacta 26520
ctccacccgc atgaattggc tcagcgccgg gcccgcgatg atctcacggg tgaatgacat 26580
ccgcgcccac cgaaaccaga tactcctaga acagtcagcg ctcaccgcca cgccccgcaa 26640
tcacctcaat ccgcgtaatt ggcccgccgc cctggtgtac caggaaattc cccagcccac 26700
```

20262014626 26 Feb 2026

gaccgtacta cttccgcgag acgcccaggc cgaagtccag ctgactaact caggtgtcca 26760
gctggcgggc ggcgccaccc tgtgtcgtca ccgccccgct cagggtataa agcggctggt 26820
gatccggggc agaggcacac agctcaacga cgaggtggtg agctcttcgc tgggtctgcg 26880
acctgacgga gtcttccaac tcgccggatc ggggagatct tccttcacgc ctcgtcaggc 26940
cgtcctgact ttggagagtt cgtcctcgca gccccgctcg ggtggcatcg gcactctcca 27000
gttcgtggag gagttcactc cctcggtcta cttcaacccc ttctccggct cccccggcca 27060
ctacccggac gagttcatcc cgaacttcga cgccatcagc gagtcggtgg acggctacga 27120
ttgaatgtcc catggtggcg cagctgacct agctcggctt cgacacctgg accactgccg 27180
ccgcttccgc tgcttcgctc gggatctcgc cgagtttgcc tactttgagc tgcccgagga 27240
gcaccctcag ggcccggccc acggagtgcg gatcgtcgtc gaaggggccc tcgactccca 27300
cctgcttcgg atcttcagcc agcgtccgat cctggtcgag cgcgagcaag gacagaccct 27360
tctgactctg tactgcatct gcaaccaccc cggcctgcat gaaagtcttt gttgtctgct 27420
gtgtactgag tataataaaa gctgagatca gcgactactc cggacttccg tgtgttcctg 27480
aatccatcaa ccagtctttg ttcttcaccg ggaacgagac cgagctccag ctccagtgta 27540
agccccacaa gaagtacctc acctggctgt tccagggctc cccgatcgcc gttgtcaacc 27600
actgcgacaa cgacggagtc ctgctgagcg gccctgccaa ccttactttt tccacccgca 27660
gaagcaagct ccagctcttc caacccttcc tccccgggac ctatcagtgc gtctcgggac 27720
cctgccatca caccttccac ctgatcccga ataccacagc gtcgctcccc gctactaaca 27780
accaaactaa cctccaccaa cgccaccgtc gcgacctttc tgaatctaat actaccaccc 27840
acaccggagg tgagctccga ggtcaaccaa cctctgggat ttactacggc ccctgggagg 27900
tggttgggtt aatagcgcta ggcctagttg cgggtgggct tttggttctc tgctacctat 27960
acctcccttg ctgttcgtac ttagtggtgc tgtgttgctg gtttaagaaa tggggaagat 28020
caccctagtg agctgcggtg cgctggtggc ggtgttgctt tcgattgtgg gactgggcgg 28080
tgcggctgta gtgaaggaga aggccgatcc ctgcttgcat ttcaatccca acaaatgcca 28140
gctgagtttt cagcccgatg gcaatcggtg cgcggtactg atcaagtgcg gatgggaatg 28200
cgagaacgtg agaatcgagt acaataacaa gactcggaac aatactctcg cgtccgtgtg 28260
gcagcccggg gaccccgagt ggtacaccgt ctctgtcccc ggtgctgacg gctccccgcg 28320
caccgtgaat aatactttca tttttgcgca catgtgcgac acggtcatgt ggatgagcaa 28380
gcagtacgat atgtggcccc ccacgaagga gaacatcgtg gtcttctcca tcgcttacag 28440
cctgtgcacg gcgctaatca ccgctatcgt gtgcctgagc attcacatgc tcatcgctat 28500
tcgccccaga aataatgccg aaaaagaaaa acagccataa cgtttttttt cacacctttt 28560
tcagaccatg gcctctgtta aatttttgct tttatttgcc agtctcattg ccgtcattca 28620
tggaatgagt aatgagaaaa ttactattta cactggcact aatcacacat tgaaaggtcc 28680
agaaaaagcc acagaagttt catggtattg ttattttaat gaatcagatg tatctactga 28740
actctgtgga aacaataaca aaaaaaatga gagcattact ctcatcaagt ttcaatgtgg 28800
atctgactta accctaatta acatcactag agactatgta ggtatgtatt atggaactac 28860
agcaggcatt tcggacatgg aattttatca agtttctgtg tctgaaccca ccacgcctag 28920
aatgaccaca accacaaaaa ctacacctgt taccactatg cagctcacta ccaataacat 28980
ttttgccatg cgtcaaatgg tcaacaatag cactcaaccc accccaccca gtgaggaaat 29040
tcccaaatcc atgattggca ttattgttgc tgtagtggtg tgcatgttga tcatcgcctt 29100
gtgcatggtg tactatgcct tctgctacag aaagcacaga ctgaacgaca agctggaaca 29160
cttactaagt gttgaatttt aatttttag aaccatgaag atcctaggcc ttttaatttt 29220
ttctatcatt acctctgctc tatgcaattc tgacaatgag gacgttactg tcgttgtcgg 29280
atcaaattat acactgaaag gtccagcgaa gggtatgctt tcgtggtatt gctattttgg 29340
atctgacact acagaaactg aattatgcaa tcttaagaat ggcaaaattc aaaattctaa 29400
aattaacaat tatatatgca atggtactga tctgatactc ctcaatatca cgaaatcata 29460
tgctggcagt tacacctgcc ctggagatga tgctgacagt atgatttttt acaaagtaac 29520
tgttgttgat cccactactc cacctccacc caccacaact actcacacca cacacacaga 29580
tcaaaccgca gcagaggagg cagcaaagtt agccttgcag gtccaagaca gttcatttgt 29640
tggcattacc cctacacctg atcagcggtg tccggggctg ctagtcagcg gcattgtcgg 29700
tgtgctttcg ggattagcag tcataatcat ctgcatgttc atttttgctt gctgctatag 29760
aaggctttac cgacaaaaat cagacccact gctgaacctc tatgtttaat tttttccaga 29820
gtcatgaagg cagttagcgc tctagttttt tgttctttga ttggcattgt tttttgcaat 29880
cctattccta aagttagctt tattaaagat gtgaatgtta ctgaggggggg caatgtgaca 29940
ctggtaggtg tagagggtgc tgaaaacacc acctggacaa aataccacct caatgggtgg 30000
aaagatattt gcaattggag tgtattagtt tatacatgtg agggagttaa tcttaccatt 30060
gtcaatgcca cctcagctca aaatggtaga attcaaggac aaagtgtcag tgtatctaat 30120
gggtatttta cccaacatac ttttatctat gacgttaaag tcataccact gcctacgcct 30180
agcccaccta gcactaccac acagacaacc cacactacac agacaaccac atacagtaca 30240
ttaaatcagc ctaccaccac tacagcagca gaggttgcca gctcgtctgg ggtccgagtg 30300
gcatttttga tgtgggcccc atctagcagt cccactgcta gtaccaatga gcagactact 30360
gaatttttgt ccactgtcga gagccacacc acagctacct ccagtgcctt ctctagcacc 30420
gccaatctct cctcgctttc ctctacacca atcagtcccg ctactactcc tagccccgct 30480
cctcttccca ctcccctgaa gcaaacagac ggcggcatgc aatggcagat caccctgctc 30540
attgtgatcg ggttggtcat cctggccgtg ttgctctact acatcttctg ccgccgcatt 30600
cccaacgcgc accgcaagcc ggtctacaag cccatcattg tcgggcagcc ggagccgctt 30660
caggtggaag ggggtctaag gaatcttctc ttctctttta cagtatggtg attgaactat 30720
gattcctaga caattcttga tcactattct tatctgcctc ctccaagtct gtgccaccct 30780
cgctctggtg gccaacgcca gtccagactg tattgggccc ttcgcctcct acgtgctctt 30840
tgccttcacc acctgcatct gctgctgtag catagtctgc ctgcttatca ccttcttcca 30900
gttcattgac tggatctttg tgcgcatcgc ctacctgcgc caccaccccc agtaccgcga 30960
ccagcgagtg gcgcggctgc tcaggctcct ctgataagca tgcgggctct gctacttctc 31020
gcgcttctgc tgttagtgct cccccgtccc gtcgacccca ggtcccccac ccagtccccc 31080
gaggaggtcc gcaaatgcaa attccaagaa ccctggaaat tcctcaaatg ctaccgccaa 31140
aaatcagaca tgcatcccag ctggatcatg atcattggga tcgtgaacat tctggcctgc 31200
accctcatct cctttgtgat ttacccctgc tttgactttg gttggaactc gccagaggcg 31260

20262014626 26 Feb 2026

ctctatctcc cgcctgaacc tgacacacca ccacagcaac ctcaggcaca cgcactacca 31320
ccactacagc ctaggccaca atacatgccc atattagact atgaggccga gccacagcga 31380
cccatgctcc ccgctattag ttacttcaat ctaaccggcg gagatgactg acccactggc 31440
caacaacaac gtcaacgacc ttctcctgga catggacggc cgcgcctcgg agcagcgact 31500
cgcccaactt cgcattcgcc agcagcagga gagagccgtc aaggagctgc aggatgcggt 31560
ggccatccac cagtgcaaga gaggcatctt ctgcctggtg aaacaggcca agatctccta 31620
cgaggtcact ccaaacgacc atcgcctctc ctacgagctc ctgcagcagc gccagaagtt 31680
cacctgcctg gtcggagtca accccatcgt catcacccag cagtctggcg ataccaaggg 31740
gtgcatccac tgctcctgcg actcccccga ctgcgtccac actctgatca agaccctctg 31800
cggcctccgc gacctcctcc ccatgaacta atcacccccc tatccagtga aataaagatc 31860
atattgatga tgattttaca gaaataaaaa ataatcattt gatttgaaat aaagatacaa 31920
tcatattgat gatttgagtt taacaaaaaa ataaagaatc acttacttga aatctgatac 31980
caggtctctg tccatgtttt ctgccaacac cacttcactc ccctcttccc agctctggta 32040
ctgcaggccc cggcgggctg caaacttcct ccacacgctg aaggggatgt caaattcctc 32100
ctgtccctca atcttcattt tatcttctat cagatgtcca aaaagcgcgt ccgggtggat 32160
gatgacttcg accccgtcta cccctacgat gcagacaacg caccgaccgt gcccttcatc 32220
aacccccccc tcgtctcttc agatggattc caagagaagc ccctgggggt gttgtccctg 32280
cgactggccg accccgtcac caccaagaac ggggaaatca ccctcaagct gggagagggg 32340
gtggacctcg attcctcggg aaaactcatc tccaacacgg ccaccaaggc cgccgcccct 32400
ctcagttttt ccaacaacac catttccctt aacatggatc acccctttta cactaaagat 32460
ggaaaattat ccttacaagt ttctccacca ttaaatatac tgagaacaag cattctaaac 32520
acactagctt taggttttgg atcaggttta ggactccgtg gctctgcctt ggcagtacag 32580
ttagtctctc cacttacatt tgatactgat ggaaacataa agcttacctt agacagaggt 32640
ttgcatgtta caacaggaga tgcaattgaa agcaacataa gctgggctaa aggtttaaaa 32700
tttgaagatg gagccatagc aaccaacatt ggaaatgggt tagagtttgg aagcagtagt 32760
acagaaacag gtgttgatga tgcttaccca atccaagtta aacttggatc tggccttagc 32820
tttgacagta caggagccat aatggctggt aacaaagaag acgataaact cactttgtgg 32880
acaacacctg atccatcacc aaactgtcaa atactcgcag aaaatgatgc aaaactaaca 32940
ctttgcttga ctaaatgtgg tagtcaaata ctggccactg tgtcagtctt agttgtagga 33000
agtggaaacc taaaccccat tactggcacc gtaagcagtg ctcaggtgtt tctacgtttt 33060
gatgcaaacg gtgttctttt aacagaacat tctacactaa aaaaatactg ggggtatagg 33120
cagggagata gcatagatgg cactccatat accaatgctg taggattcat gcccaattta 33180
aaagcttatc caaagtcaca aagttctact actaaaaata atatagtagg gcaagtatac 33240
atgaatggag atgtttcaaa acctatgctt ctcactataa ccctcaatgg tactgatgac 33300
agcaacagta catattcaat gtcattttca tacacctgga ctaatggaag ctatgttgga 33360
gcaacatttg gggctaactc ttataccttc tcatacatcg cccaagaatg aacactgtat 33420
cccaccctgc atgccaaccc ttcccacccc actctgtgga acaaactctg aaacacaaaa 33480
taaaataaag ttcaagtgtt ttattgattc aacagtttta caggattcga gcagttattt 33540
ttcctccacc ctcccaggac atggaataca ccaccctctc cccccgcaca gccttgaaca 33600
tctgaatgcc attggtgatg gacatgcttt tggtctccac gttccacaca gtttcagagc 33660
gagccagtct cgggtcggtc agggagatga aaccctccgg gcactcccgc atctgcacct 33720
cacagctcaa cagctgagga ttgtcctcgg tggtcgggat cacggttatc tggaagaagc 33780
agaagagcgg cggtgggaat catagtccgc gaacgggatc ggccggtggt gtcgcatcag 33840
gccccgcagc agtcgctgcc gccgccgctc cgtcaagctg ctgctcaggg ggtccgggtc 33900
cagggactcc ctcagcatga tgcccacggc cctcagcatc agtcgtctgg tgcggcgggc 33960
gcagcagcgc atgcggatct cgctcaggtc gctgcagtac gtgcaacaca gaaccaccag 34020
gttgttcaac agtccatagt tcaacacgct ccagccgaaa ctcatcgcgg gaaggatgct 34080
acccacgtgg ccgtcgtacc agatcctcag gtaaatcaag tggtgccccc tccagaacac 34140
gctgcccacg tacatgatct ccttgggcat gtggcggttc accacctccc ggtaccacat 34200
caccctctgg ttgaacatgc agccccggat gatcctgcgg aaccacaggg ccagcaccgc 34260
cccgccccgcc atgcagcgaa gagaccccgg gtcccggcaa tggcaatgga ggacccaccg 34320
ctcgtacccg tggatcatct gggagctgaa caagtctatg ttggcacagc acaggcatat 34380
gctcatgcat ctcttcagca ctctcaactc ctcgggggtc aaaaccatat cccagggcac 34440
ggggaactct tgcaggacag cgaaccccgc agaacagggc aatcctcgca cagaacttac 34500
attgtgcatg gacagggtat cgcaatcagg cagcaccggg tgatcctcca ccagagaagc 34560
gcgggtctcg gtctcctcac agcgtggtaa gggggccggc cgatacgggt gatggcggga 34620
cgcggctgat cgtgttcgcg accgtgtcat gatgcagttg ctttcggaca ttttcgtact 34680
tgctgtagca gaacctggtc cgggcgctgc acaccgatcg ccggcggcgg tctcggcgct 34740
tggaacgctc ggtgttgaaa ttgtaaaaca gccactctct cagaccgtgc agcagatcta 34800
gggcctcagg agtgatgaag atcccatcat gcctgatggc tctgatcaca tcgaccaccg 34860
tggaatgggc cagacccagc cagatgatgc aattttgttg ggtttcggtg acggcggggg 34920
agggaagaac aggaagaacc atgattaact tttaatccaa acggtctcgg agtacttcaa 34980
aatgaagatc gcggagatgg cacctctcgc ccccgctgtg ttggtggaaa ataacagcca 35040
ggtcaaaggt gatacggttc tcgagatgtt ccacggtggc ttccagcaaa gcctccacgc 35100
gcacatccag aaacaagaca atagcgaaag cgggagggtt ctctaattcc tcaatcatca 35160
tgttacactc ctgcaccatc cccagataat tttcattttt ccagccttga atgattcgaa 35220
ctagttcctg aggtaaatcc aagccagcca tgataaagag ctcgcgcaga gcgccctcca 35280
ccggcattct taagcacacc ctcataattc caagatattc tgctcctggt tcacctgcag 35340
cagattgaca agcggaatat caaaatctct gccgcgatcc ctgagctcct ccctcagcaa 35400
taactgtaag tactctttca tatcctctcc gaaattttta gccataggac caccaggaat 35460
aagattaggg caagccacag tacagataaa ccgaagtcct ccccagtgag cattgccaaa 35520
tgcaagactg ctataagcat gctggctaga cccggtgata tcttccagat aactggacag 35580
aaaatcgccc aggcaatttt taagaaaatc aacaaaagaa aaatcctcca ggtggacgtt 35640
tagagcctcg ggaacaacga tgaagtaaat gcaagcggtg cgttccagca tggttagtta 35700
gctgatctgt agaaaaaaca aaaatgaaca ttaaaccatg ctagcctggc gaacaggtgg 35760
gtaaatcgtt ctctccagca ccaggcaggc cacggggtct ccggcgcgac cctcgtaaaa 35820

2026201462 26 Feb 2026

		attgtcgcta tgattgaaaa ccatcacaga gagacgttcc cggtggccgg cgtgaatgat 35880 tcgacaagat gaatacaccc ccggaacatt ggcgtccgcg agtgaaaaaa agcgcccgag 35940 gaagcaataa ggcactacaa tgctcagtct caagtccagc aaagcgatgc catgcggatg 36000 aagcacaaaa ttctcaggtg cgtacaaaat gtaattactc ccctcctgca caggcagcaa 36060 agcccccgat ccctccaggt acacatacaa agcctcagcg tccatagctt accgagcagc 36120 agcacacaac aggcgcaaga gtcagagaaa ggctgagctc taacctgtcc acccgctctc 36180 tgctcaatat atagcccaga tctacactga cgtaaaggcc aaagtctaaa aatacccgcc 36240 aaataatcac acacgcccag cacacgccca gaaaccggtg acacactcaa aaaaatacgc 36300 gcacttcctc aaacgcccaa aactgccgtc atttccgggt tcccacgcta cgtcatcaaa 36360 acacgacttt caaattccgt cgaccgttaa aaacgtcacc cgccccgccc ctaacggtcg 36420 cccgtctctc agccaatcag cgccccgcat ccccaaattc aaacacctca tttgcatatt 36480 aacgcgcaca aaaagtttga ggtatattat tgatgatgg 36519
3-2	**Sequences**	
3-2-1	Sequence Number [ID]	2
3-2-2	Molecule Type	DNA
3-2-3	Length	31588
3-2-4	Features	**misc_feature 1..31588**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..31588
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-2-5	Residues	ccatcttcaa taatatacct caaacttttt gtgcgcgtta atatgcaaat gaggcgtttg 60 aatttgggga ggaagggcgg tgattggtcg agggatgagc gaccgttagg ggcggggcga 120 gtgacgtttt gatgacgtgg ttgcgaggag gagccagttt gcaagttctc gtgggaaaag 180 tgacgtcaaa cgaggtgtgg tttgaacacg gaaatactca attttcccgc gctctctgac 240 aggaaatgag gtgtttctgg gcggatgcaa gtgaaaacgg gccattttcg cgcgaaaact 300 gaatgaggaa gtgaaaatct gagtaatttc gcgtttatgg cagggaggag tatttgccga 360 gggccgagta gactttgacc gattacgtgg gggtttcgat taccgtgttt ttcacctaaa 420 tttccgcgta cggtgtcaaa gtccggtgtt tttacgtagg tgtcagctga tcgccagggt 480 atttaaacct gcgctctcca gtcaagaggc cactcttgag tgccagcgag aagagttttc 540 tcctccgcgc cgcgagtcag atctacactt tgaaagtagg gataacaggg taatgacatt 600 gattattgac tagttgttaa tagtaatcaa ttacggggtc attagttcat agcccatata 660 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 720 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 780 attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt 840 atcatatgcc aagtccgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 900 atgcccagta catgacctta cgggactttc ctacttggca gtacatctac gtattagtca 960 tcgctattac catggtgatg cggttttggc agtacaccaa tgggcgtgga tagcggtttg 1020 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 1080 aaaatcaacg ggactttcca aaatgtcgta ataaccccgc cccgttgacg caaatgggcg 1140 gtaggcgtgt acggtgggag gtctatataa gcagagctcg tttagtgaac cgtcagatcg 1200 cctggaacgc catccacgct gttttgacct ccatagaaga cagcgatcgc gccaccatgg 1260 ccgggatgtt ccaggcactg tccgaaggct gcacacccta tgatattaac cagatgctga 1320 atgtcctggg agaccaccag gtctctggcc tggagcagct ggagagcatc atcaacttcg 1380 agaagctgac cgagtggaca agctccaatg tgatgcctat cctgtcccca ctgaccaagg 1440 gcatcctggg cttcgtgttt accctgacag tgccttctga gcggggcctg tcttgcatca 1500 gcgaggcaga cgcaaccaca ccagagtccg ccaatctggg cgaggagatc ctgtctcagc 1560 tgtacctgtg gccccgggtg acatatcact ccccttctta cgcctatcac cagttcgagc 1620 ggagagccaa gtacaagaga cacttcccag gctttggcca gtctctgctg ttcggctacc 1680 ccgtgtacgt gttcggcgat tgcgtgcagg gcgactggga tgccatccgg tttagatact 1740 gcgcaccacc tggatatgca ctgctgaggt gtaacgacac caattattcc gccctgctgg 1800 cagtgggcgc cctggagggc cctcgcaatc aggattggct gggcgtgcca aggcagctgg 1860 tgacacgcat gcaggccatc cagaacgcag gcctgtgcac cctggtggca atgctggagg 1920 agacaatctt ctggctgcag gcctttctga tggccctgac cgacagcggc cccaagacaa 1980 acatcatcgt ggattcccag tacgtgatgg gcatctccaa gccttctttc caggagtttg 2040 tggactggga gaacgtgagc ccagagctga attccaccga tcagccattc tggcaggcag 2100 gaatcctggc aaggaacctg gtgcctatgg tggccacagt gcagggccag aatctgaagt 2160 accagggcca gagcctggtc atcagcgcct ccatcatcgt gtttaacctg ctggagctgg 2220 agggcgacta tcgggacgat ggcaacgtgt gggtgcacac cccactgagc cccagaacac 2280 tgaacgcctg ggtgaaggcc gtggaggaga agaagggcat cccagtgcac ctggagctgg 2340 cctccatgac caatatggag ctgatgtcta gcatcgtgca ccagcaggtg aggacatacg 2400 gacccgtgtt catgtgcctg ggaggcctgc tgaccatggt ggcaggagcc gtgtggctga 2460 cagtgcgggt gctggagctg ttcagagccg cccagctggc caacgatgtg gtgctgcaga 2520 tcatggagct gtgcggagca gcctttcgcc aggtgtgcca caccacagtg ccatggccca 2580 atgcctccct gacccccaag tggaacaatg agacaacaca gcctcagatc gccaactgta 2640 gcgtgtacga cttcttcgtg tggctgcact actatagcgt gagggatacc ctgtggcccc 2700 gcgtgacata ccacatgaat aagtacgcct atcacatgct ggagaggcgc gccaagtata 2760 agagaggccc tggcccaggc gcaaagtttg tggcagcatg gaccctgaag gccgccgccg 2820 gccccggccc cggccagtat atcaaggcta acagtaagtt cattggaatc acagagctgg 2880 gacccggacc tggataatga gtttaaactc ccatttaaat gtgagggtta atgcttcgag 2940 cagacatgat aagatacatt gatgagtttg gacaaaccac aactagaatg cagtgaaaaa 3000 aatgctttat ttgtgaaatt tgtgatgcta ttgctttatt tgtaaccatt ataagctgca 3060 ataaacaagt taacaacaac aattgcattc attttatgtt tcaggttcag ggggagatgt 3120 gggaggtttt ttaaagcaag taaaacctct acaaatgtgg taaaataact ataacggtcc 3180

2026201462 26 Feb 2026

taaggtagcg agtgagtagt gttctggggc gggggaggac ctgcatgagg gccagaataa 3240
ctgaaatctg tgcttttctg tgtgttgcag cagcatgagc ggaagcggct cctttgaggg 3300
aggggtattc agcccttatc tgacggggcg tctcccctcc tgggcgggag tgcgtcagaa 3360
tgtgatggga tccacggtgg acggccggcc cgtgcagccc gcgaactctt caaccctgac 3420
ctatgcaacc ctgagctctt cgtcgttgga cgcagctgcc gccgcagctg ctgcatctgc 3480
cgccagcgcc gtgcgcggaa tggccatggg cgccggctac tacggcactc tggtggccaa 3540
ctcgagttcc accaataatc ccgccagcct gaacgaggag aagctgttgc tgctgatggc 3600
ccagctcgag gccttgaccc agcgcctggg cgagctgacc cagcaggtgg ctcagctgca 3660
ggagcagacg cgggccgcgg ttgccacggt gaaatccaaa taaaaaatga atcaataaat 3720
aaacggagac ggttgttgat tttaacacag agtctgaatc tttatttgat ttttcgcgcg 3780
cggtaggccc tggaccaccg gtctcgatca ttgagcaccc ggtggatctt ttccaggacc 3840
cggtagaggt gggcttggat gttgaggtac atgggcatga gcccgtcccg ggggtggagg 3900
tagctccatt gcagggcctc gtgctcgggg gtggtgttgt aaatcaccca gtcatagcag 3960
gggcgcaggg catggtgttg cacaatatct ttgaggagga gactgatggc cacgggcagc 4020
cctttggtgt aggtgtttac aaatctgttg agctgggagg gatgcatgcg gggggagatg 4080
aggtgcatct tggcctggat cttgagattg gcgatgttac cgcccagatc ccgcctgggg 4140
ttcatgttgt gcaggaccac cagcacggtg tatccggtgc acttggggaa tttatcatgc 4200
aacttggaag ggaaggcgtg aaagaatttg gcgacgcctt tgtgcccgcc caggttttcc 4260
atgcactcat ccatgatgat ggcgatgggc ccgtgggcgg cggcctgggc aaagacgttt 4320
cgggggtcgg acacatcata gttgtggtcc tgggtgaggt catcataggc cattttaatg 4380
aatttggggc ggagggtgcc ggactggggg acaaaggtac cctcgatccc gggggcgtag 4440
ttcccctcac agatctgcat ctcccaggct ttgagctcgg agggggggat catgtccacc 4500
tgcggggcga taaagaacac ggtttccggg gcgggggaga tgagctgggc cgaaagcaag 4560
ttccggagca gctgggactt gccgcagccg gtggggccgt agatgacccc gatgaccggc 4620
tgcaggtggt agttgaggga gagacagctg ccgtcctccc ggaggagggg ggccacctcg 4680
ttcatcatct cgcgcacgtg catgttctcg cgcaccagtt ccgccaggag gcgctctccc 4740
cccagggata ggagctcctg gagcgaggcg aagtttttca gcggcttgag tccgtcggcc 4800
atgggcattt tggagagggt ttgttgcaag agttccaggc ggtcccagag ctcggtgatg 4860
tgctctacgg catctcgatc cagcagacct cctcgtttcg cgggttggga cggctgcggg 4920
agtagggcac cagacgatgg gcgtccagcg cagccagggt ccggtccttc cagggtcgca 4980
gcgtccgcgt cagggtggtc tccgtcacgg tgaaggggtg cgcgccgggc tgggcgcttg 5040
cgagggtgcg cttcaggctc atccggctgg tcgaaaaccg ctcccgatcg gcgccctgcg 5100
cgtcggccag gtagcaattg accatgagtt cgtagttgag cgcctcggcc gcgtggcctt 5160
tggcgcggag cttacctttg gaagtctgcc cgcaggcggg acagaggagg gacttgaggg 5220
cgtagagctt gggggcgagg aagacggact cgggggcgta ggcgtccgcg ccgcagtggg 5280
cgcagacggt ctcgcactcc acgagccagg tgaggtcggg ctggtcgggg tcaaaaacca 5340
gtttcccgcc gttctttttg atgcgtttct tacctttggt ctccatgagc tcgtgtcccc 5400
gctgggtgac aaagaggctg tccgtgtccc cgtagaccga ctttatgggc cggtcctcga 5460
gcggtgtgcc gcggtcctcc tcgtagagga accccgccca ctccgagacg aaagcccggg 5520
tccaggccag cacgaaggag gccacgtggg acgggtagcg gtcgttgtcc accagcgggt 5580
ccacctttc cagggtatgc aaacacatgt ccccctcgtc cacatccagg aaggtgattg 5640
gcttgtaagt gtaggccacg tgaccggggg tcccggccgg gggggtataa aagggtgcgg 5700
gtccctgctc gtcctcactg tcttccggat cgctgtccag gagcgccagc tgttggggta 5760
ggtattccct ctcgaaggcg ggcatgacct cggcactcag gttgtcagtt tctagaaacg 5820
aggaggattt gatattgacg gtgccggcgg agatgccttt caagagcccc tcgtccatct 5880
ggtcagaaaa gacgatcttt ttgttgtcga gcttggtggc gaaggagccg tagagggcgt 5940
tggagaggag cttggcgatg gagcgcatgg tctggttttt ttccttgtcg gcgcgctcct 6000
tggcggcgat gttgagctgc acgtactcgc gcgccacgca cttccattcg gggaagacgg 6060
tggtcagctc gtcgggcacg attctgacct gccagccccg attatgcagg gtgatgaggt 6120
ccacactggt ggccacctcg ccgcgcaggg gctcattagt ccagcagagg cgtccgccct 6180
tgcgcgagca gaaggggggc aggggtcca gcatgacctc gtcgggggggg tcggcatcga 6240
tggtgaagat gccgggcagg aggtcggggt caaagtagct gatggaagtg gccagatcgt 6300
ccagggcagc ttgccattcg cgcacggcca gcgcgcgctc gtagggactg aggggcgtgc 6360
cccagggcat gggatgggta agcgcggagg cgtacatgcc gcagatgtcg tagacgtaga 6420
ggggctcctc gaggatgccg atgtaggtgg ggtagcagcg ccccccgcgg atgctggcgc 6480
gcacgtagtc atacagctcg tgcgaggggg cgaggagccc cgggcccagg ttggtgcgac 6540
tgggcttttc ggcgcggtag acgatctggc ggaaaatggc atgcgagttg gaggagatgg 6600
tgggcctttg gaagatgttg aagtgggcgt ggggcagtcc gaccgagtcg cggatgaagt 6660
gggcgtagga gtcttgcagc ttggcgacga gctcggcggt gactaggacg tccagagcgc 6720
agtagtcgag ggtctcctgg atgatgtcat acttgagctg tccctttttgt ttccacagct 6780
cgcggttgag aaggaactct tcgcggtcct tccagtactc ttcgaggggg aacccgtcct 6840
gatctgcacg gtaagagcct agcatgtaga actggttgac ggccttgtag gcgcagcagc 6900
ccttctccac ggggagggcg taggcctggg cggccttgcg cagggaggtg tgcgtgaggg 6960
cgaaagtgtc cctgaccatg accttgagga actggtgctt gaagtcgata tcgtcgcagc 7020
ccccctgctc ccagagctgg aagtccgtgc gcttcttgta ggcggggttg ggcaaagcga 7080
aagtaacatc gttgaagagg atcttgcccg cgcggggcat aaagttgcga gtgatgcgga 7140
aaggttgggg cacctcggcc cggttgttga tgacctgggc ggcgagcacg atctcgtcga 7200
agccgttgat gttgtggccc acgatgtaga gttccacgaa tcgcggacgg cccttgacgt 7260
ggggcagttt cttgagctcc tcgtaggtga gctcgtcggg gtcgctgagc ccgtgctgct 7320
cgagcgccca gtcggcgaga tgggggttgg cgcggaggaa ggaagtccag agatccacgg 7380
ccagggcggt ttgcagacgg tcccggtact gacggaactg ctgcccgacg gccatttttt 7440
cgggggtgac gcagtagaag gtgcgggggt ccccgtgcca gcgatcccat ttgagctgga 7500
gggcgagatc gagggcgagc tcgacgagcc ggtcgtcccc ggagagtttc atgaccagca 7560
tgaaggggac gagctgcttg ccgaaggacc ccatccaggt gtaggtttcc acatcgtagg 7620
tgaggaagag cctttcggtg cgaggatgcg agccgatggg gaagaactgg atctcctgcc 7680
accaattgga ggaatggctg ttgatgtgat ggaagtagaa atgccgacgg cgcgccgaac 7740

20262014626 26 Feb 2026

actcgtgctt gtgtttatac aagcggccac agtgctcgca acgctgcacg ggatgcacgt 7800
gctgcacgag ctgtacctga gttcctttga cgaggaattt cagtgggaag tggagtcgtg 7860
gcgcctgcat ctcgtgctgt actacgtcgt ggtggtcggc ctggccctct tctgcctcga 7920
tggtggtcat gctgacgagc ccgcgcggga ggcaggtcca gacctcggcg cgagcgggtc 7980
ggagagcgag gacgagggcg cgcaggccgg agctgtccag ggtcctgaga cgctgcggag 8040
tcaggtcagt gggcagcggc ggcgcgcggt tgacttgcag gagtttttcc agggcgcgcg 8100
ggaggtccag atggtacttg atctccaccg cgccattggt ggcgacgtcg atggcttgca 8160
gggtcccgtg cccctggggt gtgaccaccg tcccccgttt cttcttgggc ggctggggcg 8220
acgggggcgg tgcctcttcc atggttagaa gcggcggcga ggacgcgcgc cgggcggcag 8280
gggcggctcg gggcccggag gcaggggcgg caggggcacg tcggcgccgc gcgcgggtag 8340
gttctggtac tgcgcccgga gaagactggc gtgagcgacg acgcgacggt tgacgtcctg 8400
gatctgacgc ctctgggtga aggccacggg acccgtgagt ttgaacctga aagagagttc 8460
gacagaatca atctcggtat cgttgacggc ggcctgccgc aggatctctt gcacgtcgcc 8520
cgagttgtcc tggtaggcga tctcggtcat gaactgctcg atctcctcct cttgaaggtc 8580
tccgcggccg gcgcgctcca cggtggccgc gaggtcgttg gagatgcggc ccatgagctg 8640
cgagaaggcg ttcatgcccg cctcgttcca gacgcggctg tagaccacga cgccctcggg 8700
atcgcgggcg cgcatgacca cctgggcgag gttgagctcc acgtggcgcg tgaagaccgc 8760
gtagttgcag aggcgctggt agaggtagtt gagcgtggtg gcgatgtgct cggtgacgaa 8820
gaaatacatg atccagcggc ggagcggcat ctcgctgacg tcgcccagcg cctccaaacg 8880
ttccatggcc tcgtaaaagt ccacggcgaa gttgaaaaac tgggagttgc gcgccgagac 8940
ggtcaactcc tcctccagaa gacggatgag ctcggcgatg gtggcgcgca cctcgcgctc 9000
gaaggccccc gggagttcct ccacttcctc ttcttcctcc tccactaaca tctcttctac 9060
ttcctcctca ggcggcagtg gtggcggggg aggggcctg cgtcgccggc ggcgcacggg 9120
cagacggtcg atgaagcgct cgatggtctc gccgcgccgg cgtcgcatgg tctcggtgac 9180
ggcgcgcccg tcctcgcggg gccgcagcgt gaagacgccg ccgcgcatct ccaggtggcc 9240
ggggggggtcc ccgttgggca gggagagggc gctgacgatg catcttatca attgccccgt 9300
agggactccg cgcaaggacc tgagcgtctc gagatccacg ggatctgaaa accgctgaac 9360
gaaggcttcg agccagtcgc agtcgcaagg taggctgagc acggtttctt ctggcgggtc 9420
atgttggttg ggagcggggc gggcgatgct gctggtgatg aagttgaaat aggcggttct 9480
gagacggcgg atggtggcga ggagcaccag gtctttgggc ccggcttgct ggatgcgcag 9540
acggtcggcc atgccccagg cgtggtcctg acacctggcc aggtccttgt agtagtcctg 9600
catgagccgc tccacgggca cctcctcctc gcccgcgcgg ccgtgcatgc gcgtgagccc 9660
gaagccgcgc tggggctgga cgagcgccag gtcggcgacg acgcgctcgg cgaggatggc 9720
ttgctggatc tgggtgaggg tggtctggaa gtcatcaaag tcgacgaagc ggtggtaggc 9780
tccggtgttg atggtgtagg agcagttggc catgacggac cagttgacgg tctggtggcc 9840
cggacgcacg agctcgtggt acttgaggcg cgagtaggcg cgcgtgtcga agatgtagtc 9900
gttgcaggtg cgcaccaggt actggtagcc gatgaggaag tgcggcggcg gctggcggta 9960
gagcggccat cgctcggtgg cgggggcgcc gggcgcgagg tcctcgagca tggtgcggtg 10020
gtagccgtag atgtacctgg acatccaggt gatgccggcg gcggtggtgg aggcgcgcgg 10080
gaactcgcgg acgcggttcc agatgttgcg cagcggcagg aagtagttca tggtgggcac 10140
ggtctggccc gtgaggcgcg cgcagtcgtg gatgctctat acgggcaaaa acgaaagcgg 10200
tcagcggctc gactccgtgg cctggaggct aagcgaacgg gttgggctgc gcgtgtaccc 10260
cggttcgaat ctcgaatcag gctggagccg cagctaacgt ggtattggca ctcccgtctc 10320
gacccaagcc tgcaccaacc ctccaggata cggaggcggg tcgttttgca actttttttt 10380
ggaggccgga tgagactagt aagcgcggaa agcggccgac cgcgatggct cgctgccgta 10440
gtctggagaa gaatcgccag ggttgcgttg cggtgtgccc cggttcgagg ccggccggat 10500
tccgcggcta acgagggcgt ggctgccccg tcgtttccaa gaccccatag ccagccgact 10560
tctccagtta cggagcgagc ccctcttttg ttttgtttgt ttttgccaga tgcatcccgt 10620
actgcggcag atgcgccccc accaccctcc accgcaacaa cagccccctc cacagccggc 10680
gcttctgccc ccgccccagc agcaacttcc agccacgacc gccgcggccg ccgtgagcgg 10740
ggctggacag agttatgatc accagctggc cttggaagag ggcgaggggc tggcgcgcct 10800
gggggcgtcg tcgccggagc ggcacccgcg cgtgcagatg aaaagggacg ctcgcgaggc 10860
ctacgtgccc aagcagaacc tgttcagaga caggagcggc gaggagcccg aggagatgcg 10920
cgcggcccgg ttccacgcgg ggcgggagct gcggcgcggc ctggaccgaa agagggtgct 10980
gagggacgag gatttcgagg cggacgagct gacggggatc agccccgcgc gcgcgcacgt 11040
ggccgcggcc aacctggtca cggcgtacga gcagaccgtg aaggaggaga gcaacttcca 11100
aaaatccttc aacaaccacg tgcgcaccct gatcgcgcgc gaggaggtga ccctgggcct 11160
gatgcacctg tgggacctgc tggaggccat cgtgcagaac cccaccagca agccgctgac 11220
ggcgcagctg ttcctggtgg tgcagcatag tcgggacaac gaagcgttca gggaggcgct 11280
gctgaatatc accgagcccg agggccgctg gctcctggac ctggtgaaca ttctgcagag 11340
catcgtggtg caggagcgcg ggctgccgct gtccgagaag ctggcggcca tcaacttctc 11400
ggtgctgagt ttgggcaagt actacgctag gaagatctac aagaccccgt acgtgcccat 11460
agacaaggag gtgaagatcg acgggtttta catgcgcatg accctgaaag tgctgaccct 11520
gagcgacgat ctgggggtgt accgcaacga caggatgcac cgtgcggtga gcgccagcag 11580
gcggcgcgag ctgagcgacc aggagctgat gcatagtctg cagcgggccc tgaccggggc 11640
cgggaccgag ggggagagct actttgacat gggcgcggac ctgcactggc agcccagccg 11700
ccgggccttg gaggcggcgg caggacccta cgtagaagag gtggacgatg aggtggacga 11760
ggagggcgag tacctggaag actgatggcg cgaccgtatt tttgctagat gcaacaacaa 11820
cagccacctc ctgatcccgc gatgcgggcg gcgctgcaga gccagccgtc cggcattaac 11880
tcctcggacg attggaccca ggccatgcaa cgcatcatgg cgctgacgac ccgcaacccc 11940
gaagccttta gacagcagcc ccaggccaac cggctctcgg ccatcctgga ggccgtggtg 12000
ccctcgcgct ccaaccccac gcacgagaag gtcctggcca tcgtgaacgc gctggtggag 12060
aacaaggcca tccgcggcga cgaggccggc ctggtgtaca acgcgctgct ggagcgcgtg 12120
gcccgctaca acagcaccaa cgtgcagacc aacctggacc gcatggtgac cgacgtgcgc 12180
gaggccgtgg cccagcgcga gcggttccac cgcgagtcca acctgggatc catggtggcg 12240
ctgaacgcct tcctcagcac ccagcccgcc aacgtgcccc ggggccagga ggactacacc 12300

20262014626 26 Feb 2026

aacttcatca gcgccctgcg cctgatggtg accgaggtgc cccagagcga ggtgtaccag 12360
tccgggccgg actacttctt ccagaccagt cgccagggct tgcagaccgt gaacctgagc 12420
caggctttca agaacttgca gggcctgtgg ggcgtgcagg ccccggtcgg ggaccgcgcg 12480
acggtgtcga gcctgctgac gccgaactcg cgcctgctgc tgctgctggt ggccccttc 12540
acggacagcg gcagcatcaa ccgcaactcg tacctgggct acctgattaa cctgtaccgc 12600
gaggccatcg gccaggcgca cgtggacgag cagacctacc aggagatcac ccacgtgagc 12660
cgcgccctgg gccaggacga cccgggcaac ctggaagcca ccctgaactt tttgctgacc 12720
aaccggtcgc agaagatccc gccccagtac gcgctcagca ccgaggagga gcgcatcctg 12780
cgttacgtgc agcagagcgt gggcctgttc ctgatgcagg agggggccac ccccagcgcc 12840
gcgctcgaca tgaccgcgcg caacatggag cccagcatgt acgccagcaa ccgcccgttc 12900
atcaataaac tgatggacta cttgcatcgg gcggccgcca tgaactctga ctatttcacc 12960
aacgccatcc tgaatcccca ctggctcccg ccgccggggt tctacacggg cgagtacgac 13020
atgcccgacc ccaatgacgg gttcctgtgg gacgatgtgg acagcagcgt gttctccccc 13080
cgaccgggtg ctaacgagcg ccccttgtgg aagaaggaag gcagcgaccg acgcccgtcc 13140
tcggcgctgt ccggccgcga gggtgctgcc gcggcggtgc ccgaggccgc cagtcctttc 13200
ccgagcttgc ccttctcgct gaacagtatc cgcagcagcg agctgggcag gatcacgcgc 13260
ccgcgcttgc tgggcgaaga ggagtacttg aatgactcgc tgttgagacc cgagcgggag 13320
aagaacttcc ccaataacgg gatagaaagc ctggtggaca agatgagccg ctggaagacg 13380
tatgcgcagg agcacaggga cgatccccgg gcgtcgcagg gggccacgag ccggggcagc 13440
gccgcccgta aacgccggtg gcacgacagg cagcggggac agatgtggga cgatgaggac 13500
tccgccgacg acagcagcgt gttggacttg ggtgggagtg gtaacccgtt cgctcacctg 13560
cgcccccgta tcgggcgcat gatgtaagag aaaccgaaaa taaatgatac tcaccaaggc 13620
catggcgacc agcgtgcgtt cgtttcttct ctgttgttgt tgtatctagt atgatgaggc 13680
gtgcgtaccc ggagggtcct cctccctcgt acgagagcgt gatgcagcag gcgatggcgg 13740
cggcggcgat gcagcccccg ctggaggctc cttacgtgcc cccgcggtac ctggcgccta 13800
cggaggggcg gaacagcatt cgttactcgg agctggcacc cttgtacgat accacccggt 13860
tgtacctggt ggacaacaag tcggcggaca tcgcctcgct gaactaccag aacgaccaca 13920
gcaacttcct gaccaccgtg gtgcagaaca atgacttcac ccccacggag gccagcaccc 13980
agaccatcaa ctttgacgag cgctcgcggt ggggcggcca gctgaaaacc atcatgcaca 14040
ccaacatgcc caacgtgaac gagttcatgt acagcaacaa gttcaaggcg cgggtgatgg 14100
tctcccgcaa gacccccaat ggggtgacag tgacagagga ttatgatggt agtcaggatg 14160
agctgaagta tgaatgggtg gaatttgagc tgcccgaagg caacttctcg gtgaccatga 14220
ccatcgacct gatgaacaac gccatcatcg acaattactt ggcggtgggg cggcagaacg 14280
gggtgctgga gagcgacatc ggcgtgaagt tcgacactag gaacttcagg ctgggctggg 14340
accccgtgac cgagctggtc atgcccgggg tgtacaccaa cgaggctttc catcccgata 14400
ttgtcttgct gcccggctgc ggggtggact tcaccgagag ccgcctcagc aacctgctgg 14460
gcattcgcaa gaggcagccc ttccaggaag gcttccagat catgtacgag gatctggagg 14520
ggggcaacat ccccgcgctc ctggatgtcg acgcctatga gaaaagcaag gaggatgcag 14580
cagctgaagc aactgcagcc gtagctaccg cctctaccga ggtcaggggc gataattttg 14640
caagcgccgc agcagtggca gcggccgagg cggctgaaac cgaaagtaag atagtcattc 14700
agccggtgga gaaggatagc aagaacagga gctacaacgt actaccggac aagataaaca 14760
ccgcctaccg cagctggtac ctagcctaca actatggcga ccccgagaag ggcgtgcgct 14820
cctggacgct gctcaccacc tcggacgtca cctgcggcgt ggagcaagtc tactggtcgc 14880
tgcccgacat gatgcaagac ccggtcacct tccgctccac gcgtcaagtt agcaactacc 14940
cggtggtggg cgccgagctc ctgcccgtct actccaagag cttcttcaac gagcaggccg 15000
tctactcgca gcagctgcgc gccttcacct cgcttacgca cgtcttcaac cgcttccccg 15060
agaaccagat cctcgtccgc ccgcccgcgc ccaccattac caccgtcagt gaaaacgttc 15120
ctgctctcac agatcacggg accctgccgc tgcgcagcag tatccgggga gtccagcgcg 15180
tgaccgttac tgacgccaga cgccgcacct gcccctacgt ctacaaggcc ctgggcatag 15240
tcgcgccgcg cgtcctctcg agccgcacct tctaaatgtc cattctcatc tcgcccagta 15300
ataacaccgg ttggggcctg cgcgcgccca gcaagatgta cggaggcgct cgccaacgct 15360
ccacgcaaca ccccgtgcgc gtgcgcgggc acttccgcgc tccctggggc gccctcaagg 15420
gccgcgtgcg gtcgcgcacc accgtcgacg acgtgatcga ccaggtggtg gccgacgcgc 15480
gcaactacac ccccgccgcc gcgcccgtct ccaccgtgga cgccgtcatc gacagcgtgg 15540
tggccgacgc gcgccggtac gcccgcgcca agagccggcg gcggcgcatc gcccggcggc 15600
accggagcac ccccgccatg cgcgcggcgc gagccttgct gcgcagggcc aggcgcacgg 15660
gacgcagggc catgctcagg gcggccagac gcgcggcttc aggcgccagc gccggcagga 15720
cccggagacg cgcggccacg gcggcggcag cggccatcgc cagcatgtcc cgcccgcggc 15780
gagggaacgt gtactgggtg cgcgacgccg ccaccggtgt gcgcgtgccc gtgcgcaccc 15840
gccccctcg cacttgaaga tgttcacttc gcgatgttga tgtgtcccag cggcgaggag 15900
gatgtccaag cgcaaattca aggaagagat gctccaggtc atcgcgcctg agatctacgg 15960
ccctgcggtg gtgaaggagg aaagaaagcc ccgcaaaatc aagcgggtca aaaaggacaa 16020
aaaggaagaa gaaagtgatg tggacggatt ggtggagttt gtgcgcgagt tcgccccccg 16080
gcggcgcgtg cagtggcgcg ggcggaaggt gcaaccggtg ctgagacccg gcaccaccgt 16140
ggtcttcacg cccggcgagc gctccggcac cgcttccaag cgctcctacg acgaggtgta 16200
cggggatgat gatattctgg agcaggcggc cgagcgcctg ggcgagtttg cttacggcaa 16260
gcgcagccgt tccgcaccga aggaagaggc ggtgtccatc ccgctggacc acggcaaccc 16320
cacgccgagc ctcaagcccg tgaccttgca gcaggtgctg ccgaccgcgg cgccgcgccg 16380
ggggttcaag cgcgagggcg aggatctgta ccccaccatg cagctgatgg tgcccaagcg 16440
ccagaagctg gaagacgtgc tggagaccat gaaggtggac ccggacgtgc agcccgaggt 16500
caaggtgcgg cccatcaagc aggtggcccc gggcctgggc gtgcagaccg tggacatcaa 16560
gattcccacg gagcccatgg aaacgcagac cgagcccatg atcaagccca gcaccagcac 16620
catggaggtg cagacggatc cctggatgcc atcggctcct agtcgaagac cccggcgcaa 16680
gtacggcgcg gccagcctgc tgatgcccaa ctacgcgctg catccttcca tcatccccac 16740
gccgggctac cgcggcacgc gcttctaccg cggtcatacc agcagccgcc gccgcaagac 16800
caccactcgc cgccgccgtc gccgcaccgc cgctgcaacc acccctgccg ccctggtgcg 16860

2026201462 26 Feb 2026

gagagtgtac cgccgcggcc gcgcacctct gaccctgccg cgcgcgcgct accacccgag 16920
catcgccatt taaactttcg cctgctttgc agatcaatgg ccctcacatg ccgccttcgc 16980
gttcccatta cgggctaccg aggaagaaaa ccgcgccgta gaaggctggc ggggaacggg 17040
atgcgtcgcc accaccaccg gcggcggcgc gccatcagca agcggttggg gggaggcttc 17100
ctgcccgcgc tgatccccat catcgccgcg gcgatcgggg cgatccccgg cattgcttcc 17160
gtggcggtgc aggcctctca gcgccactga gacacacttg gaaacatctt gtaataaacc 17220
aatggactct gacgctcctg gtcctgtgat gtgttttcgt agacagatgg aagacatcaa 17280
tttttcgtcc ctggctccgc gacacggcac gcggccgttc atgggcacct ggagcgacat 17340
cggcaccagc caactgaacg ggggcgcctt caattggagc agtctctgga gcgggcttaa 17400
gaatttcggg tccacgctta aaacctatgg cagcaaggcg tggaacagca ccacagggca 17460
ggcgctgagg gataagctga aagagcagaa cttccagcag aaggtggtcg atgggctcgc 17520
ctcgggcatc aacggggtgg tggacctggc caaccaggcc gtgcagcggc agatcaacag 17580
ccgcctggac ccggtgccgc ccgccggctc cgtggagatg ccgcaggtgg aggaggagct 17640
gcctcccctg gacaagcggg gcgagaagcg accccgcccc gatgcggagg agacgctgct 17700
gacgcacacg gacgagccgc ccccgtacga ggaggcggtg aaactgggtc tgcccaccac 17760
gcggcccatc gcgcccctgg ccaccggggt gctgaaaccc gaaaagcccg cgaccctgga 17820
cttgcctcct ccccagcctt cccgcccctc tacagtggct aagcccctgc cgccggtggc 17880
cgtggcccgc gcgcgacccg ggggcaccgc ccgccctcat gcgaactggc agagcactct 17940
gaacagcatc gtgggtctgg gagtgcagag tgtgaagcgc cgccgctgct attaaaccta 18000
ccgtagcgct taacttgctt gtctgtgtgt gtatgtatta tgtcgccgcc gccgctgtcc 18060
accagaagga ggagtgaaga ggcgcgtcgc cgagttgcaa gatggccacc ccatcgatgc 18120
tgccccagtg ggcgtacatg cacatcgccg gacaggacgc ttcggagtac ctgagtccgg 18180
gtctggtgca gtttgcccgc gccacagaca cctacttcag tctggggaac aagtttagga 18240
accccacggt ggcgcccacg cacgatgtga ccaccgaccg cagccagcgg ctgacgctgc 18300
gcttcgtgcc cgtggaccgc gaggacaaca cctactcgta caaagtgcgc tacacgctgg 18360
ccgtgggcga caaccgcgtg ctggacatgg ccagcaccta ctttgacatc cgcggcgtgc 18420
tggatcgggg ccctagcttc aaaccctact ccggcaccgc ctacaacagt ctggccccca 18480
agggagcacc caacacttgt cagtggacat ataaagccga tggtgaaact gccacagaaa 18540
aaacctatac atatggaaat gcacccgtgc agggcattaa catcacaaaa gatggtattc 18600
aacttggaac tgacaccgat gatcagccaa tctacgcaga taaaacctat cagcctgaac 18660
ctcaagtggg tgatgctgaa tggcatgaca tcactggtac tgatgaaaag tatggaggca 18720
gagctcttaa gcctgatacc aaaatgaagc cttgttatgg ttcttttgcc aagcctacta 18780
ataaagaagg aggtcaggca aatgtgaaaa caggaacagg cactactaaa gaatatgaca 18840
tagacatggc tttctttgac aacagaagtg cggctgctgc tggcctagct ccagaaattg 18900
ttttgtatac tgaaaatgtg gatttggaaa ctccagatac ccatattgta tacaaagcag 18960
gcacagatga cagcagctct tctattaatt tgggtcagca agccatgccc aacagaccta 19020
actacattgg tttcagagac aactttatcg ggctcatgta ctacaacagc actggcaata 19080
tgggggtgct ggccggtcag gcttctcagc tgaatgctgt ggttgacttg caagacagaa 19140
acaccgagct gtcctaccag ctcttgcttg actctctggg tgacagaacc cggtatttca 19200
gtatgtggaa tcaggcggtg gacagctatg atcctgatgt gcgcattatt gaaaatcatg 19260
gtgtggagga tgaacttccc aactattgtt tccctctgga tgctgttggc agaacagata 19320
cttatcaggg aattaaggct aatggaactg atcaaaccac atggaccaaa gatgacagtg 19380
tcaatgatgc taatgagata ggcaagggta atccattcgc catggaaatc aacatccaag 19440
ccaacctgtg gaggaacttc ctctacgcca acgtggccct gtacctgccc gactcttaca 19500
agtacacgcc ggccaatgtt accctgccca ccaacaccaa cacctacgat tacatgaacg 19560
gccgggtggt ggcgccctcg ctggtggact cctacatcaa catcggggcg cgctggtcgc 19620
tggatcccat ggacaacgtg aaccccttca accaccaccg caatgcgggg ctgcgctacc 19680
gctccatgct cctgggcaac gggcgctacg tgcccttcca catccaggtg ccccagaaat 19740
ttttcgccat caagagcctc ctgctcctgc ccgggtccta cacctacgag tggaacttcc 19800
gcaaggacgt caacatgatc ctgcagagct ccctcggcaa cgacctgcgc acggacgggg 19860
cctccatctc cttcaccagc atcaacctct acgccacctt cttccccatg gcgcacaaca 19920
cggcctccac gctcgaggcc atgctgcgca acgacaccaa cgaccagtcc ttcaacgact 19980
acctctcggc ggccaacatg ctctacccca tcccggccaa cgccaccaac gtgcccatct 20040
ccatcccctc gcgcaactgg gccgccttcc gcggctggtc cttcacgcgt ctcaagacca 20100
aggagacgcc ctcgctgggc tccgggttcg acccctactt cgtctactcg ggctccatcc 20160
cctacctcga cggcaccttc tacctcaacc acaccttcaa gaaggtctcc atcaccttcg 20220
actcctccgt cagctggccc ggcaacgacc ggctcctgac gcccaacgag ttcgaaatca 20280
agcgcaccgt cgacggcgag ggctacaacg tggcccagtg caacatgacc aaggactggt 20340
tcctggtcca gatgctggcc cactacaaca tcggctacca gggcttctac gtgcccgagg 20400
gctacaagga ccgcatgtac tccttcttcc gcaacttcca gcccatgagc cgccaggtgg 20460
tggacgaggt caactacaag gactaccagg ccgtcaccct ggcctaccag cacaacaact 20520
cgggcttcgt cggctacctc gcgcccacca tgcgccaggg ccagccctac cccgccaact 20580
acccctaccc gctcatcggc aagagcgccg tcaccagcgt cacccagaaa aagttcctct 20640
gcgacagggt catgtggcgc atccccttct ccagcaactt catgtccatg ggcgcgctca 20700
ccgacctcgg ccagaacatg ctctatgcca actccgccca cgcgctagac atgaatttcg 20760
aagtcgaccc catggatgag tccacccttc tctatgttgt cttcgaagtc ttcgacgtcg 20820
tccgagtgca ccagccccac cgcggcgtca tcgaggccgt ctacctgcgc acccccttct 20880
cggccggtaa cgccaccacc taagctcttg cttcttgcaa gccatggccg cgggctccgg 20940
cgagcaggag ctcagggcca tcatccgcga cctgggctgc gggccctact tcctgggcac 21000
cttcgataag cgcttcccgg gattcatggc cccgcacaag ctggcctgcg ccatcgtcaa 21060
cacggccggc cgcgagaccg ggggcgagca ctggctggcc ttcgcctgga acccgcgctc 21120
gaacacctgc tacctcttcg acccccttcgg gttctcggac gagcgcctca agcagatcta 21180
ccagttcgag tacgagggcc tgctgcgccg cagcgccctg gccaccgagg accgctgcgt 21240
caccctggaa aagtccaccc agaccgtgca gggtccgcgc tcggccgcct gcgggctctt 21300
ctgctgcatg ttcctgcacg ccttcgtgca ctggcccgac cgccccatgg acaagaaccc 21360
caccatgaac ttgctgacgg gggtgcccaa cggcatgctc cagtcgcccc aggtggaacc 21420

20262014626 26 Feb 2026

		caccctgcgc cgcaaccagg aggcgctcta ccgcttcctc aactcccact ccgcctactt 21480 tcgctcccac cgcgcgcgca tcgagaaggc caccgccttc gaccgcatga atcaagacat 21540 gtaaaccgtg tgtgtatgtt aaatgtcttt aataaacagc actttcatgt tacacatgca 21600 tctgagatga tttatttaga aatcgaaagg gttctgccgg gtctcggcat ggcccgcggg 21660 cagggacacg ttgcggaact ggtacttggc cagccacttg aactcgggga tcagcagttt 21720 gggcagcggg gtgtcgggga aggagtcggt ccacagcttc cgcgtcagtt gcagggcgcc 21780 cagcaggtcg ggcgcggaga tcttgaaatc gcagttggga cccgcgttct gcgcgcggga 21840 gttgcggtac acggggttgc agcactggaa caccatcagg gccgggtgct tcacgctcgc 21900 cagcaccgtc gcgtcggtga tgctctccac gtcgaggtcc tcggcgttgg ccatcccgaa 21960 gggggtcatc ttgcaggtct gccttcccat ggtgggcacg cacccgggct tgtggttgca 22020 atcgcagtgc agggggatca gcatcatctg ggcctggtcg gcgttcatcc ccgggtacat 22080 ggccttcatg aaagcctcca attgcctgaa cgcctgctgg gccttggctc cctcggtgaa 22140 gaagaccccg caggacttgc tagagaactg gttggtggcg cacccggcgt cgtgcacgca 22200 gcagcgcgcg tcgttgttgg ccagctgcac cacgctgcgc ccccagcggt tctgggtgat 22260 cttggcccgg tcggggttct ccttcagcgc gcgctgcccg ttctcgctcg ccacatccat 22320 ctcgatcatg tgctccttct ggatcatggt ggtcccgtgc aggcaccgca gcttgccctc 22380 ggcctcggtg cacccgtgca gccacagcgc gcacccggtg cactcccagt tcttgtgggc 22440 gatctgggaa tgcgcgtgca cgaagccctg caggaagcgg cccatcatgg tggtcagggt 22500 cttgttgcta gtgaaggtca gcggaatgcc gcggtgctcc tcgttgatgt acaggtggca 22560 gatgcggcgg tacacctcgc cctgctcggg catcagctgg aagttggctt tcaggtcggt 22620 ctccacgcgg tagcggtcca tcagcatagt catgatttcc ataccttct cccaggccga 22680 gacgatgggc aggctcatag ggttcttcac catcatctta gcgctagcag ccgcggccag 22740 ggggtcgctc tcgtccaggg tctcaaagct ccgcttgccg tccttctcgg tgatccgcac 22800 cgggggggtag ctgaagccca cggccgccag ctcctcctcg gcctgtcttt cgtcctcgct 22860 gtcctggctg acgtcctgca ggaccacatg cttggtcttg cggggtttct tcttgggcgg 22920 cagcggcggc ggagatgttg gagatggcga gggggagcgc gagttctcgc tcaccactac 22980 tatctcttcc tcttcttggt ccgaggccac gcggcggtag gtatgtctct tcgggggcag 23040 aggcggaggc gacgggctct cgccgccgcg acttggcgga tggctggcag agcccctcc 23100 gcgttcgggg gtgcgctccc ggcggcgctc tgactgactt cctccgcggc cggccattgt 23160 gttctcctag ggaggaacaa caagcatgga gactcagcca tcgccaacct cgccatctgc 23220 ccccaccgcc gacgagaagc agcagcagca gaatgaaagc ttaaccgccc cgccgcccag 23280 ccccgccacc tccgacgcgg ccgtcccaga catgcaagag atggaggaat ccatcgagat 23340 tgacctgggc tatgtgacgc ccgcggagca cgaggaggag ctggcagtgc gcttttcaca 23400 agaagagata caccaagaac agccagagca ggaagcagag aatgagcaga gtcaggctgg 23460 gctcgagcat gacggcgact acctccacct gagcgggggg gaggacgcgc tcatcaagca 23520 tctggcccgg caggccacca tcgtcaagga tgcgctgctc gaccgcaccg aggtgcccct 23580 cagcgtggag gagctcagcc gcgcctacga gttgaacctc ttctcgccgc gcgtgccccc 23640 caagcgccag cccaatggca cctgcgagcc caacccgcgc ctcaacttct acccggtctt 23700 cgcggtgccc gaggccctgg ccacctacca catctttttc aagaaccaaa agatccccgt 23760 ctcctgccgc gccaaccgca cccgcgccga cgccctttc aacctgggtc ccggcgcccg 23820 cctacctgat atcgcctcct tggaagaggt tcccaagatc ttcgagggtc tgggcagcga 23880 cgagactcgg gccgcgaacg ctctgcaagg agaaggagga gagcatgagc accacagcgc 23940 cctggtcgag ttggaaggcg acaacgcgcg gctggcggtg ctcaaacgca cggtcgagct 24000 gacccatttc gcctacccgg ctctgaacct gccccccaaa gtcatgagcg cggtcatgga 24060 ccaggtgctc atcaagcgcg cgtcgcccat ctccgaggac gagggcatgc aagactccga 24120 ggagggcaag cccgtggtca gcgacgagca gctggcccgg tggctgggtc ctaatgctag 24180 tccccagagt ttggaagagc ggcgcaaact catgatggcc gtggtcctgg tgaccgtgga 24240 gctggagtgc ctgcgccgct tcttcgccga cgcggagacc ctgcgcaagg tcgaggagaa 24300 cctgcactac ctcttcaggc acgggttcgt gcgccaggcc tgcaagatct ccaacgtgga 24360 gctgaccaac ctggtctcct acatgggcat cttgcacgag aaccgcctgg ggcagaacgt 24420 gctgcacacc accctgcgcg gggaggcccg gcgcgactac atccgcgact gcgtctacct 24480 ctacctctgc cacacctggc agacgggcat gggcgtgtgg cagcagtgtc tggaggagca 24540 gaacctgaaa gagctctgca agctcctgca gaagaacctc aagggtctgt ggaccgggtt 24600 cgacgagcgc accaccgcct cggacctggc cgacctcatt ttccccgagc gcctcaggct 24660 gacgctgcgc aacggcctgc ccgactttat gagccaaagc atgttgcaaa actttcgctc 24720 tttcatcctc gaacgctccg gaatcctgcc cgccacctgc tccgcgctgc cctcggactt 24780 cgtgccgctg accttccgcg agtgcccccc gccgctgtgg agccactgct acctgctgcg 24840 cctggccaac tacctggcct accactcgga cgtgatcgag gacgtcagcg gcgagggcct 24900 gctcgagtgc cactgccgct gcaacctctg cacgccgcac cgctccctgg cctgcaaccc 24960 ccagctgctg agcgagaccc agatcatcgg caccttcgag ttgcaagggc ccagcgaagg 25020 cgagggttca gccgccaagg ggggtctgaa actcaccccg gggctgtgga cctcggccta 25080 cttgcgcaag ttcgtgcccg aggactacca tcccttcgag atcaggttct acgaggacca 25140 atcccatccg cccaaggccg agctgtcggc ctgcgtcatc acccaggggg cgatcctggc 25200 ccaattgcaa gccatccaga aatcccgcca agaattcttg ctgaaaaagg gccgcggggt 25260 ctacctcgac ccccagaccg gtgaggagct caaccccggc ttcccccagg atgccccgag 25320 gaaacaagaa gctgaaagtg gagctgccgc ccgtggagga tttggaggaa gactgggaga 25380 acagcagtca ggcagaggag gaggagatgg aggaagactg ggacagcact caggcagagg 25440 aggacagcct gcaagacagt ctggaggaag acgaggagga ggcagaggag gaggtggaag 25500 aagcagccgc cgccagaccg tcgtcctcgg cgggggagaa agcaagcagc acggatacca 25560 tctccgctcc gggtcggggt cccgctcgac cacacagtag atgggacgag accggacgat 25620 tcccgaaccc caccacccag accggtaaga aggagcggca gggatacaag tcctggcggg 25680 ggcacaaaaa cgccatcgtc tcctgcttgc aggcctgcgg gggcaacatc tccttcaccc 25740 ggcgctacct gctcttccac cgcggggtga actttccccg caacatcttg cattactacc 25800 gtcacctcca cagcccctac tacttccaag aagaggcagc agcagcagaa aaagaccagc 25860 agaaaaccag cagctagaaa atccacagcg gcggcagcag gtggactgag gatcgcggcg 25920 aacgagccgg cgcaaacccg ggagctgagg aaccggatct ttcccaccct ctatgccatc 25980

20262014622 26 Feb 2026

ttccagcaga gtcgggggca ggagcaggaa ctgaaagtca agaaccgttc tctgcgctcg 26040
ctcacccgca gttgtctgta tcacaagagc gaagaccaac ttcagcgcac tctcgaggac 26100
gccgaggctc tcttcaacaa gtactgcgcg ctcactctta aagagtagcc cgcgcccgcc 26160
cagtcgcaga aaaaggcggg aattacgtca cctgtgccct tcgccctagc cgcctccacc 26220
catcatcatg agcaaagaga ttcccacgcc ttacatgtgg agctaccagc cccagatggg 26280
cctggccgcc ggtgccgccc aggactactc cacccgcatg aattggctca gcgccgggcc 26340
cgcgatgatc tcacgggtga atgacatccg cgcccaccga aaccagatac tcctagaaca 26400
gtcagcgctc accgccacgc cccgcaatca cctcaatccg cgtaattggc ccgccgccct 26460
ggtgtaccag gaaattcccc agcccacgac cgtactactt ccgcgagacg cccaggccga 26520
agtccagctg actaactcag gtgtccagct ggcgggcggc gccaccctgt gtcgtcaccg 26580
ccccgctcag ggtataaagc ggctggtgat ccggggcaga ggcacacagc tcaacgacga 26640
ggtggtgagc tcttcgctgg gtctgcgacc tgacggagtc ttccaactcg ccggatcggg 26700
gagatcttcc ttcacgcctc gtcaggccgt cctgactttg gagagttcgt cctcgcagcc 26760
ccgctcgggt ggcatcggca ctctccagtt cgtggaggag ttcactccct cggtctactt 26820
caaccccttc tccggctccc ccggccacta cccggacgag ttcatcccga acttcgacgc 26880
catcagcgag tcggtggacg gctacgattg aaactaatca cccccttatc cagtgaaata 26940
aagatcatat tgatgatgat tttacagaaa taaaaaataa tcatttgatt tgaaataaag 27000
atacaatcat attgatgatt tgagtttaac aaaaaaataa agaatcactt acttgaaatc 27060
tgataccagg tctctgtcca tgttttctgc caacaccact tcactcccct cttcccagct 27120
ctggtactgc aggccccggc gggctgcaaa cttcctccac acgctgaagg ggatgtcaaa 27180
ttcctcctgt ccctcaatct tcattttatc ttctatcaga tgtccaaaaa gcgcgtccgg 27240
gtggatgatg acttcgaccc cgtctacccc tacgatgcag acaacgcacc gaccgtgccc 27300
ttcatcaacc ccccccttcgt ctcttcagat ggattccaag agaagcccct gggggtgttg 27360
tccctgcgac tggccgaccc cgtcaccacc aagaacgggg aaatcaccct caagctggga 27420
gagggggtgg acctcgattc ctcgggaaaa ctcatctcca acacggccac caaggccgcc 27480
gcccctctca gtttttccaa caacaccatt tcccttaaca tggatcaccc cttttacact 27540
aaagatggaa aattatcctt acaagtttct ccaccattaa atatactgag aacaagcatt 27600
ctaaacacac tagctttagg ttttggatca ggtttaggac tccgtggctc tgccttggca 27660
gtacagttag tctctccact tacatttgat actgatggaa acataaagct taccttagac 27720
agaggtttgc atgttacaac aggagatgca attgaaagca acataagctg ggctaaaggt 27780
ttaaaatttg aagatggagc catagcaacc aacattggaa atgggttaga gtttggaagc 27840
agtagtacag aaacaggtgt tgatgatgct tacccaatcc aagttaaact tggatctggc 27900
cttagctttg acagtacagg agccataatg gctggtaaca aagaagacga taaactcact 27960
ttgtggacaa cacctgatcc atcaccaaac tgtcaaatac tcgcagaaaa tgatgcaaaa 28020
ctaacacttt gcttgactaa atgtggtagt caaatactgg ccactgtgtc agtcttagtt 28080
gtaggaagtg gaaacctaaa ccccattact ggcaccgtaa gcagtgctca ggtgtttcta 28140
cgttttgatg caaacggtgt tcttttaaca gaacattcta cactaaaaaa atactggggg 28200
tataggcagg gagatagcat agatggcact ccatatacca atgctgtagg attcatgccc 28260
aatttaaaag cttatccaaa gtcacaaagt tctactacta aaaataatat agtagggcaa 28320
gtatacatga atggagatgt ttcaaaacct atgcttctca ctataaccct caatggtact 28380
gatgacagca acagtacata ttcaatgtca ttttcataca cctggactaa tggaagctat 28440
gttggagcaa catttggggc taactcttat accttctcat acatcgccca agaatgaaca 28500
ctgtatccca ccctgcatgc caacccttcc caccccactc tgtggaacaa actctgaaac 28560
acaaaataaa ataaagttca agtgttttat tgattcaaca gttttacagg attcgagcag 28620
ttatttttcc tccaccctcc caggacatgg aatacaccac cctctccccc cgcacagcct 28680
tgaacatctg aatgccattg gtgatggaca tgcttttggt ctccacgttc cacacagttt 28740
cagagcgagc cagtctcggg tcggtcaggg agatgaaacc ctccgggcac tcccgcatct 28800
gcacctcaca gctcaacagc tgaggattgt cctcggtggt cgggatcacg gttatctgga 28860
agaagcagaa gagcggcggt gggaatcata gtccgcgaac gggatcggcc ggtggtgtcg 28920
catcaggccc cgcagcagtc gctgccgccg ccgctccgtc aagctgctgc tcaggggtc 28980
cgggtccagg gactccctca gcatgatgcc cacggccctc agcatcagtc gtctggtgcg 29040
gcgggcgcag cagcgcatgc ggatctcgct caggtcgctg cagtacgtgc aacacagaac 29100
caccaggttg ttcaacagtc catagttcaa cacgctccag ccgaaactca tcgcgggaag 29160
gatgctaccc acgtggccgt cgtaccagat cctcaggtaa atcaagtggt gccccctcca 29220
gaacacgctg cccacgtaca tgatctcctt gggcatgtgg cggttcacca cctcccggta 29280
ccacatcacc ctctggttga acatgcagcc ccggatgatc ctgcggaacc acagggccag 29340
caccgccccg cccgccatgc agcgaagaga ccccgggtcc cggcaatggc aatggaggac 29400
ccaccgctcg tacccgtgga tcatctggga gctgaacaag tctatgttgg cacagcacag 29460
gcatatgctc atgcatctct tcagcactct caactcctcg ggggtcaaaa ccatatccca 29520
gggcacgggg aactcttgca ggacagcgaa ccccgcagaa cagggcaatc ctcgcacaga 29580
acttacattg tgcatggaca gggtatcgca atcaggcagc accgggtgat cctccaccag 29640
agaagcgcgg gtctcggtct cctcacagcg tggtaagggg gccggccgat acgggtgatg 29700
gcgggacgcg gctgatcgtg ttcgcgaccg tgtcatgatg cagttgcttt cggacatttt 29760
cgtacttgct gtagcagaac ctggtccggg cgctgcacac cgatcgccgg cggcggtctc 29820
ggcgcttgga acgctcggtg ttgaaattgt aaaacagcca ctctctcaga ccgtgcagca 29880
gatctagggc ctcaggagtg atgaagatcc catcatgcct gatggctctg atcacatcga 29940
ccaccgtgga atgggccaga cccagccaga tgatgcaatt ttgttgggtt tcggtgacgg 30000
cgggggaggg aagaacagga agaaccatga ttaactttta atccaaacgg tctcggagta 30060
cttcaaaatg aagatcgcgg agatggcacc tctcgccccc gctgtgttgg tggaaaataa 30120
cagccaggtc aaaggtgata cggttctcga gatgttccac ggtggcttcc agcaaagcct 30180
ccacgcgcac atccagaaac aagacaatag cgaaagcggg agggttctct aattcctcaa 30240
tcatcatgtt acactcctgc accatcccca gataattttc atttttccag ccttgaatga 30300
ttcgaactag ttcctgaggt aaatccaagc cagccatgat aaagagctcg cgcagagcgc 30360
cctccaccgg cattcttaag cacaccctca taattccaag atattctgct cctggttcac 30420
ctgcagcaga ttgacaagcg gaatatcaaa atctctgccg cgatccctga gctcctccct 30480
cagcaataac tgtaagtact ctttcatatc ctctccgaaa tttttagcca taggaccacc 30540

2026201462 26 Feb 2026

		aggaataaga ttagggcaag ccacagtaca gataaaccga agtcctcccc agtgagcatt 30600 gccaaatgca agactgctat aagcatgctg gctagacccg gtgatatctt ccagataact 30660 ggacagaaaa tcgcccaggc aatttttaag aaaatcaaca aaagaaaaat cctccaggtg 30720 gacgtttaga gcctcgggaa caacgatgaa gtaaatgcaa gcggtgcgtt ccagcatggt 30780 tagttagctg atctgtagaa aaaacaaaaa tgaacattaa accatgctag cctggcgaac 30840 aggtgggtaa atcgttctct ccagcaccag gcaggccacg gggtctccgg cgcgaccctc 30900 gtaaaaattg tcgctatgat tgaaaaccat cacagagaga cgttcccggt ggccggcgtg 30960 aatgattcga caagatgaat acacccccgg aacattggcg tccgcgagtg aaaaaaagcg 31020 cccgaggaag caataaggca ctacaatgct cagtctcaag tccagcaaag cgatgccatg 31080 cggatgaagc acaaaattct caggtgcgta caaaatgtaa ttactcccct cctgcacagg 31140 cagcaaagcc cccgatccct ccaggtacac atacaaagcc tcagcgtcca tagcttaccg 31200 agcagcagca cacaacaggc gcaagagtca gagaaaggct gagctctaac ctgtccaccc 31260 gctctctgct caatatatag cccagatcta cactgacgta aaggccaaag tctaaaaata 31320 cccgccaaat aatcacacac gcccagcaca cgcccagaaa ccggtgacac actcaaaaaa 31380 atacgcgcac ttcctcaaac gcccaaaact gccgtcattt ccgggttccc acgctacgtc 31440 atcaaaacac gactttcaaa ttccgtcgac cgttaaaaac gtcacccgcc ccgcccctaa 31500 cggtcgcccg tctctcagcc aatcagcgcc ccgcatcccc aaattcaaac acctcatttg 31560 catattaacg cgcacaaaaa gtttgagg 31588
3-3	**Sequences**	
3-3-1	Sequence Number [ID]	3
3-3-2	Molecule Type	DNA
3-3-3	Length	11447
3-3-4	Features	**source 1..11447**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Venezuelan equine encephalitis virus
	NonEnglishQualifier Value	
3-3-5	Residues	atgggcggcg catgagagaa gcccagacca attacctacc caaaatggag aaagttcacg 60 ttgacatcga ggaagacagc ccattcctca gagctttgca gcggagcttc ccgcagtttg 120 aggtagaagc caagcaggtc actgataatg accatgctaa tgccagagcg ttttcgcatc 180 tggcttcaaa actgatcgaa acggaggtgg acccatccga cacgatcctt gacattggaa 240 gtgcgcccgc ccgcagaatg tattctaagc acaagtatca ttgtatctgt ccgatgagat 300 gtgcggaaga tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgtaagg 360 aaataactga taaggaattg gacaagaaaa tgaaggagct cgccgccgtc atgagcgacc 420 ctgacctgga aactgagact atgtgcctcc acgacgacga gtcgtgtcgc tacgaagggc 480 aagtcgctgt ttaccaggat gtatacgcgg ttgacggacc gacaagtctc tatcaccaag 540 ccaataaggg agttagagtc gcctactgga taggctttga caccacccct tttatgttta 600 agaacttggc tggagcatat ccatcatact ctaccaactg ggccgacgaa accgtgttaa 660 cggctcgtaa cataggccta tgcagctctg acgttatgga gcggtcacgt agagggatgt 720 ccattcttag aaagaagtat ttgaaaccat ccaacaatgt tctattctct gttggctcga 780 ccatctacca cgagaagagg gacttactga ggagctggca cctgccgtct gtatttcact 840 tacgtggcaa gcaaaattac acatgtcggt gtgagactat agttagttgc gacgggtacg 900 tcgttaaaag aatagctatc agtccaggcc tgtatgggaa gccttcaggc tatgctgcta 960 cgatgcaccg cgagggattc ttgtgctgca aagtgacaga cacattgaac ggggagaggg 1020 tctcttttcc cgtgtgcacg tatgtgccag ctacattgtg tgaccaaatg actggcatac 1080 tggcaacaga tgtcagtgcg gacgacgcgc aaaaactgct ggttgggctc aaccagcgta 1140 tagtcgtcaa cggtcgcacc cagagaaaca ccaataccat gaaaaattac cttttgcccg 1200 tagtggccca ggcatttgct aggtgggcaa aggaatataa ggaagatcaa gaagatgaaa 1260 ggccactagg actacgagat agacagttag tcatggggtg ttgttgggct tttagaaggc 1320 acaagataac atctatttat aagcgcccgg atacccaaac catcatcaaa gtgaacagcg 1380 atttccactc attcgtgctg cccaggatag gcagtaacac attggagatc gggctgagaa 1440 caagaatcag gaaaatgtta gaggagcaca aggagccgtc acctctcatt accgccgagg 1500 acgtacaaga agctaagtgc gcagccgatg aggctaagga ggtgcgtgaa gccgaggagt 1560 tgcgcgcagc tctaccacct ttggcagctg atgttgagga gcccactctg gaagccgatg 1620 tcgacttgat gttacaagag gctggggccg gctcagtgga gacacctcgt ggcttgataa 1680 aggttaccag ctacgctggc gaggacaaga tcggctctta cgctgtgctt tctccgcagg 1740 ctgtactcaa gagtgaaaaa ttatcttgca tccaccctct cgctgaacaa gtcatagtga 1800 taacacactc tggccgaaaa gggcgttatg ccgtggaacc ataccatggt aaagtagtgg 1860 tgccagaggg acatgcaata cccgtccagg actttcaagc tctgagtgaa agtgccacca 1920 ttgtgtacaa cgaacgtgag ttcgtaaaca ggtacctgca ccatattgcc acacatggag 1980 gagcgctgaa cactgatgaa gaatattaca aaactgtcaa gcccagcgag cacgacggcg 2040 aatacctgta cgacatcgac aggaaacagt gcgtcaagaa agaactagtc actgggctag 2100 ggctcacagg cgagctggtg gatcctccct tccatgaatt cgcctacgag agtctgagaa 2160 cacgaccagc cgctccttac caagtaccaa ccataggggt gtatggcgtg ccaggatcag 2220 gcaagtctgg catcattaaa agcgcagtca ccaaaaaaga tctagtggtg agcgccaaga 2280 aagaaaactg tgcagaaatt ataagggacg tcaagaaaat gaaagggctg gacgtcaatg 2340 ccagaactgt ggactcagtg ctcttgaatg gatgcaaaca ccccgtagag accctgtata 2400 ttgacgaagc ttttgcttgt catgcaggta ctctcagagc gctcatagcc attataagac 2460 ctaaaaaggc agtgctctgc ggggatccca aacagtgcgg ttttttaac atgatgtgcc 2520 tgaaagtgca ttttaaccac gagatttgca cacaagtctt ccacaaaagc atctctcgcc 2580 gttgcactaa atctgtgact tcggtcgtct caaccttgtt ttacgacaaa aaaatgagaa 2640 cgacgaatcc gaaagagact aagattgtga ttgacactac cggcagtacc aaacctaagc 2700 aggacgatct cattctcact tgtttcagag ggtgggtgaa gcagttgcaa atagattaca 2760 aaggcaacga aataatgacg gcagctgcct ctcaagggct gacccgtaaa ggtgtgtatg 2820 ccgttcggta caaggtgaat gaaaatcctc tgtacgcacc cacctcagaa catgtgaacg 2880 tcctactgac ccgcacggag gaccgcatcg tgtggaaaac actagccggc gacccatgga 2940

20262014626 26 Feb 2026

taaaaacact gactgccaag taccctggga atttcactgc cacgatagag gagtggcaag 3000
cagagcatga tgccatcatg aggcacatct tggagagacc ggaccctacc gacgtcttcc 3060
agaataaggc aaacgtgtgt tgggccaagg ctttagtgcc ggtgctgaag accgctggca 3120
tagacatgac cactgaacaa tggaacactg tggattattt tgaaacggac aaagctcact 3180
cagcagagat agtattgaac caactatgcg tgaggttctt tggactcgat ctggactccg 3240
gtctattttc tgcacccact gttccgttat ccattaggaa taatcactgg gataactccc 3300
cgtcgcctaa catgtacggg ctgaataaag aagtggtccg tcagctctct cgcaggtacc 3360
cacaactgcc tcgggcagtt gccactggaa gagtctatga catgaacact ggtacactgc 3420
gcaattatga tccgcgcata aacctagtac ctgtaaacag aagactgcct catgctttag 3480
tcctccacca taatgaacac ccacagagtg acttttcttc attcgtcagc aaattgaagg 3540
gcagaactgt cctggtggtc ggggaaaagt tgtccgtccc aggcaaaatg gttgactggt 3600
tgtcagaccg gcctgaggct accttcagag ctcggctgga tttaggcatc ccaggtgatg 3660
tgcccaaata tgacataata tttgttaatg tgaggacccc atataaatac catcactatc 3720
agcagtgtga agaccatgcc attaagctta gcatgttgac caagaaagct tgtctgcatc 3780
tgaatcccgg cggaacctgt gtcagcatag gttatggtta cgctgacagg gccagcgaaa 3840
gcatcattgg tgctatagcg cggcagttca agttttcccg ggtatgcaaa ccgaaatcct 3900
cacttgaaga gacggaagtt ctgtttgtat tcattgggta cgatcgcaag gcccgtacgc 3960
acaatcctta caagctttca tcaaccttga ccaacattta tacaggttcc agactccacg 4020
aagccggatg tgcaccctca tatcatgtgg tgcgagggga tattgccacg gccaccgaag 4080
gagtgattat aaatgctgct aacagcaaag gacaacctgg cggaggggtg tgcggagcgc 4140
tgtataagaa attcccggaa agcttcgatt tacagccgat cgaagtagga aaagcgcgac 4200
tggtcaaagg tgcagctaaa catatcattc atgccgtagg accaaacttc aacaaagttt 4260
cggaggttga aggtgacaaa cagttggcag aggcttatga gtccatcgct aagattgtca 4320
acgataacaa ttacaagtca gtagcgattc cactgttgtc caccggcatc ttttccggga 4380
acaaagatcg actaacccaa tcattgaacc atttgctgac agctttagac accactgatg 4440
cagatgtagc catatactgc agggacaaga aatgggaaat gactctcaag gaagcagtgg 4500
ctaggagaga agcagtggag gagatatgca tatccgacga ctcttcagtg acagaacctg 4560
atgcagagct ggtgagggtg catccgaaga gttctttggc tggaaggaag ggctacagca 4620
caagcgatgg caaaactttc tcatatttgg aagggaccaa gtttcaccag gcggccaagg 4680
atatagcaga aattaatgcc atgtggcccg ttgcaacgga ggccaatgag caggtatgca 4740
tgtatatcct cggagaaagc atgagcagta ttaggtcgaa atgccccgtc gaagagtcgg 4800
aagcctccac accacctagc acgctgcctt gcttgtgcat ccatgccatg actccagaaa 4860
gagtacagcg cctaaaagcc tcacgtccag aacaaattac tgtgtgctca tcctttccat 4920
tgccgaagta tagaatcact ggtgtgcaga agatccaatg ctcccagcct atattgttct 4980
caccgaaagt gcctgcgtat attcatccaa ggaagtatct cgtggaaaca ccaccggtag 5040
acgagactcc ggagccatcg gcagagaacc aatccacaga ggggacacct gaacaaccac 5100
cacttataac cgaggatgag accaggacta gaacgcctga gccgatcatc atcgaagagg 5160
aagaagagga tagcataagt ttgctgtcag atggcccgac ccaccaggtg ctgcaagtcg 5220
aggcagacat tcacgggccg ccctctgtat ctagctcatc ctggtccatt cctcatgcat 5280
ccgactttga tgtggacagt ttatccatac ttgacaccct ggagggagct agcgtgacca 5340
gcggggcaac gtcagccgag actaactctt acttcgcaaa gagtatggag tttctggcgc 5400
gaccggtgcc tgcgcctcga acagtattca ggaaccctcc acatcccgct ccgcgcacaa 5460
gaacaccgtc acttgcaccc agcagggcct gctcgagaac cagcctagtt tccaccccgc 5520
caggcgtgaa tagggtgatc actagagagg agctcgaggc gcttaccccg tcacgcactc 5580
ctagcaggtc ggtctcgaga accagcctgg tctccaaccc gccaggcgta aatagggtga 5640
ttacaagaga ggagtttgag gcgttcgtag cacaacaaca atgacggttt gatgcgggtg 5700
catacatctt ttcctccgac accggtcaag ggcatttaca acaaaaatca gtaaggcaaa 5760
cggtgctatc cgaagtggtg ttggagagga ccgaattgga gatttcgtat gccccgcgcc 5820
tcgaccaaga aaaagaagaa ttactacgca agaaattaca gttaaatccc acacctgcta 5880
acagaagcag ataccagtcc aggaaggtgg agaacatgaa agccataaca gctagacgta 5940
ttctgcaagg cctagggcat tatttgaagg cagaaggaaa agtggagtgc taccgaaccc 6000
tgcatcctgt tcctttgtat tcatctagtg tgaaccgtgc cttttcaagc cccaaggtcg 6060
cagtggaagc ctgtaacgcc atgttgaaag agaactttcc gactgtggct tcttactgta 6120
ttattccaga gtacgatgcc tatttggaca tggttgacgg agcttcatgc tgcttagaca 6180
ctgccagttt ttgccctgca aagctgcgca gctttccaaa gaaacactcc tatttggaac 6240
ccacaatacg atcggcagtg ccttcagcga tccagaacac gctccagaac gtcctggcag 6300
ctgccacaaa aagaaattgc aatgtcacgc aaatgagaga attgcccgta ttggattcgg 6360
cggcctttaa tgtggaatgc ttcaagaaat atgcgtgtaa taatgaatat tgggaaacgt 6420
ttaaagaaaa ccccatcagg cttactgaag aaaacgtggt aaattacatt accaaattaa 6480
aaggaccaaa agctgctgct ctttttgcga agacacataa tttgaatatg ttgcaggaca 6540
taccaatgga caggtttgta atggacttaa agagagacgt gaaagtgact ccaggaacaa 6600
aacatactga agaacggccc aaggtacagg tgatccaggc tgccgatccg ctagcaacag 6660
cgtatctgtg cggaatccac cgagagctgg ttaggagatt aaatgcggtc ctgcttccga 6720
acattcatac actgtttgat atgtcggctg aagactttga cgctattata gccgagcact 6780
tccagcctgg ggattgtgtt ctggaaactg acatcgcgtc gtttgataaa agtgaggacg 6840
acgccatggc tctgaccgcg ttaatgattc tggaagactt aggtgtggac gcagagctgt 6900
tgacgctgat tgaggcggct ttcggcgaaa tttcatcaat acatttgccc actaaaacta 6960
aatttaaatt cggagccatg atgaaatctg gaatgttcct cacactgttt gtgaacacag 7020
tcattaacat tgtaatcgca agcagagtgt tgagagaacg gctaaccgga tcaccatgtg 7080
cagcattcat tggagatgac aatatcgtga aaggagtcaa atcggacaaa ttaatggcag 7140
acaggtgcgc cacctggttg aatatggaag tcaagattat agatgctgtg gtgggcgaga 7200
aagcgcctta tttctgtgga gggtttattt tgtgtgactc cgtgaccggc acagcgtgcc 7260
gtgtggcaga ccccctaaaa aggctgttta agcttggcaa acctctggca gcagacgatg 7320
aacatgatga tgacaggaga agggcattgc atgaagagtc aacacgctgg aaccgagtgg 7380
gtattctttc agagctgtgc aaggcagtag aatcaaggta tgaaaccgta ggaacttcca 7440
tcatagttat ggccatgact actctagcta gcagtgttaa atcattcagc tacctgagag 7500

20262014462 26 Feb 2026

```
gggcccctat aactctctac ggctaacctg aatggactac gacatagtct agtccgccaa 7560
gatgttcccg ttccagccaa tgtatccgat gcagccaatg ccctatcgca acccgttcgc 7620
ggccccgcgc aggccctggt tccccagaac cgacccтttt ctggcgatgc aggtgcagga 7680
attaacccgc tcgatggcta acctgacgtt caagcaacgc cgggacgcgc cacctgaggg 7740
gccatccgct aagaaaccga agaaggaggc ctcgcaaaaa cagaaagggg gaggccaagg 7800
gaagaagaag aagaaccaag ggaagaagaa ggctaagaca gggccgccta atccgaaggc 7860
acagaatgga aacaagaaga agaccaacaa gaaaccaggc aagagacagc gcatggtcat 7920
gaaattggaa tctgacaaga cgttcccaat catgttggaa gggaagataa acggctacgc 7980
ttgtgtggtc ggagggaagt tattcaggcc gatgcatgtg gaaggcaaga tcgacaacga 8040
cgttctggcc gcgcttaaga cgaagaaagc atccaaatac gatcttgagt atgcagatgt 8100
gccacagaac atgcgggccg atacattcaa atacacccat gagaaacccc aaggctatta 8160
cagctggcat catggagcag tccaatatga aaatgggcgt ttcacggtgc cgaaaggagt 8220
tggggccaag ggagacagcg gacgacccat tctggataac cagggacggg tggtcgctat 8280
tgtgctggga ggtgtgaatg aaggatctag gacagccctt tcagtcgtca tgtggaacga 8340
gaagggagtt accgtgaagt atactccgga gaactgcgag caatggtcac tagtgaccac 8400
catgtgtctg ctcgccaatg tgacgttccc atgtgctcaa ccaccaattt gctacgacag 8460
aaaaccagca gagactttgg ccatgctcag cgttaacgtt gacaacccgg gctacgatga 8520
gctgctggaa gcagctgtta agtgccccgg aaggaaaagg agatccaccg aggagctgtt 8580
taaggagtat aagctaacgc gcccttacat ggccagatgc atcagatgtg cagttgggag 8640
ctgccatagt ccaatagcaa tcgaggcagt aaagagcgac gggcacgacg gttatgttag 8700
acttcagact tcctcgcagt atggcctgga ttcctccggc aacttaaagg gcaggaccat 8760
gcggtatgac atgcacggga ccattaaaga gataccacta catcaagtgt cactccatac 8820
atctcgcccg tgtcacattg tggatgggca cggttatttc ctgcttgcca ggtgcccggc 8880
aggggactcc atcaccatgg aatttaagaa agattccgtc acacactcct gctcggtgcc 8940
gtatgaagtg aaatttaatc ctgtaggcag agaactctat actcatcccc cagaacacgg 9000
agtagagcaa gcgtgccaag tctacgcaca tgatgcacag aacagaggag cttatgtcga 9060
gatgcacctc ccgggctcag aagtggacag cagtttggtt tccttgagcg gcagttcagt 9120
caccgtgaca cctcctgttg ggactagcgc cctggtggaa tgcgagtgtg gcggcacaaa 9180
gatctccgag accatcaaca agacaaaaca gttcagccag tgcacaaaga aggagcagtg 9240
cagagcatat cggctgcaga acgataagtg ggtgtataat tctgacaaac tgcccaaagc 9300
agcgggagcc accttaaaag gaaaactgca tgtcccattc ttgctggcag acggcaaatg 9360
caccgtgcct ctagcaccag aacctatgat aacctttggt ttcagatcag tgtcactgaa 9420
actgcaccct aagaatccca catatctaac cacccgccaa cttgctgatg agcctcacta 9480
cacgcacgag ctcatatctg aaccagctgt taggaatttt accgtcaccg aaaaagggtg 9540
ggagtttgta tggggaaacc acccgccgaa aaggttttgg gcacaggaaa cagcacccgg 9600
aaatccacat gggctaccgc acgaggtgat aactcattat taccacagat accctatgtc 9660
caccatcctg ggtttgtcaa tttgtgccgc cattgcaacc gtttccgttg cagcgtctac 9720
ctggctgttt tgcagatcta gagttgcgtg cctaactcct taccggctaa cacctaacgc 9780
taggatacca ttttgtctgg ctgtgctttg ctgcgcccgc actgcccggg ccgagaccac 9840
ctgggagtcc ttggatcacc tatggaacaa taaccaacag atgttctgga ttcaattgct 9900
gatccctctg gccgccttga tcgtagtgac tcgcctgctc aggtgcgtgt gctgtgtcgt 9960
gccttttta gtcatggccg gcgccgcagg cgccggcgcc tacgagcacg cgaccacgat 10020
gccgagccaa gcgggaatct cgtataacac tatagtcaac agagcaggct acgcaccact 10080
ccctatcagc ataacaccaa caaagatcaa gctgatacct acagtgaact tggagtacgt 10140
cacctgccac tacaaaacag gaatggattc accagccatc aaatgctgcg gatctcagga 10200
atgcactcca acttacaggc ctgatgaaca gtgcaaagtc ttcacagggg tttacccgtt 10260
catgtggggt ggtgcatatt gcttttgcga cactgagaac acccaagtca gcaaggccta 10320
cgtaatgaaa tctgacgact gccttgcgga tcatgctgaa gcatataaag cgcacacagc 10380
ctcagtgcag gcgttcctca acatcacagt gggagaacac tctattgtga ctaccgtgta 10440
tgtgaatgga gaaactcctg tgaatttcaa tggggtcaaa ttaactgcag gtccgctttc 10500
cacagcttgg acacccтttg atcgcaaaat cgtgcagtat gccggggaga tctataatta 10560
tgattttcct gagtatgggg caggacaacc aggagcattt ggagatatac aatccagaac 10620
agtctcaagc tcagatctgt atgccaatac caacctagtg ctgcagagac ccaaagcagg 10680
agcgatccac gtgccataca ctcaggcacc ttcgggtttt gagcaatgga agaaagataa 10740
agctccatca ttgaaattta ccgccccttt cggatgcgaa atatatacaa accccattcg 10800
cgccgaaaac tgtgctgtag ggtcaattcc attagccttt gacattcccg acgccttgtt 10860
caccagggtg tcagaaacac cgacactttc agcggccgaa tgcactctta acgagtgcgt 10920
gtattcttcc gactttggtg ggatcgccac ggtcaagtac tcggccagca agtcaggcaa 10980
gtgcgcagtc catgtgccat cagggactgc taccctaaaa gaagcagcag tcgagctaac 11040
cgagcaaggg tcggcgacta tccatttctc gaccgcaaat atccacccgg agttcaggct 11100
ccaaatatgc acatcatatg ttacgtgcaa aggtgattgt caccccccga aagaccatat 11160
tgtgacacac cctcagtatc acgcccaaac atttacagcc gcggtgtcaa aaaccgcgtg 11220
gacgtggtta acatccctgc tgggaggatc agccgtaatt attataattg gcttggtgct 11280
ggctactatt gtggccatgt acgtgctgac caaccagaaa cataattgaa tacagcagca 11340
attggcaagc tgcttacata gaactcgcgg cgattggcat gccgccttaa aatttttatt 11400
ttatttttтc ttttcttttc cgaatcggat tttgttttta atatttc              11447
```

3-4	**Sequences**	
3-4-1	Sequence Number [ID]	4
3-4-2	Molecule Type	DNA
3-4-3	Length	9577
3-4-4	Features	**misc_feature 1..9577**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..9577
		mol_type=other DNA
		organism=synthetic construct

20262014 62 26 Feb 2026

	NonEnglishQualifier Value	
3-4-5	Residues	atgggcggcg catgagagaa gcccagacca attacctacc caaaatggag aaagttcacg 60 ttgacatcga ggaagacagc ccattcctca gagctttgca gcggagcttc ccgcagtttg 120 aggtagaagc caagcaggtc actgataatg accatgctaa tgccagagcg ttttcgcatc 180 tggcttcaaa actgatcgaa acggaggtgg acccatccga cacgatcctt gacattggaa 240 gtgcgcccgc ccgcagaatg tattctaagc acaagtatca ttgtatctgt ccgatgagat 300 gtgcggaaga tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgtaagg 360 aaataactga taaggaattg gacaagaaaa tgaaggagct cgccgccgtc atgagcgacc 420 ctgacctgga aactgagact atgtgcctcc acgacgacga gtcgtgtcgc tacgaagggc 480 aagtcgctgt ttaccaggat gtatacgcgg ttgacggacc gacaagtctc tatcaccaag 540 ccaataaggg agttagagtc gcctactgga taggctttga caccacccct tttatgttta 600 agaacttggc tggagcatat ccatcatact ctaccaactg ggccgacgaa accgtgttaa 660 cggctcgtaa cataggccta tgcagctctg acgttatgga gcggtcacgt agagggatgt 720 ccattcttag aaagaagtat ttgaaaccat ccaacaatgt tctattctct gttggctcga 780 ccatctacca cgagaagagg gacttactga ggagctggca cctgccgtct gtatttcact 840 tacgtggcaa gcaaaattac acatgtcggt gtgagactat agttagttgc gacgggtacg 900 tcgttaaaag aatagctatc agtccaggcc tgtatgggaa gccttcaggc tatgctgcta 960 cgatgcaccg cgagggattc ttgtgctgca aagtgacaga cacattgaac ggggagaggg 1020 tctcttttcc cgtgtgcacg tatgtgccag ctacattgtg tgaccaaatg actggcatac 1080 tggcaacaga tgtcagtgcg gacgacgcgc aaaaactgct ggttgggctc aaccagcgta 1140 tagtcgtcaa cggtcgcacc cagagaaaca ccaataccat gaaaaattac cttttgcccg 1200 tagtggccca ggcatttgct aggtgggcaa aggaatataa ggaagatcaa gaagatgaaa 1260 ggccactagg actacgagat agacagttag tcatggggtg ttgttgggct tttagaaggc 1320 acaagataac atctatttat aagcgcccgg atacccaaac catcatcaaa gtgaacagcg 1380 atttccactc attcgtgctg cccaggatag gcagtaacac attggagatc gggctgagaa 1440 caagaatcag gaaaatgtta gaggagcaca aggagccgtc acctctcatt accgccgagg 1500 acgtacaaga agctaagtgc gcagccgatg aggctaagga ggtgcgtgaa gccgaggagt 1560 tgcgcgcagc tctaccacct ttggcagctg atgttgagga gcccactctg gaagccgatg 1620 tcgacttgat gttacaagag gctggggccg gctcagtgga gacacctcgt ggcttgataa 1680 aggttaccag ctacgctggc gaggacaaga tcggctctta cgctgtgctt tctccgcagg 1740 ctgtactcaa gagtgaaaaa ttatcttgca tccaccctct cgctgaacaa gtcatagtga 1800 taacacactc tggccgaaaa gggcgttatg ccgtggaacc ataccatggt aaagtagtgg 1860 tgccagaggg acatgcaata cccgtccagg actttcaagc tctgagtgaa agtgccacca 1920 ttgtgtacaa cgaacgtgag ttcgtaaaca ggtacctgca ccatattgcc acacatggag 1980 gagcgctgaa cactgatgaa gaatattaca aaactgtcaa gcccagcgag cacgacggcg 2040 aatacctgta cgacatcgac aggaaacagt gcgtcaagaa agaactagtc actgggctag 2100 ggctcacagg cgagctggtg gatcctccct tccatgaatt cgcctacgag agtctgagaa 2160 cacgaccagc cgctccttac caagtaccaa ccataggggt gtatggcgtg ccaggatcag 2220 gcaagtctgg catcattaaa agcgcagtca ccaaaaaaga tctagtggtg agcgccaaga 2280 aagaaaactg tgcagaaatt ataagggacg tcaagaaaat gaaagggctg gacgtcaatg 2340 ccagaactgt ggactcagtg ctcttgaatg gatgcaaaca ccccgtagag accctgtata 2400 ttgacgaagc ttttgcttgt catgcaggta ctctcagagc gctcatagcc attataagac 2460 ctaaaaaggc agtgctctgc ggggatccca aacagtgcgg ttttttaac atgatgtgcc 2520 tgaaagtgca ttttaaccac gagatttgca cacaagtctt ccacaaaagc atctctcgcc 2580 gttgcactaa atctgtgact tcggtcgtct caaccttgtt ttacgacaaa aaaatgagaa 2640 cgacgaatcc gaaagagact aagattgtga ttgacactac cggcagtacc aaacctaagc 2700 aggacgatct cattctcact tgtttcagag ggtgggtgaa gcagttgcaa atagattaca 2760 aaggcaacga aataatgacg gcagctgcct ctcaagggct gacccgtaaa ggtgtgtatg 2820 ccgttcggta caaggtgaat gaaaatcctc tgtacgcacc cacctcagaa catgtgaacg 2880 tcctactgac ccgcacggag gaccgcatcg tgtggaaaac actagccggc gacccatgga 2940 taaaaacact gactgccaag taccctggga atttcactgc cacgatagag gagtggcaag 3000 cagagcatga tgccatcatg aggcacatct tggagagacc ggaccctacc gacgtcttcc 3060 agaataaggc aaacgtgtgt tgggccaagg ctttagtgcc ggtgctgaag accgctggca 3120 tagacatgac cactgaacaa tggaacactg tggattattt tgaaacggac aaagctcact 3180 cagcagagat agtattgaac caactatgcg tgaggttctt tggactcgat ctggactccg 3240 gtctattttc tgcacccact gttccgttat ccattaggaa taatcactgg gataactccc 3300 cgtcgcctaa catgtacggg ctgaataaag aagtggtccg tcagctctct cgcaggtacc 3360 cacaactgcc tcgggcagtt gccactggaa gagtctatga catgaacact ggtacactgc 3420 gcaattatga tccgcgcata aacctagtac ctgtaaacag aagactgcct catgctttag 3480 tcctccacca taatgaacac ccacagagtg acttttcttc attcgtcagc aaattgaagg 3540 gcagaactgt cctggtggtc ggggaaaagt tgtccgtccc aggcaaaatg gttgactggt 3600 tgtcagaccg gcctgaggct accttcagag ctcggctgga tttaggcatc ccaggtgatg 3660 tgcccaaata tgacataata tttgttaatg tgaggacccc atataaatac catcactatc 3720 agcagtgtga agaccatgcc attaagctta gcatgttgac caagaaagct tgtctgcatc 3780 tgaatcccgg cggaacctgt gtcagcatag gttatggtta cgctgacagg gccagcgaaa 3840 gcatcattgg tgctatagcg cggcagttca agttttcccg ggtatgcaaa ccgaaatcct 3900 cacttgaaga gacggaagtt ctgtttgtat tcattgggta cgatcgcaag gcccgtacgc 3960 acaatcctta caagctttca tcaaccttga ccaacattta tacaggttcc agactccacg 4020 aagccggatg tgcaccctca tatcatgtgg tgcgagggga tattgccacg gccaccgaag 4080 gagtgattat aaatgctgct aacagcaaag gacaacctgg cggaggggtg tgcggagcgc 4140 tgtataagaa attcccggaa agcttcgatt tacagccgat cgaagtagga aaagcgcgac 4200 tggtcaaagg tgcagctaaa catatcattc atgccgtagg accaaacttc aacaaagttt 4260 cggaggttga aggtgacaaa cagttggcag aggcttatga gtccatcgct aagattgtca 4320 acgataacaa ttacaagtca gtagcgattc cactgttgtc caccggcatc ttttccggga 4380 acaaagatcg actaacccaa tcattgaacc atttgctgac agctttagac accactgatg 4440 cagatgtagc catatactgc agggacaaga aatgggaaat gactctcaag gaagcagtgg 4500

20262014626 26 Feb 2026

ctaggagaga agcagtggag gagatatgca tatccgacga ctcttcagtg acagaacctg 4560
atgcagagct ggtgagggtg catccgaaga gttctttggc tggaaggaag ggctacagca 4620
caagcgatgg caaaactttc tcatatttgg aagggaccaa gtttcaccag gcggccaagg 4680
atatagcaga aattaatgcc atgtggcccg ttgcaacgga ggccaatgag caggtatgca 4740
tgtatatcct cggagaaagc atgagcagta ttaggtcgaa atgccccgtc gaagagtcgg 4800
aagcctccac accacctagc acgctgcctt gcttgtgcat ccatgccatg actccagaaa 4860
gagtacagcg cctaaaagcc tcacgtccag aacaaattac tgtgtgctca tcctttccat 4920
tgccgaagta tagaatcact ggtgtgcaga agatccaatg ctcccagcct atattgttct 4980
caccgaaagt gcctgcgtat attcatccaa ggaagtatct cgtggaaaca ccaccggtag 5040
acgagactcc ggagccatcg gcagagaacc aatccacaga ggggacacct gaacaaccac 5100
cacttataac cgaggatgag accaggacta gaacgcctga gccgatcatc atcgaagagg 5160
aagaagagga tagcataagt ttgctgtcag atggcccgac ccaccaggtg ctgcaagtcg 5220
aggcagacat tcacgggccg ccctctgtat ctagctcatc ctggtccatt cctcatgcat 5280
ccgactttga tgtggacagt ttatccatac ttgacaccct ggagggagct agcgtgacca 5340
gcggggcaac gtcagccgag actaactctt acttcgcaaa gagtatggag tttctggcgc 5400
gaccggtgcc tgcgcctcga acagtattca ggaaccctcc acatcccgct ccgcgcacaa 5460
gaacaccgtc acttgcaccc agcagggcct gctcgagaac cagcctagtt tccaccccgc 5520
caggcgtgaa tagggtgatc actagagagg agctcgaggc gcttaccccg tcacgcactc 5580
ctagcaggtc ggtctcgaga accagcctgg tctccaaccc gccaggcgta aatagggtga 5640
ttacaagaga ggagtttgag gcgttcgtag cacaacaaca atgacggttt gatgcgggtg 5700
catacatctt ttcctccgac accggtcaag ggcatttaca acaaaaatca gtaaggcaaa 5760
cggtgctatc cgaagtggtg ttggagagga ccgaattgga gatttcgtat gccccgcgcc 5820
tcgaccaaga aaaagaagaa ttactacgca agaaattaca gttaaatccc acacctgcta 5880
acagaagcag ataccagtcc aggaaggtgg agaacatgaa agccataaca gctagacgta 5940
ttctgcaagg cctagggcat tatttgaagg cagaaggaaa agtggagtgc taccgaaccc 6000
tgcatcctgt tcctttgtat tcatctagtg tgaaccgtgc cttttcaagc cccaaggtcg 6060
cagtggaagc ctgtaacgcc atgttgaaag agaactttcc gactgtggct tcttactgta 6120
ttattccaga gtacgatgcc tatttggaca tggttgacgg agcttcatgc tgcttagaca 6180
ctgccagttt ttgccctgca aagctgcgca gctttccaaa gaaacactcc tatttggaac 6240
ccacaatacg atcggcagtg ccttcagcga tccagaacac gctccagaac gtcctggcag 6300
ctgccacaaa aagaaattgc aatgtcacgc aaatgagaga attgcccgta ttggattcgg 6360
cggcctttaa tgtggaatgc ttcaagaaat atgcgtgtaa taatgaatat tgggaaacgt 6420
ttaaagaaaa ccccatcagg cttactgaag aaaacgtggt aaattacatt accaaattaa 6480
aaggaccaaa agctgctgct ctttttgcga agacacataa tttgaatatg ttgcaggaca 6540
taccaatgga caggtttgta atggacttaa agagagacgt gaaagtgact ccaggaacaa 6600
aacatactga agaacggccc aaggtacagg tgatccaggc tgccgatccg ctagcaacag 6660
cgtatctgtg cggaatccac cgagagctgg ttaggagatt aaatgcggtc ctgcttccga 6720
acattcatac actgtttgat atgtcggctg aagactttga cgctattata gccgagcact 6780
tccagcctgg ggattgtgtt ctggaaactg acatcgcgtc gtttgataaa agtgaggacg 6840
acgccatggc tctgaccgcg ttaatgattc tggaagactt aggtgtggac gcagagctgt 6900
tgacgctgat tgaggcggct ttcggcgaaa tttcatcaat acatttgccc actaaaacta 6960
aatttaaatt cggagccatg atgaaatctg gaatgttcct cacactgttt gtgaacacag 7020
tcattaacat tgtaatcgca agcagagtgt tgagagaacg gctaaccgga tcaccatgtg 7080
cagcattcat tggagatgac aatatcgtga aaggagtcaa atcggacaaa ttaatggcag 7140
acaggtgcgc cacctggttg aatatggaag tcaagattat agatgctgtg gtgggcgaga 7200
aagcgcctta tttctgtgga gggtttattt tgtgtgactc cgtgaccggc acagcgtgcc 7260
gtgtggcaga ccccctaaaa aggctgttta agcttggcaa acctctggca gcagacgatg 7320
aacatgatga tgacaggaga agggcattgc atgaagagtc aacacgctgg aaccgagtgg 7380
gtattctttc agagctgtgc aaggcagtag aatcaaggta tgaaaccgta ggaacttcca 7440
tcatagttat ggccatgact actctagcta gcagtgttaa atcattcagc tacctgagag 7500
gggcccctat aactctctac ggctaacctg aatggactac gactctagaa tagtctttaa 7560
ttaagccacc atggcaggca tgtttcaggc gctgagcgaa ggctgcaccc cgtatgatat 7620
taaccagatg ctgaacgtgc tgggcgatca tcaggtctca ggccttgagc agcttgagag 7680
tataatcaac tttgaaaaac tgactgaatg gaccagttct aatgttatgc ctatcctgtc 7740
tcctctgaca aagggcatcc tgggcttcgt gtttaccctg accgtgcctt ctgagagagg 7800
acttagctgc attagcgaag cggatgcgac caccccggaa agcgcgaacc tgggcgaaga 7860
aattctgagc cagctgtatc tttggccaag ggtgacctac cattccccta gttatgctta 7920
ccaccaattt gaaagacgag ccaaatataa aagacacttc cccggctttg gccagagcct 7980
gctgtttggc taccctgtgt acgtgttcgg cgattgcgtg cagggcgatt gggatgcgat 8040
tcgctttcgc tattgcgcgc cgccgggcta tgcgctgctg cgctgcaacg ataccaacta 8100
tagcgctctg ctggctgtgg gggccctaga aggacccagg aatcaggact ggcttggtgt 8160
cccaagacaa cttgtaactc ggatgcaggc tattcagaat gccggcctgt gtaccctggt 8220
ggccatgctg gaagagacaa tcttctggct gcaagcgttt ctgatggcgc tgaccgatag 8280
cggcccgaaa accaacatta ttgtggatag ccagtatgtg atgggcatta gcaaaccgag 8340
ctttcaggaa tttgtggatt gggaaaacgt gagcccggaa ctgaacagca ccgatcagcc 8400
gttttggcaa gccggaatcc tggccagaaa tctggtgcct atggtggcca cagtgcaggg 8460
ccagaacctg aagtaccagg gtcagtcact agtcatctct gcttctatca ttgtcttcaa 8520
cctgctggaa ctggaaggtg attatcgaga tgatggcaac gtgtgggtgc ataccccgct 8580
gagcccgcgc accctgaacg cgtgggtgaa agcggtggaa gaaaaaaaag gtattccagt 8640
tcacctagag ctggccagta tgaccaacat ggagctcatg agcagtattg tgcatcagca 8700
ggtcagaaca tacggccccg tgttcatgtg tctcggcgga ctgcttacaa tggtggctgg 8760
tgctgtgtgg ctgacagtgc gagtgctcga gctgttccgg gccgcgcagc tggccaacga 8820
cgtggtcctc cagatcatgg agctttgtgg tgcagcgttt cgccaggtgt gccataccac 8880
cgtgccgtgg ccgaacgcga gcctgacccc gaaatggaac aacgaaacca cccagcccca 8940
gatcgccaac tgcagcgtgt atgacttttt tgtgtggctc cattattatt ctgttcgaga 9000
cacactttgg ccaagggtga cctaccatat gaacaaatat gcgtatcata tgctggaaag 9060

20262014 62 26 Feb 2026

		acgagccaaa tataaaagag gaccaggacc tggcgctaaa tttgtggccg cctggacact 9120 gaaagccgct gctggtcctg gacctggcca gtacatcaag gccaacagca agttcatcgg 9180 catcaccgaa ctcggacccg gaccaggctg atgattcgaa cggccgtatc acgcccaaac 9240 atttacagcc gcggtgtcaa aaaccgcgtg gacgtggtta acatccctgc tgggaggatc 9300 agccgtaatt attataattg gcttggtgct ggctactatt gtggccatgt acgtgctgac 9360 caaccagaaa cataattgaa tacagcagca attggcaagc tgcttacata gaactcgcgg 9420 cgattggcat gccgccttaa aatttttatt ttatttttc ttttcttttc cgaatcggat 9480 tttgttttta atatttcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 9540 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 9577
3-5	**Sequences**	
3-5-1	Sequence Number [ID]	5
3-5-2	Molecule Type	DNA
3-5-3	Length	11447
3-5-4	Features	**source 1..11447**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Venezuelan equine encephalitis virus
	NonEnglishQualifier Value	
3-5-5	Residues	atgggcggcg catgagagaa gcccagacca attacctacc caaaatggag aaagttcacg 60 ttgacatcga ggaagacagc ccattcctca gagctttgca gcggagcttc ccgcagtttg 120 aggtagaagc caagcaggtc actgataatg accatgctaa tgccagagcg ttttcgcatc 180 tggcttcaaa actgatcgaa acggaggtgg acccatccga cacgatcctt gacattggaa 240 gtgcgcccgc ccgcagaatg tattctaagc acaagtatca ttgtatctgt ccgatgagat 300 gtgcggaaga tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgtaagg 360 aaataactga taaggaattg gacaagaaaa tgaaggagct cgccgccgtc atgagcgacc 420 ctgacctgga aactgagact atgtgcctcc acgacgacga gtcgtgtcgc tacgaagggc 480 aagtcgctgt ttaccaggat gtatacgcgg ttgacggacc gacaagtctc tatcaccaag 540 ccaataaggg agttagagtc gcctactgga taggctttga caccacccct tttatgttta 600 agaacttggc tggagcatat ccatcatact ctaccaactg ggccgacgaa accgtgttaa 660 cggctcgtaa cataggccta tgcagctctg acgttatgga gcggtcacgt agagggatgt 720 ccattcttag aaagaagtat ttgaaaccat ccaacaatgt tctattctct gttggctcga 780 ccatctacca cgagaagagg gacttactga ggagctggca cctgccgtct gtatttcact 840 tacgtggcaa gcaaaattac acatgtcggt gtgagactat agttagttgc gacgggtacg 900 tcgttaaaag aatagctatc agtccaggcc tgtatgggaa gccttcaggc tatgctgcta 960 cgatgcaccg cgagggattc ttgtgctgca aagtgacaga cacattgaac ggggagaggg 1020 tctcttttcc cgtgtgcacg tatgtgccag ctacattgtg tgaccaaatg actggcatac 1080 tggcaacaga tgtcagtgcg gacgacgcgc aaaaactgct ggttgggctc aaccagcgta 1140 tagtcgtcaa cggtcgcacc cagagaaaca ccaataccat gaaaaattac cttttgcccg 1200 tagtggccca ggcatttgct aggtgggcaa aggaatataa ggaagatcaa gaagatgaaa 1260 ggccactagg actacgagat agacagttag tcatggggtg ttgttgggct tttagaaggc 1320 acaagataac atctatttat aagcgcccgg atacccaaac catcatcaaa gtgaacagcg 1380 atttccactc attcgtgctg cccaggatag gcagtaacac attggagatc gggctgagaa 1440 caagaatcag gaaaatgtta gaggagcaca aggagccgtc acctctcatt accgccgagg 1500 acgtacaaga agctaagtgc gcagccgatg aggctaagga ggtgcgtgaa gccgaggagt 1560 tgcgcgcagc tctaccacct ttggcagctg atgttgagga gcccactctg gaagccgatg 1620 tcgacttgat gttacaagag gctggggccg gctcagtgga gacacctcgt ggcttgataa 1680 aggttaccag ctacgctggc gaggacaaga tcggctctta cgctgtgctt tctccgcagg 1740 ctgtactcaa gagtgaaaaa ttatcttgca tccaccctct cgctgaacaa gtcatagtga 1800 taacacactc tggccgaaaa gggcgttatg ccgtggaacc ataccatggt aaagtagtgg 1860 tgccagaggg acatgcaata cccgtccagg actttcaagc tctgagtgaa agtgccacca 1920 ttgtgtacaa cgaacgtgag ttcgtaaaca ggtacctgca ccatattgcc acacatggag 1980 gagcgctgaa cactgatgaa gaatattaca aaactgtcaa gcccagcgag cacgacggcg 2040 aatacctgta cgacatcgac aggaaacagt gcgtcaagaa agaactagtc actgggctag 2100 ggctcacagg cgagctggtg gatcctccct tccatgaatt cgcctacgag agtctgagaa 2160 cacgaccagc cgctccttac caagtaccaa ccataggggt gtatggcgtg ccaggatcag 2220 gcaagtctgg catcattaaa agcgcagtca ccaaaaaaga tctagtggtg agcgccaaga 2280 aagaaaactg tgcagaaatt ataagggacg tcaagaaaat gaaagggctg gacgtcaatg 2340 ccagaactgt ggactcagtg ctcttgaatg gatgcaaaca ccccgtagag accctgtata 2400 ttgacgaagc ttttgcttgt catgcaggta ctctcagagc gctcatagcc attataagac 2460 ctaaaaaggc agtgctctgc ggggatccca aacagtgcgg ttttttaac atgatgtgcc 2520 tgaaagtgca ttttaaccac gagatttgca cacaagtctt ccacaaaagc atctctcgcc 2580 gttgcactaa atctgtgact tcggtcgtct caaccttgtt ttacgacaaa aaaatgagaa 2640 cgacgaatcc gaaagagact aagattgtga ttgacactac cggcagtacc aaacctaagc 2700 aggacgatct cattctcact tgtttcagag ggtgggtgaa gcagttgcaa atagattaca 2760 aaggcaacga aataatgacg gcagctgcct ctcaagggct gacccgtaaa ggtgtgtatg 2820 ccgttcggta caaggtgaat gaaaatcctc tgtacgcacc cacctcagaa catgtgaacg 2880 tcctactgac ccgcacggag gaccgcatcg tgtggaaaac actagccggc gacccatgga 2940 taaaaacact gactgccaag taccctggga atttcactgc cacgatagag gagtggcaag 3000 cagagcatga tgccatcatg aggcacatct tggagagacc ggaccctacc gacgtcttcc 3060 agaataaggc aaacgtgtgt tgggccaagg ctttagtgcc ggtgctgaag accgctggca 3120 tagacatgac cactgaacaa tggaacactg tggattattt tgaaacggac aaagctcact 3180 cagcagagat agtattgaac caactatgcg tgaggttctt tggactcgat ctggactccg 3240 gtctattttc tgcacccact gttccgttat ccattaggaa taatcactgg gataactccc 3300 cgtcgcctaa catgtacggg ctgaataaag aagtggtccg tcagctctct cgcaggtacc 3360 cacaactgcc tcgggcagtt gccactggaa gagtctatga catgaacact ggtacactgc 3420 gcaattatga tccgcgcata aacctagtac ctgtaaacag aagactgcct catgctttag 3480

20262014626 26 Feb 2026

tcctccacca taatgaacac ccacagagtg acttttcttc attcgtcagc aaattgaagg 3540
gcagaactgt cctggtggtc ggggaaaagt tgtccgtccc aggcaaaatg gttgactggt 3600
tgtcagaccg gcctgaggct accttcagag ctcggctgga tttaggcatc ccaggtgatg 3660
tgcccaaata tgacataata tttgttaatg tgaggacccc atataaatac catcactatc 3720
agcagtgtga agaccatgcc attaagctta gcatgttgac caagaaagct tgtctgcatc 3780
tgaatcccgg cggaacctgt gtcagcatag gttatggtta cgctgacagg gccagcgaaa 3840
gcatcattgg tgctatagcg cggcagttca agttttcccg ggtatgcaaa ccgaaatcct 3900
cacttgaaga gacggaagtt ctgtttgtat tcattgggta cgatcgcaag gcccgtacgc 3960
acaatcctta caagctttca tcaaccttga ccaacattta tacaggttcc agactccacg 4020
aagccggatg tgcaccctca tatcatgtgg tgcgagggga tattgccacg gccaccgaag 4080
gagtgattat aaatgctgct aacagcaaag gacaacctgg cggaggggtg tgcggagcgc 4140
tgtataagaa attcccggaa agcttcgatt tacagccgat cgaagtagga aaagcgcgac 4200
tggtcaaagg tgcagctaaa catatcattc atgccgtagg accaaacttc aacaaagttt 4260
cggaggttga aggtgacaaa cagttggcag aggcttatga gtccatcgct aagattgtca 4320
acgataacaa ttacaagtca gtagcgattc cactgttgtc caccggcatc ttttccggga 4380
acaaagatcg actaacccaa tcattgaacc atttgctgac agctttagac accactgatg 4440
cagatgtagc catatactgc agggacaaga aatgggaaat gactctcaag gaagcagtgg 4500
ctaggagaga agcagtggag gagatatgca tatccgacga ctcttcagtg acagaacctg 4560
atgcagagct ggtgagggtg catccgaaga gttctttggc tggaaggaag ggctacagca 4620
caagcgatgg caaaactttc tcatatttgg aagggaccaa gtttcaccag gcggccaagg 4680
atatagcaga aattaatgcc atgtggcccg ttgcaacgga ggccaatgag caggtatgca 4740
tgtatatcct cggagaaagc atgagcagta ttaggtcgaa atgccccgtc gaagagtcgg 4800
aagcctccac accacctagc acgctgcctt gcttgtgcat ccatgccatg actccagaaa 4860
gagtacagcg cctaaaagcc tcacgtccag aacaaattac tgtgtgctca tcctttccat 4920
tgccgaagta tagaatcact ggtgtgcaga agatccaatg ctcccagcct atattgttct 4980
caccgaaagt gcctgcgtat attcatccaa ggaagtatct cgtggaaaca ccaccggtag 5040
acgagactcc ggagccatcg gcagagaacc aatccacaga ggggacacct gaacaaccac 5100
cacttataac cgaggatgag accaggacta gaacgcctga gccgatcatc atcgaagagg 5160
aagaagagga tagcataagt ttgctgtcag atggcccgac ccaccaggtg ctgcaagtcg 5220
aggcagacat tcacgggccg ccctctgtat ctagctcatc ctggtccatt cctcatgcat 5280
ccgactttga tgtggacagt ttatccatac ttgacaccct ggagggagct agcgtgacca 5340
gcggggcaac gtcagccgag actaactctt acttcgcaaa gagtatggag tttctggcgc 5400
gaccggtgcc tgcgcctcga acagtattca ggaaccctcc acatcccgct ccgcgcacaa 5460
gaacaccgtc acttgcaccc agcagggcct gctcgagaac cagcctagtt tccaccccgc 5520
caggcgtgaa tagggtgatc actagagagg agctcgaggc gcttaccccg tcacgcactc 5580
ctagcaggtc ggtctcgaga accagcctgg tctccaaccc gccaggcgta aatagggtga 5640
ttacaagaga ggagtttgag gcgttcgtag cacaacaaca atgacggttt gatgcgggtg 5700
catacatctt ttcctccgac accggtcaag ggcatttaca acaaaaatca gtaaggcaaa 5760
cggtgctatc cgaagtggtg ttggagagga ccgaattgga gatttcgtat gccccgcgcc 5820
tcgaccaaga aaaagaagaa ttactacgca agaaattaca gttaaatccc acacctgcta 5880
acagaagcag ataccagtcc aggaaggtgg agaacatgaa agccataaca gctagacgta 5940
ttctgcaagg cctagggcat tatttgaagg cagaaggaaa agtggagtgc taccgaaccc 6000
tgcatcctgt tcctttgtat tcatctagtg tgaaccgtgc cttttcaagc cccaaggtcg 6060
cagtggaagc ctgtaacgcc atgttgaaag agaactttcc gactgtggct tcttactgta 6120
ttattccaga gtacgatgcc tatttggaca tggttgacgg agcttcatgc tgcttagaca 6180
ctgccagttt ttgccctgca aagctgcgca gctttccaaa gaaacactcc tatttggaac 6240
ccacaatacg atcggcagtg ccttcagcga tccagaacac gctccagaac gtcctggcag 6300
ctgccacaaa aagaaattgc aatgtcacgc aaatgagaga attgcccgta ttggattcgg 6360
cggcctttaa tgtggaatgc ttcaagaaat atgcgtgtaa taatgaatat tgggaaacgt 6420
ttaaagaaaa ccccatcagg cttactgaag aaaacgtggt aaattacatt accaaattaa 6480
aaggaccaaa agctgctgct ctttttgcga agacacataa tttgaatatg ttgcaggaca 6540
taccaatgga caggtttgta atggacttaa agagagacgt gaaagtgact ccaggaacaa 6600
aacatactga agaacggccc aaggtacagg tgatccaggc tgccgatccg ctagcaacag 6660
cgtatctgtg cggaatccac cgagagctgg ttaggagatt aaatgcggtc ctgcttccga 6720
acattcatac actgtttgat atgtcggctg aagactttga cgctattata gccgagcact 6780
tccagcctgg ggattgtgtt ctggaaactg acatcgcgtc gtttgataaa agtgaggacg 6840
acgccatggc tctgaccgcg ttaatgattc tggaagactt aggtgtggac gcagagctgt 6900
tgacgctgat tgaggcggct ttcggcgaaa tttcatcaat acatttgccc actaaaacta 6960
aatttaaatt cggagccatg atgaaatctg gaatgttcct cacactgttt gtgaacacag 7020
tcattaacat tgtaatcgca agcagagtgt tgagagaacg gctaaccgga tcaccatgtg 7080
cagcattcat tggagatgac aatatcgtga aaggagtcaa atcggacaaa ttaatggcag 7140
acaggtgcgc cacctggttg aatatggaag tcaagattat agatgctgtg gtgggcgaga 7200
aagcgcctta tttctgtgga gggtttattt tgtgtgactc cgtgaccggc acagcgtgcc 7260
gtgtggcaga ccccctaaaa aggctgttta agcttggcaa acctctggca gcagacgatg 7320
aacatgatga tgacaggaga agggcattgc atgaagagtc aacacgctgg aaccgagtgg 7380
gtattctttc agagctgtgc aaggcagtag aatcaaggta tgaaaccgta ggaacttcca 7440
tcatagttat ggccatgact actctagcta gcagtgttaa atcattcagc tacctgagag 7500
gggcccctat aactctctac ggctaacctg aatggactac gacatagtct agtccgccaa 7560
gatgttcccg ttccagccaa tgtatccgat gcagccaatg ccctatcgca acccgttcgc 7620
ggccccgcgc aggccctggt tccccagaac cgacccttttt ctggcgatgc aggtgcagga 7680
attaacccgc tcgatggcta acctgacgtt caagcaacgc cgggacgcgc cacctgaggg 7740
gccatccgct aagaaaccga agaaggaggc ctcgcaaaaa cagaaagggg gaggccaagg 7800
gaagaagaag aagaaccaag ggaagaagaa ggctaagaca gggccgccta atccgaaggc 7860
acagaatgga aacaagaaga agaccaacaa gaaaccaggc aagagacagc gcatggtcat 7920
gaaattggaa tctgacaaga cgttcccaat catgttggaa gggaagataa acggctacgc 7980
ttgtgtggtc ggagggaagt tattcaggcc gatgcatgtg gaaggcaaga tcgacaacga 8040

2026201462 26 Feb 2026

		cgttctggcc gcgcttaaga cgaagaaagc atccaaatac gatcttgagt atgcagatgt 8100 gccacagaac atgcgggccg atacattcaa atacacccat gagaaacccc aaggctatta 8160 cagctggcat catggagcag tccaatatga aaatgggcgt ttcacggtgc cgaaaggagt 8220 tggggccaag ggagacagcg gacgacccat tctggataac cagggacggg tggtcgctat 8280 tgtgctggga ggtgtgaatg aaggatctag gacagccctt tcagtcgtca tgtggaacga 8340 gaagggagtt accgtgaagt atactccgga gaactgcgag caatggtcac tagtgaccac 8400 catgtgtctg ctcgccaatg tgacgttccc atgtgctcaa ccaccaattt gctacgacag 8460 aaaaccagca gagactttgg ccatgctcag cgttaacgtt gacaacccgg gctacgatga 8520 gctgctggaa gcagctgtta agtgccccgg aaggaaaagg agatccaccg aggagctgtt 8580 taaggagtat aagctaacgc gcccttacat ggccagatgc atcagatgtg cagttgggag 8640 ctgccatagt ccaatagcaa tcgaggcagt aaagagcgac gggcacgacg gttatgttag 8700 acttcagact tcctcgcagt atggcctgga ttcctccggc aacttaaagg gcaggaccat 8760 gcggtatgac atgcacggga ccattaaaga gataccacta catcaagtgt cactccatac 8820 atctcgcccg tgtcacattg tggatgggca cggttatttc ctgcttgcca ggtgcccggc 8880 aggggactcc atcaccatgg aatttaagaa agattccgtc acacactcct gctcggtgcc 8940 gtatgaagtg aaatttaatc ctgtaggcag agaactctat actcatcccc cagaacacgg 9000 agtagagcaa gcgtgccaag tctacgcaca tgatgcacag aacagaggag cttatgtcga 9060 gatgcacctc ccgggctcag aagtggacag cagtttggtt tccttgagcg gcagttcagt 9120 caccgtgaca cctcctgttg ggactagcgc cctggtggaa tgcgagtgtg gcggcacaaa 9180 gatctccgag accatcaaca agacaaaaca gttcagccag tgcacaaaga aggagcagtg 9240 cagagcatat cggctgcaga acgataagtg ggtgtataat tctgacaaac tgcccaaagc 9300 agcgggagcc accttaaaag gaaaactgca tgtcccattc ttgctggcag acggcaaatg 9360 caccgtgcct ctagcaccag aacctatgat aacctttggt ttcagatcag tgtcactgaa 9420 actgcaccct aagaatccca catatctaac cacccgccaa cttgctgatg agcctcacta 9480 cacgcacgag ctcatatctg aaccagctgt taggaatttt accgtcaccg aaaaagggtg 9540 ggagtttgta tggggaaacc acccgccgaa aaggttttgg gcacaggaaa cagcacccgg 9600 aaatccacat gggctaccgc acgaggtgat aactcattat taccacagat accctatgtc 9660 caccatcctg ggtttgtcaa tttgtgccgc cattgcaacc gtttccgttg cagcgtctac 9720 ctggctgttt tgcagatcta gagttgcgtg cctaactcct taccggctaa cacctaacgc 9780 taggatacca ttttgtctgg ctgtgctttg ctgcgcccgc actgcccggg ccgagaccac 9840 ctgggagtcc ttggatcacc tatggaacaa taaccaacag atgttctgga ttcaattgct 9900 gatccctctg gccgccttga tcgtagtgac tcgcctgctc aggtgcgtgt gctgtgtcgt 9960 gccttttta gtcatggccg gcgccgcagg cgccggcgcc tacgagcacg cgaccacgat 10020 gccgagccaa gcgggaatct cgtataacac tatagtcaac agagcaggct acgcaccact 10080 ccctatcagc ataacaccaa caaagatcaa gctgatacct acagtgaact tggagtacgt 10140 cacctgccac tacaaaacag gaatggattc accagccatc aaatgctgcg gatctcagga 10200 atgcactcca acttacaggc ctgatgaaca gtgcaaagtc ttcacagggg tttacccgtt 10260 catgtggggt ggtgcatatt gcttttgcga cactgagaac acccaagtca gcaaggccta 10320 cgtaatgaaa tctgacgact gccttgcgga tcatgctgaa gcatataaag cgcacacagc 10380 ctcagtgcag gcgttcctca acatcacagt gggagaacac tctattgtga ctaccgtgta 10440 tgtgaatgga gaaactcctg tgaatttcaa tggggtcaaa ttaactgcag gtccgctttc 10500 cacagcttgg acacccttg atcgcaaaat cgtgcagtat gccggggaga tctataatta 10560 tgattttcct gagtatgggg caggacaacc aggagcattt ggagatatac aatccagaac 10620 agtctcaagc tcagatctgt atgccaatac caacctagtg ctgcagagac ccaaagcagg 10680 agcgatccac gtgccataca ctcaggcacc ttcgggtttt gagcaatgga agaaagataa 10740 agctccatca ttgaaattta ccgccccttt cggatgcgaa atatatacaa accccattcg 10800 cgccgaaaac tgtgctgtag ggtcaattcc attagccttt gacattcccg acgccttgtt 10860 caccagggtg tcagaaacac cgacactttc agcggccgaa tgcactctta acgagtgcgt 10920 gtattcttcc gactttggtg ggatcgccac ggtcaagtac tcggccagca agtcaggcaa 10980 gtgcgcagtc catgtgccat cagggactgc taccctaaaa gaagcagcag tcgagctaac 11040 cgagcaaggg tcggcgacta tccatttctc gaccgcaaat atccacccgg agttcaggct 11100 ccaaatatgc acatcatatg ttacgtgcaa aggtgattgt caccccccga aagaccatat 11160 tgtgacacac cctcagtatc acgcccaaac atttacagcc gcggtgtcaa aaaccgcgtg 11220 gacgtggtta acatccctgc tgggaggatc agccgtaatt attataattg gcttggtgct 11280 ggctactatt gtggccatgt acgtgctgac caaccagaaa cataattgaa tacagcagca 11340 attggcaagc tgcttacata gaactcgcgg cgattggcat gccgccttaa aatttttatt 11400 ttatttttc ttttcttttc cgaatcggat tttgttttta atatttc 11447
3-6	**Sequences**	
3-6-1	Sequence Number [ID]	6
3-6-2	Molecule Type	DNA
3-6-3	Length	7894
3-6-4	Features	**misc_feature 1..7894**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide **source 1..7894** mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-6-5	Residues	atgggcggcg catgagagaa gcccagacca attacctacc caaaatggag aaagttcacg 60 ttgacatcga ggaagacagc ccattcctca gagctttgca gcggagcttc ccgcagtttg 120 aggtagaagc caagcaggtc actgataatg accatgctaa tgccagagcg ttttcgcatc 180 tggcttcaaa actgatcgaa acggaggtgg acccatccga cacgatcctt gacattggaa 240 gtgcgcccgc ccgcagaatg tattctaagc acaagtatca ttgtatctgt ccgatgagat 300 gtgcggaaga tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgtaagg 360 aaataactga taaggaattg gacaagaaaa tgaaggagct cgccgccgtc atgagcgacc 420 ctgacctgga aactgagact atgtgcctcc acgacgacga gtcgtgtcgc tacgaagggc 480

20262014626 26 Feb 2026

aagtcgctgt ttaccaggat gtatacgcgg ttgacggacc gacaagtctc tatcaccaag 540
ccaataaggg agttagagtc gcctactgga taggctttga caccacccct tttatgttta 600
agaacttggc tggagcatat ccatcatact ctaccaactg ggccgacgaa accgtgttaa 660
cggctcgtaa cataggccta tgcagctctg acgttatgga gcggtcacgt agagggatgt 720
ccattcttag aaagaagtat ttgaaaccat ccaacaatgt tctattctct gttggctcga 780
ccatctacca cgagaagagg gacttactga ggagctggca cctgccgtct gtatttcact 840
tacgtggcaa gcaaaattac acatgtcggt gtgagactat agttagttgc gacgggtacg 900
tcgttaaaag aatagctatc agtccaggcc tgtatgggaa gccttcaggc tatgctgcta 960
cgatgcaccg cgagggattc ttgtgctgca aagtgacaga cacattgaac ggggagaggg 1020
tctcttttcc cgtgtgcacg tatgtgccag ctacattgtg tgaccaaatg actggcatac 1080
tggcaacaga tgtcagtgcg gacgacgcgc aaaaactgct ggttgggctc aaccagcgta 1140
tagtcgtcaa cggtcgcacc cagagaaaca ccaataccat gaaaaattac cttttgcccg 1200
tagtggccca ggcatttgct aggtgggcaa aggaatataa ggaagatcaa gaagatgaaa 1260
ggccactagg actacgagat agacagttag tcatggggtg ttgttgggct tttagaaggc 1320
acaagataac atctatttat aagcgcccgg atacccaaac catcatcaaa gtgaacagcg 1380
atttccactc attcgtgctg cccaggatag gcagtaacac attggagatc gggctgagaa 1440
caagaatcag gaaaatgtta gaggagcaca aggagccgtc acctctcatt accgccgagg 1500
acgtacaaga agctaagtgc gcagccgatg aggctaagga ggtgcgtgaa gccgaggagt 1560
tgcgcgcagc tctaccacct ttggcagctg atgttgagga gcccactctg gaagccgatg 1620
tcgacttgat gttacaagag gctggggccg gctcagtgga gacacctcgt ggcttgataa 1680
aggttaccag ctacgctggc gaggacaaga tcggctctta cgctgtgctt tctccgcagg 1740
ctgtactcaa gagtgaaaaa ttatcttgca tccaccctct cgctgaacaa gtcatagtga 1800
taacacactc tggccgaaaa gggcgttatg ccgtggaacc ataccatggt aaagtagtgg 1860
tgccagaggg acatgcaata cccgtccagg actttcaagc tctgagtgaa agtgccacca 1920
ttgtgtacaa cgaacgtgag ttcgtaaaca ggtacctgca ccatattgcc acacatggag 1980
gagcgctgaa cactgatgaa gaatattaca aaactgtcaa gcccagcgag cacgacggcg 2040
aatacctgta cgacatcgac aggaaacagt gcgtcaagaa agaactagtc actgggctag 2100
ggctcacagg cgagctggtg gatcctccct tccatgaatt cgcctacgag agtctgagaa 2160
cacgaccagc cgctccttac caagtaccaa ccataggggt gtatggcgtg ccaggatcag 2220
gcaagtctgg catcattaaa agcgcagtca ccaaaaaaga tctagtggtg agcgccaaga 2280
aagaaaactg tgcagaaatt ataagggacg tcaagaaaat gaaagggctg gacgtcaatg 2340
ccagaactgt ggactcagtg ctcttgaatg gatgcaaaca ccccgtagag accctgtata 2400
ttgacgaagc ttttgcttgt catgcaggta ctctcagagc gctcatagcc attataagac 2460
ctaaaaaggc agtgctctgc ggggatccca aacagtgcgg ttttttaac atgatgtgcc 2520
tgaaagtgca ttttaaccac gagatttgca cacaagtctt ccacaaaagc atctctcgcc 2580
gttgcactaa atctgtgact tcggtcgtct caaccttgtt ttacgacaaa aaaatgagaa 2640
cgacgaatcc gaaagagact aagattgtga ttgacactac cggcagtacc aaacctaagc 2700
aggacgatct cattctcact tgtttcagag ggtgggtgaa gcagttgcaa atagattaca 2760
aaggcaacga aataatgacg gcagctgcct ctcaagggct gacccgtaaa ggtgtgtatg 2820
ccgttcggta caaggtgaat gaaaatcctc tgtacgcacc cacctcagaa catgtgaacg 2880
tcctactgac ccgcacggag gaccgcatcg tgtggaaaac actagccggc gacccatgga 2940
taaaaacact gactgccaag taccctggga atttcactgc cacgatagag gagtggcaag 3000
cagagcatga tgccatcatg aggcacatct tggagagacc ggaccctacc gacgtcttcc 3060
agaataaggc aaacgtgtgt tgggccaagg ctttagtgcc ggtgctgaag accgctggca 3120
tagacatgac cactgaacaa tggaacactg tggattattt tgaaacggac aaagctcact 3180
cagcagagat agtattgaac caactatgcg tgaggttctt tggactcgat ctggactccg 3240
gtctattttc tgcacccact gttccgttat ccattaggaa taatcactgg gataactccc 3300
cgtcgcctaa catgtacggg ctgaataaag aagtggtccg tcagctctct cgcaggtacc 3360
cacaactgcc tcgggcagtt gccactggaa gagtctatga catgaacact ggtacactgc 3420
gcaattatga tccgcgcata aacctagtac ctgtaaacag aagactgcct catgctttag 3480
tcctccacca taatgaacac ccacagagtg acttttcttc attcgtcagc aaattgaagg 3540
gcagaactgt cctggtggtc ggggaaaagt tgtccgtccc aggcaaaatg gttgactggt 3600
tgtcagaccg gcctgaggct accttcagag ctcggctgga tttaggcatc ccaggtgatg 3660
tgcccaaata tgacataata tttgttaatg tgaggacccc atataaatac catcactatc 3720
agcagtgtga agaccatgcc attaagctta gcatgttgac caagaaagct tgtctgcatc 3780
tgaatcccgg cggaacctgt gtcagcatag gttatggtta cgctgacagg gccagcgaaa 3840
gcatcattgg tgctatagcg cggcagttca agttttcccg ggtatgcaaa ccgaaatcct 3900
cacttgaaga gacggaagtt ctgtttgtat tcattgggta cgatcgcaag gcccgtacgc 3960
acaatcctta caagctttca tcaaccttga ccaacattta tacaggttcc agactccacg 4020
aagccggatg tgcaccctca tatcatgtgg tgcgagggga tattgccacg gccaccgaag 4080
gagtgattat aaatgctgct aacagcaaag gacaacctgg cggaggggtg tgcggagcgc 4140
tgtataagaa attcccggaa agcttcgatt tacagccgat cgaagtagga aaagcgcgac 4200
tggtcaaagg tgcagctaaa catatcattc atgccgtagg accaaacttc aacaaagttt 4260
cggaggttga aggtgacaaa cagttggcag aggcttatga gtccatcgct aagattgtca 4320
acgataacaa ttacaagtca gtagcgattc cactgttgtc caccggcatc ttttccggga 4380
acaaagatcg actaacccaa tcattgaacc atttgctgac agctttagac accactgatg 4440
cagatgtagc catatactgc agggacaaga aatgggaaat gactctcaag gaagcagtgg 4500
ctaggagaga agcagtggag gagatatgca tatccgacga ctcttcagtg acagaacctg 4560
atgcagagct ggtgagggtg catccgaaga gttctttggc tggaaggaag ggctacagca 4620
caagcgatgg caaaactttc tcatatttgg aagggaccaa gtttcaccag gcggccaagg 4680
atatagcaga aattaatgcc atgtggcccg ttgcaacgga ggccaatgag caggtatgca 4740
tgtatatcct cggagaaagc atgagcagta ttaggtcgaa atgccccgtc gaagagtcgg 4800
aagcctccac accacctagc acgctgcctt gcttgtgcat ccatgccatg actccagaaa 4860
gagtacagcg cctaaaagcc tcacgtccag aacaaattac tgtgtgctca tcctttccat 4920
tgccgaagta tagaatcact ggtgtgcaga agatccaatg ctcccagcct atattgttct 4980
caccgaaagt gcctgcgtat attcatccaa ggaagtatct cgtggaaaca ccaccggtag 5040

2026201462 26 Feb 2026

		acgagactcc ggagccatcg gcagagaacc aatccacaga ggggacacct gaacaaccac 5100 cacttataac cgaggatgag accaggacta gaacgcctga gccgatcatc atcgaagagg 5160 aagaagagga tagcataagt ttgctgtcag atggcccgac ccaccaggtg ctgcaagtcg 5220 aggcagacat tcacgggccg ccctctgtat ctagctcatc ctggtccatt cctcatgcat 5280 ccgactttga tgtggacagt ttatccatac ttgacaccct ggagggagct agcgtgacca 5340 gcggggcaac gtcagccgag actaactctt acttcgcaaa gagtatggag tttctggcgc 5400 gaccggtgcc tgcgcctcga acagtattca ggaaccctcc acatcccgct ccgcgcacaa 5460 gaacaccgtc acttgcaccc agcagggcct gctcgagaac cagcctagtt tccaccccgc 5520 caggcgtgaa tagggtgatc actagagagg agctcgaggc gcttaccccg tcacgcactc 5580 ctagcaggtc ggtctcgaga accagcctgg tctccaaccc gccaggcgta aatagggtga 5640 ttacaagaga ggagtttgag gcgttcgtag cacaacaaca atgacggttt gatgcgggtg 5700 catacatctt ttcctccgac accggtcaag ggcatttaca acaaaaatca gtaaggcaaa 5760 cggtgctatc cgaagtggtg ttggagagga ccgaattgga gatttcgtat gccccgcgcc 5820 tcgaccaaga aaaagaagaa ttactacgca agaaattaca gttaaatccc acacctgcta 5880 acagaagcag ataccagtcc aggaaggtgg agaacatgaa agccataaca gctagacgta 5940 ttctgcaagg cctagggcat tatttgaagg cagaaggaaa agtggagtgc taccgaaccc 6000 tgcatcctgt tcctttgtat tcatctagtg tgaaccgtgc cttttcaagc cccaaggtcg 6060 cagtggaagc ctgtaacgcc atgttgaaag agaactttcc gactgtggct tcttactgta 6120 ttattccaga gtacgatgcc tatttggaca tggttgacgg agcttcatgc tgcttagaca 6180 ctgccagttt ttgccctgca aagctgcgca gctttccaaa gaaacactcc tatttggaac 6240 ccacaatacg atcggcagtg ccttcagcga tccagaacac gctccagaac gtcctggcag 6300 ctgccacaaa aagaaattgc aatgtcacgc aaatgagaga attgcccgta ttggattcgg 6360 cggcctttaa tgtggaatgc ttcaagaaat atgcgtgtaa taatgaatat tgggaaacgt 6420 ttaaagaaaa ccccatcagg cttactgaag aaaacgtggt aaattacatt accaaattaa 6480 aaggaccaaa agctgctgct ctttttgcga agacacataa tttgaatatg ttgcaggaca 6540 taccaatgga caggtttgta atggacttaa agagagacgt gaaagtgact ccaggaacaa 6600 aacatactga agaacggccc aaggtacagg tgatccaggc tgccgatccg ctagcaacag 6660 cgtatctgtg cggaatccac cgagagctgg ttaggagatt aaatgcggtc ctgcttccga 6720 acattcatac actgtttgat atgtcggctg aagactttga cgctattata gccgagcact 6780 tccagcctgg ggattgtgtt ctggaaactg acatcgcgtc gtttgataaa agtgaggacg 6840 acgccatggc tctgaccgcg ttaatgattc tggaagactt aggtgtggac gcagagctgt 6900 tgacgctgat tgaggcggct ttcggcgaaa tttcatcaat acatttgccc actaaaacta 6960 aatttaaatt cggagccatg atgaaatctg gaatgttcct cacactgttt gtgaacacag 7020 tcattaacat tgtaatcgca agcagagtgt tgagagaacg gctaaccgga tcaccatgtg 7080 cagcattcat tggagatgac aatatcgtga aaggagtcaa atcggacaaa ttaatggcag 7140 acaggtgcgc cacctggttg aatatggaag tcaagattat agatgctgtg gtgggcgaga 7200 aagcgcctta tttctgtgga gggtttattt tgtgtgactc cgtgaccggc acagcgtgcc 7260 gtgtggcaga ccccctaaaa aggctgttta agcttggcaa acctctggca gcagacgatg 7320 aacatgatga tgacaggaga agggcattgc atgaagagtc aacacgctgg aaccgagtgg 7380 gtattctttc agagctgtgc aaggcagtag aatcaaggta tgaaaccgta ggaacttcca 7440 tcatagttat ggccatgact actctagcta gcagtgttaa atcattcagc tacctgagag 7500 gggcccctat aactctctac ggctaacctg aatggactac gactatcacg cccaaacatt 7560 tacagccgcg gtgtcaaaaa ccgcgtggac gtggttaaca tccctgctgg gaggatcagc 7620 cgtaattatt ataattggct tggtgctggc tactattgtg gccatgtacg tgctgaccaa 7680 ccagaaacat aattgaatac agcagcaatt ggcaagctgc ttacatagaa ctcgcggcga 7740 ttggcatgcc gccttaaaat ttttatttta ttttttcttt tcttttccga atcggatttt 7800 gtttttaata tttcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 7860 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 7894
3-7	**Sequences**	
3-7-1	Sequence Number [ID]	7
3-7-2	Molecule Type	DNA
3-7-3	Length	7893
3-7-4	Features	**misc_feature 1..7893**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..7893
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-7-5	Residues	ataggcggcg catgagagaa gcccagacca attacctacc caaaatggag aaagttcacg 60 ttgacatcga ggaagacagc ccattcctca gagctttgca gcggagcttc ccgcagtttg 120 aggtagaagc caagcaggtc actgataatg accatgctaa tgccagagcg ttttcgcatc 180 tggcttcaaa actgatcgaa acggaggtgg acccatccga cacgatcctt gacattggaa 240 gtgcgcccgc ccgcagaatg tattctaagc acaagtatca ttgtatctgt ccgatgagat 300 gtgcggaaga tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgtaagg 360 aaataactga taaggaattg gacaagaaaa tgaaggagct cgccgccgtc atgagcgacc 420 ctgacctgga aactgagact atgtgcctcc acgacgacga gtcgtgtcgc tacgaagggc 480 aagtcgctgt ttaccaggat gtatacgcgg ttgacggacc gacaagtctc tatcaccaag 540 ccaataaggg agttagagtc gcctactgga taggctttga caccacccct tttatgttta 600 agaacttggc tggagcatat ccatcatact ctaccaactg ggccgacgaa accgtgttaa 660 cggctcgtaa cataggccta tgcagctctg acgttatgga gcggtcacgt agagggatgt 720 ccattcttag aaagaagtat ttgaaaccat ccaacaatgt tctattctct gttggctcga 780 ccatctacca cgagaagagg gacttactga ggagctggca cctgccgtct gtatttcact 840 tacgtggcaa gcaaaattac acatgtcggt gtgagactat agttagttgc gacgggtacg 900 tcgttaaaag aatagctatc agtccaggcc tgtatgggaa gccttcaggc tatgctgcta 960 cgatgcaccg cgagggattc ttgtgctgca aagtgacaga cacattgaac ggggagaggg 1020

2026201462 26 Feb 2026

tctcttttcc cgtgtgcacg tatgtgccag ctacattgtg tgaccaaatg actggcatac 1080
tggcaacaga tgtcagtgcg gacgacgcgc aaaaactgct ggttgggctc aaccagcgta 1140
tagtcgtcaa cggtcgcacc cagagaaaca ccaataccat gaaaaattac cttttgcccg 1200
tagtggccca ggcatttgct aggtgggcaa aggaatataa ggaagatcaa gaagatgaaa 1260
ggccactagg actacgagat agacagttag tcatggggtg ttgttgggct tttagaaggc 1320
acaagataac atctatttat aagcgcccgg atacccaaac catcatcaaa gtgaacagcg 1380
atttccactc attcgtgctg cccaggatag gcagtaacac attggagatc gggctgagaa 1440
caagaatcag gaaaatgtta gaggagcaca aggagccgtc acctctcatt accgccgagg 1500
acgtacaaga agctaagtgc gcagccgatg aggctaagga ggtgcgtgaa gccgaggagt 1560
tgcgcgcagc tctaccacct ttggcagctg atgttgagga gcccactctg gaagccgatg 1620
tcgacttgat gttacaagag gctggggccg gctcagtgga gacacctcgt ggcttgataa 1680
aggttaccag ctacgatggc gaggacaaga tcggctctta cgctgtgctt tctccgcagg 1740
ctgtactcaa gagtgaaaaa ttatcttgca tccaccctct cgctgaacaa gtcatagtga 1800
taacacactc tggccgaaaa gggcgttatg ccgtggaacc ataccatggt aaagtagtgg 1860
tgccagaggg acatgcaata cccgtccagg actttcaagc tctgagtgaa agtgccacca 1920
ttgtgtacaa cgaacgtgag ttcgtaaaca ggtacctgca ccatattgcc acacatggag 1980
gagcgctgaa cactgatgaa gaatattaca aaactgtcaa gcccagcgag cacgacggcg 2040
aatacctgta cgacatcgac aggaaacagt gcgtcaagaa agaactagtc actgggctag 2100
ggctcacagg cgagctggtg gatcctccct tccatgaatt cgcctacgag agtctgagaa 2160
cacgaccagc cgctccttac caagtaccaa ccataggggt gtatggcgtg ccaggatcag 2220
gcaagtctgg catcattaaa agcgcagtca ccaaaaaaga tctagtggtg agcgccaaga 2280
aagaaaactg tgcagaaatt ataagggacg tcaagaaaat gaaagggctg gacgtcaatg 2340
ccagaactgt ggactcagtg ctcttgaatg gatgcaaaca ccccgtagag accctgtata 2400
ttgacgaagc ttttgcttgt catgcaggta ctctcagagc gctcatagcc attataagac 2460
ctaaaaaggc agtgctctgc ggggatccca aacagtgcgg ttttttaac atgatgtgcc 2520
tgaaagtgca ttttaaccac gagatttgca cacaagtctt ccacaaaagc atctctcgcc 2580
gttgcactaa atctgtgact tcggtcgtct caaccttgtt ttacgacaaa aaaatgagaa 2640
cgacgaatcc gaaagagact aagattgtga ttgacactac cggcagtacc aaacctaagc 2700
aggacgatct cattctcact tgtttcagag ggtgggtgaa gcagttgcaa atagattaca 2760
aaggcaacga aataatgacg gcagctgcct ctcaagggct gacccgtaaa ggtgtgtatg 2820
ccgttcggta caaggtgaat gaaaatcctc tgtacgcacc cacctcagaa catgtgaacg 2880
tcctactgac ccgcacggag gaccgcatcg tgtggaaaac actagccggc gacccatgga 2940
taaaaacact gactgccaag taccctggga atttcactgc cacgatagag gagtggcaag 3000
cagagcatga tgccatcatg aggcacatct tggagagacc ggaccctacc gacgtcttcc 3060
agaataaggc aaacgtgtgt tgggccaagg ctttagtgcc ggtgctgaag accgctggca 3120
tagacatgac cactgaacaa tggaacactg tggattattt tgaaacggac aaagctcact 3180
cagcagagat agtattgaac caactatgcg tgaggttctt tggactcgat ctggactccg 3240
gtctattttc tgcacccact gttccgttat ccattaggaa taatcactgg gataactccc 3300
cgtcgcctaa catgtacggg ctgaataaag aagtggtccg tcagctctct cgcaggtacc 3360
cacaactgcc tcgggcagtt gccactggaa gagtctatga catgaacact ggtacactgc 3420
gcaattatga tccgcgcata aacctagtac ctgtaaacag aagactgcct catgctttag 3480
tcctccacca taatgaacac ccacagagtg acttttcttc attcgtcagc aaattgaagg 3540
gcagaactgt cctggtggtc ggggaaaagt tgtccgtccc aggcaaaatg gttgactggt 3600
tgtcagaccg gcctgaggct accttcagag ctcggctgga tttaggcatc ccaggtgatg 3660
tgcccaaata tgacataata tttgttaatg tgaggacccc atataaatac catcactatc 3720
agcagtgtga agaccatgcc attaagctta gcatgttgac caagaaagct tgtctgcatc 3780
tgaatcccgg cggaacctgt gtcagcatag gttatggtta cgctgacagg gccagcgaaa 3840
gcatcattgg tgctatagcg cggcagttca agttttcccg ggtatgcaaa ccgaaatcct 3900
cacttgaaga gacggaagtt ctgtttgtat tcattgggta cgatcgcaag gcccgtacgc 3960
acaatcctta caagctttca tcaaccttga ccaacattta tacaggttcc agactccacg 4020
aagccggatg tgcaccctca tatcatgtgg tgcgagggga tattgccacg gccaccgaag 4080
gagtgattat aaatgctgct aacagcaaag gacaacctgg cggaggggtg tgcggagcgc 4140
tgtataagaa attcccggaa agcttcgatt tacagccgat cgaagtagga aaagcgcgac 4200
tggtcaaagg tgcagctaaa catatcattc atgccgtagg accaaacttc aacaaagttt 4260
cggaggttga aggtgacaaa cagttggcag aggcttatga gtccatcgct aagattgtca 4320
acgataacaa ttacaagtca gtagcgattc cactgttgtc caccggcatc ttttccggga 4380
acaaagatcg actaacccaa tcattgaacc atttgctgac agctttagac accactgatg 4440
cagatgtagc catatactgc agggacaaga aatgggaaat gactctcaag gaagcagtgg 4500
ctaggagaga agcagtggag gagatatgca tatccgacga ctcttcagtg acagaacctg 4560
atgcagagct ggtgagggtg catccgaaga gttctttggc tggaaggaag ggctacagca 4620
caagcgatgg caaaactttc tcatatttgg aagggaccaa gtttcaccag gcggccaagg 4680
atatagcaga aattaatgcc atgtggcccg ttgcaacgga ggccaatgag caggtatgca 4740
tgtatatcct cggagaaagc atgagcagta ttaggtcgaa atgccccgtc gaagagtcgg 4800
aagcctccac accacctagc acgctgcctt gcttgtgcat ccatgccatg actccagaaa 4860
gagtacagcg cctaaaagcc tcacgtccag aacaaattac tgtgtgctca tcctttccat 4920
tgccgaagta tagaatcact ggtgtgcaga agatccaatg ctcccagcct atattgttct 4980
caccgaaagt gcctgcgtat attcatccaa ggaagtatct cgtggaaaca ccaccggtag 5040
acgagactcc ggagccatcg gcagagaacc aatccacaga ggggacacct gaacaaccac 5100
cacttataac cgaggatgag accaggacta gaacgcctga gccgatcatc atcgaagagg 5160
aagaagagga tagcataagt ttgctgtcag atggcccgac ccaccaggtg ctgcaagtcg 5220
aggcagacat tcacgggccg ccctctgtat ctagctcatc ctggtccatt cctcatgcat 5280
ccgactttga tgtggacagt ttatccatac ttgacaccct ggagggagct agcgtgacca 5340
gcggggcaac gtcagccgag actaactctt acttcgcaaa gagtatggag tttctggcgc 5400
gaccggtgcc tgcgcctcga acagtattca ggaaccctcc acatcccgct ccgcgcacaa 5460
gaacaccgtc acttgcaccc agcagggcct gctcgagaac cagcctagtt tccaccccgc 5520
caggcgtgaa tagggtgatc actagagagg agctcgaggc gcttaccccg tcacgcactc 5580

2026201462 26 Feb 2026

		ctagcaggtc ggtctcgaga accagcctgg tctccaaccc gccaggcgta aatagggtga 5640 ttacaagaga ggagtttgag gcgttcgtag cacaacaaca atgacggttt gatgcgggtg 5700 catacatctt ttcctccgac accggtcaag ggcatttaca acaaaaatca gtaaggcaaa 5760 cggtgctatc cgaagtggtg ttggagagga ccgaattgga gatttcgtat gccccgcgcc 5820 tcgaccaaga aaaagaagaa ttactacgca agaaattaca gttaaatccc acacctgcta 5880 acagaagcag ataccagtcc aggaaggtgg agaacatgaa agccataaca gctagacgta 5940 ttctgcaagg cctagggcat tatttgaagg cagaaggaaa agtggagtgc taccgaaccc 6000 tgcatcctgt tcctttgtat tcatctagtg tgaaccgtgc cttttcaagc cccaaggtcg 6060 cagtggaagc ctgtaacgcc atgttgaaag agaactttcc gactgtggct tcttactgta 6120 ttattccaga gtacgatgcc tatttggaca tggttgacgg agcttcatgc tgcttagaca 6180 ctgccagttt ttgccctgca aagctgcgca gctttccaaa gaaacactcc tatttggaac 6240 ccacaatacg atcggcagtg ccttcagcga tccagaacac gctccagaac gtcctggcag 6300 ctgccacaaa aagaaattgc aatgtcacgc aaatgagaga attgcccgta ttggattcgg 6360 cggcctttaa tgtggaatgc ttcaagaaat atgcgtgtaa taatgaatat tgggaaacgt 6420 ttaaagaaaa ccccatcagg cttactgaag aaaacgtggt aaattacatt accaaattaa 6480 aaggaccaaa agctgctgct ctttttgcga agacacataa tttgaatatg ttgcaggaca 6540 taccaatgga caggtttgta atggacttaa agagagacgt gaaagtgact ccaggaacaa 6600 aacatactga agaacggccc aaggtacagg tgatccaggc tgccgatccg ctagcaacag 6660 cgtatctgtg cggaatccac cgagagctgg ttaggagatt aaatgcggtc ctgcttccga 6720 acattcatac actgtttgat atgtcggctg aagactttga cgctattata gccgagcact 6780 tccagcctgg ggattgtgtt ctggaaactg acatcgcgtc gtttgataaa agtgaggacg 6840 acgccatggc tctgaccgcg ttaatgattc tggaagactt aggtgtggac gcagagctgt 6900 tgacgctgat tgaggcggct ttcggcgaaa tttcatcaat acatttgccc actaaaacta 6960 aatttaaatt cggagccatg atgaaatctg gaatgttcct cacactgttt gtgaacacag 7020 tcattaacat tgtaatcgca agcagagtgt tgagagaacg gctaaccgga tcaccatgtg 7080 cagcattcat tggagatgac aatatcgtga aaggagtcaa atcggacaaa ttaatggcag 7140 acaggtgcgc cacctggttg aatatggaag tcaagattat agatgctgtg gtgggcgaga 7200 aagcgcctta tttctgtgga gggtttattt tgtgtgactc cgtgaccggc acagcgtgcc 7260 gtgtggcaga ccccctaaaa aggctgttta agcttggcaa acctctggca gcagacgatg 7320 aacatgatga tgacaggaga agggcattgc atgaagagtc aacacgctgg aaccgagtgg 7380 gtattctttc agagctgtgc aaggcagtag aatcaaggta tgaaaccgta ggaacttcca 7440 tcatagttat ggccatgact actctagcta gcagtgttaa atcattcagc tacctgagag 7500 gggcccctat aactctctac ggctaacctg aatggactac gactatcacg cccaaacatt 7560 tacagccgcg gtgtcaaaaa ccgcgtggac gtggttaaca tccctgctgg gaggatcagc 7620 cgtaattatt ataattggct tggtgctggc tactattgtg gccatgtacg tgctgaccaa 7680 ccagaaacat aattgaatac agcagcaatt ggcaagctgc ttacatagaa ctcgcggcga 7740 ttggcatgcc gccttaaaat ttttatttta tttttctttt cttttccgaa tcggattttg 7800 tttttaatat ttcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 7860 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 7893
3-8	**Sequences**	
3-8-1	Sequence Number [ID]	8
3-8-2	Molecule Type	DNA
3-8-3	Length	7927
3-8-4	Features	**misc_feature 1..7927**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide **source 1..7927** mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-8-5	Residues	taatacgact cactatagga tgggcggcgc atgagagaag cccagaccaa ttacctaccc 60 aaaatggaga aagttcacgt tgacatcgag gaagacagcc cattcctcag agctttgcag 120 cggagcttcc cgcagtttga ggtagaagcc aagcaggtca ctgataatga ccatgctaat 180 gccagagcgt tttcgcatct ggcttcaaaa ctgatcgaaa cggaggtgga cccatccgac 240 acgatccttg acattggaag tgcgcccgcc cgcagaatgt attctaagca caagtatcat 300 tgtatctgtc cgatgagatg tgcggaagat ccggacagat tgtataagta tgcaactaag 360 ctgaagaaaa actgtaagga aataactgat aaggaattgg acaagaaaat gaaggagctc 420 gccgccgtca tgagcgaccc tgacctggaa actgagacta tgtgcctcca cgacgacgag 480 tcgtgtcgct acgaagggca agtcgctgtt taccaggatg tatacgcggt tgacggaccg 540 acaagtctct atcaccaagc caataaggga gttagagtcg cctactggat aggctttgac 600 accacccctt ttatgtttaa gaacttggct ggagcatatc catcatactc taccaactgg 660 gccgacgaaa ccgtgttaac ggctcgtaac ataggcctat gcagctctga cgttatggag 720 cggtcacgta gagggatgtc cattcttaga aagaagtatt tgaaaccatc caacaatgtt 780 ctattctctg ttggctcgac catctaccac gagaagaggg acttactgag gagctggcac 840 ctgccgtctg tatttcactt acgtggcaag caaaattaca catgtcggtg tgagactata 900 gttagttgcg acgggtacgt cgttaaaaga atagctatca gtccaggcct gtatgggaag 960 ccttcaggct atgctgctac gatgcaccgc gagggattct tgtgctgcaa agtgacagac 1020 acattgaacg gggagagggt ctcttttccc gtgtgcacgt atgtgccagc tacattgtgt 1080 gaccaaatga ctggcatact ggcaacagat gtcagtgcgg acgacgcgca aaaactgctg 1140 gttgggctca accagcgtat agtcgtcaac ggtcgcaccc agagaaacac caataccatg 1200 aaaaattacc ttttgcccgt agtggcccag gcatttgcta ggtgggcaaa ggaatataag 1260 gaagatcaag aagatgaaag gccactagga ctacgagata gacagttagt catggggtgt 1320 tgttgggctt ttagaaggca caagataaca tctatttata agcgcccgga tacccaaacc 1380 atcatcaaag tgaacagcga tttccactca ttcgtgctgc ccaggatagg cagtaacaca 1440 ttggagatcg ggctgagaac aagaatcagg aaaatgttag aggagcacaa ggagccgtca 1500 cctctcatta ccgccgagga cgtacaagaa gctaagtgcg cagccgatga ggctaaggag 1560

20262014622 26 Feb 2026

gtgcgtgaag ccgaggagtt gcgcgcagct ctaccacctt tggcagctga tgttgaggag 1620
cccactctgg aagccgatgt cgacttgatg ttacaagagg ctggggccgg ctcagtggag 1680
acacctcgtg gcttgataaa ggttaccagc tacgctggcg aggacaagat cggctcttac 1740
gctgtgcttt ctccgcaggc tgtactcaag agtgaaaaat tatcttgcat ccacctctc 1800
gctgaacaag tcatagtgat aacacactct ggccgaaaag ggcgttatgc cgtggaacca 1860
taccatggta aagtagtggt gccagaggga catgcaatac ccgtccagga ctttcaagct 1920
ctgagtgaaa gtgccaccat tgtgtacaac gaacgtgagt tcgtaaacag gtacctgcac 1980
catattgcca cacatggagg agcgctgaac actgatgaag aatattacaa aactgtcaag 2040
cccagcgagc acgacggcga atacctgtac gacatcgaca ggaaacagtg cgtcaagaaa 2100
gaactagtca ctgggctagg gctcacaggc gagctggtgg atcctccctt ccatgaattc 2160
gcctacgaga gtctgagaac acgaccagcc gctccttacc aagtaccaac cataggggtg 2220
tatggcgtgc caggatcagg caagtctggc atcattaaaa gcgcagtcac caaaaaagat 2280
ctagtggtga gcgccaagaa agaaaactgt gcagaaatta taagggacgt caagaaaatg 2340
aaagggctgg acgtcaatgc cagaactgtg gactcagtgc tcttgaatgg atgcaaacac 2400
cccgtagaga ccctgtatat tgacgaagct tttgcttgtc atgcaggtac tctcagagcg 2460
ctcatagcca ttataagacc taaaaaggca gtgctctgcg gggatcccaa acagtgcggt 2520
ttttttaaca tgatgtgcct gaaagtgcat tttaaccacg agatttgcac acaagtcttc 2580
cacaaaagca tctctcgccg ttgcactaaa tctgtgactt cggtcgtctc aaccttgttt 2640
tacgacaaaa aaatgagaac gacgaatccg aaagagacta agattgtgat tgacactacc 2700
ggcagtacca aacctaagca ggacgatctc attctcactt gtttcagagg gtgggtgaag 2760
cagttgcaaa tagattacaa aggcaacgaa ataatgacgg cagctgcctc tcaagggctg 2820
acccgtaaag gtgtgtatgc cgttcggtac aaggtgaatg aaaatcctct gtacgcaccc 2880
acctcagaac atgtgaacgt cctactgacc cgcacggagg accgcatcgt gtggaaaaca 2940
ctagccggcg acccatggat aaaaacactg actgccaagt accctgggaa tttcactgcc 3000
acgatagagg agtggcaagc agagcatgat gccatcatga ggcacatctt ggagagaccg 3060
gaccctaccg acgtcttcca gaataaggca aacgtgtgtt gggccaaggc tttagtgccg 3120
gtgctgaaga ccgctggcat agacatgacc actgaacaat ggaacactgt ggattatttt 3180
gaaacggaca aagctcactc agcagagata gtattgaacc aactatgcgt gaggttcttt 3240
ggactcgatc tggactccgg tctattttct gcacccactg ttccgttatc cattaggaat 3300
aatcactggg ataactcccc gtcgcctaac atgtacgggc tgaataaaga agtggtccgt 3360
cagctctctc gcaggtaccc acaactgcct cgggcagttg ccactggaag agtctatgac 3420
atgaacactg gtacactgcg caattatgat ccgcgcataa acctagtacc tgtaaacaga 3480
agactgcctc atgctttagt cctccaccat aatgaacacc cacagagtga cttttcttca 3540
ttcgtcagca aattgaaggg cagaactgtc ctggtggtcg gggaaaagtt gtccgtccca 3600
ggcaaaatgg ttgactggtt gtcagaccgg cctgaggcta ccttcagagc tcggctggat 3660
ttaggcatcc caggtgatgt gcccaaatat gacataatat ttgttaatgt gaggacccca 3720
tataaatacc atcactatca gcagtgtgaa gaccatgcca ttaagcttag catgttgacc 3780
aagaaagctt gtctgcatct gaatcccggc ggaacctgtg tcagcatagg ttatggttac 3840
gctgacaggg ccagcgaaag catcattggt gctatagcgc ggcagttcaa gttttcccgg 3900
gtatgcaaac cgaaatcctc acttgaagag acggaagttc tgtttgtatt cattgggtac 3960
gatcgcaagg cccgtacgca caatccttac aagctttcat caaccttgac caacatttat 4020
acaggttcca gactccacga agccggatgt gcaccctcat atcatgtggt gcgaggggat 4080
attgccacgg ccaccgaagg agtgattata aatgctgcta acagcaaagg acaacctggc 4140
ggaggggtgt gcggagcgct gtataagaaa ttcccggaaa gcttcgattt acagccgatc 4200
gaagtaggaa aagcgcgact ggtcaaaggt gcagctaaac atatcattca tgccgtagga 4260
ccaaacttca acaaagtttc ggaggttgaa ggtgacaaac agttggcaga ggcttatgag 4320
tccatcgcta agattgtcaa cgataacaat tacaagtcag tagcgattcc actgttgtcc 4380
accggcatct tttccgggaa caaagatcga ctaacccaat cattgaacca tttgctgaca 4440
gctttagaca ccactgatgc agatgtagcc atatactgca gggacaagaa atgggaaatg 4500
actctcaagg aagcagtggc taggagagaa gcagtggagg agatatgcat atccgacgac 4560
tcttcagtga cagaacctga tgcagagctg gtgagggtgc atccgaagag ttctttggct 4620
ggaaggaagg gctacagcac aagcgatggc aaaactttct catatttgga agggaccaag 4680
tttcaccagg cggccaagga tatagcagaa attaatgcca tgtggcccgt tgcaacggag 4740
gccaatgagc aggtatgcat gtatatcctc ggagaaagca tgagcagtat taggtcgaaa 4800
tgccccgtcg aagagtcgga agcctccaca ccacctagca cgctgccttg cttgtgcatc 4860
catgccatga ctccagaaag agtacagcgc ctaaaagcct cacgtccaga acaaattact 4920
gtgtgctcat cctttccatt gccgaagtat agaatcactg gtgtgcagaa gatccaatgc 4980
tcccagccta tattgttctc accgaaagtg cctgcgtata ttcatccaag gaagtatctc 5040
gtggaaacac caccggtaga cgagactccg gagccatcgg cagagaacca atccacagag 5100
gggacacctg aacaaccacc acttataacc gaggatgaga ccaggactag aacgcctgag 5160
ccgatcatca tcgaagagga agaagaggat agcataagtt tgctgtcaga tggcccgacc 5220
caccaggtgc tgcaagtcga ggcagacatt cacgggccgc cctctgtatc tagctcatcc 5280
tggtccattc ctcatgcatc cgactttgat gtggacagtt tatccatact tgacaccctg 5340
gagggagcta gcgtgaccag cggggcaacg tcagccgaga ctaactctta cttcgcaaag 5400
agtatggagt ttctggcgcg accggtgcct gcgcctcgaa cagtattcag gaaccctcca 5460
catcccgctc cgcgcacaag aacaccgtca cttgcaccca gcagggcctg ctcgagaacc 5520
agcctagttt ccacccccgcc aggcgtgaat agggtgatca ctagagagga gctcgaggcg 5580
cttaccccgt cacgcactcc tagcaggtcg gtctcgagaa ccagcctggt ctccaacccg 5640
ccaggcgtaa atagggtgat tacaagagag gagtttgagg cgttcgtagc acaacaacaa 5700
tgacggtttg atgcgggtgc atacatcttt tcctccgaca ccggtcaagg gcatttacaa 5760
caaaaatcag taaggcaaac ggtgctatcc gaagtggtgt tggagaggac cgaattggag 5820
atttcgtatg ccccgcgcct cgaccaagaa aaagaagaat tactacgcaa gaaattacag 5880
ttaaatccca cacctgctaa cagaagcaga taccagtcca ggaaggtgga gaacatgaaa 5940
gccataacag ctagacgtat tctgcaaggc ctagggcatt atttgaaggc agaaggaaaa 6000
gtggagtgct accgaaccct gcatcctgtt cctttgtatt catctagtgt gaaccgtgcc 6060
ttttcaagcc ccaaggtcgc agtggaagcc tgtaacgcca tgttgaaaga gaactttccg 6120

2026201462 26 Feb 2026

		actgtggctt cttactgtat tattccagag tacgatgcct atttggacat ggttgacgga 6180 gcttcatgct gcttagacac tgccagtttt tgccctgcaa agctgcgcag ctttccaaag 6240 aaacactcct atttggaacc cacaatacga tcggcagtgc cttcagcgat ccagaacacg 6300 ctccagaacg tcctggcagc tgccacaaaa agaaattgca atgtcacgca aatgagagaa 6360 ttgcccgtat tggattcggc ggcctttaat gtggaatgct tcaagaaata tgcgtgtaat 6420 aatgaatatt gggaaacgtt taaagaaaac cccatcaggc ttactgaaga aaacgtggta 6480 aattacatta ccaaattaaa aggaccaaaa gctgctgctc tttttgcgaa gacacataat 6540 ttgaatatgt tgcaggacat accaatggac aggtttgtaa tggacttaaa gagagacgtg 6600 aaagtgactc caggaacaaa acatactgaa gaacggccca aggtacaggt gatccaggct 6660 gccgatccgc tagcaacagc gtatctgtgc ggaatccacc gagagctggt taggagatta 6720 aatgcggtcc tgcttccgaa cattcataca ctgtttgata tgtcggctga agactttgac 6780 gctattatag ccgagcactt ccagcctggg gattgtgttc tggaaactga catcgcgtcg 6840 tttgataaaa gtgaggacga cgccatggct ctgaccgcgt taatgattct ggaagactta 6900 ggtgtggacg cagagctgtt gacgctgatt gaggcggctt tcggcgaaat ttcatcaata 6960 catttgccca ctaaaactaa atttaaattc ggagccatga tgaaatctgg aatgttcctc 7020 acactgtttg tgaacacagt cattaacatt gtaatcgcaa gcagagtgtt gagagaacgg 7080 ctaaccggat caccatgtgc agcattcatt ggagatgaca atatcgtgaa aggagtcaaa 7140 tcggacaaat taatggcaga caggtgcgcc acctggttga atatggaagt caagattata 7200 gatgctgtgg tgggcgagaa agcgccttat ttctgtggag ggtttatttt gtgtgactcc 7260 gtgaccggca cagcgtgccg tgtggcagac cccctaaaaa ggctgtttaa gcttggcaaa 7320 cctctggcag cagacgatga acatgatgat gacaggagaa gggcattgca tgaagagtca 7380 acacgctgga accgagtggg tattctttca gagctgtgca aggcagtaga atcaaggtat 7440 gaaaccgtag gaacttccat catagttatg gccatgacta ctctagctag cagtgttaaa 7500 tcattcagct acctgagagg ggcccctata actctctacg gctaacctga atggactacg 7560 actatcacgc ccaaacattt acagccgcgg tgtcaaaaac cgcgtggacg tggttaacat 7620 ccctgctggg aggatcagcc gtaattatta taattggctt ggtgctggct actattgtgg 7680 ccatgtacgt gctgaccaac cagaaacata attgaataca gcagcaattg gcaagctgct 7740 tacatagaac tcgcggcgat tggcatgccg ccttaaaatt tttattttat tttttctttt 7800 cttttccgaa tcggattttg tttttaatat ttcaaaaaaa aaaaaaaaaa aaaaaaaaaa 7860 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaatacgtag 7920 tttaaac 7927
3-9	**Sequences**	
3-9-1	Sequence Number [ID]	9
3-9-2	Molecule Type	DNA
3-9-3	Length	7926
3-9-4	Features	**misc_feature 1..7926**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..7926
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-9-5	Residues	taatacgact cactatagga taggcggcgc atgagagaag cccagaccaa ttacctaccc 60 aaaatggaga aagttcacgt tgacatcgag gaagacagcc cattcctcag agctttgcag 120 cggagcttcc cgcagtttga ggtagaagcc aagcaggtca ctgataatga ccatgctaat 180 gccagagcgt tttcgcatct ggcttcaaaa ctgatcgaaa cggaggtgga cccatccgac 240 acgatccttg acattggaag tgcgcccgcc cgcagaatgt attctaagca caagtatcat 300 tgtatctgtc cgatgagatg tgcggaagat ccggacagat tgtataagta tgcaactaag 360 ctgaagaaaa actgtaagga aataactgat aaggaattgg acaagaaaat gaaggagctc 420 gccgccgtca tgagcgaccc tgacctggaa actgagacta tgtgcctcca cgacgacgag 480 tcgtgtcgct acgaagggca agtcgctgtt taccaggatg tatacgcggt tgacggaccg 540 acaagtctct atcaccaagc caataaggga gttagagtcg cctactggat aggctttgac 600 accacccctt ttatgtttaa gaacttggct ggagcatatc catcatactc taccaactgg 660 gccgacgaaa ccgtgttaac ggctcgtaac ataggcctat gcagctctga cgttatggag 720 cggtcacgta gagggatgtc cattcttaga aagaagtatt tgaaaccatc caacaatgtt 780 ctattctctg ttggctcgac catctaccac gagaagaggg acttactgag gagctggcac 840 ctgccgtctg tatttcactt acgtggcaag caaaattaca catgtcggtg tgagactata 900 gttagttgcg acgggtacgt cgttaaaaga atagctatca gtccaggcct gtatgggaag 960 ccttcaggct atgctgctac gatgcaccgc gagggattct tgtgctgcaa agtgacagac 1020 acattgaacg gggagagggt ctcttttccc gtgtgcacgt atgtgccagc tacattgtgt 1080 gaccaaatga ctggcatact ggcaacagat gtcagtgcgg acgacgcgca aaaactgctg 1140 gttgggctca accagcgtat agtcgtcaac ggtcgcaccc agagaaacac caataccatg 1200 aaaaattacc ttttgcccgt agtggcccag gcatttgcta ggtgggcaaa ggaatataag 1260 gaagatcaag aagatgaaag gccactagga ctacgagata gacagttagt catggggtgt 1320 tgttgggctt ttagaaggca caagataaca tctatttata agcgcccgga tacccaaacc 1380 atcatcaaag tgaacagcga tttccactca ttcgtgctgc ccaggatagg cagtaacaca 1440 ttggagatcg ggctgagaac aagaatcagg aaaatgttag aggagcacaa ggagccgtca 1500 cctctcatta ccgccgagga cgtacaagaa gctaagtgcg cagccgatga ggctaaggag 1560 gtgcgtgaag ccgaggagtt gcgcgcagct ctaccacctt tggcagctga tgttgaggag 1620 cccactctgg aagccgatgt cgacttgatg ttacaagagg ctggggccgg ctcagtggag 1680 acacctcgtg gcttgataaa ggttaccagc tacgatggcg aggacaagat cggctcttac 1740 gctgtgcttt ctccgcaggc tgtactcaag agtgaaaaat tatcttgcat ccaccctctc 1800 gctgaacaag tcatagtgat aacacactct ggccgaaaag ggcgttatgc cgtggaacca 1860 taccatggta aagtagtggt gccagaggga catgcaatac ccgtccagga ctttcaagct 1920 ctgagtgaaa gtgccaccat tgtgtacaac gaacgtgagt tcgtaaacag gtacctgcac 1980 catattgcca cacatggagg agcgctgaac actgatgaag aatattacaa aactgtcaag 2040

20262014626 26 Feb 2026

cccagcgagc acgacggcga atacctgtac gacatcgaca ggaaacagtg cgtcaagaaa 2100
gaactagtca ctgggctagg gctcacaggc gagctggtgg atcctccctt ccatgaattc 2160
gcctacgaga gtctgagaac acgaccagcc gctccttacc aagtaccaac cataggggtg 2220
tatggcgtgc caggatcagg caagtctggc atcattaaaa gcgcagtcac caaaaaagat 2280
ctagtggtga gcgccaagaa agaaaactgt gcagaaatta taagggacgt caagaaaatg 2340
aaagggctgg acgtcaatgc cagaactgtg gactcagtgc tcttgaatgg atgcaaacac 2400
cccgtagaga ccctgtatat tgacgaagct tttgcttgtc atgcaggtac tctcagagcg 2460
ctcatagcca ttataagacc taaaaaggca gtgctctgcg gggatcccaa acagtgcggt 2520
ttttttaaca tgatgtgcct gaaagtgcat tttaaccacg agatttgcac acaagtcttc 2580
cacaaaagca tctctcgccg ttgcactaaa tctgtgactt cggtcgtctc aaccttgttt 2640
tacgacaaaa aaatgagaac gacgaatccg aaagagacta agattgtgat tgacactacc 2700
ggcagtacca aacctaagca ggacgatctc attctcactt gtttcagagg gtgggtgaag 2760
cagttgcaaa tagattacaa aggcaacgaa ataatgacgg cagctgcctc tcaagggctg 2820
acccgtaaag gtgtgtatgc cgttcggtac aaggtgaatg aaaatcctct gtacgcaccc 2880
acctcagaac atgtgaacgt cctactgacc cgcacggagg accgcatcgt gtggaaaaca 2940
ctagccggcg acccatggat aaaaacactg actgccaagt accctgggaa tttcactgcc 3000
acgatagagg agtggcaagc agagcatgat gccatcatga ggcacatctt ggagagaccg 3060
gaccctaccg acgtcttcca gaataaggca aacgtgtgtt gggccaaggc tttagtgccg 3120
gtgctgaaga ccgctggcat agacatgacc actgaacaat ggaacactgt ggattatttt 3180
gaaacggaca aagctcactc agcagagata gtattgaacc aactatgcgt gaggttcttt 3240
ggactcgatc tggactccgg tctattttct gcacccactg ttccgttatc cattaggaat 3300
aatcactggg ataactcccc gtcgcctaac atgtacgggc tgaataaaga agtggtccgt 3360
cagctctctc gcaggtaccc acaactgcct cgggcagttg ccactggaag agtctatgac 3420
atgaacactg gtacactgcg caattatgat ccgcgcataa acctagtacc tgtaaacaga 3480
agactgcctc atgctttagt cctccaccat aatgaacacc cacagagtga cttttcttca 3540
ttcgtcagca aattgaaggg cagaactgtc ctggtggtcg gggaaaagtt gtccgtccca 3600
ggcaaaatgg ttgactggtt gtcagaccgg cctgaggcta ccttcagagc tcggctggat 3660
ttaggcatcc caggtgatgt gcccaaatat gacataatat ttgttaatgt gaggacccca 3720
tataaatacc atcactatca gcagtgtgaa gaccatgcca ttaagcttag catgttgacc 3780
aagaaagctt gtctgcatct gaatcccggc ggaacctgtg tcagcatagg ttatggttac 3840
gctgacaggg ccagcgaaag catcattggt gctatagcgc ggcagttcaa gttttcccgg 3900
gtatgcaaac cgaaatcctc acttgaagag acggaagttc tgtttgtatt cattgggtac 3960
gatcgcaagg cccgtacgca caatccttac aagctttcat caaccttgac caacatttat 4020
acaggttcca gactccacga agccggatgt gcaccctcat atcatgtggt gcgaggggat 4080
attgccacgg ccaccgaagg agtgattata aatgctgcta acagcaaagg acaacctggc 4140
ggaggggtgt gcggagcgct gtataagaaa ttcccggaaa gcttcgattt acagccgatc 4200
gaagtaggaa aagcgcgact ggtcaaaggt gcagctaaac atatcattca tgccgtagga 4260
ccaaacttca acaaagtttc ggaggttgaa ggtgacaaac agttggcaga ggcttatgag 4320
tccatcgcta agattgtcaa cgataacaat tacaagtcag tagcgattcc actgttgtcc 4380
accggcatct tttccgggaa caaagatcga ctaacccaat cattgaacca tttgctgaca 4440
gctttagaca ccactgatgc agatgtagcc atatactgca gggacaagaa atgggaaatg 4500
actctcaagg aagcagtggc taggagagaa gcagtggagg agatatgcat atccgacgac 4560
tcttcagtga cagaacctga tgcagagctg gtgagggtgc atccgaagag ttctttggct 4620
ggaaggaagg gctacagcac aagcgatggc aaaactttct catatttgga agggaccaag 4680
tttcaccagg cggccaagga tatagcagaa attaatgcca tgtggcccgt tgcaacggag 4740
gccaatgagc aggtatgcat gtatatcctc ggagaaagca tgagcagtat taggtcgaaa 4800
tgccccgtcg aagagtcgga agcctccaca ccacctagca cgctgccttg cttgtgcatc 4860
catgccatga ctccagaaag agtacagcgc ctaaaagcct cacgtccaga acaaattact 4920
gtgtgctcat cctttccatt gccgaagtat agaatcactg gtgtgcagaa gatccaatgc 4980
tcccagccta tattgttctc accgaaagtg cctgcgtata ttcatccaag gaagtatctc 5040
gtggaaacac caccggtaga cgagactccg gagccatcgg cagagaacca atccacagag 5100
gggacacctg aacaaccacc acttataacc gaggatgaga ccaggactag aacgcctgag 5160
ccgatcatca tcgaagagga agaagaggat agcataagtt tgctgtcaga tggcccgacc 5220
caccaggtgc tgcaagtcga ggcagacatt cacgggccgc cctctgtatc tagctcatcc 5280
tggtccattc ctcatgcatc cgactttgat gtggacagtt tatccatact tgacaccctg 5340
gagggagcta gcgtgaccag cggggcaacg tcagccgaga ctaactctta cttcgcaaag 5400
agtatggagt ttctggcgcg accggtgcct gcgcctcgaa cagtattcag gaaccctcca 5460
catcccgctc cgcgcacaag aacaccgtca cttgcaccca gcagggcctg ctcgagaacc 5520
agcctagttt ccacccccgcc aggcgtgaat agggtgatca ctagagagga gctcgaggcg 5580
cttaccccgt cacgcactcc tagcaggtcg gtctcgagaa ccagcctggt ctccaacccg 5640
ccaggcgtaa atagggtgat tacaagagag gagtttgagg cgttcgtagc acaacaacaa 5700
tgacggtttg atgcgggtgc atacatcttt tcctccgaca ccggtcaagg gcatttacaa 5760
caaaaatcag taaggcaaac ggtgctatcc gaagtggtgt tggagaggac cgaattggag 5820
atttcgtatg ccccgcgcct cgaccaagaa aaagaagaat tactacgcaa gaaattacag 5880
ttaaatccca cacctgctaa cagaagcaga taccagtcca ggaaggtgga gaacatgaaa 5940
gccataacag ctagacgtat tctgcaaggc ctagggcatt atttgaaggc agaaggaaaa 6000
gtggagtgct accgaaccct gcatcctgtt cctttgtatt catctagtgt gaaccgtgcc 6060
ttttcaagcc ccaaggtcgc agtggaagcc tgtaacgcca tgttgaaaga gaactttccg 6120
actgtggctt cttactgtat tattccagag tacgatgcct atttggacat ggttgacgga 6180
gcttcatgct gcttagacac tgccagtttt tgccctgcaa agctgcgcag ctttccaaag 6240
aaacactcct atttggaacc cacaatacga tcggcagtgc cttcagcgat ccagaacacg 6300
ctccagaacg tcctggcagc tgccacaaaa agaaattgca atgtcacgca aatgagagaa 6360
ttgcccgtat tggattcggc ggcctttaat gtggaatgct tcaagaaata tgcgtgtaat 6420
aatgaatatt gggaaacgtt taaagaaaac cccatcaggc ttactgaaga aaacgtggta 6480
aattacatta ccaaattaaa aggaccaaaa gctgctgctc tttttgcgaa gacacataat 6540
ttgaatatgt tgcaggacat accaatggac aggtttgtaa tggacttaaa gagagacgtg 6600

2026201462 26 Feb 2026

		aaagtgactc caggaacaaa acatactgaa gaacggccca aggtacaggt gatccaggct 6660 gccgatccgc tagcaacagc gtatctgtgc ggaatccacc gagagctggt taggagatta 6720 aatgcggtcc tgcttccgaa cattcataca ctgtttgata tgtcggctga agactttgac 6780 gctattatag ccgagcactt ccagcctggg gattgtgttc tggaaactga catcgcgtcg 6840 tttgataaaa gtgaggacga cgccatggct ctgaccgcgt taatgattct ggaagactta 6900 ggtgtggacg cagagctgtt gacgctgatt gaggcggctt tcggcgaaat ttcatcaata 6960 catttgccca ctaaaactaa atttaaattc ggagccatga tgaaatctgg aatgttcctc 7020 acactgtttg tgaacacagt cattaacatt gtaatcgcaa gcagagtgtt gagagaacgg 7080 ctaaccggat caccatgtgc agcattcatt ggagatgaca atatcgtgaa aggagtcaaa 7140 tcggacaaat taatggcaga caggtgcgcc acctggttga atatggaagt caagattata 7200 gatgctgtgg tgggcgagaa agcgccttat ttctgtggag ggtttatttt gtgtgactcc 7260 gtgaccggca cagcgtgccg tgtggcagac cccctaaaaa ggctgtttaa gcttggcaaa 7320 cctctggcag cagacgatga acatgatgat gacaggagaa gggcattgca tgaagagtca 7380 acacgctgga accgagtggg tattctttca gagctgtgca aggcagtaga atcaaggtat 7440 gaaaccgtag gaacttccat catagttatg gccatgacta ctctagctag cagtgttaaa 7500 tcattcagct acctgagagg ggcccctata actctctacg gctaacctga atggactacg 7560 actatcacgc ccaaacattt acagccgcgg tgtcaaaaac cgcgtggacg tggttaacat 7620 ccctgctggg aggatcagcc gtaattatta taattggctt ggtgctggct actattgtgg 7680 ccatgtacgt gctgaccaac cagaaacata attgaataca gcagcaattg gcaagctgct 7740 tacatagaac tcgcggcgat tggcatgccg ccttaaaatt tttattttat ttttcttttc 7800 ttttccgaat cggattttgt ttttaatatt tcaaaaaaaa aaaaaaaaaa aaaaaaaaaa 7860 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aatacgtagt 7920 ttaaac 7926
3-10	**Sequences**	
3-10-1	Sequence Number [ID]	10
3-10-2	Molecule Type	DNA
3-10-3	Length	36519
3-10-4	Features	**misc_feature 1..36519**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide **source 1..36519** mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-10-5	Residues	ccatcttcaa taatatacct caaacttttt gtgcgcgtta atatgcaaat gaggcgtttg 60 aatttgggga ggaagggcgg tgattggtcg agggatgagc gaccgttagg ggcggggcga 120 gtgacgtttt gatgacgtgg ttgcgaggag gagccagttt gcaagttctc gtgggaaaag 180 tgacgtcaaa cgaggtgtgg tttgaacacg gaaatactca attttcccgc gctctctgac 240 aggaaatgag gtgtttctgg gcggatgcaa gtgaaaacgg gccattttcg cgcgaaaact 300 gaatgaggaa gtgaaaatct gagtaatttc gcgtttatgg cagggaggag tatttgccga 360 gggccgagta gactttgacc gattacgtgg gggtttcgat taccgtgttt ttcacctaaa 420 tttccgcgta cggtgtcaaa gtccggtgtt tttacgtagg tgtcagctga tcgccagggt 480 atttaaacct gcgctctcca gtcaagaggc cactcttgag tgccagcgag aagagttttc 540 tcctccgcgc cgcgagtcag atctacactt tgaaagatga ggcacctgag agacctgccc 600 gatgagaaaa tcatcatcgc ttccgggaac gagattctgg aactggtggt aaatgccatg 660 atgggcgacg accctccgga gccccccacc ccatttgaga caccttcgct gcacgatttg 720 tatgatctgg aggtggatgt gcccgaggac gatcccaatg aggaggcggt aaatgatttt 780 tttagcgatg ccgcgctgct agctgccgag gaggcttcga gctctagctc agacagcgac 840 tcttcactgc ataccctag acccggcaga ggtgagaaaa agatccccga gcttaaaggg 900 gaagagatgg acttgcgctg ctatgaggaa tgcttgcccc cgagcgatga tgaggacgag 960 caggcgatcc agaacgcagc gagccaggga gtgcaagccg ccagcgagag ctttgcgctg 1020 gactgcccgc ctctgcccgg acacggctgt aagtcttgtg aatttcatcg catgaatact 1080 ggagataaag ctgtgttgtg tgcactttgc tatatgagag cttacaacca ttgtgtttac 1140 agtaagtgtg attaagttga actttagagg gaggcagaga gcagggtgac tgggcgatga 1200 ctggtttatt tatgtatata tgttctttat ataggtcccg tctctgacgc agatgatgag 1260 acccccacta caaagtccac ttcgtcaccc ccagaaattg gcacatctcc acctgagaat 1320 attgttagac cagttcctgt tagagccact gggaggagag cagctgtgga atgtttggat 1380 gacttgctac agggtggggt tgaacctttg gacttgtgta cccggaaacg ccccaggcac 1440 taagtgccac acatgtgtgt ttacttgagg tgatgtcagt atttataggg tgtggagtgc 1500 aataaaaaat gtgttgactt taagtgcgtg gtttatgact caggggtggg gactgtgagt 1560 atataagcag gtgcagacct gtgtggttag ctcagagcgg catggagatt tggacggtct 1620 tggaagactt tcacaagact agacagctgc tagagaacgc ctcgaacgga gtctcttacc 1680 tgtggagatt ctgcttcggt ggcgacctag ctaggctagt ctacagggcc aaacaggatt 1740 atagtgaaca atttgaggtt attttgagag agtgttctgg tctttttgac gctcttaact 1800 tgggccatca gtctcacttt aaccagagga tttcgagagc ccttgatttt actactcctg 1860 gcagaaccac tgcagcagta gccttttttg cttttattct tgacaaatgg agtcaagaaa 1920 cccatttcag cagggattac cagctggatt tcttagcagt agctttgtgg agaacatgga 1980 agtgccagcg cctgaatgca atctccggct acttgccggt acagccgcta gacactctga 2040 ggatcctgaa tctccaggag agtcccaggg cacgccaacg tcgccagcag cagcagcagg 2100 aggaggatca agaagagaac ccgagagccg gcctggaccc tccggcggag gaggaggagt 2160 agctgacctg tttcctgaac tgcgccgggt gctgactagg tcttcgagtg gtcgggagag 2220 ggggattaag cgggagaggc atgatgagac taatcacaga actgaactga ctgtgggtct 2280 gatgagtcgc aagcgcccag aaacagtgtg gtggcatgag gtgcagtcga ctggcacaga 2340 tgaggtgtcg gtgatgcatg agaggttttc tctagaacaa gtcaagactt gttggttaga 2400 gcctgaggat gattgggagg tagccatcag gaattatgcc aagctggctc tgaggccaga 2460 caagaagtac aagattacta agctgataaa tatcagaaat gcctgctaca tctcagggaa 2520

20262014622 26 Feb 2026

tggggctgaa gtggagatct gtctccagga aagggtggct ttcagatgct gcatgatgaa 2580
tatgtacccg ggagtggtgg gcatggatgg ggttaccttt atgaacatga ggttcagggg 2640
agatgggtat aatggcacgg tctttatggc caataccaag ctgacagtcc atggctgctc 2700
cttctttggg tttaataaca cctgcatcga ggcctggggt caggtcggtg tgaggggctg 2760
cagtttttca gccaactgga tgggggtcgt gggcaggacc aagagtatgc tgtccgtgaa 2820
gaaatgcttg tttgagaggt gccacctggg ggtgatgagc gagggcgaag ccagaatccg 2880
ccactgcgcc tctaccgaga cgggctgctt tgtgctgtgc aagggcaatg ctaagatcaa 2940
gcataatatg atctgtggag cctcggacga gcgcggctac cagatgctga cctgcgccgg 3000
cgggaacagc catatgctgg ccaccgtaca tgtggcttcc catgctcgca agccctggcc 3060
cgagttcgag cacaatgtca tgaccaggtg caatatgcat ctggggtccc gccgaggcat 3120
gttcatgccc taccagtgca acctgaatta tgtgaaggtg ctgctggagc ccgatgccat 3180
gtccagagtg agcctgacgg gggtgtttga catgaatgtg gaggtgtgga agattctgag 3240
atatgatgaa tccaagacca ggtgccgagc ctgcgagtgc ggagggaagc atgccaggtt 3300
ccagcccgtg tgtgtggatg tgacggagga cctgcgaccc gatcatttgg tgttgccctg 3360
caccgggacg gagttcggtt ccagcgggga agaatctgac tagagtgagt agtgttctgg 3420
ggcgggggag gacctgcatg agggccagaa taactgaaat ctgtgctttt ctgtgtgttg 3480
cagcagcatg agcggaagcg gctcctttga gggaggggta ttcagccctt atctgacggg 3540
gcgtctcccc tcctgggcgg gagtgcgtca gaatgtgatg ggatccacgg tggacggccg 3600
gcccgtgcag cccgcgaact cttcaaccct gacctatgca accctgagct cttcgtcgtt 3660
ggacgcagct gccgccgcag ctgctgcatc tgccgccagc gccgtgcgcg gaatggccat 3720
gggcgccggc tactacggca ctctggtggc caactcgagt tccaccaata atcccgccag 3780
cctgaacgag gagaagctgt tgctgctgat ggcccagctc gaggccttga cccagcgcct 3840
gggcgagctg acccagcagg tggctcagct gcaggagcag acgcgggccg cggttgccac 3900
ggtgaaatcc aaataaaaaa tgaatcaata aataaacgga gacggttgtt gattttaaca 3960
cagagtctga atctttattt gatttttcgc gcgcggtagg ccctggacca ccggtctcga 4020
tcattgagca cccggtggat cttttccagg acccggtaga ggtgggcttg gatgttgagg 4080
tacatgggca tgagcccgtc ccgggggtgg aggtagctcc attgcagggc ctcgtgctcg 4140
ggggtggtgt tgtaaatcac ccagtcatag caggggcgca gggcatggtg ttgcacaata 4200
tctttgagga ggagactgat ggccacgggc agcccttttgg tgtaggtgtt tacaaatctg 4260
ttgagctggg agggatgcat gcgggggggag atgaggtgca tcttggcctg gatcttgaga 4320
ttggcgatgt taccgcccag atcccgcctg gggttcatgt tgtgcaggac caccagcacg 4380
gtgtatccgg tgcacttggg gaatttatca tgcaacttgg aagggaaggc gtgaaagaat 4440
ttggcgacgc ctttgtgccc gcccaggttt tccatgcact catccatgat gatggcgatg 4500
ggcccgtggg cggcggcctg ggcaaagacg tttcgggggt cggacacatc atagttgtgg 4560
tcctgggtga ggtcatcata ggccatttta atgaatttgg ggcggagggt gccggactgg 4620
gggacaaagg taccctcgat cccgggggcg tagttcccct cacagatctg catctcccag 4680
gctttgagct cggaggggggg gatcatgtcc acctgcgggg cgataaagaa cacggtttcc 4740
ggggcggggg agatgagctg ggccgaaagc aagttccgga gcagctggga cttgccgcag 4800
ccggtggggc cgtagatgac cccgatgacc ggctgcaggt ggtagttgag ggagagacag 4860
ctgccgtcct cccggaggag gggggccacc tcgttcatca tctcgcgcac gtgcatgttc 4920
tcgcgcacca gttccgccag gaggcgctct ccccccaggg ataggagctc ctggagcgag 4980
gcgaagtttt tcagcggctt gagtccgtcg gccatgggca ttttggagag ggtttgttgc 5040
aagagttcca ggcggtccca gagctcggtg atgtgctcta cggcatctcg atccagcaga 5100
cctcctcgtt tcgcgggttg ggacggctgc gggagtaggg caccagacga tgggcgtcca 5160
gcgcagccag ggtccggtcc ttccagggtc gcagcgtccg cgtcagggtg gtctccgtca 5220
cggtgaaggg gtgcgcgccg ggctgggcgc ttgcgagggt gcgcttcagg ctcatccggc 5280
tggtcgaaaa ccgctcccga tcggcgccct gcgcgtcggc caggtagcaa ttgaccatga 5340
gttcgtagtt gagcgcctcg gccgcgtggc ctttggcgcg gagcttacct ttggaagtct 5400
gcccgcaggc gggacagagg agggacttga gggcgtagag cttgggggcg aggaagacgg 5460
actcgggggc gtaggcgtcc gcgccgcagt gggcgcagac ggtctcgcac tccacgagcc 5520
aggtgaggtc gggctggtcg gggtcaaaaa ccagtttccc gccgttcttt ttgatgcgtt 5580
tcttaccttt ggtctccatg agctcgtgtc cccgctgggt gacaaagagg ctgtccgtgt 5640
ccccgtagac cgactttatg ggccggtcct cgagcggtgt gccgcggtcc tcctcgtaga 5700
ggaaccccgc ccactccgag acgaaagccc gggtccaggc cagcacgaag gaggccacgt 5760
gggacgggta gcggtcgttg tccaccagcg ggtccacctt ttccagggta tgcaaacaca 5820
tgtccccctc gtccacatcc aggaaggtga ttggcttgta agtgtaggcc acgtgaccgg 5880
gggtcccggc cgggggggta taaaagggtg cgggtccctg ctcgtcctca ctgtcttccg 5940
gatcgctgtc caggagcgcc agctgttggg gtaggtattc cctctcgaag gcgggcatga 6000
cctcggcact caggttgtca gtttctagaa acgaggagga tttgatattg acggtgccgg 6060
cggagatgcc tttcaagagc ccctcgtcca tctggtcaga aaagacgatc tttttgttgt 6120
cgagcttggt ggcgaaggag ccgtagaggg cgttggagag gagcttggcg atggagcgca 6180
tggtctggtt tttttccttg tcggcgcgct ccttggcggc gatgttgagc tgcacgtact 6240
cgcgcgccac gcacttccat tcggggaaga cggtggtcag ctcgtcgggc acgattctga 6300
cctgccagcc ccgattatgc agggtgatga ggtccacact ggtggccacc tcgccgcgca 6360
ggggctcatt agtccagcag aggcgtccgc ccttgcgcga gcagaagggg ggcaggggt 6420
ccagcatgac ctcgtcgggg gggtcggcat cgatggtgaa gatgccgggc aggaggtcgg 6480
ggtcaaagta gctgatggaa gtggccagat cgtccagggc agcttgccat tcgcgcacgg 6540
ccagcgcgcg ctcgtaggga ctgaggggcg tgccccaggg catgggatgg gtaagcgcgg 6600
aggcgtacat gccgcagatg tcgtagacgt agaggggctc ctcgaggatg ccgatgtagg 6660
tggggtagca gcgccccccg cggatgctgg cgcgcacgta gtcatacagc tcgtgcgagg 6720
gggcgaggag ccccgggccc aggttggtgc gactgggctt ttcggcgcgg tagacgatct 6780
ggcggaaaat ggcatgcgag ttggaggaga tggtgggcct ttggaagatg ttgaagtggg 6840
cgtggggcag tccgaccgag tcgcggatga agtgggcgta ggagtcttgc agcttggcga 6900
cgagctcggc ggtgactagg acgtccagag cgcagtagtc gagggtctcc tggatgatgt 6960
catacttgag ctgtcccttt tgtttccaca gctcgcggtt gagaaggaac tcttcgcggt 7020
ccttccagta ctcttcgagg gggaacccgt cctgatctgc acggtaagag cctagcatgt 7080

20262014626 26 Feb 2026

agaactggtt gacggccttg taggcgcagc agcccttctc cacggggagg gcgtaggcct 7140
gggcggcctt gcgcagggag gtgtgcgtga gggcgaaagt gtccctgacc atgaccttga 7200
ggaactggtg cttgaagtcg atatcgtcgc agccccccctg ctcccagagc tggaagtccg 7260
tgcgcttctt gtaggcgggg ttgggcaaag cgaaagtaac atcgttgaag aggatcttgc 7320
ccgcgcgggg cataaagttg cgagtgatgc ggaaaggttg gggcacctcg gcccggttgt 7380
tgatgacctg ggcggcgagc acgatctcgt cgaagccgtt gatgttgtgg cccacgatgt 7440
agagttccac gaatcgcgga cggcccttga cgtggggcag tttcttgagc tcctcgtagg 7500
tgagctcgtc ggggtcgctg agcccgtgct gctcgagcgc ccagtcggcg agatgggggt 7560
tggcgcggag gaaggaagtc cagagatcca cggccagggc ggtttgcaga cggtcccggt 7620
actgacggaa ctgctgcccg acggccattt tttcgggggt gacgcagtag aaggtgcggg 7680
ggtccccgtg ccagcgatcc catttgagct ggagggcgag atcgagggcg agctcgacga 7740
gccggtcgtc cccggagagt ttcatgacca gcatgaaggg gacgagctgc ttgccgaagg 7800
accccatcca ggtgtaggtt tccacatcgt aggtgaggaa gagcctttcg gtgcgaggat 7860
gcgagccgat ggggaagaac tggatctcct gccaccaatt ggaggaatgg ctgttgatgt 7920
gatggaagta gaaatgccga cggcgcgccg aacactcgtg cttgtgttta tacaagcggc 7980
cacagtgctc gcaacgctgc acgggatgca cgtgctgcac gagctgtacc tgagttcctt 8040
tgacgaggaa tttcagtggg aagtggagtc gtggcgcctg catctcgtgc tgtactacgt 8100
cgtggtggtc ggcctggccc tcttctgcct cgatggtggt catgctgacg agcccgcgcg 8160
ggaggcaggt ccagacctcg gcgcgagcgg gtcggagagc gaggacgagg gcgcgcaggc 8220
cggagctgtc cagggtcctg agacgctgcg gagtcaggtc agtgggcagc ggcggcgcgc 8280
ggttgacttg caggagtttt tccagggcgc gcgggaggtc cagatggtac ttgatctcca 8340
ccgcgccatt ggtggcgacg tcgatggctt gcagggtccc gtgcccctgg ggtgtgacca 8400
ccgtcccccg tttcttcttg ggcggctggg gcgacggggg cggtgcctct tccatggtta 8460
gaagcggcgg cgaggacgcg cgccgggcgg caggggcggc tcggggcccg gaggcagggg 8520
cggcaggggc acgtcggcgc cgcgcgcggg taggttctgg tactgcgccc ggagaagact 8580
ggcgtgagcg acgacgcgac ggttgacgtc ctggatctga cgcctctggg tgaaggccac 8640
gggacccgtg agtttgaacc tgaaagagag ttcgacagaa tcaatctcgg tatcgttgac 8700
ggcggcctgc cgcaggatct cttgcacgtc gcccgagttg tcctggtagg cgatctcggt 8760
catgaactgc tcgatctcct cctcttgaag gtctccgcgg ccggcgcgct ccacggtggc 8820
cgcgaggtcg ttggagatgc ggcccatgag ctgcgagaag gcgttcatgc ccgcctcgtt 8880
ccagacgcgg ctgtagacca cgacgccctc gggatcgcgg gcgcgcatga ccacctgggc 8940
gaggttgagc tccacgtggc gcgtgaagac cgcgtagttg cagaggcgct ggtagaggta 9000
gttgagcgtg gtggcgatgt gctcggtgac gaagaaatac atgatccagc ggcggagcgg 9060
catctcgctg acgtcgccca gcgcctccaa acgttccatg gcctcgtaaa agtccacggc 9120
gaagttgaaa aactgggagt tgcgcgccga gacggtcaac tcctcctcca gaagacggat 9180
gagctcggcg atggtggcgc gcacctcgcg ctcgaaggcc cccgggagtt cctccacttc 9240
ctcttcttcc tcctccacta acatctcttc tacttcctcc tcaggcggca gtggtggcgg 9300
gggaggggggc ctgcgtcgcc ggcggcgcac gggcagacgg tcgatgaagc gctcgatggt 9360
ctcgccgcgc cggcgtcgca tggtctcggt gacggcgcgc ccgtcctcgc ggggccgcag 9420
cgtgaagacg ccgccgcgca tctccaggtg gccgggggggg tccccgttgg gcagggagag 9480
ggcgctgacg atgcatctta tcaattgccc cgtagggact ccgcgcaagg acctgagcgt 9540
ctcgagatcc acgggatctg aaaaccgctg aacgaaggct tcgagccagt cgcagtcgca 9600
aggtaggctg agcacggttt cttctggcgg gtcatgttgg ttgggagcgg ggcgggcgat 9660
gctgctggtg atgaagttga aataggcggt tctgagacgg cggatggtgg cgaggagcac 9720
caggtctttg ggcccggctt gctggatgcg cagacggtcg gccatgcccc aggcgtggtc 9780
ctgacacctg gccaggtcct tgtagtagtc ctgcatgagc cgctccacgg gcacctcctc 9840
ctcgcccgcg cggccgtgca tgcgcgtgag cccgaagccg cgctggggct ggacgagcgc 9900
caggtcggcg acgacgcgct cggcgaggat ggcttgctgg atctgggtga gggtggtctg 9960
gaagtcatca aagtcgacga agcggtggta ggctccggtg ttgatggtgt aggagcagtt 10020
ggccatgacg gaccagttga cggtctggtg gcccggacgc acgagctcgt ggtacttgag 10080
gcgcgagtag gcgcgcgtgt cgaagatgta gtcgttgcag gtgcgcacca ggtactggta 10140
gccgatgagg aagtgcggcg gcggctggcg gtagagcggc catcgctcgg tggcgggggc 10200
gccgggcgcg aggtcctcga gcatggtgcg gtggtagccg tagatgtacc tggacatcca 10260
ggtgatgccg gcggcggtgg tggaggcgcg cgggaactcg cggacgcggt tccagatgtt 10320
gcgcagcggc aggaagtagt tcatggtggg cacggtctgg cccgtgaggc gcgcgcagtc 10380
gtggatgctc tatacgggca aaaacgaaag cggtcagcgg ctcgactccg tggcctggag 10440
gctaagcgaa cgggttgggc tgcgcgtgta ccccggttcg aatctcgaat caggctggag 10500
ccgcagctaa cgtggtattg gcactcccgt ctcgacccaa gcctgcacca accctccagg 10560
atacggaggc gggtcgtttt gcaacttttt tttggaggcc ggatgagact agtaagcgcg 10620
gaaagcggcc gaccgcgatg gctcgctgcc gtagtctgga gaagaatcgc cagggttgcg 10680
ttgcggtgtg ccccggttcg aggccggccg gattccgcgg ctaacgaggg cgtggctgcc 10740
ccgtcgtttc caagacccca tagccagccg acttctccag ttacggagcg agcccctctt 10800
ttgttttgtt tgtttttgcc agatgcatcc cgtactgcgg cagatgcgcc cccaccaccc 10860
tccaccgcaa caacagcccc ctccacagcc ggcgcttctg cccccgcccc agcagcaact 10920
tccagccacg accgccgcgg ccgccgtgag cggggctgga cagagttatg atcaccagct 10980
ggccttggaa gagggcgagg ggctggcgcg cctgggggcg tcgtcgccgg agcggcaccc 11040
gcgcgtgcag atgaaaaggg acgctcgcga ggcctacgtg cccaagcaga acctgttcag 11100
agacaggagc ggcgaggagc ccgaggagat gcgcgcggcc cggttccacg cggggcggga 11160
gctgcggcgc ggcctggacc gaaagagggt gctgagggac gaggatttcg aggcggacga 11220
gctgacgggg atcagccccg cgcgcgcgca cgtggccgcg gccaacctgg tcacggcgta 11280
cgagcagacc gtgaaggagg agagcaactt ccaaaaatcc ttcaacaacc acgtgcgcac 11340
cctgatcgcg cgcgaggagg tgaccctggg cctgatgcac ctgtgggacc tgctggaggc 11400
catcgtgcag aaccccacca gcaagccgct gacggcgcag ctgttcctgg tggtgcagca 11460
tagtcgggac aacgaagcgt tcagggaggc gctgctgaat atcaccgagc ccgagggccg 11520
ctggctcctg gacctggtga acattctgca gagcatcgtg gtgcaggagc gcgggctgcc 11580
gctgtccgag aagctggcgg ccatcaactt ctcggtgctg agtttgggca agtactacgc 11640

20262014626 26 Feb 2026

taggaagatc tacaagaccc cgtacgtgcc catagacaag gaggtgaaga tcgacgggtt 11700
ttacatgcgc atgaccctga aagtgctgac cctgagcgac gatctggggg tgtaccgcaa 11760
cgacaggatg caccgtgcgg tgagcgccag caggcggcgc gagctgagcg accaggagct 11820
gatgcatagt ctgcagcggg ccctgaccgg ggccgggacc gaggggaga gctactttga 11880
catgggcgcg gacctgcact ggcagcccag ccgccgggcc ttggaggcgg cggcaggacc 11940
ctacgtagaa gaggtggacg atgaggtgga cgaggagggc gagtacctgg aagactgatg 12000
gcgcgaccgt atttttgcta gatgcaacaa caacagccac ctcctgatcc cgcgatgcgg 12060
gcggcgctgc agagccagcc gtccggcatt aactcctcgg acgattggac ccaggccatg 12120
caacgcatca tggcgctgac gacccgcaac cccgaagcct ttagacagca gccccaggcc 12180
aaccggctct cggccatcct ggaggccgtg gtgccctcgc gctccaaccc cacgcacgag 12240
aaggtcctgg ccatcgtgaa cgcgctggtg gagaacaagg ccatccgcgg cgacgaggcc 12300
ggcctggtgt acaacgcgct gctggagcgc gtggcccgct acaacagcac caacgtgcag 12360
accaacctgg accgcatggt gaccgacgtg cgcgaggccg tggcccagcg cgagcggttc 12420
caccgcgagt ccaacctggg atccatggtg gcgctgaacg ccttcctcag cacccagccc 12480
gccaacgtgc cccggggcca ggaggactac accaacttca tcagcgccct gcgcctgatg 12540
gtgaccgagg tgccccagag cgaggtgtac cagtccgggc cggactactt cttccagacc 12600
agtcgccagg gcttgcagac cgtgaacctg agccaggctt tcaagaactt gcagggcctg 12660
tggggcgtgc aggccccggt cggggaccgc gcgacggtgt cgagcctgct gacgccgaac 12720
tcgcgcctgc tgctgctgct ggtggccccc ttcacggaca gcggcagcat caaccgcaac 12780
tcgtacctgg gctacctgat taacctgtac cgcgaggcca tcggccaggc gcacgtggac 12840
gagcagacct accaggagat cacccacgtg agccgcgccc tgggccagga cgacccgggc 12900
aacctggaag ccaccctgaa ctttttgctg accaaccggt cgcagaagat cccgccccag 12960
tacgcgctca gcaccgagga ggagcgcatc ctgcgttacg tgcagcagag cgtgggcctg 13020
ttcctgatgc aggagggggc cacccccagc gccgcgctcg acatgaccgc gcgcaacatg 13080
gagcccagca tgtacgccag caaccgcccg ttcatcaata aactgatgga ctacttgcat 13140
cgggcggccg ccatgaactc tgactatttc accaacgcca tcctgaatcc ccactggctc 13200
ccgccgccgg ggttctacac gggcgagtac gacatgcccg accccaatga cgggttcctg 13260
tgggacgatg tggacagcag cgtgttctcc ccccgaccgg gtgctaacga gcgccccttg 13320
tggaagaagg aaggcagcga ccgacgcccg tcctcggcgc tgtccggccg cgagggtgct 13380
gccgcggcgg tgcccgaggc cgccagtcct ttcccgagct tgcccttctc gctgaacagt 13440
atccgcagca gcgagctggg caggatcacg cgcccgcgct tgctgggcga agaggagtac 13500
ttgaatgact cgctgttgag acccgagcgg gagaagaact tccccaataa cgggatagaa 13560
agcctggtgg acaagatgag ccgctggaag acgtatgcgc aggagcacag ggacgatccc 13620
cgggcgtcgc agggggccac gagccggggc agcgccgccc gtaaacgccg gtggcacgac 13680
aggcagcggg gacagatgtg ggacgatgag gactccgccg acgacagcag cgtgttggac 13740
ttgggtggga gtggtaaccc gttcgctcac ctgcgccccc gtatcgggcg catgatgtaa 13800
gagaaaccga aaataaatga tactcaccaa ggccatggcg accagcgtgc gttcgtttct 13860
tctctgttgt tgttgtatct agtatgatga ggcgtgcgta cccggagggt cctcctccct 13920
cgtacgagag cgtgatgcag caggcgatgg cggcggcggc gatgcagccc ccgctggagg 13980
ctccttacgt gcccccgcgg tacctggcgc ctacggaggg gcggaacagc attcgttact 14040
cggagctggc acccttgtac gataccaccc ggttgtacct ggtggacaac aagtcggcgg 14100
acatcgcctc gctgaactac cagaacgacc acagcaactt cctgaccacc gtggtgcaga 14160
acaatgactt caccccacg gaggccagca cccagaccat caactttgac gagcgctcgc 14220
ggtggggcgg ccagctgaaa accatcatgc acaccaacat gcccaacgtg aacgagttca 14280
tgtacagcaa caagttcaag gcgcgggtga tggtctcccg caagacccca aatggggtga 14340
cagtgacaga ggattatgat ggtagtcagg atgagctgaa gtatgaatgg gtggaatttg 14400
agctgcccga aggcaacttc tcggtgacca tgaccatcga cctgatgaac aacgccatca 14460
tcgacaatta cttggcggtg gggcggcaga acggggtgct ggagagcgac atcggcgtga 14520
agttcgacac taggaacttc aggctgggct gggaccccgt gaccgagctg gtcatgcccg 14580
gggtgtacac caacgaggct ttccatcccg atattgtctt gctgcccggc tgcggggtgg 14640
acttcaccga gagccgcctc agcaacctgc tgggcattcg caagaggcag cccttccagg 14700
aaggcttcca gatcatgtac gaggatctgg agggggcaa catccccgcg ctcctggatg 14760
tcgacgccta tgagaaaagc aaggaggatg cagcagctga agcaactgca gccgtagcta 14820
ccgcctctac cgaggtcagg ggcgataatt ttgcaagcgc cgcagcagtg gcagcggccg 14880
aggcggctga aaccgaaagt aagatagtca ttcagccggt ggagaaggat agcaagaaca 14940
ggagctacaa cgtactaccg gacaagataa acaccgccta ccgcagctgg tacctagcct 15000
acaactatgg cgaccccgag aagggcgtgc gctcctggac gctgctcacc acctcggacg 15060
tcacctgcgg cgtggagcaa gtctactggt cgctgcccga catgatgcaa gacccggtca 15120
ccttccgctc cacgcgtcaa gttagcaact acccggtggt gggcgccgag ctcctgcccg 15180
tctactccaa gagcttcttc aacgagcagg ccgtctactc gcagcagctg cgcgccttca 15240
cctcgcttac gcacgtcttc aaccgcttcc ccgagaacca gatcctcgtc cgcccgcccg 15300
cgcccaccat taccaccgtc agtgaaaacg ttcctgctct cacagatcac gggaccctgc 15360
cgctgcgcag cagtatccgg ggagtccagc gcgtgaccgt tactgacgcc agacgccgca 15420
cctgccccta cgtctacaag gccctgggca tagtcgcgcc gcgcgtcctc tcgagccgca 15480
ccttctaaat gtccattctc atctcgccca gtaataacac cggttggggc ctgcgcgcgc 15540
ccagcaagat gtacggaggc gctcgccaac gctccacgca acaccccgtg cgcgtgcgcg 15600
ggcacttccg cgctccctgg ggcgccctca agggccgcgt gcggtcgcgc accaccgtcg 15660
acgacgtgat cgaccaggtg gtggccgacg cgcgcaacta cacccccgcc gccgcgcccg 15720
tctccaccgt ggacgccgtc atcgacagcg tggtggccga cgcgcgccgg tacgcccgcg 15780
ccaagagccg gcggcggcgc atcgcccggc ggcaccggag cacccccgcc atgcgcgcgg 15840
cgcgagcctt gctgcgcagg gccaggcgca cgggacgcag ggccatgctc agggcggcca 15900
gacgcgcggc ttcaggcgcc agcgccggca ggacccggag acgcgcggcc acggcggcgg 15960
cagcggccat cgccagcatg tcccgcccgc ggcgagggaa cgtgtactgg gtgcgcgacg 16020
ccgccaccgg tgtgcgcgtg cccgtgcgca cccgcccccc tcgcacttga agatgttcac 16080
ttcgcgatgt tgatgtgtcc cagcggcgag gaggatgtcc aagcgcaaat tcaaggaaga 16140
gatgctccag gtcatcgcgc ctgagatcta cggccctgcg gtggtgaagg aggaaagaaa 16200

20262014626 26 Feb 2026

gccccgcaaa atcaagcggg tcaaaaagga caaaaaggaa gaagaaagtg atgtggacgg 16260
attggtggag tttgtgcgcg agttcgcccc ccggcggcgc gtgcagtggc gcgggcggaa 16320
ggtgcaaccg gtgctgagac ccggcaccac cgtggtcttc acgcccggcg agcgctccgg 16380
caccgcttcc aagcgctcct acgacgaggt gtacggggat gatgatattc tggagcaggc 16440
ggccgagcgc ctgggcgagt ttgcttacgg caagcgcagc cgttccgcac cgaaggaaga 16500
ggcggtgtcc atcccgctgg accacggcaa ccccacgccg agcctcaagc ccgtgacctt 16560
gcagcaggtg ctgccgaccg cggcgccgcg ccgggggttc aagcgcgagg gcgaggatct 16620
gtaccccacc atgcagctga tggtgcccaa gcgccagaag ctggaagacg tgctggagac 16680
catgaaggtg gacccggacg tgcagcccga ggtcaaggtg cggcccatca agcaggtggc 16740
cccgggcctg ggcgtgcaga ccgtggacat caagattccc acggagccca tggaaacgca 16800
gaccgagccc atgatcaagc ccagcaccag caccatggag gtgcagacgg atccctggat 16860
gccatcggct cctagtcgaa gaccccggcg caagtacggc gcggccagcc tgctgatgcc 16920
caactacgcg ctgcatcctt ccatcatccc cacgccgggc taccgcggca cgcgcttcta 16980
ccgcggtcat accagcagcc gccgccgcaa gaccaccact cgccgccgcc gtcgccgcac 17040
cgccgctgca accacccctg ccgccctggt gcggagagtg taccgccgcg gccgcgcacc 17100
tctgaccctg ccgcgcgcgc gctaccaccc gagcatcgcc atttaaactt tcgcctgctt 17160
tgcagatcaa tggccctcac atgccgcctt cgcgttccca ttacgggcta ccgaggaaga 17220
aaaccgcgcc gtagaaggct ggcggggaac gggatgcgtc gccaccacca ccggcggcgg 17280
cgcgccatca gcaagcggtt gggggggaggc ttcctgcccg cgctgatccc catcatcgcc 17340
gcggcgatcg gggcgatccc cggcattgct tccgtggcgg tgcaggcctc tcagcgccac 17400
tgagacacac ttggaaacat cttgtaataa accaatggac tctgacgctc ctggtcctgt 17460
gatgtgtttt cgtagacaga tggaagacat caatttttcg tccctggctc cgcgacacgg 17520
cacgcggccg ttcatgggca cctggagcga catcggcacc agccaactga acgggggcgc 17580
cttcaattgg agcagtctct ggagcgggct taagaatttc gggtccacgc ttaaaaccta 17640
tggcagcaag gcgtggaaca gcaccacagg gcaggcgctg agggataagc tgaaagagca 17700
gaacttccag cagaaggtgg tcgatgggct cgcctcgggc atcaacgggg tggtggacct 17760
ggccaaccag gccgtgcagc ggcagatcaa cagccgcctg gacccggtgc cgcccgccgg 17820
ctccgtggag atgccgcagg tggaggagga gctgcctccc ctggacaagc ggggcgagaa 17880
gcgaccccgc cccgatgcgg aggagacgct gctgacgcac acggacgagc cgcccccgta 17940
cgaggaggcg gtgaaactgg gtctgcccac cacgcggccc atcgcgcccc tggccaccgg 18000
ggtgctgaaa cccgaaaagc ccgcgaccct ggacttgcct cctccccagc cttcccgccc 18060
ctctacagtg gctaagcccc tgccgccggt ggccgtggcc cgcgcgcgac ccgggggcac 18120
cgcccgccct catgcgaact ggcagagcac tctgaacagc atcgtgggtc tgggagtgca 18180
gagtgtgaag cgccgccgct gctattaaac ctaccgtagc gcttaacttg cttgtctgtg 18240
tgtgtatgta ttatgtcgcc gccgccgctg tccaccagaa ggaggagtga agaggcgcgt 18300
cgccgagttg caagatggcc accccatcga tgctgcccca gtgggcgtac atgcacatcg 18360
ccggacagga cgcttcggag tacctgagtc cgggtctggt gcagtttgcc cgcgccacag 18420
acacctactt cagtctgggg aacaagttta ggaaccccac ggtggcgccc acgcacgatg 18480
tgaccaccga ccgcagccag cggctgacgc tgcgcttcgt gcccgtggac cgcgaggaca 18540
acacctactc gtacaaagtg cgctacacgc tggccgtggg cgacaaccgc gtgctggaca 18600
tggccagcac ctactttgac atccgcggcg tgctggatcg gggccctagc ttcaaaccct 18660
actccggcac cgcctacaac agtctggccc ccaagggagc acccaacact tgtcagtgga 18720
catataaagc cgatggtgaa actgccacag aaaaaaccta tacatatgga aatgcacccg 18780
tgcagggcat taacatcaca aaagatggta ttcaacttgg aactgacacc gatgatcagc 18840
caatctacgc agataaaacc tatcagcctg aacctcaagt gggtgatgct gaatggcatg 18900
acatcactgg tactgatgaa aagtatggag gcagagctct taagcctgat accaaaatga 18960
agccttgtta tggttctttt gccaagccta ctaataaaga aggaggtcag gcaaatgtga 19020
aaacaggaac aggcactact aaagaatatg acatagacat ggctttcttt gacaacagaa 19080
gtgcggctgc tgctggccta gctccagaaa ttgttttgta tactgaaaat gtggatttgg 19140
aaactccaga tacccatatt gtatacaaag caggcacaga tgacagcagc tcttctatta 19200
atttgggtca gcaagccatg cccaacagac ctaactacat tggtttcaga gacaacttta 19260
tcgggctcat gtactacaac agcactggca atatgggggt gctggccggt caggcttctc 19320
agctgaatgc tgtggttgac ttgcaagaca gaaacaccga gctgtcctac cagctcttgc 19380
ttgactctct gggtgacaga acccggtatt tcagtatgtg gaatcaggcg gtggacagct 19440
atgatcctga tgtgcgcatt attgaaaatc atggtgtgga ggatgaactt cccaactatt 19500
gtttccctct ggatgctgtt ggcagaacag atacttatca gggaattaag gctaatggaa 19560
ctgatcaaac cacatggacc aaagatgaca gtgtcaatga tgctaatgag ataggcaagg 19620
gtaatccatt cgccatggaa atcaacatcc aagccaacct gtggaggaac ttcctctacg 19680
ccaacgtggc cctgtacctg cccgactctt acaagtacac gccggccaat gttaccctgc 19740
ccaccaacac caacacctac gattacatga acggccgggt ggtggcgccc tcgctggtgg 19800
actcctacat caacatcggg gcgcgctggt cgctggatcc catggacaac gtgaacccct 19860
tcaaccacca ccgcaatgcg gggctgcgct accgctccat gctcctgggc aacgggcgct 19920
acgtgccctt ccacatccag gtgccccaga aatttttcgc catcaagagc ctcctgctcc 19980
tgcccgggtc ctacacctac gagtggaact tccgcaagga cgtcaacatg atcctgcaga 20040
gctccctcgg caacgacctg cgcacggacg gggcctccat ctccttcacc agcatcaacc 20100
tctacgccac cttcttcccc atggcgcaca acacggcctc cacgctcgag gccatgctgc 20160
gcaacgacac caacgaccag tccttcaacg actacctctc ggcggccaac atgctctacc 20220
ccatcccggc caacgccacc aacgtgccca tctccatccc ctcgcgcaac tgggccgcct 20280
tccgcggctg gtccttcacg cgtctcaaga ccaaggagac gccctcgctg ggctccgggt 20340
tcgaccccta cttcgtctac tcgggctcca tcccctacct cgacggcacc ttctacctca 20400
accacacctt caagaaggtc tccatcacct tcgactcctc cgtcagctgg cccggcaacg 20460
accggctcct gacgcccaac gagttcgaaa tcaagcgcac cgtcgacggc gagggctaca 20520
acgtggccca gtgcaacatg accaaggact ggttcctggt ccagatgctg gcccactaca 20580
acatcggcta ccagggcttc tacgtgcccg agggctacaa ggaccgcatg tactccttct 20640
tccgcaactt ccagcccatg agccgccagg tggtggacga ggtcaactac aaggactacc 20700
aggccgtcac cctggcctac cagcacaaca actcgggctt cgtcggctac ctcgcgccca 20760

2026201462 26 Feb 2026

ccatgcgcca gggccagccc taccccgcca actaccccta cccgctcatc ggcaagagcg 20820
ccgtcaccag cgtcacccag aaaaagttcc tctgcgacag ggtcatgtgg cgcatcccct 20880
tctccagcaa cttcatgtcc atgggcgcgc tcaccgacct cggccagaac atgctctatg 20940
ccaactccgc ccacgcgcta gacatgaatt tcgaagtcga ccccatggat gagtccaccc 21000
ttctctatgt tgtcttcgaa gtcttcgacg tcgtccgagt gcaccagccc caccgcggcg 21060
tcatcgaggc cgtctacctg cgcaccccct tctcggccgg taacgccacc acctaagctc 21120
ttgcttcttg caagccatgg ccgcgggctc cggcgagcag gagctcaggg ccatcatccg 21180
cgacctgggc tgcgggccct acttcctggg caccttcgat aagcgcttcc cgggattcat 21240
ggccccgcac aagctggcct gcgccatcgt caacacggcc ggccgcgaga ccgggggcga 21300
gcactggctg gccttcgcct ggaacccgcg ctcgaacacc tgctacctct tcgacccctt 21360
cgggttctcg gacgagcgcc tcaagcagat ctaccagttc gagtacgagg gcctgctgcg 21420
ccgcagcgcc ctggccaccg aggaccgctg cgtcaccctg gaaaagtcca cccagaccgt 21480
gcagggtccg cgctcggccg cctgcgggct cttctgctgc atgttcctgc acgccttcgt 21540
gcactggccc gaccgcccca tggacaagaa ccccaccatg aacttgctga cgggggtgcc 21600
caacggcatg ctccagtcgc cccaggtgga acccaccctg cgccgcaacc aggaggcgct 21660
ctaccgcttc ctcaactccc actccgccta ctttcgctcc caccgcgcgc gcatcgagaa 21720
ggccaccgcc ttcgaccgca tgaatcaaga catgtaaacc gtgtgtgtat gttaaatgtc 21780
tttaataaac agcactttca tgttacacat gcatctgaga tgatttattt agaaatcgaa 21840
agggttctgc cgggtctcgg catggcccgc gggcagggac acgttgcgga actggtactt 21900
ggccagccac ttgaactcgg ggatcagcag tttgggcagc ggggtgtcgg ggaaggagtc 21960
ggtccacagc ttccgcgtca gttgcagggc gcccagcagg tcgggcgcgg agatcttgaa 22020
atcgcagttg ggacccgcgt tctgcgcgcg ggagttgcgg tacacggggt tgcagcactg 22080
gaacaccatc agggccgggt gcttcacgct cgccagcacc gtcgcgtcgg tgatgctctc 22140
cacgtcgagg tcctcggcgt tggccatccc gaagggggtc atcttgcagg tctgccttcc 22200
catggtgggc acgcacccgg gcttgtggtt gcaatcgcag tgcaggggga tcagcatcat 22260
ctgggcctgg tcggcgttca tccccgggta catggccttc atgaaagcct ccaattgcct 22320
gaacgcctgc tgggccttgg ctccctcggt gaagaagacc ccgcaggact tgctagagaa 22380
ctggttggtg gcgcacccgg cgtcgtgcac gcagcagcgc gcgtcgttgt tggccagctg 22440
caccacgctg cgcccccagc ggttctgggt gatcttggcc cggtcggggt tctccttcag 22500
cgcgcgctgc ccgttctcgc tcgccacatc catctcgatc atgtgctcct tctggatcat 22560
ggtggtcccg tgcaggcacc gcagcttgcc ctcggcctcg gtgcacccgt gcagccacag 22620
cgcgcacccg gtgcactccc agttcttgtg ggcgatctgg gaatgcgcgt gcacgaagcc 22680
ctgcaggaag cggcccatca tggtggtcag ggtcttgttg ctagtgaagg tcagcggaat 22740
gccgcggtgc tcctcgttga tgtacaggtg gcagatgcgg cggtacacct cgccctgctc 22800
gggcatcagc tggaagttgg ctttcaggtc ggtctccacg cggtagcggt ccatcagcat 22860
agtcatgatt tccataccct tctcccaggc cgagacgatg ggcaggctca tagggttctt 22920
caccatcatc ttagcgctag cagccgcggc caggggtcg ctctcgtcca gggtctcaaa 22980
gctccgcttg ccgtccttct cggtgatccg caccgggggg tagctgaagc ccacggccgc 23040
cagctcctcc tcggcctgtc tttcgtcctc gctgtcctgg ctgacgtcct gcaggaccac 23100
atgcttggtc ttgcggggtt tcttcttggg cggcagcggc ggcggagatg ttggagatgg 23160
cgaggggggag cgcgagttct cgctcaccac tactatctct tcctcttctt ggtccgaggc 23220
cacgcggcgg taggtatgtc tcttcggggg cagaggcgga ggcgacgggc tctcgccgcc 23280
gcgacttggc ggatggctgg cagagcccct tccgcgttcg ggggtgcgct cccggcggcg 23340
ctctgactga cttcctccgc ggccggccat tgtgttctcc tagggaggaa caacaagcat 23400
ggagactcag ccatcgccaa cctcgccatc tgcccccacc gccgacgaga agcagcagca 23460
gcagaatgaa agcttaaccg ccccgccgcc cagccccgcc acctccgacg cggccgtccc 23520
agacatgcaa gagatggagg aatccatcga gattgacctg ggctatgtga cgcccgcgga 23580
gcacgaggag gagctggcag tgcgcttttc acaagaagag atacaccaag aacagccaga 23640
gcaggaagca gagaatgagc agagtcaggc tgggctcgag catgacggcg actacctcca 23700
cctgagcggg ggggaggacg cgctcatcaa gcatctggcc cggcaggcca ccatcgtcaa 23760
ggatgcgctg ctcgaccgca ccgaggtgcc cctcagcgtg gaggagctca gccgcgccta 23820
cgagttgaac ctcttctcgc cgcgcgtgcc ccccaagcgc cagcccaatg gcacctgcga 23880
gcccaacccg cgcctcaact tctacccggt cttcgcggtg cccgaggccc tggccaccta 23940
ccacatcttt ttcaagaacc aaaagatccc cgtctcctgc cgcgccaacc gcacccgcgc 24000
cgacgccctt ttcaacctgg gtcccggcgc ccgcctacct gatatcgcct ccttggaaga 24060
ggttcccaag atcttcgagg gtctgggcag cgacgagact cgggccgcga acgctctgca 24120
aggagaagga ggagagcatg agcaccacag cgccctggtc gagttggaag gcgacaacgc 24180
gcggctggcg gtgctcaaac gcacggtcga gctgacccat ttcgcctacc cggctctgaa 24240
cctgcccccc aaagtcatga gcgcggtcat ggaccaggtg ctcatcaagc gcgcgtcgcc 24300
catctccgag gacgagggca tgcaagactc cgaggagggc aagcccgtgg tcagcgacga 24360
gcagctggcc cggtggctgg gtcctaatgc tagtccccag agtttggaag agcggcgcaa 24420
actcatgatg gccgtggtcc tggtgaccgt ggagctggag tgcctgcgcc gcttcttcgc 24480
cgacgcggag accctgcgca aggtcgagga gaacctgcac tacctcttca ggcacgggtt 24540
cgtgcgccag gcctgcaaga tctccaacgt ggagctgacc aacctggtct cctacatggg 24600
catcttgcac gagaaccgcc tggggcagaa cgtgctgcac accaccctgc gcggggaggc 24660
ccggcgcgac tacatccgcg actgcgtcta cctctacctc tgccacacct ggcagacggg 24720
catgggcgtg tggcagcagt gtctggagga gcagaacctg aaagagctct gcaagctcct 24780
gcagaagaac ctcaagggtc tgtggaccgg gttcgacgag cgcaccaccg cctcggacct 24840
ggccgacctc attttccccg agcgcctcag gctgacgctg cgcaacggcc tgcccgactt 24900
tatgagccaa agcatgttgc aaaactttcg ctctttcatc ctcgaacgct ccggaatcct 24960
gcccgccacc tgctccgcgc tgccctcgga cttcgtgccg ctgaccttcc gcgagtgccc 25020
cccgccgctg tggagccact gctacctgct gcgcctggcc aactacctgg cctaccactc 25080
ggacgtgatc gaggacgtca gcggcgaggg cctgctcgag tgccactgcc gctgcaacct 25140
ctgcacgccg caccgctccc tggcctgcaa cccccagctg ctgagcgaga cccagatcat 25200
cggcaccttc gagttgcaag ggcccagcga aggcgagggt tcagccgcca agggggggtct 25260
gaaactcacc ccggggctgt ggacctcggc ctacttgcgc aagttcgtgc ccgaggacta 25320

20262014626 26 Feb 2026

ccatcccttc gagatcaggt tctacgagga ccaatcccat ccgcccaagg ccgagctgtc 25380
ggcctgcgtc atcacccagg gggcgatcct ggcccaattg caagccatcc agaaatcccg 25440
ccaagaattc ttgctgaaaa agggccgcgg ggtctacctc gacccccaga ccggtgagga 25500
gctcaacccc ggcttccccc aggatgcccc gaggaaacaa gaagctgaaa gtggagctgc 25560
cgcccgtgga ggatttggag gaagactggg agaacagcag tcaggcagag gaggaggaga 25620
tggaggaaga ctgggacagc actcaggcag aggaggacag cctgcaagac agtctggagg 25680
aagacgagga ggaggcagag gaggaggtgg aagaagcagc cgccgccaga ccgtcgtcct 25740
cggcggggga gaaagcaagc agcacggata ccatctccgc tccgggtcgg ggtcccgctc 25800
gaccacacag tagatgggac gagaccggac gattcccgaa ccccaccacc cagaccggta 25860
agaaggagcg gcagggatac aagtcctggc gggggcacaa aaacgccatc gtctcctgct 25920
tgcaggcctg cgggggcaac atctccttca cccggcgcta cctgctcttc caccgcgggg 25980
tgaactttcc ccgcaacatc ttgcattact accgtcacct ccacagcccc tactacttcc 26040
aagaagaggc agcagcagca gaaaaagacc agcagaaaac cagcagctag aaaatccaca 26100
gcggcggcag caggtggact gaggatcgcg gcgaacgagc cggcgcaaac ccgggagctg 26160
aggaaccgga tctttcccac cctctatgcc atcttccagc agagtcgggg gcaggagcag 26220
gaactgaaag tcaagaaccg ttctctgcgc tcgctcaccc gcagttgtct gtatcacaag 26280
agcgaagacc aacttcagcg cactctcgag gacgccgagg ctctcttcaa caagtactgc 26340
gcgctcactc ttaaagagta gcccgcgccc gcccagtcgc agaaaaaggc gggaattacg 26400
tcacctgtgc ccttcgccct agccgcctcc acccatcatc atgagcaaag agattcccac 26460
gccttacatg tggagctacc agccccagat gggcctggcc gccggtgccg cccaggacta 26520
ctccacccgc atgaattggc tcagcgccgg gcccgcgatg atctcacggg tgaatgacat 26580
ccgcgcccac cgaaaccaga tactcctaga acagtcagcg ctcaccgcca cgccccgcaa 26640
tcacctcaat ccgcgtaatt ggcccgccgc cctggtgtac caggaaattc cccagcccac 26700
gaccgtacta cttccgcgag acgcccaggc cgaagtccag ctgactaact caggtgtcca 26760
gctggcgggc ggcgccaccc tgtgtcgtca ccgccccgct cagggtataa agcggctggt 26820
gatccggggc agaggcacac agctcaacga cgaggtggtg agctcttcgc tgggtctgcg 26880
acctgacgga gtcttccaac tcgccggatc ggggagatct tccttcacgc ctcgtcaggc 26940
cgtcctgact ttggagagtt cgtcctcgca gccccgctcg ggtggcatcg gcactctcca 27000
gttcgtggag gagttcactc cctcggtcta cttcaacccc ttctccggct cccccggcca 27060
ctacccggac gagttcatcc cgaacttcga cgccatcagc gagtcggtgg acggctacga 27120
ttgaatgtcc catggtggcg cagctgacct agctcggctt cgacacctgg accactgccg 27180
ccgcttccgc tgcttcgctc gggatctcgc cgagtttgcc tactttgagc tgcccgagga 27240
gcaccctcag ggcccggccc acggagtgcg gatcgtcgtc gaaggggccc tcgactccca 27300
cctgcttcgg atcttcagcc agcgtccgat cctggtcgag cgcgagcaag gacagaccct 27360
tctgactctg tactgcatct gcaaccaccc cggcctgcat gaaagtcttt gttgtctgct 27420
gtgtactgag tataataaaa gctgagatca gcgactactc cggacttccg tgtgttcctg 27480
aatccatcaa ccagtctttg ttcttcaccg ggaacgagac cgagctccag ctccagtgta 27540
agccccacaa gaagtacctc acctggctgt tccagggctc cccgatcgcc gttgtcaacc 27600
actgcgacaa cgacggagtc ctgctgagcg gccctgccaa ccttactttt tccacccgca 27660
gaagcaagct ccagctcttc caacccttcc tccccgggac ctatcagtgc gtctcgggac 27720
cctgccatca caccttccac ctgatcccga ataccacagc gtcgctcccc gctactaaca 27780
accaaactaa cctccaccaa cgccaccgtc gcgacctttc tgaatctaat actaccaccc 27840
acaccggagg tgagctccga ggtcaaccaa cctctgggat ttactacggc ccctgggagg 27900
tggttgggtt aatagcgcta ggcctagttg cgggtgggct tttggttctc tgctacctat 27960
acctcccttg ctgttcgtac ttagtggtgc tgtgttgctg gtttaagaaa tggggaagat 28020
caccctagtg agctgcggtg cgctggtggc ggtgttgctt tcgattgtgg gactgggcgg 28080
tgcggctgta gtgaaggaga aggccgatcc ctgcttgcat ttcaatccca acaaatgcca 28140
gctgagtttt cagcccgatg gcaatcggtg cgcggtactg atcaagtgcg gatgggaatg 28200
cgagaacgtg agaatcgagt acaataacaa gactcggaac aatactctcg cgtccgtgtg 28260
gcagcccggg gaccccgagt ggtacaccgt ctctgtcccc ggtgctgacg gctccccgcg 28320
caccgtgaat aatactttca tttttgcgca catgtgcgac acggtcatgt ggatgagcaa 28380
gcagtacgat atgtggcccc ccacgaagga gaacatcgtg gtcttctcca tcgcttacag 28440
cctgtgcacg gcgctaatca ccgctatcgt gtgcctgagc attcacatgc tcatcgctat 28500
tcgccccaga aataatgccg aaaaagaaaa acagccataa cgttttttt cacacctttt 28560
tcagaccatg gcctctgtta aatttttgct tttatttgcc agtctcattg ccgtcattca 28620
tggaatgagt aatgagaaaa ttactattta cactggcact aatcacacat tgaaaggtcc 28680
agaaaaagcc acagaagttt catggtattg ttattttaat gaatcagatg tatctactga 28740
actctgtgga aacaataaca aaaaaaatga gagcattact ctcatcaagt ttcaatgtgg 28800
atctgactta accctaatta acatcactag agactatgta ggtatgtatt atggaactac 28860
agcaggcatt tcggacatgg aattttatca agtttctgtg tctgaaccca ccacgcctag 28920
aatgaccaca accacaaaaa ctacacctgt taccactatg cagctcacta ccaataacat 28980
ttttgccatg cgtcaaatgg tcaacaatag cactcaaccc accccaccca gtgaggaaat 29040
tcccaaatcc atgattggca ttattgttgc tgtagtggtg tgcatgttga tcatcgcctt 29100
gtgcatggtg tactatgcct tctgctacag aaagcacaga ctgaacgaca agctggaaca 29160
cttactaagt gttgaatttt aatttttag aaccatgaag atcctaggcc ttttaatttt 29220
ttctatcatt acctctgctc tatgcaattc tgacaatgag gacgttactg tcgttgtcgg 29280
atcaaattat acactgaaag gtccagcgaa gggtatgctt tcgtggtatt gctattttgg 29340
atctgacact acagaaactg aattatgcaa tcttaagaat ggcaaaattc aaaattctaa 29400
aattaacaat tatatatgca atggtactga tctgatactc ctcaatatca cgaaatcata 29460
tgctggcagt tacacctgcc ctggagatga tgctgacagt atgatttttt acaaagtaac 29520
tgttgttgat cccactactc cacctccacc caccacaact actcacacca cacacacaga 29580
tcaaaccgca gcagaggagg cagcaaagtt agccttgcag gtccaagaca gttcatttgt 29640
tggcattacc cctacacctg atcagcggtg tccggggctg ctagtcagcg gcattgtcgg 29700
tgtgctttcg ggattagcag tcataatcat ctgcatgttc atttttgctt gctgctatag 29760
aaggctttac cgacaaaaat cagacccact gctgaacctc tatgtttaat tttttccaga 29820
gtcatgaagg cagttagcgc tctagttttt tgttctttga ttggcattgt tttttgcaat 29880

20262014626 26 Feb 2026

cctattccta aagttagctt tattaaagat gtgaatgtta ctgaggggg caatgtgaca 29940
ctggtaggtg tagagggtgc tgaaaacacc acctggacaa aataccacct caatgggtgg 30000
aaagatattt gcaattggag tgtattagtt tatacatgtg agggagttaa tcttaccatt 30060
gtcaatgcca cctcagctca aaatggtaga attcaaggac aaagtgtcag tgtatctaat 30120
gggtatttta cccaacatac ttttatctat gacgttaaag tcataccact gcctacgcct 30180
agcccaccta gcactaccac acagacaacc cacactacac agacaaccac atacagtaca 30240
ttaaatcagc ctaccaccac tacagcagca gaggttgcca gctcgtctgg ggtccgagtg 30300
gcatttttga tgttggcccc atctagcagt cccactgcta gtaccaatga gcagactact 30360
gaatttttgt ccactgtcga gagccacacc acagctacct ccagtgcctt ctctagcacc 30420
gccaatctct cctcgctttc ctctacacca atcagtcccg ctactactcc tagccccgct 30480
cctcttccca ctcccctgaa gcaaacagac ggcggcatgc aatggcagat caccctgctc 30540
attgtgatcg ggttggtcat cctggccgtg ttgctctact acatcttctg ccgccgcatt 30600
cccaacgcgc accgcaagcc ggtctacaag cccatcattg tcgggcagcc ggagccgctt 30660
caggtggaag ggggtctaag gaatcttctc ttctctttta cagtatggtg attgaactat 30720
gattcctaga caattcttga tcactattct tatctgcctc ctccaagtct gtgccaccct 30780
cgctctggtg gccaacgcca gtccagactg tattgggccc ttcgcctcct acgtgctctt 30840
tgccttcacc acctgcatct gctgctgtag catagtctgc ctgcttatca ccttcttcca 30900
gttcattgac tggatctttg tgcgcatcgc ctacctgcgc caccaccccc agtaccgcga 30960
ccagcgagtg gcgcggctgc tcaggctcct ctgataagca tgcgggctct gctacttctc 31020
gcgcttctgc tgttagtgct cccccgtccc gtcgacccca ggtcccccac ccagtccccc 31080
gaggaggtcc gcaaatgcaa attccaagaa ccctggaaat tcctcaaatg ctaccgccaa 31140
aaatcagaca tgcatcccag ctggatcatg atcattggga tcgtgaacat tctggcctgc 31200
accctcatct cctttgtgat ttacccctgc tttgactttg gttggaactc gccagaggcg 31260
ctctatctcc cgcctgaacc tgacacacca ccacagcaac ctcaggcaca cgcactacca 31320
ccactacagc ctaggccaca atacatgccc atattagact atgaggccga gccacagcga 31380
cccatgctcc ccgctattag ttacttcaat ctaaccggcg gagatgactg acccactggc 31440
caacaacaac gtcaacgacc ttctcctgga catggacggc cgcgcctcgg agcagcgact 31500
cgcccaactt cgcattcgcc agcagcagga gagagccgtc aaggagctgc aggatgcggt 31560
ggccatccac cagtgcaaga gaggcatctt ctgcctggtg aaacaggcca agatctccta 31620
cgaggtcact ccaaacgacc atcgcctctc ctacgagctc ctgcagcagc gccagaagtt 31680
cacctgcctg gtcggagtca accccatcgt catcacccag cagtctggcg ataccaaggg 31740
gtgcatccac tgctcctgcg actcccccga ctgcgtccac actctgatca agaccctctg 31800
cggcctccgc gacctcctcc ccatgaacta atcacccccc tatccagtga aataaagatc 31860
atattgatga tgattttaca gaaataaaaa ataatcattt gatttgaaat aaagatacaa 31920
tcatattgat gatttgagtt taacaaaaaa ataaagaatc acttacttga aatctgatac 31980
caggtctctg tccatgtttt ctgccaacac cacttcactc ccctcttccc agctctggta 32040
ctgcaggccc cggcgggctg caaacttcct ccacacgctg aaggggatgt caaattcctc 32100
ctgtccctca atcttcattt tatcttctat cagatgtcca aaaagcgcgt ccgggtggat 32160
gatgacttcg accccgtcta cccctacgat gcagacaacg caccgaccgt gcccttcatc 32220
aacccccccc tcgtctcttc agatggattc caagagaagc ccctgggggt gttgtccctg 32280
cgactggccg accccgtcac caccaagaac ggggaaatca ccctcaagct gggagagggg 32340
gtggacctcg attcctcggg aaaactcatc tccaacacgg ccaccaaggc cgccgcccct 32400
ctcagttttt ccaacaacac catttccctt aacatggatc acccctttta cactaaagat 32460
ggaaaattat ccttacaagt ttctccacca ttaaatatac tgagaacaag cattctaaac 32520
acactagctt taggttttgg atcaggttta ggactccgtg gctctgcctt ggcagtacag 32580
ttagtctctc cacttacatt tgatactgat ggaaacataa agcttacctt agacagaggt 32640
ttgcatgtta caacaggaga tgcaattgaa agcaacataa gctgggctaa aggtttaaaa 32700
tttgaagatg gagccatagc aaccaacatt ggaaatgggt tagagtttgg aagcagtagt 32760
acagaaacag gtgttgatga tgcttaccca atccaagtta aacttggatc tggccttagc 32820
tttgacagta caggagccat aatggctggt aacaaagaag acgataaact cactttgtgg 32880
acaacacctg atccatcacc aaactgtcaa atactcgcag aaaatgatgc aaaactaaca 32940
ctttgcttga ctaaatgtgg tagtcaaata ctggccactg tgtcagtctt agttgtagga 33000
agtggaaacc taaaccccat tactggcacc gtaagcagtg ctcaggtgtt tctacgtttt 33060
gatgcaaacg gtgttctttt aacagaacat tctacactaa aaaaatactg ggggtatagg 33120
cagggagata gcatagatgg cactccatat accaatgctg taggattcat gcccaattta 33180
aaagcttatc caaagtcaca aagttctact actaaaaata atatagtagg gcaagtatac 33240
atgaatggag atgtttcaaa acctatgctt ctcactataa ccctcaatgg tactgatgac 33300
agcaacagta catattcaat gtcattttca tacacctgga ctaatggaag ctatgttgga 33360
gcaacatttg gggctaactc ttataccttc tcatacatcg cccaagaatg aacactgtat 33420
cccaccctgc atgccaaccc ttcccacccc actctgtgga acaaactctg aaacacaaaa 33480
taaaataaag ttcaagtgtt ttattgattc aacagtttta caggattcga gcagttattt 33540
ttcctccacc ctcccaggac atggaataca ccaccctctc cccccgcaca gccttgaaca 33600
tctgaatgcc attggtgatg gacatgcttt tggtctccac gttccacaca gtttcagagc 33660
gagccagtct cgggtcggtc agggagatga aaccctccgg gcactcccgc atctgcacct 33720
cacagctcaa cagctgagga ttgtcctcgg tggtcgggat cacggttatc tggaagaagc 33780
agaagagcgg cggtgggaat catagtccgc gaacgggatc ggccggtggt gtcgcatcag 33840
gccccgcagc agtcgctgcc gccgccgctc cgtcaagctg ctgctcaggg ggtccgggtc 33900
cagggactcc ctcagcatga tgcccacggc cctcagcatc agtcgtctgg tgcggcgggc 33960
gcagcagcgc atgcggatct cgctcaggtc gctgcagtac gtgcaacaca gaaccaccag 34020
gttgttcaac agtccatagt tcaacacgct ccagccgaaa ctcatcgcgg gaaggatgct 34080
acccacgtgg ccgtcgtacc agatcctcag gtaaatcaag tggtgccccc tccagaacac 34140
gctgcccacg tacatgatct ccttgggcat gtggcggttc accacctccc ggtaccacat 34200
caccctctgg ttgaacatgc agccccggat gatcctgcgg aaccacaggg ccagcaccgc 34260
cccgcccgcc atgcagcgaa gagaccccgg gtcccggcaa tggcaatgga ggacccaccg 34320
ctcgtacccg tggatcatct gggagctgaa caagtctatg ttggcacagc acaggcatat 34380
gctcatgcat ctcttcagca ctctcaactc ctcgggggtc aaaaccatat cccagggcac 34440

20262014462 26 Feb 2026

		ggggaactct tgcaggacag cgaaccccgc agaacagggc aatcctcgca cagaacttac 34500 attgtgcatg gacagggtat cgcaatcagg cagcaccggg tgatcctcca ccagagaagc 34560 gcgggtctcg gtctcctcac agcgtggtaa gggggccggc cgatacgggt gatggcggga 34620 cgcggctgat cgtgttcgcg accgtgtcat gatgcagttg ctttcggaca ttttcgtact 34680 tgctgtagca gaacctggtc cgggcgctgc acaccgatcg ccggcggcgg tctcggcgct 34740 tggaacgctc ggtgttgaaa ttgtaaaaca gccactctct cagaccgtgc agcagatcta 34800 gggcctcagg agtgatgaag atcccatcat gcctgatggc tctgatcaca tcgaccaccg 34860 tggaatgggc cagacccagc cagatgatgc aattttgttg ggtttcggtg acggcggggg 34920 agggaagaac aggaagaacc atgattaact tttaatccaa acggtctcgg agtacttcaa 34980 aatgaagatc gcggagatgg cacctctcgc ccccgctgtg ttggtggaaa ataacagcca 35040 ggtcaaaggt gatacggttc tcgagatgtt ccacggtggc ttccagcaaa gcctccacgc 35100 gcacatccag aaacaagaca atagcgaaag cgggagggtt ctctaattcc tcaatcatca 35160 tgttacactc ctgcaccatc cccagataat tttcattttt ccagccttga atgattcgaa 35220 ctagttcctg aggtaaatcc aagccagcca tgataaagag ctcgcgcaga gcgccctcca 35280 ccggcattct taagcacacc ctcataattc caagatattc tgctcctggt tcacctgcag 35340 cagattgaca agcggaatat caaaatctct gccgcgatcc ctgagctcct ccctcagcaa 35400 taactgtaag tactctttca tatcctctcc gaaattttta gccataggac caccaggaat 35460 aagattaggg caagccacag tacagataaa ccgaagtcct ccccagtgag cattgccaaa 35520 tgcaagactg ctataagcat gctggctaga cccggtgata tcttccagat aactggacag 35580 aaaatcgccc aggcaatttt taagaaaatc aacaaaagaa aaatcctcca ggtggacgtt 35640 tagagcctcg ggaacaacga tgaagtaaat gcaagcggtg cgttccagca tggttagtta 35700 gctgatctgt agaaaaaaca aaaatgaaca ttaaaccatg ctagcctggc gaacaggtgg 35760 gtaaatcgtt ctctccagca ccaggcaggc cacggggtct ccggcgcgac cctcgtaaaa 35820 attgtcgcta tgattgaaaa ccatcacaga gagacgttcc cggtggccgg cgtgaatgat 35880 tcgacaagat gaatacaccc ccggaacatt ggcgtccgcg agtgaaaaaa agcgcccgag 35940 gaagcaataa ggcactacaa tgctcagtct caagtccagc aaagcgatgc catgcggatg 36000 aagcacaaaa ttctcaggtg cgtacaaaat gtaattactc ccctcctgca caggcagcaa 36060 agcccccgat ccctccaggt acacatacaa agcctcagcg tccatagctt accgagcagc 36120 agcacacaac aggcgcaaga gtcagagaaa ggctgagctc taacctgtcc acccgctctc 36180 tgctcaatat atagcccaga tctacactga cgtaaaggcc aaagtctaaa aatacccgcc 36240 aaataatcac acacgcccag cacacgccca gaaaccggtg acacactcaa aaaaatacgc 36300 gcacttcctc aaacgcccaa aactgccgtc atttccgggt tcccacgcta cgtcatcaaa 36360 acacgacttt caaattccgt cgaccgttaa aaacgtcacc cgccccgccc ctaacggtcg 36420 cccgtctctc agccaatcag cgccccgcat ccccaaattc aaacacctca tttgcatatt 36480 aacgcgcaca aaaagtttga ggtatattat tgatgatgg 36519
3-11	**Sequences**	
3-11-1	Sequence Number [ID]	11
3-11-2	Molecule Type	DNA
3-11-3	Length	31867
3-11-4	Features	**misc_feature 1..31867**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide **source 1..31867** mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-11-5	Residues	ccatcttcaa taatatacct caaacttttt gtgcgcgtta atatgcaaat gaggcgtttg 60 aatttgggga ggaagggcgg tgattggtcg agggatgagc gaccgttagg ggcggggcga 120 gtgacgtttt gatgacgtgg ttgcgaggag gagccagttt gcaagttctc gtgggaaaag 180 tgacgtcaaa cgaggtgtgg tttgaacacg gaaatactca attttcccgc gctctctgac 240 aggaaatgag gtgtttctgg gcggatgcaa gtgaaaacgg gccattttcg cgcgaaaact 300 gaatgaggaa gtgaaaatct gagtaatttc gcgtttatgg cagggaggag tatttgccga 360 gggccgagta gactttgacc gattacgtgg gggtttcgat taccgtgttt ttcacctaaa 420 tttccgcgta cggtgtcaaa gtccggtgtt tttacgtagg tgtcagctga tcgccagggt 480 atttaaacct gcgctctcca gtcaagaggc cactcttgag tgccagcgag aagagttttc 540 tcctccgcgc cgcgagtcag atctacactt tgaaagtagg gataacaggg taatgacatt 600 gattattgac tagttgttaa tagtaatcaa ttacggggtc attagttcat agcccatata 660 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 720 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 780 attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt 840 atcatatgcc aagtccgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 900 atgcccagta catgacctta cgggactttc ctacttggca gtacatctac gtattagtca 960 tcgctattac catggtgatg cggttttggc agtacaccaa tgggcgtgga tagcggtttg 1020 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 1080 aaaatcaacg ggactttcca aaatgtcgta ataaccccgc cccgttgacg caaatgggcg 1140 gtaggcgtgt acggtgggag gtctatataa gcagagctcg tttagtgaac cgtcagatcg 1200 cctggaacgc catccacgct gttttgacct ccatagaaga cagcgatcgc gccaccatgg 1260 tgagcaaggg cgaggagctg ttcaccgggg tggtgcccat cctggtcgag ctggacggcg 1320 acgtaaacgg ccacaagttc agcgtgtccg gcgagggcga gggcgatgcc acctacggca 1380 agctgaccct gaagttcatc tgcaccaccg gcaagctgcc cgtgccctgg cccaccctcg 1440 tgaccaccct gacctacggc gtgcagtgct tcagccgcta ccccgaccac atgaagcagc 1500 acgacttctt caagtccgcc atgcccgaag gctacgtcca ggagcgcacc atcttcttca 1560 aggacgacgg caactacaag acccgcgccg aggtgaagtt cgagggcgac accctggtga 1620 accgcatcga gctgaagggc atcgacttca aggaggacgg caacatcctg gggcacaagc 1680 tggagtacaa ctacaacagc cacaacgtct atatcatggc cgacaagcag aagaacggca 1740 tcaaggtgaa cttcaagatc cgccacaaca tcgaggacgg cagcgtgcag ctcgccgacc 1800

20262014626 26 Feb 2026

actaccagca gaacaccccc atcggcgacg gccccgtgct gctgcccgac aaccactacc 1860
tgagcaccca gtccgccctg agcaaagacc ccaacgagaa gcgcgatcac atggtcctgc 1920
tggagttcgt gaccgccgcc gggatcactc tcggcatgga cgagctttac aagtagtgag 1980
tttaaactcc catttaaatg tgagggttaa tgcttcgagc agacatgata agatacattg 2040
atgagtttgg acaaaccaca actagaatgc agtgaaaaaa atgctttatt tgtgaaattt 2100
gtgatgctat tgctttattt gtaaccatta taagctgcaa taaacaagtt aacaacaaca 2160
attgcattca ttttatgttt caggttcagg gggagatgtg ggaggttttt taaagcaagt 2220
aaaacctcta caaatgtggt aaaataacta taacggtcct aaggtagcga gtgagtagtg 2280
ttctggggcg ggggaggacc tgcatgaggg ccagaataac tgaaatctgt gcttttctgt 2340
gtgttgcagc agcatgagcg gaagcggctc ctttgaggga ggggtattca gcccttatct 2400
gacggggcgt ctcccctcct gggcgggagt gcgtcagaat gtgatgggat ccacggtgga 2460
cggccggccc gtgcagcccg cgaactcttc aaccctgacc tatgcaaccc tgagctcttc 2520
gtcgttggac gcagctgccg ccgcagctgc tgcatctgcc gccagcgccg tgcgcggaat 2580
ggccatgggc gccggctact acggcactct ggtggccaac tcgagttcca ccaataatcc 2640
cgccagcctg aacgaggaga agctgttgct gctgatggcc cagctcgagg ccttgaccca 2700
gcgcctgggc gagctgaccc agcaggtggc tcagctgcag gagcagacgc gggccgcggt 2760
tgccacggtg aaatccaaat aaaaaatgaa tcaataaata aacggagacg gttgttgatt 2820
ttaacacaga gtctgaatct ttatttgatt tttcgcgcgc ggtaggccct ggaccaccgg 2880
tctcgatcat tgagcacccg gtggatcttt tccaggaccc ggtagaggtg ggcttggatg 2940
ttgaggtaca tgggcatgag cccgtcccgg gggtggaggt agctccattg cagggcctcg 3000
tgctcggggg tggtgttgta aatcacccag tcatagcagg ggcgcagggc atggtgttgc 3060
acaatatctt tgaggaggag actgatggcc acgggcagcc ctttggtgta ggtgtttaca 3120
aatctgttga gctgggaggg atgcatgcgg ggggagatga ggtgcatctt ggcctggatc 3180
ttgagattgg cgatgttacc gcccagatcc cgcctggggt tcatgttgtg caggaccacc 3240
agcacggtgt atccggtgca cttggggaat ttatcatgca acttggaagg gaaggcgtga 3300
aagaatttgg cgacgccttt gtgcccgccc aggttttcca tgcactcatc catgatgatg 3360
gcgatgggcc cgtgggcggc ggcctgggca aagacgtttc gggggtcgga cacatcatag 3420
ttgtggtcct gggtgaggtc atcataggcc attttaatga atttggggcg gagggtgccg 3480
gactgggga caaaggtacc ctcgatcccg ggggcgtagt tcccctcaca gatctgcatc 3540
tcccaggctt tgagctcgga ggggggggatc atgtccacct gcggggcgat aaagaacacg 3600
gtttccgggg cgggggagat gagctgggcc gaaagcaagt tccggagcag ctgggacttg 3660
ccgcagccgg tggggccgta gatgaccccg atgaccggct gcaggtggta gttgagggag 3720
agacagctgc cgtcctcccg gaggaggggg gccacctcgt tcatcatctc gcgcacgtgc 3780
atgttctcgc gcaccagttc cgccaggagg cgctctcccc ccagggatag gagctcctgg 3840
agcgaggcga agtttttcag cggcttgagt ccgtcggcca tgggcatttt ggagagggtt 3900
tgttgcaaga gttccaggcg gtcccagagc tcggtgatgt gctctacggc atctcgatcc 3960
agcagacctc ctcgtttcgc gggttgggac ggctgcggga gtagggcacc agacgatggg 4020
cgtccagcgc agccagggtc cggtccttcc agggtcgcag cgtccgcgtc agggtggtct 4080
ccgtcacggt gaaggggtgc gcgccgggct gggcgcttgc gagggtgcgc ttcaggctca 4140
tccggctggt cgaaaaccgc tcccgatcgg cgccctgcgc gtcggccagg tagcaattga 4200
ccatgagttc gtagttgagc gcctcggccg cgtggccttt ggcgcggagc ttacctttgg 4260
aagtctgccc gcaggcggga cagaggaggg acttgagggc gtagagcttg ggggcgagga 4320
agacggactc gggggcgtag gcgtccgcgc cgcagtgggc gcagacggtc tcgcactcca 4380
cgagccaggt gaggtcgggc tggtcggggt caaaaaccag tttcccgccg ttctttttga 4440
tgcgtttctt acctttggtc tccatgagct cgtgtccccg ctgggtgaca aagaggctgt 4500
ccgtgtcccc gtagaccgac tttatgggcc ggtcctcgag cggtgtgccg cggtcctcct 4560
cgtagaggaa ccccgcccac tccgagacga aagcccgggt ccaggccagc acgaaggagg 4620
ccacgtggga cgggtagcgg tcgttgtcca ccagcgggtc cacctttcc agggtatgca 4680
aacacatgtc cccctcgtcc acatccagga aggtgattgg cttgtaagtg taggccacgt 4740
gaccgggggt cccggccggg ggggtataaa agggtgcggg tccctgctcg tcctcactgt 4800
cttccggatc gctgtccagg agcgccagct gttggggtag gtattccctc tcgaaggcgg 4860
gcatgacctc ggcactcagg ttgtcagttt ctagaaacga ggaggatttg atattgacgg 4920
tgccggcgga gatgcctttc aagagcccct cgtccatctg gtcagaaaag acgatctttt 4980
tgttgtcgag cttggtggcg aaggagccgt agagggcgtt ggagaggagc ttggcgatgg 5040
agcgcatggt ctggtttttt tccttgtcgg cgcgctcctt ggcggcgatg ttgagctgca 5100
cgtactcgcg cgccacgcac ttccattcgg ggaagacggt ggtcagctcg tcgggcacga 5160
ttctgacctg ccagccccga ttatgcaggg tgatgaggtc cacactggtg gccacctcgc 5220
cgcgcagggg ctcattagtc cagcagaggc gtccgccctt gcgcgagcag aaggggggca 5280
gggggtccag catgacctcg tcgggggggt cggcatcgat ggtgaagatg ccgggcagga 5340
ggtcggggtc aaagtagctg atggaagtgg ccagatcgtc cagggcagct tgccattcgc 5400
gcacggccag cgcgctctcg tagggactga ggggcgtgcc ccagggcatg ggatgggtaa 5460
gcgcggaggc gtacatgccg cagatgtcgt agacgtagag gggctcctcg aggatgccga 5520
tgtaggtggg gtagcagcgc cccccgcgga tgctggcgcg cacgtagtca tacagctcgt 5580
gcgagggggc gaggagcccc gggcccaggt tggtgcgact gggcttttcg gcgcggtaga 5640
cgatctggcg gaaaatggca tgcgagttgg aggagatggt gggcctttgg aagatgttga 5700
agtgggcgtg gggcagtccg accgagtcgc ggatgaagtg ggcgtaggag tcttgcagct 5760
tggcgacgag ctcggcggtg actaggacgt ccagagcgca gtagtcgagg gtctcctgga 5820
tgatgtcata cttgagctgt ccctttttgtt tccacagctc gcggttgaga aggaactctt 5880
cgcggtcctt ccagtactct tcgaggggga acccgtcctg atctgcacgg taagagccta 5940
gcatgtagaa ctggttgacg gccttgtagg cgcagcagcc cttctccacg gggagggcgt 6000
aggcctgggc ggccttgcgc agggaggtgt gcgtgagggc gaaagtgtcc ctgaccatga 6060
ccttgaggaa ctggtgcttg aagtcgatat cgtcgcagcc cccctgctcc cagagctgga 6120
agtccgtgcg cttcttgtag gcggggttgg gcaaagcgaa agtaacatcg ttgaagagga 6180
tcttgcccgc gcggggcata aagttgcgag tgatgcggaa aggttggggc acctcggccc 6240
ggttgttgat gacctgggcg gcgagcacga tctcgtcgaa gccgttgatg ttgtggccca 6300
cgatgtagag ttccacgaat cgcggacggc ccttgacgtg gggcagtttc ttgagctcct 6360

20262014626 26 Feb 2026

```
cgtaggtgag ctcgtcgggg tcgctgagcc cgtgctgctc gagcgcccag tcggcgagat 6420
gggggttggc gcggaggaag gaagtccaga gatccacggc cagggcggtt tgcagacggt 6480
cccggtactg acggaactgc tgcccgacgg ccatttttc gggggtgacg cagtagaagg 6540
tgcgggggtc cccgtgccag cgatcccatt tgagctggag ggcgagatcg agggcgagct 6600
cgacgagccg gtcgtccccg gagagtttca tgaccagcat gaaggggacg agctgcttgc 6660
cgaaggaccc catccaggtg taggtttcca catcgtaggt gaggaagagc ctttcggtgc 6720
gaggatgcga gccgatgggg aagaactgga tctcctgcca ccaattggag gaatggctgt 6780
tgatgtgatg gaagtagaaa tgccgacggc gcgccgaaca ctcgtgcttg tgtttataca 6840
agcggccaca gtgctcgcaa cgctgcacgg gatgcacgtg ctgcacgagc tgtacctgag 6900
ttcctttgac gaggaatttc agtgggaagt ggagtcgtgg cgcctgcatc tcgtgctgta 6960
ctacgtcgtg gtggtcggcc tggccctctt ctgcctcgat ggtggtcatg ctgacgagcc 7020
cgcgcgggag gcaggtccag acctcggcgc gagcgggtcg gagagcgagg acgagggcgc 7080
gcaggccgga gctgtccagg gtcctgagac gctgcggagt caggtcagtg ggcagcggcg 7140
gcgcgcggtt gacttgcagg agtttttcca gggcgcgcgg gaggtccaga tggtacttga 7200
tctccaccgc gccattggtg gcgacgtcga tggcttgcag ggtcccgtgc ccctggggtg 7260
tgaccaccgt cccccgtttc ttcttgggcg gctggggcga cgggggcggt gcctcttcca 7320
tggttagaag cggcggcgag gacgcgcgcc gggcggcagg ggcggctcgg ggcccggagg 7380
caggggcggc aggggcacgt cggcgccgcg cgcgggtagg ttctggtact gcgcccggag 7440
aagactggcg tgagcgacga cgcgacggtt gacgtcctgg atctgacgcc tctgggtgaa 7500
ggccacggga cccgtgagtt tgaacctgaa agagagttcg acagaatcaa tctcggtatc 7560
gttgacggcg gcctgccgca ggatctcttg cacgtcgccc gagttgtcct ggtaggcgat 7620
ctcggtcatg aactgctcga tctcctcctc ttgaaggtct ccgcggccgg cgcgctccac 7680
ggtggccgcg aggtcgttgg agatgcggcc catgagctgc gagaaggcgt tcatgcccgc 7740
ctcgttccag acgcggctgt agaccacgac gccctcggga tcgcgggcgc gcatgaccac 7800
ctgggcgagg ttgagctcca cgtggcgcgt gaagaccgcg tagttgcaga ggcgctggta 7860
gaggtagttg agcgtggtgg cgatgtgctc ggtgacgaag aaatacatga tccagcggcg 7920
gagcggcatc tcgctgacgt cgcccagcgc ctccaaacgt tccatggcct cgtaaaagtc 7980
cacggcgaag ttgaaaaact gggagttgcg cgccgagacg gtcaactcct cctccagaag 8040
acggatgagc tcggcgatgg tggcgcgcac ctcgcgctcg aaggcccccg ggagttcctc 8100
cacttcctct tcttcctcct ccactaacat ctcttctact tcctcctcag gcggcagtgg 8160
tggcggggga gggggcctgc gtcgccggcg gcgcacgggc agacggtcga tgaagcgctc 8220
gatggtctcg ccgcgccggc gtcgcatggt ctcggtgacg gcgcgcccgt cctcgcgggg 8280
ccgcagcgtg aagacgccgc cgcgcatctc caggtggccg ggggggtccc cgttgggcag 8340
ggagagggcg ctgacgatgc atcttatcaa ttgccccgta gggactccgc gcaaggacct 8400
gagcgtctcg agatccacgg gatctgaaaa ccgctgaacg aaggcttcga gccagtcgca 8460
gtcgcaaggt aggctgagca cggtttcttc tggcgggtca tgttggttgg gagcggggcg 8520
ggcgatgctg ctggtgatga agttgaaata ggcggttctg agacggcgga tggtggcgag 8580
gagcaccagg tctttgggcc cggcttgctg gatgcgcaga cggtcggcca tgccccaggc 8640
gtggtcctga cacctggcca ggtccttgta gtagtcctgc atgagccgct ccacgggcac 8700
ctcctcctcg cccgcgcggc cgtgcatgcg cgtgagcccg aagccgcgct ggggctggac 8760
gagcgccagg tcggcgacga cgcgctcggc gaggatggct tgctggatct gggtgagggt 8820
ggtctggaag tcatcaaagt cgacgaagcg gtggtaggct ccggtgttga tggtgtagga 8880
gcagttggcc atgacggacc agttgacggt ctggtggccc ggacgcacga gctcgtggta 8940
cttgaggcgc gagtaggcgc gcgtgtcgaa gatgtagtcg ttgcaggtgc gcaccaggta 9000
ctggtagccg atgaggaagt gcggcggcgg ctggcggtag agcggccatc gctcggtggc 9060
gggggcgccg ggcgcgaggt cctcgagcat ggtgcggtgg tagccgtaga tgtacctgga 9120
catccaggtg atgccggcgg cggtggtgga ggcgcgcggg aactcgcgga cgcggttcca 9180
gatgttgcgc agcggcagga agtagttcat ggtgggcacg gtctggcccg tgaggcgcgc 9240
gcagtcgtgg atgctctata cgggcaaaaa cgaaagcggt cagcggctcg actccgtggc 9300
ctggaggcta agcgaacggg ttgggctgcg cgtgtacccc ggttcgaatc tcgaatcagg 9360
ctggagccgc agctaacgtg gtattggcac tcccgtctcg acccaagcct gcaccaaccc 9420
tccaggatac ggaggcgggt cgttttgcaa ctttttttg gaggccggat gagactagta 9480
agcgcggaaa gcggccgacc gcgatggctc gctgccgtag tctggagaag aatcgccagg 9540
gttgcgttgc ggtgtgcccc ggttcgaggc cggccggatt ccgcggctaa cgagggcgtg 9600
gctgccccgt cgtttccaag accccatagc cagccgactt ctccagttac ggagcgagcc 9660
cctcttttgt tttgtttgtt tttgccagat gcatcccgta ctgcggcaga tgcgccccca 9720
ccaccctcca ccgcaacaac agccccctcc acagccggcg cttctgcccc cgccccagca 9780
gcaacttcca gccacgaccg ccgcggccgc cgtgagcggg gctggacaga gttatgatca 9840
ccagctggcc ttggaagagg gcgaggggct ggcgcgcctg ggggcgtcgt cgccggagcg 9900
gcacccgcgc gtgcagatga aaagggacgc tcgcgaggcc tacgtgccca agcagaacct 9960
gttcagagac aggagcggcg aggagcccga ggagatgcgc gcggcccggt tccacgcggg 10020
gcgggagctg cggcgcggcc tggaccgaaa gagggtgctg agggacgagg atttcgaggc 10080
ggacgagctg acggggatca gccccgcgcg cgcgcacgtg gccgcggcca acctggtcac 10140
ggcgtacgag cagaccgtga aggaggagag caacttccaa aaatccttca acaaccacgt 10200
gcgcaccctg atcgcgcgcg aggaggtgac cctgggcctg atgcacctgt gggacctgct 10260
ggaggccatc gtgcagaacc ccaccagcaa gccgctgacg gcgcagctgt tcctggtggt 10320
gcagcatagt cgggacaacg aagcgttcag ggaggcgctg ctgaatatca ccgagcccga 10380
gggccgctgg ctcctggacc tggtgaacat tctgcagagc atcgtggtgc aggagcgcgg 10440
gctgccgctg tccgagaagc tggcggccat caacttctcg gtgctgagtt tgggcaagta 10500
ctacgctagg aagatctaca agaccccgta cgtgcccata gacaaggagg tgaagatcga 10560
cgggttttac atgcgcatga ccctgaaagt gctgaccctg agcgacgatc tgggggtgta 10620
ccgcaacgac aggatgcacc gtgcggtgag cgccagcagg cggcgcgagc tgagcgacca 10680
ggagctgatg catagtctgc agcgggccct gaccggggcc gggaccgagg gggagagcta 10740
ctttgacatg ggcgcggacc tgcactggca gcccagccgc cgggccttgg aggcggcggc 10800
aggaccctac gtagaagagg tggacgatga ggtggacgag gagggcgagt acctggaaga 10860
ctgatggcgc gaccgtattt ttgctagatg caacaacaac agccacctcc tgatcccgcg 10920
```

20262014626 26 Feb 2026

atgcgggcgg cgctgcagag ccagccgtcc ggcattaact cctcggacga ttggacccag 10980
gccatgcaac gcatcatggc gctgacgacc cgcaaccccg aagcctttag acagcagccc 11040
caggccaacc ggctctcggc catcctggag gccgtggtgc cctcgcgctc caaccccacg 11100
cacgagaagg tcctggccat cgtgaacgcg ctggtggaga acaaggccat ccgcggcgac 11160
gaggccggcc tggtgtacaa cgcgctgctg gagcgcgtgg cccgctacaa cagcaccaac 11220
gtgcagacca acctggaccg catggtgacc gacgtgcgcg aggccgtggc ccagcgcgag 11280
cggttccacc gcgagtccaa cctgggatcc atggtggcgc tgaacgcctt cctcagcacc 11340
cagcccgcca acgtgccccg gggccaggag gactacacca acttcatcag cgccctgcgc 11400
ctgatggtga ccgaggtgcc ccagagcgag gtgtaccagt ccgggccgga ctacttcttc 11460
cagaccagtc gccagggctt gcagaccgtg aacctgagcc aggctttcaa gaacttgcag 11520
ggcctgtggg gcgtgcaggc cccggtcggg gaccgcgcga cggtgtcgag cctgctgacg 11580
ccgaactcgc gcctgctgct gctgctggtg gccccccttca cggacagcgg cagcatcaac 11640
cgcaactcgt acctgggcta cctgattaac ctgtaccgcg aggccatcgg ccaggcgcac 11700
gtggacgagc agacctacca ggagatcacc cacgtgagcc gcgccctggg ccaggacgac 11760
ccgggcaacc tggaagccac cctgaacttt ttgctgacca accggtcgca gaagatcccg 11820
ccccagtacg cgctcagcac cgaggaggag cgcatcctgc gttacgtgca gcagagcgtg 11880
ggcctgttcc tgatgcagga gggggccacc cccagcgccg cgctcgacat gaccgcgcgc 11940
aacatggagc ccagcatgta cgccagcaac cgcccgttca tcaataaact gatggactac 12000
ttgcatcggg cggccgccat gaactctgac tatttcacca acgccatcct gaatccccac 12060
tggctcccgc cgccggggtt ctacacgggc gagtacgaca tgcccgaccc caatgacggg 12120
ttcctgtggg acgatgtgga cagcagcgtg ttctcccccc gaccgggtgc taacgagcgc 12180
cccttgtgga agaaggaagg cagcgaccga cgcccgtcct cggcgctgtc cggccgcgag 12240
ggtgctgccg cggcggtgcc cgaggccgcc agtcctttcc cgagcttgcc cttctcgctg 12300
aacagtatcc gcagcagcga gctgggcagg atcacgcgcc cgcgcttgct gggcgaagag 12360
gagtacttga atgactcgct gttgagaccc gagcgggaga agaacttccc caataacggg 12420
atagaaagcc tggtggacaa gatgagccgc tggaagacgt atgcgcagga gcacagggac 12480
gatccccggg cgtcgcaggg ggccacgagc cggggcagcg ccgcccgtaa acgccggtgg 12540
cacgacaggc agcggggaca gatgtgggac gatgaggact ccgccgacga cagcagcgtg 12600
ttggacttgg gtgggagtgg taacccgttc gctcacctgc gcccccgtat cgggcgcatg 12660
atgtaagaga aaccgaaaat aaatgatact caccaaggcc atggcgacca gcgtgcgttc 12720
gtttcttctc tgttgttgtt gtatctagta tgatgaggcg tgcgtacccg gagggtcctc 12780
ctccctcgta cgagagcgtg atgcagcagg cgatggcggc ggcggcgatg cagcccccgc 12840
tggaggctcc ttacgtgccc ccgcggtacc tggcgcctac ggaggggcgg aacagcattc 12900
gttactcgga gctggcaccc ttgtacgata ccacccggtt gtacctggtg gacaacaagt 12960
cggcggacat cgcctcgctg aactaccaga acgaccacag caacttcctg accaccgtgg 13020
tgcagaacaa tgacttcacc cccacggagg ccagcaccca gaccatcaac tttgacgagc 13080
gctcgcggtg gggcggccag ctgaaaacca tcatgcacac caacatgccc aacgtgaacg 13140
agttcatgta cagcaacaag ttcaaggcgc gggtgatggt ctcccgcaag acccccaatg 13200
gggtgacagt gacagaggat tatgatggta gtcaggatga gctgaagtat gaatgggtgg 13260
aatttgagct gcccgaaggc aacttctcgg tgaccatgac catcgacctg atgaacaacg 13320
ccatcatcga caattacttg gcggtggggc ggcagaacgg ggtgctggag agcgacatcg 13380
gcgtgaagtt cgacactagg aacttcaggc tgggctggga ccccgtgacc gagctggtca 13440
tgcccggggt gtacaccaac gaggctttcc atcccgatat tgtcttgctg cccggctgcg 13500
gggtggactt caccgagagc cgcctcagca acctgctggg cattcgcaag aggcagccct 13560
tccaggaagg cttccagatc atgtacgagg atctggaggg gggcaacatc cccgcgctcc 13620
tggatgtcga cgcctatgag aaaagcaagg aggatgcagc agctgaagca actgcagccg 13680
tagctaccgc ctctaccgag gtcaggggcg ataattttgc aagcgccgca gcagtggcag 13740
cggccgaggc ggctgaaacc gaaagtaaga tagtcattca gccggtggag aaggatagca 13800
agaacaggag ctacaacgta ctaccggaca agataaacac cgcctaccgc agctggtacc 13860
tagcctacaa ctatggcgac cccgagaagg gcgtgcgctc ctggacgctg ctcaccacct 13920
cggacgtcac ctgcggcgtg gagcaagtct actggtcgct gcccgacatg atgcaagacc 13980
cggtcacctt ccgctccacg cgtcaagtta gcaactaccc ggtggtgggc gccgagctcc 14040
tgcccgtcta ctccaagagc ttcttcaacg agcaggccgt ctactcgcag cagctgcgcg 14100
ccttcacctc gcttacgcac gtcttcaacc gcttccccga gaaccagatc ctcgtccgcc 14160
cgcccgcgcc caccattacc accgtcagtg aaaacgttcc tgctctcaca gatcacggga 14220
ccctgccgct gcgcagcagt atccggggag tccagcgcgt gaccgttact gacgccagac 14280
gccgcacctg cccctacgtc tacaaggccc tgggcatagt cgcgccgcgc gtcctctcga 14340
gccgcacctt ctaaatgtcc attctcatct cgcccagtaa taacaccggt tggggcctgc 14400
gcgcgcccag caagatgtac ggaggcgctc gccaacgctc cacgcaacac cccgtgcgcg 14460
tgcgcgggca cttccgcgct ccctggggcg ccctcaaggg ccgcgtgcgg tcgcgcacca 14520
ccgtcgacga cgtgatcgac caggtggtgg ccgacgcgcg caactacacc cccgccgccg 14580
cgcccgtctc caccgtggac gccgtcatcg acagcgtggt ggccgacgcg cgccggtacg 14640
cccgcgccaa gagccggcgg cggcgcatcg cccggcggca ccggagcacc cccgccatgc 14700
gcgcggcgcg agccttgctg cgcagggcca ggcgcacggg acgcagggcc atgctcaggg 14760
cggccagacg cgcggcttca ggcgccagcg ccggcaggac ccggagacgc gcggccacgg 14820
cggcggcagc ggccatcgcc agcatgtccc gcccgcggcg agggaacgtg tactgggtgc 14880
gcgacgccgc caccggtgtg cgcgtgcccg tgcgcacccg ccccccctcgc acttgaagat 14940
gttcacttcg cgatgttgat gtgtcccagc ggcgaggagg atgtccaagc gcaaattcaa 15000
ggaagagatg ctccaggtca tcgcgcctga gatctacggc cctgcggtgg tgaaggagga 15060
aagaaagccc cgcaaaatca agcgggtcaa aaaggacaaa aaggaagaag aaagtgatgt 15120
ggacggattg gtggagtttg tgcgcgagtt cgccccccgg cggcgcgtgc agtggcgcgg 15180
gcggaaggtg caaccggtgc tgagacccgg caccaccgtg gtcttcacgc ccggcgagcg 15240
ctccggcacc gcttccaagc gctcctacga cgaggtgtac ggggatgatg atattctgga 15300
gcaggcggcc gagcgcctgg gcgagtttgc ttacggcaag cgcagccgtt ccgcaccgaa 15360
ggaagaggcg gtgtccatcc cgctggacca cggcaacccc acgccgagcc tcaagcccgt 15420
gaccttgcag caggtgctgc cgaccgcggc gccgcgccgg gggttcaagc gcgagggcga 15480

20262014622 26 Feb 2026

ggatctgtac cccaccatgc agctgatggt gcccaagcgc cagaagctgg aagacgtgct 15540
ggagaccatg aaggtggacc cggacgtgca gcccgaggtc aaggtgcggc ccatcaagca 15600
ggtggccccg ggcctgggcg tgcagaccgt ggacatcaag attcccacgg agcccatgga 15660
aacgcagacc gagcccatga tcaagcccag caccagcacc atggaggtgc agacggatcc 15720
ctggatgcca tcggctccta gtcgaagacc ccggcgcaag tacggcgcgg ccagcctgct 15780
gatgcccaac tacgcgctgc atccttccat catccccacg ccgggctacc gcggcacgcg 15840
cttctaccgc ggtcatacca gcagccgccg ccgcaagacc accactcgcc gccgccgtcg 15900
ccgcaccgcc gctgcaacca cccctgccgc cctggtgcgg agagtgtacc gccgcggccg 15960
cgcacctctg accctgccgc gcgcgcgcta ccacccgagc atcgccattt aaactttcgc 16020
ctgctttgca gatcaatggc cctcacatgc cgccttcgcg ttcccattac gggctaccga 16080
ggaagaaaac cgcgccgtag aaggctggcg gggaacggga tgcgtcgcca ccaccaccgg 16140
cggcggcgcg ccatcagcaa gcggttgggg ggaggcttcc tgcccgcgct gatccccatc 16200
atcgccgcgg cgatcggggc gatccccggc attgcttccg tggcggtgca ggcctctcag 16260
cgccactgag acacacttgg aaacatcttg taataaacca atggactctg acgctcctgg 16320
tcctgtgatg tgttttcgta gacagatgga agacatcaat ttttcgtccc tggctccgcg 16380
acacggcacg cggccgttca tgggcacctg gagcgacatc ggcaccagcc aactgaacgg 16440
gggcgccttc aattggagca gtctctggag cgggcttaag aatttcgggt ccacgcttaa 16500
aacctatggc agcaaggcgt ggaacagcac cacagggcag gcgctgaggg ataagctgaa 16560
agagcagaac ttccagcaga aggtggtcga tgggctcgcc tcgggcatca acggggtggt 16620
ggacctggcc aaccaggccg tgcagcggca gatcaacagc cgcctggacc cggtgccgcc 16680
cgccggctcc gtggagatgc cgcaggtgga ggaggagctg cctcccctgg acaagcgggg 16740
cgagaagcga ccccgccccg atgcggagga gacgctgctg acgcacacgg acgagccgcc 16800
cccgtacgag gaggcggtga aactgggtct gcccaccacg cggcccatcg cgcccctggc 16860
caccggggtg ctgaaacccg aaaagcccgc gaccctggac ttgcctcctc cccagccttc 16920
ccgcccctct acagtggcta agcccctgcc gccggtggcc gtggcccgcg cgcgacccgg 16980
gggcaccgcc cgccctcatg cgaactggca gagcactctg aacagcatcg tgggtctggg 17040
agtgcagagt gtgaagcgcc gccgctgcta ttaaacctac cgtagcgctt aacttgcttg 17100
tctgtgtgtg tatgtattat gtcgccgccg ccgctgtcca ccagaaggag gagtgaagag 17160
gcgcgtcgcc gagttgcaag atggccaccc catcgatgct gccccagtgg gcgtacatgc 17220
acatcgccgg acaggacgct tcggagtacc tgagtccggg tctggtgcag tttgcccgcg 17280
ccacagacac ctacttcagt ctggggaaca agtttaggaa ccccacggtg gcgcccacgc 17340
acgatgtgac caccgaccgc agccagcggc tgacgctgcg cttcgtgccc gtggaccgcg 17400
aggacaacac ctactcgtac aaagtgcgct acacgctggc cgtgggcgac aaccgcgtgc 17460
tggacatggc cagcacctac tttgacatcc gcggcgtgct ggatcggggc cctagcttca 17520
aaccctactc cggcaccgcc tacaacagtc tggcccccaa gggagcaccc aacacttgtc 17580
agtggacata taaagccgat ggtgaaactg ccacagaaaa aacctataca tatggaaatg 17640
cacccgtgca gggcattaac atcacaaaag atggtattca acttggaact gacaccgatg 17700
atcagccaat ctacgcagat aaaacctatc agcctgaacc tcaagtgggt gatgctgaat 17760
ggcatgacat cactggtact gatgaaaagt atggaggcag agctcttaag cctgatacca 17820
aaatgaagcc ttgttatggt tcttttgcca agcctactaa taaagaagga ggtcaggcaa 17880
atgtgaaaac aggaacaggc actactaaag aatatgacat agacatggct ttctttgaca 17940
acagaagtgc ggctgctgct ggcctagctc cagaaattgt tttgtatact gaaaatgtgg 18000
atttggaaac tccagatacc catattgtat acaaagcagg cacagatgac agcagctctt 18060
ctattaattt gggtcagcaa gccatgccca acagacctaa ctacattggt ttcagagaca 18120
actttatcgg gctcatgtac tacaacagca ctggcaatat gggggtgctg gccggtcagg 18180
cttctcagct gaatgctgtg gttgacttgc aagacagaaa caccgagctg tcctaccagc 18240
tcttgcttga ctctctgggt gacagaaccc ggtatttcag tatgtggaat caggcggtgg 18300
acagctatga tcctgatgtg cgcattattg aaaatcatgg tgtggaggat gaacttccca 18360
actattgttt ccctctggat gctgttggca gaacagatac ttatcaggga attaaggcta 18420
atggaactga tcaaaccaca tggaccaaag atgacagtgt caatgatgct aatgagatag 18480
gcaagggtaa tccattcgcc atggaaatca acatccaagc caacctgtgg aggaacttcc 18540
tctacgccaa cgtggccctg tacctgcccg actcttacaa gtacacgccg gccaatgtta 18600
ccctgcccac caacaccaac acctacgatt acatgaacgg ccgggtggtg gcgccctcgc 18660
tggtggactc ctacatcaac atcggggcgc gctggtcgct ggatcccatg gacaacgtga 18720
acccccttcaa ccaccaccgc aatgcggggc tgcgctaccg ctccatgctc ctgggcaacg 18780
ggcgctacgt gcccttccac atccaggtgc cccagaaatt tttcgccatc aagagcctcc 18840
tgctcctgcc cgggtcctac acctacgagt ggaacttccg caaggacgtc aacatgatcc 18900
tgcagagctc cctcggcaac gacctgcgca cggacggggc ctccatctcc ttcaccagca 18960
tcaacctcta cgccaccttc ttccccatgg cgcacaacac ggcctccacg ctcgaggcca 19020
tgctgcgcaa cgacaccaac gaccagtcct tcaacgacta cctctcggcg gccaacatgc 19080
tctaccccat cccggccaac gccaccaacg tgcccatctc catcccctcg cgcaactggg 19140
ccgccttccg cggctggtcc ttcacgcgtc tcaagaccaa ggagacgccc tcgctgggct 19200
ccgggttcga cccctacttc gtctactcgg gctccatccc ctacctcgac ggcaccttct 19260
acctcaacca caccttcaag aaggtctcca tcaccttcga ctcctccgtc agctggcccg 19320
gcaacgaccg gctcctgacg cccaacgagt tcgaaatcaa gcgcaccgtc gacggcgagg 19380
gctacaacgt ggcccagtgc aacatgacca aggactggtt cctggtccag atgctggccc 19440
actacaacat cggctaccag ggcttctacg tgcccgaggg ctacaaggac cgcatgtact 19500
ccttcttccg caacttccag cccatgagcc gccaggtggt ggacgaggtc aactacaagg 19560
actaccaggc cgtcaccctg gcctaccagc acaacaactc gggcttcgtc ggctacctcg 19620
cgcccaccat gcgccagggc cagccctacc ccgccaacta cccctacccg ctcatcggca 19680
agagcgccgt caccagcgtc acccagaaaa agttcctctg cgacagggtc atgtggcgca 19740
tcccccttctc cagcaacttc atgtccatgg gcgcgctcac cgacctcggc cagaacatgc 19800
tctatgccaa ctccgcccac gcgctagaca tgaatttcga agtcgacccc atggatgagt 19860
ccacccttct ctatgttgtc ttcgaagtct tcgacgtcgt ccgagtgcac cagccccacc 19920
gcggcgtcat cgaggccgtc tacctgcgca ccccccttctc ggccggtaac gccaccacct 19980
aagctcttgc ttcttgcaag ccatggccgc gggctccggc gagcaggagc tcagggccat 20040

20262014626 26 Feb 2026

catccgcgac ctgggctgcg ggccctactt cctgggcacc ttcgataagc gcttcccggg 20100
attcatggcc ccgcacaagc tggcctgcgc catcgtcaac acggccggcc gcgagaccgg 20160
gggcgagcac tggctggcct tcgcctggaa cccgcgctcg aacacctgct acctcttcga 20220
ccccttcggg ttctcggacg agcgcctcaa gcagatctac cagttcgagt acgagggcct 20280
gctgcgccgc agcgccctgg ccaccgagga ccgctgcgtc accctggaaa agtccaccca 20340
gaccgtgcag ggtccgcgct cggccgcctg cgggctcttc tgctgcatgt tcctgcacgc 20400
cttcgtgcac tggcccgacc gccccatgga caagaacccc accatgaact tgctgacggg 20460
ggtgcccaac ggcatgctcc agtcgcccca ggtggaaccc accctgcgcc gcaaccagga 20520
ggcgctctac cgcttcctca actcccactc cgcctacttt cgctcccacc gcgcgcgcat 20580
cgagaaggcc accgccttcg accgcatgaa tcaagacatg taaaccgtgt gtgtatgtta 20640
aatgtcttta ataaacagca ctttcatgtt acacatgcat ctgagatgat ttatttagaa 20700
atcgaaaggg ttctgccggg tctcggcatg gcccgcgggc agggacacgt tgcggaactg 20760
gtacttggcc agccacttga actcggggat cagcagtttg ggcagcgggg tgtcggggaa 20820
ggagtcggtc cacagcttcc gcgtcagttg cagggcgccc agcaggtcgg gcgcggagat 20880
cttgaaatcg cagttgggac ccgcgttctg cgcgcgggag ttgcggtaca cggggttgca 20940
gcactggaac accatcaggg ccgggtgctt cacgctcgcc agcaccgtcg cgtcggtgat 21000
gctctccacg tcgaggtcct cggcgttggc catcccgaag ggggtcatct tgcaggtctg 21060
ccttcccatg gtgggcacgc acccgggctt gtggttgcaa tcgcagtgca gggggatcag 21120
catcatctgg gcctggtcgg cgttcatccc cgggtacatg gccttcatga aagcctccaa 21180
ttgcctgaac gcctgctggg ccttggctcc ctcggtgaag aagaccccgc aggacttgct 21240
agagaactgg ttggtggcgc acccggcgtc gtgcacgcag cagcgcgcgt cgttgttggc 21300
cagctgcacc acgctgcgcc cccagcggtt ctgggtgatc ttggcccggt cggggttctc 21360
cttcagcgcg cgctgcccgt tctcgctcgc cacatccatc tcgatcatgt gctccttctg 21420
gatcatggtg gtcccgtgca ggcaccgcag cttgccctcg gcctcggtgc acccgtgcag 21480
ccacagcgcg cacccggtgc actcccagtt cttgtgggcg atctgggaat gcgcgtgcac 21540
gaagccctgc aggaagcggc ccatcatggt ggtcagggtc ttgttgctag tgaaggtcag 21600
cggaatgccg cggtgctcct cgttgatgta caggtggcag atgcggcggt acacctcgcc 21660
ctgctcgggc atcagctgga agttggcttt caggtcggtc tccacgcggt agcggtccat 21720
cagcatagtc atgatttcca taccttctc ccaggccgag acgatgggca ggctcatagg 21780
gttcttcacc atcatcttag cgctagcagc cgcggccagg gggtcgctct cgtccagggt 21840
ctcaaagctc cgcttgccgt ccttctcggt gatccgcacc ggggggtagc tgaagcccac 21900
ggccgccagc tcctcctcgg cctgtctttc gtcctcgctg tcctggctga cgtcctgcag 21960
gaccacatgc ttggtcttgc ggggtttctt cttgggcggc agcggcggcg gagatgttgg 22020
agatggcgag ggggagcgcg agttctcgct caccactact atctcttcct cttcttggtc 22080
cgaggccacg cggcggtagg tatgtctctt cgggggcaga ggcggaggcg acgggctctc 22140
gccgccgcga cttggcggat ggctggcaga gcccttccg cgttcggggg tgcgctcccg 22200
gcggcgctct gactgacttc ctccgcggcc ggccattgtg ttctcctagg gaggaacaac 22260
aagcatggag actcagccat cgccaacctc gccatctgcc cccaccgccg acgagaagca 22320
gcagcagcag aatgaaagct taaccgcccc gccgcccagc cccgccacct ccgacgcggc 22380
cgtcccagac atgcaagaga tggaggaatc catcgagatt gacctgggct atgtgacgcc 22440
cgcggagcac gaggaggagc tggcagtgcg cttttcacaa gaagagatac accaagaaca 22500
gccagagcag gaagcagaga atgagcagag tcaggctggg ctcgagcatg acggcgacta 22560
cctccacctg agcgggggggg aggacgcgct catcaagcat ctggcccggc aggccaccat 22620
cgtcaaggat gcgctgctcg accgcaccga ggtgcccctc agcgtggagg agctcagccg 22680
cgcctacgag ttgaacctct tctcgccgcg cgtgcccccc aagcgccagc ccaatggcac 22740
ctgcgagccc aacccgcgcc tcaacttcta cccggtcttc gcggtgcccg aggccctggc 22800
cacctaccac atctttttca agaaccaaaa gatccccgtc tcctgccgcg ccaaccgcac 22860
ccgcgccgac gccctttca acctgggtcc cggcgcccgc ctacctgata tcgcctcctt 22920
ggaagaggtt cccaagatct tcgagggtct gggcagcgac gagactcggg ccgcgaacgc 22980
tctgcaagga gaaggaggag agcatgagca ccacagcgcc ctggtcgagt tggaaggcga 23040
caacgcgcgg ctggcggtgc tcaaacgcac ggtcgagctg acccatttcg cctacccggc 23100
tctgaacctg ccccccaaag tcatgagcgc ggtcatggac caggtgctca tcaagcgcgc 23160
gtcgcccatc tccgaggacg agggcatgca agactccgag gagggcaagc ccgtggtcag 23220
cgacgagcag ctggcccggt ggctgggtcc taatgctagt ccccagagtt tggaagagcg 23280
gcgcaaactc atgatggccg tggtcctggt gaccgtggag ctggagtgcc tgcgccgctt 23340
cttcgccgac gcggagaccc tgcgcaaggt cgaggagaac ctgcactacc tcttcaggca 23400
cgggttcgtg cgccaggcct gcaagatctc caacgtggag ctgaccaacc tggtctccta 23460
catgggcatc ttgcacgaga accgcctggg gcagaacgtg ctgcacacca ccctgcgcgg 23520
ggaggcccgg cgcgactaca tccgcgactg cgtctacctc tacctctgcc acacctggca 23580
gacgggcatg ggcgtgtggc agcagtgtct ggaggagcag aacctgaaag agctctgcaa 23640
gctcctgcag aagaacctca agggtctgtg gaccgggttc gacgagcgca ccaccgcctc 23700
ggacctggcc gacctcattt tccccgagcg cctcaggctg acgctgcgca acggcctgcc 23760
cgactttatg agccaaagca tgttgcaaaa ctttcgctct ttcatcctcg aacgctccgg 23820
aatcctgccc gccacctgct ccgcgctgcc ctcggacttc gtgccgctga ccttccgcga 23880
gtgccccccg ccgctgtgga gccactgcta cctgctgcgc ctggccaact acctggccta 23940
ccactcggac gtgatcgagg acgtcagcgg cgagggcctg ctcgagtgcc actgccgctg 24000
caacctctgc acgccgcacc gctccctggc ctgcaacccc cagctgctga gcgagaccca 24060
gatcatcggc accttcgagt tgcaagggcc cagcgaaggc gagggttcag ccgccaaggg 24120
gggtctgaaa ctcaccccgg ggctgtggac ctcggcctac ttgcgcaagt tcgtgcccga 24180
ggactaccat cccttcgaga tcaggttcta cgaggaccaa tcccatccgc ccaaggccga 24240
gctgtcggcc tgcgtcatca cccagggggc gatcctggcc caattgcaag ccatccagaa 24300
atcccgccaa gaattcttgc tgaaaaaggg ccgcggggtc tacctcgacc cccagaccgg 24360
tgaggagctc aaccccggct tcccccagga tgccccgagg aaacaagaag ctgaaagtgg 24420
agctgccgcc cgtggaggat ttggaggaag actgggagaa cagcagtcag gcagaggagg 24480
aggagatgga ggaagactgg gacagcactc aggcagagga ggacagcctg caagacagtc 24540
tggaggaaga cgaggaggag gcagaggagg aggtggaaga agcagccgcc gccagaccgt 24600

20262014626 26 Feb 2026

cgtcctcggc gggggagaaa gcaagcagca cggataccat ctccgctccg ggtcggggtc 24660
ccgctcgacc acacagtaga tgggacgaga ccggacgatt cccgaacccc accacccaga 24720
ccggtaagaa ggagcggcag ggatacaagt cctggcgggg gcacaaaaac gccatcgtct 24780
cctgcttgca ggcctgcggg ggcaacatct ccttcacccg gcgctacctg ctcttccacc 24840
gcggggtgaa ctttccccgc aacatcttgc attactaccg tcacctccac agcccctact 24900
acttccaaga agaggcagca gcagcagaaa aagaccagca gaaaaccagc agctagaaaa 24960
tccacagcgg cggcagcagg tggactgagg atcgcggcga acgagccggc gcaaacccgg 25020
gagctgagga accggatctt tcccaccctc tatgccatct tccagcagag tcgggggcag 25080
gagcaggaac tgaaagtcaa gaaccgttct ctgcgctcgc tcacccgcag ttgtctgtat 25140
cacaagagcg aagaccaact tcagcgcact ctcgaggacg ccgaggctct cttcaacaag 25200
tactgcgcgc tcactcttaa agagtagccc gcgcccgccc agtcgcagaa aaaggcggga 25260
attacgtcac ctgtgccctt cgccctagcc gcctccaccc atcatcatga gcaaagagat 25320
tcccacgcct tacatgtgga gctaccagcc ccagatgggc ctggccgccg gtgccgccca 25380
ggactactcc acccgcatga attggctcag cgccgggccc gcgatgatct cacgggtgaa 25440
tgacatccgc gcccaccgaa accagatact cctagaacag tcagcgctca ccgccacgcc 25500
ccgcaatcac ctcaatccgc gtaattggcc cgccgccctg gtgtaccagg aaattcccca 25560
gcccacgacc gtactacttc cgcgagacgc ccaggccgaa gtccagctga ctaactcagg 25620
tgtccagctg gcgggcggcg ccaccctgtg tcgtcaccgc cccgctcagg gtataaagcg 25680
gctggtgatc cggggcagag gcacacagct caacgacgag gtggtgagct cttcgctggg 25740
tctgcgacct gacggagtct tccaactcgc cggatcgggg agatcttcct tcacgcctcg 25800
tcaggccgtc ctgactttgg agagttcgtc ctcgcagccc cgctcgggtg gcatcggcac 25860
tctccagttc gtggaggagt tcactccctc ggtctacttc aacccctttct ccggctcccc 25920
cggccactac ccggacgagt tcatcccgaa cttcgacgcc atcagcgagt cggtggacgg 25980
ctacgattga atgtcccatg gtggcgcagc tgacctagct cggcttcgac acctggacca 26040
ctgccgccgc ttccgctgct tcgctcggga tctcgccgag tttgcctact ttgagctgcc 26100
cgaggagcac cctcagggcc cggcccacgg agtgcggatc gtcgtcgaag ggggcctcga 26160
ctcccacctg cttcggatct tcagccagcg tccgatcctg gtcgagcgcg agcaaggaca 26220
gacccttctg actctgtact gcatctgcaa ccaccccggc ctgcatgaaa gtctttgttg 26280
tctgctgtgt actgagtata ataaaagctg agatcagcga ctactccgga cttccgtgtg 26340
ttcctgaatc catcaaccag tctttgttct tcaccgggaa cgagaccgag ctccagctcc 26400
agtgtaagcc ccacaagaag tacctcacct ggctgttcca gggctccccg atcgccgttg 26460
tcaaccactg cgacaacgac ggagtcctgc tgagcggccc tgccaacctt acttttcca 26520
cccgcagaag caagctccag ctcttccaac ccttcctccc cgggacctat cagtgcgtct 26580
cgggaccctg ccatcacacc ttccacctga tcccgaatac cacagcgtcg ctccccgcta 26640
ctaacaacca aactaacctc caccaacgcc accgtcgcga cggccacaat acatgcccat 26700
attagactat gaggccgagc cacagcgacc catgctcccc gctattagtt acttcaatct 26760
aaccggcgga gatgactgac ccactggcca acaacaacgt caacgacctt ctcctggaca 26820
tggacggccg cgcctcggag cagcgactcg cccaacttcg cattcgccag cagcaggaga 26880
gagccgtcaa ggagctgcag gatgcggtgg ccatccacca gtgcaagaga ggcatcttct 26940
gcctggtgaa acaggccaag atctcctacg aggtcactcc aaacgaccat cgcctctcct 27000
acgagctcct gcagcagcgc cagaagttca cctgcctggt cggagtcaac cccatcgtca 27060
tcacccagca gtctggcgat accaaggggt gcatccactg ctcctgcgac tcccccgact 27120
gcgtccacac tctgatcaag accctctgcg gcctccgcga cctcctcccc atgaactaat 27180
caccccctta tccagtgaaa taaagatcat attgatgatg attttacaga aataaaaaat 27240
aatcatttga tttgaaataa agatacaatc atattgatga tttgagttta acaaaaaaat 27300
aaagaatcac ttacttgaaa tctgatacca ggtctctgtc catgttttct gccaacacca 27360
cttcactccc ctcttcccag ctctggtact gcaggccccg gcgggctgca aacttcctcc 27420
acacgctgaa ggggatgtca aattcctcct gtccctcaat cttcatttta tcttctatca 27480
gatgtccaaa aagcgcgtcc gggtggatga tgacttcgac cccgtctacc cctacgatgc 27540
agacaacgca ccgaccgtgc ccttcatcaa ccccccccttc gtctcttcag atggattcca 27600
agagaagccc ctgggggtgt tgtccctgcg actggccgac cccgtcacca ccaagaacgg 27660
ggaaatcacc ctcaagctgg gagagggggt ggacctcgat tcctcgggaa aactcatctc 27720
caacacggcc accaaggccg ccgcccctct cagtttttcc aacaacacca tttcccttaa 27780
catggatcac ccctttttaca ctaaagatgg aaaattatcc ttacaagttt ctccaccatt 27840
aaatatactg agaacaagca ttctaaacac actagcttta ggttttggat caggtttagg 27900
actccgtggc tctgccttgg cagtacagtt agtctctcca cttacatttg atactgatgg 27960
aaacataaag cttaccttag acagaggttt gcatgttaca acaggagatg caattgaaag 28020
caacataagc tgggctaaag gtttaaaatt tgaagatgga gccatagcaa ccaacattgg 28080
aaatgggtta gagtttggaa gcagtagtac agaaacaggt gttgatgatg cttacccaat 28140
ccaagttaaa cttggatctg gccttagctt tgacagtaca ggagccataa tggctggtaa 28200
caaagaagac gataaactca ctttgtggac aacacctgat ccatcaccaa actgtcaaat 28260
actcgcagaa aatgatgcaa aactaacact ttgcttgact aaatgtggta gtcaaatact 28320
ggccactgtg tcagtcttag ttgtaggaag tggaaaccta aaccccatta ctggcaccgt 28380
aagcagtgct caggtgtttc tacgttttga tgcaaacggt gttcttttaa cagaacattc 28440
tacactaaaa aaatactggg ggtataggca gggagatagc atagatggca ctccatatac 28500
caatgctgta ggattcatgc ccaatttaaa agcttatcca aagtcacaaa gttctactac 28560
taaaaataat atagtagggc aagtatacat gaatggagat gtttcaaaac ctatgcttct 28620
cactataacc ctcaatggta ctgatgacag caacagtaca tattcaatgt cattttcata 28680
cacctggact aatggaagct atgttggagc aacatttggg gctaactctt ataccttctc 28740
atacatcgcc caagaatgaa cactgtatcc caccctgcat gccaaccctt cccaccccac 28800
tctgtggaac aaactctgaa acacaaaata aaataaagtt caagtgtttt attgattcaa 28860
cagttttaca ggattcgagc agttattttt cctccaccct cccaggacat ggaatacacc 28920
accctctccc cccgcacagc cttgaacatc tgaatgccat tggtgatgga catgcttttg 28980
gtctccacgt tccacacagt ttcagagcga gccagtctcg ggtcggtcag ggagatgaaa 29040
ccctccgggc actcccgcat ctgcacctca cagctcaaca gctgaggatt gtcctcggtg 29100
gtcgggatca cggttatctg gaagaagcag aagagcggcg gtgggaatca tagtccgcga 29160

2026201462 26 Feb 2026

		acgggatcgg ccggtggtgt cgcatcaggc cccgcagcag tcgctgccgc cgccgctccg 29220 tcaagctgct gctcaggggg tccgggtcca gggactccct cagcatgatg cccacggccc 29280 tcagcatcag tcgtctggtg cggcgggcgc agcagcgcat gcggatctcg ctcaggtcgc 29340 tgcagtacgt gcaacacaga accaccaggt tgttcaacag tccatagttc aacacgctcc 29400 agccgaaact catcgcggga aggatgctac ccacgtggcc gtcgtaccag atcctcaggt 29460 aaatcaagtg gtgccccctc cagaacacgc tgcccacgta catgatctcc ttgggcatgt 29520 ggcggttcac cacctcccgg taccacatca ccctctggtt gaacatgcag ccccggatga 29580 tcctgcggaa ccacagggcc agcaccgccc cgcccgccat gcagcgaaga gaccccgggt 29640 cccggcaatg gcaatggagg acccaccgct cgtacccgtg gatcatctgg gagctgaaca 29700 agtctatgtt ggcacagcac aggcatatgc tcatgcatct cttcagcact ctcaactcct 29760 cgggggtcaa aaccatatcc cagggcacgg ggaactcttg caggacagcg aaccccgcag 29820 aacagggcaa tcctcgcaca gaacttacat tgtgcatgga cagggtatcg caatcaggca 29880 gcaccgggtg atcctccacc agagaagcgc gggtctcggt ctcctcacag cgtggtaagg 29940 gggccggccg atacgggtga tggcgggacg cggctgatcg tgttcgcgac cgtgtcatga 30000 tgcagttgct ttcggacatt ttcgtacttg ctgtagcaga acctggtccg ggcgctgcac 30060 accgatcgcc ggcggcggtc tcggcgcttg gaacgctcgg tgttgaaatt gtaaaacagc 30120 cactctctca gaccgtgcag cagatctagg gcctcaggag tgatgaagat cccatcatgc 30180 ctgatggctc tgatcacatc gaccaccgtg gaatgggcca gacccagcca gatgatgcaa 30240 ttttgttggg tttcggtgac ggcgggggag ggaagaacag gaagaaccat gattaacttt 30300 taatccaaac ggtctcggag tacttcaaaa tgaagatcgc ggagatggca cctctcgccc 30360 ccgctgtgtt ggtggaaaat aacagccagg tcaaaggtga tacggttctc gagatgttcc 30420 acggtggctt ccagcaaagc ctccacgcgc acatccagaa acaagacaat agcgaaagcg 30480 ggagggttct ctaattcctc aatcatcatg ttacactcct gcaccatccc cagataattt 30540 tcatttttcc agccttgaat gattcgaact agttcgtgag gtaaatccaa gccagccatg 30600 ataaagagct cgcgcagagc gccctccacc ggcattctta agcacaccct cataattcca 30660 agatattctg ctcctggttc acctgcagca gattgacaag cggaatatca aaatctctgc 30720 cgcgatccct gagctcctcc ctcagcaata actgtaagta ctctttcata tcctctccga 30780 aatttttagc cataggacca ccaggaataa gattagggca agccacagta cagataaacc 30840 gaagtcctcc ccagtgagca ttgccaaatg caagactgct ataagcatgc tggctagacc 30900 cggtgatatc ttccagataa ctggacagaa aatcgcccag gcaattttta agaaaatcaa 30960 caaaagaaaa atcctccagg tggacgttta gagcctcggg aacaacgatg aagtaaatgc 31020 aagcggtgcg ttccagcatg gttagttagc tgatctgtag aaaaaacaaa aatgaacatt 31080 aaaccatgct agcctggcga acaggtgggt aaatcgttct ctccagcacc aggcaggcca 31140 cggggtctcc ggcgcgaccc tcgtaaaaat tgtcgctatg attgaaaacc atcacagaga 31200 gacgttcccg gtggccggcg tgaatgattc gacaagatga atacaccccc ggaacattgg 31260 cgtccgcgag tgaaaaaaag cgcccgagga agcaataagg cactacaatg ctcagtctca 31320 agtccagcaa agcgatgcca tgcggatgaa gcacaaaatt ctcaggtgcg tacaaaatgt 31380 aattactccc ctcctgcaca ggcagcaaag cccccgatcc ctccaggtac acatacaaag 31440 cctcagcgtc catagcttac cgagcagcag cacacaacag gcgcaagagt cagagaaagg 31500 ctgagctcta acctgtccac ccgctctctg ctcaatatat agcccagatc tacactgacg 31560 taaaggccaa agtctaaaaa tacccgccaa ataatcacac acgcccagca cacgcccaga 31620 aaccggtgac acactcaaaa aaatacgcgc acttcctcaa acgcccaaaa ctgccgtcat 31680 ttccgggttc ccacgctacg tcatcaaaac acgactttca aattccgtcg accgttaaaa 31740 acgtcacccg ccccgcccct aacggtcgcc cgtctctcag ccaatcagcg ccccgcatcc 31800 ccaaattcaa acacctcatt tgcatattaa cgcgcacaaa aagtttgagg tatattattg 31860 atgatgg 31867
3-12	**Sequences**	
3-12-1	Sequence Number [ID]	12
3-12-2	Molecule Type	DNA
3-12-3	Length	32788
3-12-4	Features	**misc_feature 1..32788**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..32788
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-12-5	Residues	ccatcttcaa taatatacct caaacttttt gtgcgcgtta atatgcaaat gaggcgtttg 60 aatttgggga ggaagggcgg tgattggtcg agggatgagc gaccgttagg ggcggggcga 120 gtgacgtttt gatgacgtgg ttgcgaggag gagccagttt gcaagttctc gtgggaaaag 180 tgacgtcaaa cgaggtgtgg tttgaacacg gaaatactca attttcccgc gctctctgac 240 aggaaatgag gtgtttctgg gcggatgcaa gtgaaaacgg gccattttcg cgcgaaaact 300 gaatgaggaa gtgaaaatct gagtaatttc gcgtttatgg cagggaggag tatttgccga 360 gggccgagta gactttgacc gattacgtgg gggtttcgat taccgtgttt ttcacctaaa 420 tttccgcgta cggtgtcaaa gtccggtgtt tttacgtagg tgtcagctga tcgccagggt 480 atttaaacct gcgctctcca gtcaagaggc cactcttgag tgccagcgag aagagttttc 540 tcctccgcgc cgcgagtcag atctacactt tgaaagtagg gataacaggg taatgacatt 600 gattattgac tagttgttaa tagtaatcaa ttacggggtc attagttcat agcccatata 660 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 720 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 780 attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt 840 atcatatgcc aagtccgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 900 atgcccagta catgacctta cgggactttc ctacttggca gtacatctac gtattagtca 960 tcgctattac catggtgatg cggttttggc agtacaccaa tgggcgtgga tagcggtttg 1020 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 1080 aaaatcaacg ggactttcca aaatgtcgta ataaccccgc cccgttgacg caaatgggcg 1140

20262014626 26 Feb 2026

```
gtaggcgtgt acggtgggag gtctatataa gcagagctcg tttagtgaac cgtcagatcg 1200
cctggaacgc catccacgct gttttgacct ccatagaaga cagcgatcgc gccaccatgg 1260
ccgggatgtt ccaggcactg tccgaaggct gcacacccta tgatattaac cagatgctga 1320
atgtcctggg agaccaccag gtctctggcc tggagcagct ggagagcatc atcaacttcg 1380
agaagctgac cgagtggaca agctccaatg tgatgcctat cctgtcccca ctgaccaagg 1440
gcatcctggg cttcgtgttt accctgacag tgccttctga gcggggcctg tcttgcatca 1500
gcgaggcaga cgcaaccaca ccagagtccg ccaatctggg cgaggagatc ctgtctcagc 1560
tgtacctgtg gccccgggtg acatatcact ccccttctta cgcctatcac cagttcgagc 1620
ggagagccaa gtacaagaga cacttcccag gctttggcca gtctctgctg ttcggctacc 1680
ccgtgtacgt gttcggcgat tgcgtgcagg gcgactggga tgccatccgg tttagatact 1740
gcgcaccacc tggatatgca ctgctgaggt gtaacgacac caattattcc gccctgctgg 1800
cagtgggcgc cctggagggc cctcgcaatc aggattggct gggcgtgcca aggcagctgg 1860
tgacacgcat gcaggccatc cagaacgcag gcctgtgcac cctggtggca atgctggagg 1920
agacaatctt ctggctgcag gcctttctga tggccctgac cgacagcggc cccaagacaa 1980
acatcatcgt ggattcccag tacgtgatgg gcatctccaa gccttctttc caggagtttg 2040
tggactggga gaacgtgagc ccagagctga attccaccga tcagccattc tggcaggcag 2100
gaatcctggc aaggaacctg gtgcctatgg tggccacagt gcagggccag aatctgaagt 2160
accagggcca gagcctggtc atcagcgcct ccatcatcgt gtttaacctg ctggagctgg 2220
agggcgacta tcgggacgat ggcaacgtgt gggtgcacac cccactgagc cccagaacac 2280
tgaacgcctg ggtgaaggcc gtggaggaga agaagggcat cccagtgcac ctggagctgg 2340
cctccatgac caatatggag ctgatgtcta gcatcgtgca ccagcaggtg aggacatacg 2400
gacccgtgtt catgtgcctg ggaggcctgc tgaccatggt ggcaggagcc gtgtggctga 2460
cagtgcgggt gctggagctg ttcagagccg cccagctggc caacgatgtg gtgctgcaga 2520
tcatggagct gtgcggagca gcctttcgcc aggtgtgcca caccacagtg ccatggccca 2580
atgcctccct gacccccaag tggaacaatg agacaacaca gcctcagatc gccaactgta 2640
gcgtgtacga cttcttcgtg tggctgcact actatagcgt gagggatacc ctgtggcccc 2700
gcgtgacata ccacatgaat aagtacgcct atcacatgct ggagaggcgc gccaagtata 2760
agagaggccc tggcccaggc gcaaagtttg tggcagcatg gaccctgaag gccgccgccg 2820
gccccggccc cggccagtat atcaaggcta acagtaagtt cattggaatc acagagctgg 2880
gacccggacc tggataatga gtttaaactc ccatttaaat gtgagggtta atgcttcgag 2940
cagacatgat aagatacatt gatgagtttg gacaaaccac aactagaatg cagtgaaaaa 3000
aatgctttat ttgtgaaatt tgtgatgcta ttgctttatt tgtaaccatt ataagctgca 3060
ataaacaagt taacaacaac aattgcattc attttatgtt tcaggttcag ggggagatgt 3120
gggaggtttt ttaaagcaag taaaacctct acaaatgtgg taaaataact ataacggtcc 3180
taaggtagcg agtgagtagt gttctggggc gggggaggac ctgcatgagg gccagaataa 3240
ctgaaatctg tgcttttctg tgtgttgcag cagcatgagc ggaagcggct cctttgaggg 3300
aggggtattc agcccttatc tgacggggcg tctcccctcc tgggcgggag tgcgtcagaa 3360
tgtgatggga tccacggtgg acggccggcc cgtgcagccc gcgaactctt caaccctgac 3420
ctatgcaacc ctgagctctt cgtcgttgga cgcagctgcc gccgcagctg ctgcatctgc 3480
cgccagcgcc gtgcgcggaa tggccatggg cgccggctac tacggcactc tggtggccaa 3540
ctcgagttcc accaataatc ccgccagcct gaacgaggag aagctgttgc tgctgatggc 3600
ccagctcgag gccttgaccc agcgcctggg cgagctgacc cagcaggtgg ctcagctgca 3660
ggagcagacg cgggccgcgg ttgccacggt gaaatccaaa taaaaaatga atcaataaat 3720
aaacggagac ggttgttgat tttaacacag agtctgaatc tttatttgat ttttcgcgcg 3780
cggtaggccc tggaccaccg gtctcgatca ttgagcaccc ggtggatctt ttccaggacc 3840
cggtagaggt gggcttggat gttgaggtac atgggcatga gcccgtcccg ggggtggagg 3900
tagctccatt gcagggcctc gtgctcgggg gtggtgttgt aaatcaccca gtcatagcag 3960
gggcgcaggg catggtgttg cacaatatct ttgaggagga gactgatggc cacgggcagc 4020
cctttggtgt aggtgtttac aaatctgttg agctgggagg gatgcatgcg gggggagatg 4080
aggtgcatct tggcctggat cttgagattg gcgatgttac cgcccagatc ccgcctgggg 4140
ttcatgttgt gcaggaccac cagcacggtg tatccggtgc acttggggaa tttatcatgc 4200
aacttggaag ggaaggcgtg aaagaatttg gcgacgcctt tgtgcccgcc caggttttcc 4260
atgcactcat ccatgatgat ggcgatgggc ccgtgggcgg cggcctgggc aaagacgttt 4320
cgggggtcgg acacatcata gttgtggtcc tgggtgaggt catcataggc cattttaatg 4380
aatttggggc ggagggtgcc ggactggggg acaaaggtac cctcgatccc gggggcgtag 4440
ttcccctcac agatctgcat ctcccaggct ttgagctcgg agggggggat catgtccacc 4500
tgcggggcga taaagaacac ggtttccggg gcgggggaga tgagctgggc cgaaagcaag 4560
ttccggagca gctgggactt gccgcagccg gtggggccgt agatgacccc gatgaccggc 4620
tgcaggtggt agttgaggga gagacagctg ccgtcctccc ggaggagggg ggccacctcg 4680
ttcatcatct cgcgcacgtg catgttctcg cgcaccagtt ccgccaggag gcgctctccc 4740
cccagggata ggagctcctg gagcgaggcg aagtttttca gcggcttgag tccgtcggcc 4800
atgggcattt tggagagggt ttgttgcaag agttccaggc ggtcccagag ctcggtgatg 4860
tgctctacgg catctcgatc cagcagacct cctcgtttcg cgggttggga cggctgcggg 4920
agtagggcac cagacgatgg gcgtccagcg cagccagggt ccggtccttc cagggtcgca 4980
gcgtccgcgt cagggtggtc tccgtcacgg tgaaggggtg cgcgccgggc tgggcgcttg 5040
cgagggtgcg cttcaggctc atccggctgg tcgaaaaccg ctcccgatcg gcgccctgcg 5100
cgtcggccag gtagcaattg accatgagtt cgtagttgag cgcctcggcc gcgtggcctt 5160
tggcgcggag cttacctttg gaagtctgcc cgcaggcggg acagaggagg gacttgaggg 5220
cgtagagctt gggggcgagg aagacggact cgggggcgta ggcgtccgcg ccgcagtggg 5280
cgcagacggt ctcgcactcc acgagccagg tgaggtcggg ctggtcgggg tcaaaaacca 5340
gtttcccgcc gttctttttg atgcgtttct tacctttggt ctccatgagc tcgtgtcccc 5400
gctgggtgac aaagaggctg tccgtgtccc cgtagaccga ctttatgggc cggtcctcga 5460
gcggtgtgcc gcggtcctcc tcgtagagga accccgccca ctccgagacg aaagcccggg 5520
tccaggccag cacgaaggag gccacgtggg acgggtagcg gtcgttgtcc accagcgggt 5580
ccacctttc cagggtatgc aaacacatgt ccccctcgtc cacatccagg aaggtgattg 5640
gcttgtaagt gtaggccacg tgaccggggg tcccggccgg gggggtataa aagggtgcgg 5700
```

20262014626 26 Feb 2026

gtccctgctc gtcctcactg tcttccggat cgctgtccag gagcgccagc tgttggggta 5760
ggtattccct ctcgaaggcg ggcatgacct cggcactcag gttgtcagtt tctagaaacg 5820
aggaggattt gatattgacg gtgccggcgg agatgccttt caagagcccc tcgtccatct 5880
ggtcagaaaa gacgatcttt ttgttgtcga gcttggtggc gaaggagccg tagagggcgt 5940
tggagaggag cttggcgatg gagcgcatgg tctggttttt ttccttgtcg gcgcgctcct 6000
tggcggcgat gttgagctgc acgtactcgc gcgccacgca cttccattcg gggaagacgg 6060
tggtcagctc gtcgggcacg attctgacct gccagccccg attatgcagg gtgatgaggt 6120
ccacactggt ggccacctcg ccgcgcaggg gctcattagt ccagcagagg cgtccgccct 6180
tgcgcgagca gaaggggggc agggggtcca gcatgacctc gtcgggggggg tcggcatcga 6240
tggtgaagat gccgggcagg aggtcggggt caaagtagct gatggaagtg gccagatcgt 6300
ccagggcagc ttgccattcg cgcacggcca gcgcgctctc gtagggactg aggggcgtgc 6360
cccagggcat gggatgggta agcgcggagg cgtacatgcc gcagatgtcg tagacgtaga 6420
ggggctcctc gaggatgccg atgtaggtgg ggtagcagcg ccccccgcgg atgctggcgc 6480
gcacgtagtc atacagctcg tgcgaggggg cgaggagccc cgggcccagg ttggtgcgac 6540
tgggcttttc ggcgcggtag acgatctggc ggaaaatggc atgcgagttg gaggagatgg 6600
tgggcctttg gaagatgttg aagtgggcgt ggggcagtcc gaccgagtcg cggatgaagt 6660
gggcgtagga gtcttgcagc ttggcgacga gctcggcggt gactaggacg tccagagcgc 6720
agtagtcgag ggtctcctgg atgatgtcat acttgagctg tccctttttgt ttccacagct 6780
cgcggttgag aaggaactct tcgcggtcct tccagtactc ttcgaggggg aacccgtcct 6840
gatctgcacg gtaagagcct agcatgtaga actggttgac ggccttgtag gcgcagcagc 6900
ccttctccac ggggagggcg taggcctggg cggccttgcg cagggaggtg tgcgtgaggg 6960
cgaaagtgtc cctgaccatg accttgagga actggtgctt gaagtcgata tcgtcgcagc 7020
ccccctgctc ccagagctgg aagtccgtgc gcttcttgta ggcggggttg ggcaaagcga 7080
aagtaacatc gttgaagagg atcttgcccg cgcggggcat aaagttgcga gtgatgcgga 7140
aaggttgggg cacctcggcc cggttgttga tgacctgggc ggcgagcacg atctcgtcga 7200
agccgttgat gttgtggccc acgatgtaga gttccacgaa tcgcggacgg cccttgacgt 7260
ggggcagttt cttgagctcc tcgtaggtga gctcgtcggg gtcgctgagc ccgtgctgct 7320
cgagcgccca gtcggcgaga tgggggttgg cgcggaggaa ggaagtccag agatccacgg 7380
ccagggcggt ttgcagacgg tcccggtact gacggaactg ctgcccgacg gccatttttt 7440
cgggggtgac gcagtagaag gtgcgggggt ccccgtgcca gcgatcccat ttgagctgga 7500
gggcgagatc gagggcgagc tcgacgagcc ggtcgtcccc ggagagtttc atgaccagca 7560
tgaaggggac gagctgcttg ccgaaggacc ccatccaggt gtaggtttcc acatcgtagg 7620
tgaggaagag cctttcggtg cgaggatgcg agccgatggg gaagaactgg atctcctgcc 7680
accaattgga ggaatggctg ttgatgtgat ggaagtagaa atgccgacgg cgcgccgaac 7740
actcgtgctt gtgtttatac aagcggccac agtgctcgca acgctgcacg ggatgcacgt 7800
gctgcacgag ctgtacctga gttcctttga cgaggaattt cagtgggaag tggagtcgtg 7860
gcgcctgcat ctcgtgctgt actacgtcgt ggtggtcggc ctggccctct tctgcctcga 7920
tggtggtcat gctgacgagc ccgcgcggga ggcaggtcca gacctcggcg cgagcgggtc 7980
ggagagcgag gacgagggcg cgcaggccgg agctgtccag ggtcctgaga cgctgcggag 8040
tcaggtcagt gggcagcggc ggcgcgcggt tgacttgcag gagtttttcc agggcgcgcg 8100
ggaggtccag atggtacttg atctccaccg cgccattggt ggcgacgtcg atggcttgca 8160
gggtcccgtg cccctggggt gtgaccaccg tcccccgttt cttcttgggc ggctggggcg 8220
acgggggcgg tgcctcttcc atggttagaa gcggcggcga ggacgcgcgc cgggcggcag 8280
gggcggctcg gggcccggag gcaggggcgg caggggcacg tcggcgccgc gcgcgggtag 8340
gttctggtac tgcgcccgga gaagactggc gtgagcgacg acgcgacggt tgacgtcctg 8400
gatctgacgc ctctgggtga aggccacggg acccgtgagt ttgaacctga aagagagttc 8460
gacagaatca atctcggtat cgttgacggc ggcctgccgc aggatctctt gcacgtcgcc 8520
cgagttgtcc tggtaggcga tctcggtcat gaactgctcg atctcctcct cttgaaggtc 8580
tccgcggccg gcgcgctcca cggtggccgc gaggtcgttg gagatgcggc ccatgagctg 8640
cgagaaggcg ttcatgcccg cctcgttcca gacgcggctg tagaccacga cgccctcggg 8700
atcgcgggcg cgcatgacca cctgggcgag gttgagctcc acgtggcgcg tgaagaccgc 8760
gtagttgcag aggcgctggt agaggtagtt gagcgtggtg gcgatgtgct cggtgacgaa 8820
gaaatacatg atccagcggc ggagcggcat ctcgctgacg tcgcccagcg cctccaaacg 8880
ttccatggcc tcgtaaaagt ccacggcgaa gttgaaaaac tgggagttgc gcgccgagac 8940
ggtcaactcc tcctccagaa gacggatgag ctcggcgatg gtggcgcgca cctcgcgctc 9000
gaaggccccc gggagttcct ccacttcctc ttcttcctcc tccactaaca tctcttctac 9060
ttcctcctca ggcggcagtg gtggcggggg agggggcctg cgtcgccggc ggcgcacggg 9120
cagacggtcg atgaagcgct cgatggtctc gccgcgccgg cgtcgcatgg tctcggtgac 9180
ggcgcgcccg tcctcgcggg gccgcagcgt gaagacgccg ccgcgcatct ccaggtggcc 9240
ggggggggtcc ccgttgggca gggagagggc gctgacgatg catcttatca attgccccgt 9300
agggactccg cgcaaggacc tgagcgtctc gagatccacg ggatctgaaa accgctgaac 9360
gaaggcttcg agccagtcgc agtcgcaagg taggctgagc acggtttctt ctggcgggtc 9420
atgttggttg ggagcggggc gggcgatgct gctggtgatg aagttgaaat aggcggttct 9480
gagacggcgg atggtggcga ggagcaccag gtctttgggc ccggcttgct ggatgcgcag 9540
acggtcggcc atgccccagg cgtggtcctg acacctggcc aggtccttgt agtagtcctg 9600
catgagccgc tccacgggca cctcctcctc gcccgcgcgg ccgtgcatgc gcgtgagccc 9660
gaagccgcgc tggggctgga cgagcgccag gtcggcgacg acgcgctcgg cgaggatggc 9720
ttgctggatc tgggtgaggg tggtctggaa gtcatcaaag tcgacgaagc ggtggtaggc 9780
tccggtgttg atggtgtagg agcagttggc catgacggac cagttgacgg tctggtggcc 9840
cggacgcacg agctcgtggt acttgaggcg cgagtaggcg cgcgtgtcga agatgtagtc 9900
gttgcaggtg cgcaccaggt actggtagcc gatgaggaag tgcggcggcg gctggcggta 9960
gagcggccat cgctcggtgg cgggggcgcc gggcgcgagg tcctcgagca tggtgcggtg 10020
gtagccgtag atgtacctgg acatccaggt gatgccggcg gcggtggtgg aggcgcgcgg 10080
gaactcgcgg acgcggttcc agatgttgcg cagcggcagg aagtagttca tggtgggcac 10140
ggtctggccc gtgaggcgcg cgcagtcgtg gatgctctat acgggcaaaa acgaaagcgg 10200
tcagcggctc gactccgtgg cctggaggct aagcgaacgg gttgggctgc gcgtgtaccc 10260

20262014626 26 Feb 2026

cggttcgaat ctcgaatcag gctggagccg cagctaacgt ggtattggca ctcccgtctc 10320
gacccaagcc tgcaccaacc ctccaggata cggaggcggg tcgttttgca actttttttt 10380
ggaggccgga tgagactagt aagcgcggaa agcggccgac cgcgatggct cgctgccgta 10440
gtctggagaa gaatcgccag ggttgcgttg cggtgtgccc cggttcgagg ccggccggat 10500
tccgcggcta acgagggcgt ggctgccccg tcgtttccaa gaccccatag ccagccgact 10560
tctccagtta cggagcgagc ccctcttttg ttttgtttgt ttttgccaga tgcatcccgt 10620
actgcggcag atgcgccccc accaccctcc accgcaacaa cagccccctc cacagccggc 10680
gcttctgccc ccgccccagc agcaacttcc agccacgacc gccgcggccg ccgtgagcgg 10740
ggctggacag agttatgatc accagctggc cttggaagag ggcgaggggc tggcgcgcct 10800
gggggcgtcg tcgccggagc ggcacccgcg cgtgcagatg aaaagggacg ctcgcgaggc 10860
ctacgtgccc aagcagaacc tgttcagaga caggagcggc gaggagcccg aggagatgcg 10920
cgcggcccgg ttccacgcgg ggcgggagct gcggcgcggc ctggaccgaa agagggtgct 10980
gagggacgag gatttcgagg cggacgagct gacggggatc agccccgcgc gcgcgcacgt 11040
ggccgcggcc aacctggtca cggcgtacga gcagaccgtg aaggaggaga gcaacttcca 11100
aaaatccttc aacaaccacg tgcgcaccct gatcgcgcgc gaggaggtga ccctgggcct 11160
gatgcacctg tgggacctgc tggaggccat cgtgcagaac cccaccagca agccgctgac 11220
ggcgcagctg ttcctggtgg tgcagcatag tcgggacaac gaagcgttca gggaggcgct 11280
gctgaatatc accgagcccg agggccgctg gctcctggac ctggtgaaca ttctgcagag 11340
catcgtggtg caggagcgcg ggctgccgct gtccgagaag ctggcggcca tcaacttctc 11400
ggtgctgagt ttgggcaagt actacgctag gaagatctac aagaccccgt acgtgcccat 11460
agacaaggag gtgaagatcg acgggtttta catgcgcatg accctgaaag tgctgaccct 11520
gagcgacgat ctgggggtgt accgcaacga caggatgcac cgtgcggtga gcgccagcag 11580
gcggcgcgag ctgagcgacc aggagctgat gcatagtctg cagcgggccc tgaccggggc 11640
cgggaccgag ggggagagct actttgacat gggcgcggac ctgcactggc agcccagccg 11700
ccgggccttg gaggcggcgg caggacccta cgtagaagag gtggacgatg aggtggacga 11760
ggagggcgag tacctggaag actgatggcg cgaccgtatt tttgctagat gcaacaacaa 11820
cagccacctc ctgatcccgc gatgcgggcg gcgctgcaga gccagccgtc cggcattaac 11880
tcctcggacg attggaccca ggccatgcaa cgcatcatgg cgctgacgac ccgcaacccc 11940
gaagccttta gacagcagcc ccaggccaac cggctctcgg ccatcctgga ggccgtggtg 12000
ccctcgcgct ccaaccccac gcacgagaag gtcctggcca tcgtgaacgc gctggtggag 12060
aacaaggcca tccgcggcga cgaggccggc ctggtgtaca acgcgctgct ggagcgcgtg 12120
gcccgctaca acagcaccaa cgtgcagacc aacctggacc gcatggtgac cgacgtgcgc 12180
gaggccgtgg cccagcgcga gcggttccac cgcgagtcca acctgggatc catggtggcg 12240
ctgaacgcct tcctcagcac ccagcccgcc aacgtgcccc ggggccagga ggactacacc 12300
aacttcatca gcgccctgcg cctgatggtg accgaggtgc cccagagcga ggtgtaccag 12360
tccgggccgg actacttctt ccagaccagt cgccagggct tgcagaccgt gaacctgagc 12420
caggctttca agaacttgca gggcctgtgg ggcgtgcagg ccccggtcgg ggaccgcgcg 12480
acggtgtcga gcctgctgac gccgaactcg cgcctgctgc tgctgctggt ggccccccttc 12540
acggacagcg gcagcatcaa ccgcaactcg tacctgggct acctgattaa cctgtaccgc 12600
gaggccatcg gccaggcgca cgtggacgag cagacctacc aggagatcac ccacgtgagc 12660
cgcgccctgg gccaggacga cccgggcaac ctggaagcca ccctgaactt tttgctgacc 12720
aaccggtcgc agaagatccc gccccagtac gcgctcagca ccgaggagga gcgcatcctg 12780
cgttacgtgc agcagagcgt gggcctgttc ctgatgcagg agggggccac ccccagcgcc 12840
gcgctcgaca tgaccgcgcg caacatggag cccagcatgt acgccagcaa ccgcccgttc 12900
atcaataaac tgatggacta cttgcatcgg gcggccgcca tgaactctga ctatttcacc 12960
aacgccatcc tgaatcccca ctggctcccg ccgccggggt tctacacggg cgagtacgac 13020
atgcccgacc ccaatgacgg gttcctgtgg gacgatgtgg acagcagcgt gttcctcccc 13080
cgaccgggtg ctaacgagcg ccccttgtgg aagaaggaag gcagcgaccg acgcccgtcc 13140
tcggcgctgt ccggccgcga gggtgctgcc gcggcggtgc ccgaggccgc cagtcctttc 13200
ccgagcttgc ccttctcgct gaacagtatc cgcagcagcg agctgggcag gatcacgcgc 13260
ccgcgcttgc tgggcgaaga ggagtacttg aatgactcgc tgttgagacc cgagcgggag 13320
aagaacttcc ccaataacgg gatagaaagc ctggtggaca agatgagccg ctggaagacg 13380
tatgcgcagg agcacaggga cgatccccgg gcgtcgcagg gggccacgag ccggggcagc 13440
gccgcccgta aacgccggtg gcacgacagg cagcggggac agatgtggga cgatgaggac 13500
tccgccgacg acagcagcgt gttggacttg ggtgggagtg gtaacccgtt cgctcacctg 13560
cgcccccgta tcgggcgcat gatgtaagag aaaccgaaaa taaatgatac tcaccaaggc 13620
catggcgacc agcgtgcgtt cgtttcttct ctgttgttgt tgtatctagt atgatgaggc 13680
gtgcgtaccc ggagggtcct cctccctcgt acgagagcgt gatgcagcag gcgatggcgg 13740
cggcggcgat gcagcccccg ctggaggctc cttacgtgcc cccgcggtac ctggcgccta 13800
cggaggggcg gaacagcatt cgttactcgg agctggcacc cttgtacgat accacccggt 13860
tgtacctggt ggacaacaag tcggcggaca tcgcctcgct gaactaccag aacgaccaca 13920
gcaacttcct gaccaccgtg gtgcagaaca atgacttcac ccccacggag gccagcaccc 13980
agaccatcaa ctttgacgag cgctcgcggt ggggcggcca gctgaaaacc atcatgcaca 14040
ccaacatgcc caacgtgaac gagttcatgt acagcaacaa gttcaaggcg cgggtgatgg 14100
tctcccgcaa gacccccaat ggggtgacag tgacagagga ttatgatggt agtcaggatg 14160
agctgaagta tgaatgggtg gaatttgagc tgcccgaagg caacttctcg gtgaccatga 14220
ccatcgacct gatgaacaac gccatcatcg acaattactt ggcggtgggg cggcagaacg 14280
gggtgctgga gagcgacatc ggcgtgaagt tcgacactag gaacttcagg ctgggctggg 14340
accccgtgac cgagctggtc atgcccgggg tgtacaccaa cgaggctttc catcccgata 14400
ttgtcttgct gcccggctgc ggggtggact tcaccgagag ccgcctcagc aacctgctgg 14460
gcattcgcaa gaggcagccc ttccaggaag gcttccagat catgtacgag gatctggagg 14520
ggggcaacat ccccgcgctc ctggatgtcg acgcctatga gaaaagcaag gaggatgcag 14580
cagctgaagc aactgcagcc gtagctaccg cctctaccga ggtcaggggc gataattttg 14640
caagcgccgc agcagtggca gcggccgagg cggctgaaac cgaaagtaag atagtcattc 14700
agccggtgga gaaggatagc aagaacagga gctacaacgt actaccggac aagataaaca 14760
ccgcctaccg cagctggtac ctagcctaca actatggcga ccccgagaag ggcgtgcgct 14820

20262014626 26 Feb 2026

cctggacgct gctcaccacc tcggacgtca cctgcggcgt ggagcaagtc tactggtcgc 14880
tgcccgacat gatgcaagac ccggtcacct tccgctccac gcgtcaagtt agcaactacc 14940
cggtggtggg cgccgagctc ctgcccgtct actccaagag cttcttcaac gagcaggccg 15000
tctactcgca gcagctgcgc gccttcacct cgcttacgca cgtcttcaac cgcttccccg 15060
agaaccagat cctcgtccgc ccgcccgcgc ccaccattac caccgtcagt gaaaacgttc 15120
ctgctctcac agatcacggg accctgccgc tgcgcagcag tatccgggga gtccagcgcg 15180
tgaccgttac tgacgccaga cgccgcacct gcccctacgt ctacaaggcc ctgggcatag 15240
tcgcgccgcg cgtcctctcg agccgcacct tctaaatgtc cattctcatc tcgcccagta 15300
ataacaccgg ttggggcctg cgcgcgccca gcaagatgta cggaggcgct cgccaacgct 15360
ccacgcaaca ccccgtgcgc gtgcgcgggc acttccgcgc tccctggggc gccctcaagg 15420
gccgcgtgcg gtcgcgcacc accgtcgacg acgtgatcga ccaggtggtg gccgacgcgc 15480
gcaactacac ccccgccgcc gcgcccgtct ccaccgtgga cgccgtcatc gacagcgtgg 15540
tggccgacgc gcgccggtac gcccgcgcca agagccggcg gcggcgcatc gcccggcggc 15600
accggagcac ccccgccatg cgcgcggcgc gagccttgct gcgcagggcc aggcgcacgg 15660
gacgcagggc catgctcagg gcggccagac gcgcggcttc aggcgccagc gccggcagga 15720
cccggagacg cgcggccacg gcggcggcag cggccatcgc cagcatgtcc cgcccgcggc 15780
gagggaacgt gtactgggtg cgcgacgccg ccaccggtgt gcgcgtgccc gtgcgcaccc 15840
gccccctcg cacttgaaga tgttcacttc gcgatgttga tgtgtcccag cggcgaggag 15900
gatgtccaag cgcaaattca aggaagagat gctccaggtc atcgcgcctg agatctacgg 15960
ccctgcggtg gtgaaggagg aaagaaagcc ccgcaaaatc aagcgggtca aaaaggacaa 16020
aaaggaagaa gaaagtgatg tggacggatt ggtggagttt gtgcgcgagt tcgccccccg 16080
gcggcgcgtg cagtggcgcg ggcggaaggt gcaaccggtg ctgagacccg gcaccaccgt 16140
ggtcttcacg cccggcgagc gctccggcac cgcttccaag cgctcctacg acgaggtgta 16200
cggggatgat gatattctgg agcaggcggc cgagcgcctg ggcgagtttg cttacggcaa 16260
gcgcagccgt tccgcaccga aggaagaggc ggtgtccatc ccgctggacc acggcaaccc 16320
cacgccgagc ctcaagcccg tgaccttgca gcaggtgctg ccgaccgcgg cgccgcgccg 16380
ggggttcaag cgcgagggcg aggatctgta ccccaccatg cagctgatgg tgcccaagcg 16440
ccagaagctg gaagacgtgc tggagaccat gaaggtggac ccggacgtgc agcccgaggt 16500
caaggtgcgg cccatcaagc aggtggcccc gggcctgggc gtgcagaccg tggacatcaa 16560
gattcccacg gagcccatgg aaacgcagac cgagcccatg atcaagccca gcaccagcac 16620
catggaggtg cagacggatc cctggatgcc atcggctcct agtcgaagac cccggcgcaa 16680
gtacggcgcg gccagcctgc tgatgcccaa ctacgcgctg catccttcca tcatccccac 16740
gccgggctac cgcggcacgc gcttctaccg cggtcatacc agcagccgcc gccgcaagac 16800
caccactcgc cgccgccgtc gccgcaccgc cgctgcaacc acccctgccg ccctggtgcg 16860
gagagtgtac cgccgcggcc gcgcacctct gaccctgccg cgcgcgcgct accacccgag 16920
catcgccatt taaactttcg cctgctttgc agatcaatgg ccctcacatg ccgccttcgc 16980
gttcccatta cgggctaccg aggaagaaaa ccgcgccgta gaaggctggc ggggaacggg 17040
atgcgtcgcc accaccaccg gcggcggcgc gccatcagca agcggttggg gggaggcttc 17100
ctgcccgcgc tgatccccat catcgccgcg gcgatcgggg cgatccccgg cattgcttcc 17160
gtggcggtgc aggcctctca gcgccactga gacacacttg gaaacatctt gtaataaacc 17220
aatggactct gacgctcctg gtcctgtgat gtgttttcgt agacagatgg aagacatcaa 17280
tttttcgtcc ctggctccgc gacacggcac gcggccgttc atgggcacct ggagcgacat 17340
cggcaccagc caactgaacg ggggcgcctt caattggagc agtctctgga gcgggcttaa 17400
gaatttcggg tccacgctta aaacctatgg cagcaaggcg tggaacagca ccacagggca 17460
ggcgctgagg gataagctga aagagcagaa cttccagcag aaggtggtcg atgggctcgc 17520
ctcgggcatc aacggggtgg tggacctggc caaccaggcc gtgcagcggc agatcaacag 17580
ccgcctggac ccggtgccgc ccgccggctc cgtggagatg ccgcaggtgg aggaggagct 17640
gcctcccctg gacaagcggg gcgagaagcg accccgcccc gatgcggagg agacgctgct 17700
gacgcacacg gacgagccgc ccccgtacga ggaggcggtg aaactgggtc tgcccaccac 17760
gcggcccatc gcgcccctgg ccaccggggt gctgaaaccc gaaaagcccg cgaccctgga 17820
cttgcctcct ccccagcctt cccgcccctc tacagtggct aagcccctgc cgccggtggc 17880
cgtggcccgc gcgcgacccg ggggcaccgc ccgccctcat gcgaactggc agagcactct 17940
gaacagcatc gtgggtctgg gagtgcagag tgtgaagcgc cgccgctgct attaaaccta 18000
ccgtagcgct taacttgctt gtctgtgtgt gtatgtatta tgtcgccgcc gccgctgtcc 18060
accagaagga ggagtgaaga ggcgcgtcgc cgagttgcaa gatggccacc ccatcgatgc 18120
tgccccagtg ggcgtacatg cacatcgccg gacaggacgc ttcggagtac ctgagtccgg 18180
gtctggtgca gtttgcccgc gccacagaca cctacttcag tctggggaac aagtttagga 18240
accccacggt ggcgcccacg cacgatgtga ccaccgaccg cagccagcgg ctgacgctgc 18300
gcttcgtgcc cgtggaccgc gaggacaaca cctactcgta caaagtgcgc tacacgctgg 18360
ccgtgggcga caaccgcgtg ctggacatgg ccagcaccta ctttgacatc cgcggcgtgc 18420
tggatcgggg ccctagcttc aaaccctact ccggcaccgc ctacaacagt ctggccccca 18480
agggagcacc caacacttgt cagtggacat ataaagccga tggtgaaact gccacagaaa 18540
aaacctatac atatggaaat gcacccgtgc agggcattaa catcacaaaa gatggtattc 18600
aacttggaac tgacaccgat gatcagccaa tctacgcaga taaaacctat cagcctgaac 18660
ctcaagtggg tgatgctgaa tggcatgaca tcactggtac tgatgaaaag tatggaggca 18720
gagctcttaa gcctgatacc aaaatgaagc cttgttatgg ttcttttgcc aagcctacta 18780
ataaagaagg aggtcaggca aatgtgaaaa caggaacagg cactactaaa gaatatgaca 18840
tagacatggc tttctttgac aacagaagtg cggctgctgc tggcctagct ccagaaattg 18900
ttttgtatac tgaaaatgtg gatttggaaa ctccagatac ccatattgta tacaaagcag 18960
gcacagatga cagcagctct tctattaatt tgggtcagca agccatgccc aacagaccta 19020
actacattgg tttcagagac aactttatcg ggctcatgta ctacaacagc actggcaata 19080
tgggggtgct ggccggtcag gcttctcagc tgaatgctgt ggttgacttg caagacagaa 19140
acaccgagct gtcctaccag ctcttgcttg actctctggg tgacagaacc cggtatttca 19200
gtatgtggaa tcaggcggtg gacagctatg atcctgatgt gcgcattatt gaaaatcatg 19260
gtgtggagga tgaacttccc aactattgtt tccctctgga tgctgttggc agaacagata 19320
cttatcaggg aattaaggct aatggaactg atcaaaccac atggaccaaa gatgacagtg 19380

20262014626 26 Feb 2026

tcaatgatgc taatgagata ggcaagggta atccattcgc catggaaatc aacatccaag 19440
ccaacctgtg gaggaacttc ctctacgcca acgtggccct gtacctgccc gactcttaca 19500
agtacacgcc ggccaatgtt accctgccca ccaacaccaa cacctacgat tacatgaacg 19560
gccgggtggt ggcgccctcg ctggtggact cctacatcaa catcggggcg cgctggtcgc 19620
tggatcccat ggacaacgtg aaccccttca accaccaccg caatgcgggg ctgcgctacc 19680
gctccatgct cctgggcaac gggcgctacg tgcccttcca catccaggtg ccccagaaat 19740
ttttcgccat caagagcctc ctgctcctgc ccgggtccta cacctacgag tggaacttcc 19800
gcaaggacgt caacatgatc ctgcagagct ccctcggcaa cgacctgcgc acggacgggg 19860
cctccatctc cttcaccagc atcaacctct acgccacctt cttccccatg gcgcacaaca 19920
cggcctccac gctcgaggcc atgctgcgca acgacaccaa cgaccagtcc ttcaacgact 19980
acctctcggc ggccaacatg ctctacccca tcccggccaa cgccaccaac gtgcccatct 20040
ccatcccctc gcgcaactgg gccgccttcc gcggctggtc cttcacgcgt ctcaagacca 20100
aggagacgcc ctcgctgggc tccgggttcg acccctactt cgtctactcg ggctccatcc 20160
cctacctcga cggcaccttc tacctcaacc acaccttcaa gaaggtctcc atcaccttcg 20220
actcctccgt cagctggccc ggcaacgacc ggctcctgac gcccaacgag ttcgaaatca 20280
agcgcaccgt cgacggcgag ggctacaacg tggcccagtg caacatgacc aaggactggt 20340
tcctggtcca gatgctggcc cactacaaca tcggctacca gggcttctac gtgcccgagg 20400
gctacaagga ccgcatgtac tccttcttcc gcaacttcca gcccatgagc cgccaggtgg 20460
tggacgaggt caactacaag gactaccagg ccgtcaccct ggcctaccag cacaacaact 20520
cgggcttcgt cggctacctc gcgcccacca tgcgccaggg ccagccctac cccgccaact 20580
acccctaccc gctcatcggc aagagcgccg tcaccagcgt cacccagaaa aagttcctct 20640
gcgacagggt catgtggcgc atccccttct ccagcaactt catgtccatg ggcgcgctca 20700
ccgacctcgg ccagaacatg ctctatgcca actccgccca cgcgctagac atgaatttcg 20760
aagtcgaccc catggatgag tccacccttc tctatgttgt cttcgaagtc ttcgacgtcg 20820
tccgagtgca ccagccccac cgcggcgtca tcgaggccgt ctacctgcgc acccccttct 20880
cggccggtaa cgccaccacc taagctcttg cttcttgcaa gccatggccg cgggctccgg 20940
cgagcaggag ctcagggcca tcatccgcga cctgggctgc gggccctact tcctgggcac 21000
cttcgataag cgcttcccgg gattcatggc cccgcacaag ctggcctgcg ccatcgtcaa 21060
cacggccggc cgcgagaccg ggggcgagca ctggctggcc ttcgcctgga acccgcgctc 21120
gaacacctgc tacctcttcg acccccttcgg gttctcggac gagcgcctca agcagatcta 21180
ccagttcgag tacgagggcc tgctgcgccg cagcgccctg gccaccgagg accgctgcgt 21240
caccctggaa aagtccaccc agaccgtgca gggtccgcgc tcggccgcct gcgggctctt 21300
ctgctgcatg ttcctgcacg ccttcgtgca ctggcccgac cgccccatgg acaagaaccc 21360
caccatgaac ttgctgacgg gggtgcccaa cggcatgctc cagtcgcccc aggtggaacc 21420
caccctgcgc cgcaaccagg aggcgctcta ccgcttcctc aactcccact ccgcctactt 21480
tcgctcccac cgcgcgcgca tcgagaaggc caccgccttc gaccgcatga atcaagacat 21540
gtaaaccgtg tgtgtatgtt aaatgtcttt aataaacagc actttcatgt tacacatgca 21600
tctgagatga tttatttaga aatcgaaagg gttctgccgg gtctcggcat ggcccgcggg 21660
cagggacacg ttgcggaact ggtacttggc cagccacttg aactcgggga tcagcagttt 21720
gggcagcggg gtgtcgggga aggagtcggt ccacagcttc cgcgtcagtt gcagggcgcc 21780
cagcaggtcg ggcgcggaga tcttgaaatc gcagttggga cccgcgttct gcgcgcggga 21840
gttgcggtac acggggttgc agcactggaa caccatcagg gccgggtgct tcacgctcgc 21900
cagcaccgtc gcgtcggtga tgctctccac gtcgaggtcc tcggcgttgg ccatcccgaa 21960
gggggtcatc ttgcaggtct gccttcccat ggtgggcacg cacccgggct tgtggttgca 22020
atcgcagtgc agggggatca gcatcatctg ggcctggtcg gcgttcatcc ccgggtacat 22080
ggccttcatg aaagcctcca attgcctgaa cgcctgctgg gccttggctc cctcggtgaa 22140
gaagaccccg caggacttgc tagagaactg gttggtggcg cacccggcgt cgtgcacgca 22200
gcagcgcgcg tcgttgttgg ccagctgcac cacgctgcgc ccccagcggt tctgggtgat 22260
cttggcccgg tcggggttct ccttcagcgc gcgctgcccg ttctcgctcg ccacatccat 22320
ctcgatcatg tgctccttct ggatcatggt ggtcccgtgc aggcaccgca gcttgccctc 22380
ggcctcggtg cacccgtgca gccacagcgc gcacccggtg cactcccagt tcttgtgggc 22440
gatctgggaa tgcgcgtgca cgaagccctg caggaagcgg cccatcatgg tggtcagggt 22500
cttgttgcta gtgaaggtca gcggaatgcc gcggtgctcc tcgttgatgt acaggtggca 22560
gatgcggcgg tacacctcgc cctgctcggg catcagctgg aagttggctt tcaggtcggt 22620
ctccacgcgg tagcggtcca tcagcatagt catgatttcc ataccttct cccaggccga 22680
gacgatgggc aggctcatag ggttcttcac catcatctta gcgctagcag ccgcggccag 22740
ggggtcgctc tcgtccaggg tctcaaagct ccgcttgccg tccttctcgg tgatccgcac 22800
cgggggtag ctgaagccca cggccgccag ctcctcctcg gcctgtcttt cgtcctcgct 22860
gtcctggctg acgtcctgca ggaccacatg cttggtcttg cggggtttct tcttgggcgg 22920
cagcggcggc ggagatgttg gagatggcga gggggagcgc gagttctcgc tcaccactac 22980
tatctcttcc tcttcttggt ccgaggccac gcggcggtag gtatgtctct tcgggggcag 23040
aggcggaggc gacgggctct cgccgccgcg acttggcgga tggctggcag agccccttcc 23100
gcgttcgggg gtgcgctccc ggcggcgctc tgactgactt cctccgcggc cggccattgt 23160
gttctcctag ggaggaacaa caagcatgga gactcagcca tcgccaacct cgccatctgc 23220
ccccaccgcc gacgagaagc agcagcagca gaatgaaagc ttaaccgccc cgccgcccag 23280
ccccgccacc tccgacgcgg ccgtcccaga catgcaagag atggaggaat ccatcgagat 23340
tgacctgggc tatgtgacgc ccgcggagca cgaggaggag ctggcagtgc gcttttcaca 23400
agaagagata caccaagaac agccagagca ggaagcagag aatgagcaga gtcaggctgg 23460
gctcgagcat gacggcgact acctccacct gagcgggggg gaggacgcgc tcatcaagca 23520
tctggcccgg caggccacca tcgtcaagga tgcgctgctc gaccgcaccg aggtgcccct 23580
cagcgtggag gagctcagcc gcgcctacga gttgaacctc ttctcgccgc gcgtgccccc 23640
caagcgccag cccaatggca cctgcgagcc caacccgcgc ctcaacttct acccggtctt 23700
cgcggtgccc gaggccctgg ccacctacca catctttttc aagaaccaaa agatccccgt 23760
ctcctgccgc gccaaccgca cccgcgccga cgccctttc aacctgggtc ccggcgcccg 23820
cctacctgat atcgcctcct tggaagaggt tcccaagatc ttcgagggtc tgggcagcga 23880
cgagactcgg gccgcgaacg ctctgcaagg agaaggagga gagcatgagc accacagcgc 23940

20262014626 26 Feb 2026

cctggtcgag ttggaaggcg acaacgcgcg gctggcggtg ctcaaacgca cggtcgagct 24000
gacccatttc gcctacccgg ctctgaacct gccccccaaa gtcatgagcg cggtcatgga 24060
ccaggtgctc atcaagcgcg cgtcgcccat ctccgaggac gagggcatgc aagactccga 24120
ggagggcaag cccgtggtca gcgacgagca gctggcccgg tggctgggtc ctaatgctag 24180
tccccagagt ttggaagagc ggcgcaaact catgatggcc gtggtcctgg tgaccgtgga 24240
gctggagtgc ctgcgccgct tcttcgccga cgcggagacc ctgcgcaagg tcgaggagaa 24300
cctgcactac ctcttcaggc acgggttcgt gcgccaggcc tgcaagatct ccaacgtgga 24360
gctgaccaac ctggtctcct acatgggcat cttgcacgag aaccgcctgg ggcagaacgt 24420
gctgcacacc accctgcgcg gggaggcccg gcgcgactac atccgcgact gcgtctacct 24480
ctacctctgc cacacctggc agacgggcat gggcgtgtgg cagcagtgtc tggaggagca 24540
gaacctgaaa gagctctgca agctcctgca gaagaacctc aagggtctgt ggaccgggtt 24600
cgacgagcgc accaccgcct cggacctggc cgacctcatt ttccccgagc gcctcaggct 24660
gacgctgcgc aacggcctgc ccgactttat gagccaaagc atgttgcaaa actttcgctc 24720
tttcatcctc gaacgctccg gaatcctgcc cgccacctgc tccgcgctgc cctcggactt 24780
cgtgccgctg accttccgcg agtgcccccc gccgctgtgg agccactgct acctgctgcg 24840
cctggccaac tacctggcct accactcgga cgtgatcgag gacgtcagcg gcgagggcct 24900
gctcgagtgc cactgccgct gcaacctctg cacgccgcac cgctccctgg cctgcaaccc 24960
ccagctgctg agcgagaccc agatcatcgg caccttcgag ttgcaagggc ccagcgaagg 25020
cgagggttca gccgccaagg ggggtctgaa actcaccccg gggctgtgga cctcggccta 25080
cttgcgcaag ttcgtgcccg aggactacca tcccttcgag atcaggttct acgaggacca 25140
atcccatccg cccaaggccg agctgtcggc ctgcgtcatc acccaggggg cgatcctggc 25200
ccaattgcaa gccatccaga aatcccgcca agaattcttg ctgaaaaagg gccgcggggt 25260
ctacctcgac ccccagaccg gtgaggagct caaccccggc ttcccccagg atgccccgag 25320
gaaacaagaa gctgaaagtg gagctgccgc ccgtggagga tttggaggaa gactgggaga 25380
acagcagtca ggcagaggag gaggagatgg aggaagactg ggacagcact caggcagagg 25440
aggacagcct gcaagacagt ctggaggaag acgaggagga ggcagaggag gaggtggaag 25500
aagcagccgc cgccagaccg tcgtcctcgg cgggggagaa agcaagcagc acggatacca 25560
tctccgctcc gggtcggggt cccgctcgac cacacagtag atgggacgag accggacgat 25620
tcccgaaccc caccacccag accggtaaga aggagcggca gggatacaag tcctggcggg 25680
ggcacaaaaa cgccatcgtc tcctgcttgc aggcctgcgg gggcaacatc tccttcaccc 25740
ggcgctacct gctcttccac cgcggggtga actttccccg caacatcttg cattactacc 25800
gtcacctcca cagcccctac tacttccaag aagaggcagc agcagcagaa aaagaccagc 25860
agaaaaccag cagctagaaa atccacagcg gcggcagcag gtggactgag gatcgcggcg 25920
aacgagccgg cgcaaacccg ggagctgagg aaccggatct ttcccaccct ctatgccatc 25980
ttccagcaga gtcgggggca ggagcaggaa ctgaaagtca agaaccgttc tctgcgctcg 26040
ctcacccgca gttgtctgta tcacaagagc gaagaccaac ttcagcgcac tctcgaggac 26100
gccgaggctc tcttcaacaa gtactgcgcg ctcactctta aagagtagcc cgcgcccgcc 26160
cagtcgcaga aaaaggcggg aattacgtca cctgtgccct tcgccctagc cgcctccacc 26220
catcatcatg agcaaagaga ttcccacgcc ttacatgtgg agctaccagc cccagatggg 26280
cctggccgcc ggtgccgccc aggactactc cacccgcatg aattggctca gcgccgggcc 26340
cgcgatgatc tcacgggtga atgacatccg cgcccaccga aaccagatac tcctagaaca 26400
gtcagcgctc accgccacgc cccgcaatca cctcaatccg cgtaattggc ccgccgccct 26460
ggtgtaccag gaaattcccc agcccacgac cgtactactt ccgcgagacg cccaggccga 26520
agtccagctg actaactcag gtgtccagct ggcgggcggc gccaccctgt gtcgtcaccg 26580
ccccgctcag ggtataaagc ggctggtgat ccggggcaga ggcacacagc tcaacgacga 26640
ggtggtgagc tcttcgctgg gtctgcgacc tgacggagtc ttccaactcg ccggatcggg 26700
gagatcttcc ttcacgcctc gtcaggccgt cctgactttg gagagttcgt cctcgcagcc 26760
ccgctcgggt ggcatcggca ctctccagtt cgtggaggag ttcactccct cggtctactt 26820
caaccccttc tccggctccc ccggccacta cccggacgag ttcatcccga acttcgacgc 26880
catcagcgag tcggtggacg gctacgattg aatgtcccat ggtggcgcag ctgacctagc 26940
tcggcttcga cacctggacc actgccgccg cttccgctgc ttcgctcggg atctcgccga 27000
gtttgcctac tttgagctgc ccgaggagca ccctcagggc ccggcccacg gagtgcggat 27060
cgtcgtcgaa gggggcctcg actcccacct gcttcggatc ttcagccagc gtccgatcct 27120
ggtcgagcgc gagcaaggac agacccttct gactctgtac tgcatctgca accaccccgg 27180
cctgcatgaa agtctttgtt gtctgctgtg tactgagtat aataaaagct gagatcagcg 27240
actactccgg acttccgtgt gttcctgaat ccatcaacca gtctttgttc ttcaccggga 27300
acgagaccga gctccagctc cagtgtaagc cccacaagaa gtacctcacc tggctgttcc 27360
agggctcccc gatcgccgtt gtcaaccact gcgacaacga cggagtcctg ctgagcggcc 27420
ctgccaacct tacttttttcc acccgcagaa gcaagctcca gctcttccaa cccttcctcc 27480
ccgggaccta tcagtgcgtc tcgggaccct gccatcacac cttccacctg atcccgaata 27540
ccacagcgtc gctccccgct actaacaacc aaactaacct ccaccaacgc caccgtcgcg 27600
acggccacaa tacatgccca tattagacta tgaggccgag ccacagcgac ccatgctccc 27660
cgctattagt tacttcaatc taaccggcgg agatgactga cccactggcc aacaacaacg 27720
tcaacgacct tctcctggac atggacggcc gcgcctcgga gcagcgactc gcccaacttc 27780
gcattcgcca gcagcaggag agagccgtca aggagctgca ggatgcggtg gccatccacc 27840
agtgcaagag aggcatcttc tgcctggtga aacaggccaa gatctcctac gaggtcactc 27900
caaacgacca tcgcctctcc tacgagctcc tgcagcagcg ccagaagttc acctgcctgg 27960
tcggagtcaa ccccatcgtc atcacccagc agtctggcga taccaagggg tgcatccact 28020
gctcctgcga ctccccgac tgcgtccaca ctctgatcaa gaccctctgc ggcctccgcg 28080
acctcctccc catgaactaa tcacccccctt atccagtgaa ataaagatca tattgatgat 28140
gattttacag aaataaaaaa taatcatttg atttgaaata aagatacaat catattgatg 28200
atttgagttt aacaaaaaaa taaagaatca cttacttgaa atctgatacc aggtctctgt 28260
ccatgttttc tgccaacacc acttcactcc cctcttccca gctctggtac tgcaggcccc 28320
ggcgggctgc aaacttcctc cacacgctga aggggatgtc aaattcctcc tgtccctcaa 28380
tcttcatttt atcttctatc agatgtccaa aaagcgcgtc cgggtggatg atgacttcga 28440
ccccgtctac ccctacgatg cagacaacgc accgaccgtg cccttcatca acccccccctt 28500

2026201462 26 Feb 2026

		cgtctcttca gatggattcc aagagaagcc cctgggggtg ttgtccctgc gactggccga 28560 ccccgtcacc accaagaacg gggaaatcac cctcaagctg ggagaggggg tggacctcga 28620 ttcctcggga aaactcatct ccaacacggc caccaaggcc gccgcccctc tcagtttttc 28680 caacaacacc atttccctta acatggatca ccccttttac actaaagatg gaaaattatc 28740 cttacaagtt tctccaccat taaatatact gagaacaagc attctaaaca cactagcttt 28800 aggttttgga tcaggtttag gactccgtgg ctctgccttg gcagtacagt tagtctctcc 28860 acttacattt gatactgatg gaaacataaa gcttacctta gacagaggtt tgcatgttac 28920 aacaggagat gcaattgaaa gcaacataag ctgggctaaa ggtttaaaat ttgaagatgg 28980 agccatagca accaacattg gaaatgggtt agagtttgga agcagtagta cagaaacagg 29040 tgttgatgat gcttacccaa tccaagttaa acttggatct ggccttagct ttgacagtac 29100 aggagccata atggctggta acaaagaaga cgataaactc actttgtgga caacacctga 29160 tccatcacca aactgtcaaa tactcgcaga aaatgatgca aaactaacac tttgcttgac 29220 taaatgtggt agtcaaatac tggccactgt gtcagtctta gttgtaggaa gtggaaacct 29280 aaaccccatt actggcaccg taagcagtgc tcaggtgttt ctacgttttg atgcaaacgg 29340 tgttctttta acagaacatt ctacactaaa aaaatactgg gggtataggc agggagatag 29400 catagatggc actccatata ccaatgctgt aggattcatg cccaatttaa aagcttatcc 29460 aaagtcacaa agttctacta ctaaaaataa tatagtaggg caagtataca tgaatggaga 29520 tgtttcaaaa cctatgcttc tcactataac cctcaatggt actgatgaca gcaacagtac 29580 atattcaatg tcattttcat acacctggac taatggaagc tatgttggag caacatttgg 29640 ggctaactct tataccttct catacatcgc ccaagaatga acactgtatc ccaccctgca 29700 tgccaaccct tcccacccca ctctgtggaa caaactctga aacacaaaat aaaataaagt 29760 tcaagtgttt tattgattca acagttttac aggattcgag cagttatttt tcctccaccc 29820 tcccaggaca tggaatacac caccctctcc ccccgcacag ccttgaacat ctgaatgcca 29880 ttggtgatgg acatgctttt ggtctccacg ttccacacag tttcagagcg agccagtctc 29940 gggtcggtca gggagatgaa accctccggg cactcccgca tctgcacctc acagctcaac 30000 agctgaggat tgtcctcggt ggtcgggatc acggttatct ggaagaagca gaagagcggc 30060 ggtgggaatc atagtccgcg aacgggatcg gccggtggtg tcgcatcagg ccccgcagca 30120 gtcgctgccg ccgccgctcc gtcaagctgc tgctcagggg gtccgggtcc agggactccc 30180 tcagcatgat gcccacggcc ctcagcatca gtcgtctggt gcggcgggcg cagcagcgca 30240 tgcggatctc gctcaggtcg ctgcagtacg tgcaacacag aaccaccagg ttgttcaaca 30300 gtccatagtt caacacgctc cagccgaaac tcatcgcggg aaggatgcta cccacgtggc 30360 cgtcgtacca gatcctcagg taaatcaagt ggtgccccct ccagaacacg ctgcccacgt 30420 acatgatctc cttgggcatg tggcggttca ccacctcccg gtaccacatc accctctggt 30480 tgaacatgca gccccggatg atcctgcgga accacagggc cagcaccgcc ccgcccgcca 30540 tgcagcgaag agaccccggg tcccggcaat ggcaatggag gacccaccgc tcgtacccgt 30600 ggatcatctg ggagctgaac aagtctatgt tggcacagca caggcatatg ctcatgcatc 30660 tcttcagcac tctcaactcc tcgggggtca aaaccatatc ccagggcacg gggaactctt 30720 gcaggacagc gaaccccgca gaacagggca atcctcgcac agaacttaca ttgtgcatgg 30780 acagggtatc gcaatcaggc agcaccgggt gatcctccac cagagaagcg cgggtctcgg 30840 tctcctcaca gcgtggtaag ggggccggcc gatacgggtg atggcgggac gcggctgatc 30900 gtgttcgcga ccgtgtcatg atgcagttgc tttcggacat tttcgtactt gctgtagcag 30960 aacctggtcc gggcgctgca caccgatcgc cggcggcggt ctcggcgctt ggaacgctcg 31020 gtgttgaaat tgtaaaacag ccactctctc agaccgtgca gcagatctag ggcctcagga 31080 gtgatgaaga tcccatcatg cctgatggct ctgatcacat cgaccaccgt ggaatgggcc 31140 agacccagcc agatgatgca attttgttgg gtttcggtga cggcggggga gggaagaaca 31200 ggaagaacca tgattaactt ttaatccaaa cggtctcgga gtacttcaaa atgaagatcg 31260 cggagatggc acctctcgcc cccgctgtgt tggtggaaaa taacagccag gtcaaaggtg 31320 atacggttct cgagatgttc cacggtggct tccagcaaag cctccacgcg cacatccaga 31380 aacaagacaa tagcgaaagc gggagggttc tctaattcct caatcatcat gttacactcc 31440 tgcaccatcc ccagataatt ttcatttttc cagccttgaa tgattcgaac tagttcgtga 31500 ggtaaatcca agccagccat gataaagagc tcgcgcagag cgccctccac cggcattctt 31560 aagcacaccc tcataattcc aagatattct gctcctggtt cacctgcagc agattgacaa 31620 gcggaatatc aaaatctctg ccgcgatccc tgagctcctc cctcagcaat aactgtaagt 31680 actctttcat atcctctccg aaatttttag ccataggacc accaggaata agattagggc 31740 aagccacagt acagataaac cgaagtcctc cccagtgagc attgccaaat gcaagactgc 31800 tataagcatg ctggctagac ccggtgatat cttccagata actggacaga aaatcgccca 31860 ggcaattttt aagaaaatca acaaaagaaa aatcctccag gtggacgttt agagcctcgg 31920 gaacaacgat gaagtaaatg caagcggtgc gttccagcat ggttagttag ctgatctgta 31980 gaaaaaacaa aaatgaacat taaaccatgc tagcctggcg aacaggtggg taaatcgttc 32040 tctccagcac caggcaggcc acggggtctc cggcgcgacc ctcgtaaaaa ttgtcgctat 32100 gattgaaaac catcacagag agacgttccc ggtggccggc gtgaatgatt cgacaagatg 32160 aatacacccc cggaacattg gcgtccgcga gtgaaaaaaa gcgcccgagg aagcaataag 32220 gcactacaat gctcagtctc aagtccagca aagcgatgcc atgcggatga agcacaaaat 32280 tctcaggtgc gtacaaaatg taattactcc cctcctgcac aggcagcaaa gcccccgatc 32340 cctccaggta cacatacaaa gcctcagcgt ccatagctta ccgagcagca gcacacaaca 32400 ggcgcaagag tcagagaaag gctgagctct aacctgtcca cccgctctct gctcaatata 32460 tagcccagat ctacactgac gtaaaggcca aagtctaaaa atacccgcca aataatcaca 32520 cacgcccagc acacgcccag aaaccggtga cacactcaaa aaaatacgcg cacttcctca 32580 aacgcccaaa actgccgtca tttccgggtt cccacgctac gtcatcaaaa cacgactttc 32640 aaattccgtc gaccgttaaa aacgtcaccc gccccgcccc taacggtcgc ccgtctctca 32700 gccaatcagc gccccgcatc cccaaattca aacacctcat ttgcatatta acgcgcacaa 32760 aaagtttgag gtatattatt gatgatgg 32788
3-13	**Sequences**	
3-13-1	Sequence Number [ID]	13
3-13-2	Molecule Type	DNA

2026201462 26 Feb 2026

3-13-3	Length	30684
3-13-4	Features	**misc_feature 1..30684**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..30684
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-13-5	Residues	ccatcttcaa taatatacct caaacttttt gtgcgcgtta atatgcaaat gaggcgtttg 60 aatttgggga ggaagggcgg tgattggtcg agggatgagc gaccgttagg ggcggggcga 120 gtgacgtttt gatgacgtgg ttgcgaggag gagccagttt gcaagttctc gtgggaaaag 180 tgacgtcaaa cgaggtgtgg tttgaacacg gaaatactca attttcccgc gctctctgac 240 aggaaatgag gtgtttctgg gcggatgcaa gtgaaaacgg gccattttcg cgcgaaaact 300 gaatgaggaa gtgaaaatct gagtaatttc gcgtttatgg cagggaggag tatttgccga 360 gggccgagta gactttgacc gattacgtgg gggtttcgat taccgtgttt ttcacctaaa 420 tttccgcgta cggtgtcaaa gtccggtgtt tttacgtagg tgtcagctga tcgccagggt 480 atttaaacct gcgctctcca gtcaagaggc cactcttgag tgccagcgag aagagttttc 540 tcctccgcgc cgcgagtcag atctacactt tgaaagtagg gataacaggg taatgacatt 600 gattattgac tagttgttaa tagtaatcaa ttacggggtc attagttcat agcccatata 660 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 720 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 780 attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt 840 atcatatgcc aagtccgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 900 atgcccagta catgacctta cgggactttc ctacttggca gtacatctac gtattagtca 960 tcgctattac catggtgatg cggttttggc agtacaccaa tgggcgtgga tagcggtttg 1020 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 1080 aaaatcaacg ggactttcca aaatgtcgta ataaccccgc cccgttgacg caaatgggcg 1140 gtaggcgtgt acggtgggag gtctatataa gcagagctcg tttagtgaac cgtcagatcg 1200 cctggaacgc catccacgct gttttgacct ccatagaaga cagcgatcgc gccaccatgg 1260 tgagcaaggg cgaggagctg ttcaccgggg tggtgcccat cctggtcgag ctggacggcg 1320 acgtaaacgg ccacaagttc agcgtgtccg gcgagggcga gggcgatgcc acctacggca 1380 agctgaccct gaagttcatc tgcaccaccg gcaagctgcc cgtgccctgg cccaccctcg 1440 tgaccaccct gacctacggc gtgcagtgct tcagccgcta ccccgaccac atgaagcagc 1500 acgacttctt caagtccgcc atgcccgaag gctacgtcca ggagcgcacc atcttcttca 1560 aggacgacgg caactacaag acccgcgccg aggtgaagtt cgagggcgac accctggtga 1620 accgcatcga gctgaagggc atcgacttca aggaggacgg caacatcctg gggcacaagc 1680 tggagtacaa ctacaacagc cacaacgtct atatcatggc cgacaagcag aagaacggca 1740 tcaaggtgaa cttcaagatc cgccacaaca tcgaggacgg cagcgtgcag ctcgccgacc 1800 actaccagca gaacaccccc atcggcgacg gccccgtgct gctgcccgac aaccactacc 1860 tgagcaccca gtccgccctg agcaaagacc ccaacgagaa gcgcgatcac atggtcctgc 1920 tggagttcgt gaccgccgcc gggatcactc tcggcatgga cgagctttac aagtagtgag 1980 tttaaactcc catttaaatg tgagggttaa tgcttcgagc agacatgata agatacattg 2040 atgagtttgg acaaaccaca actagaatgc agtgaaaaaa atgctttatt tgtgaaattt 2100 gtgatgctat tgctttattt gtaaccatta taagctgcaa taaacaagtt aacaacaaca 2160 attgcattca ttttatgttt caggttcagg gggagatgtg ggaggttttt taaagcaagt 2220 aaaacctcta caaatgtggt aaaataacta taacggtcct aaggtagcga gtgagtagtg 2280 ttctggggcg ggggaggacc tgcatgaggg ccagaataac tgaaatctgt gcttttctgt 2340 gtgttgcagc agcatgagcg gaagcggctc ctttgaggga ggggtattca gcccttatct 2400 gacggggcgt ctcccctcct gggcgggagt gcgtcagaat gtgatgggat ccacggtgga 2460 cggccggccc gtgcagcccg cgaactcttc aaccctgacc tatgcaaccc tgagctcttc 2520 gtcgttggac gcagctgccg ccgcagctgc tgcatctgcc gccagcgccg tgcgcggaat 2580 ggccatgggc gccggctact acggcactct ggtggccaac tcgagttcca ccaataatcc 2640 cgccagcctg aacgaggaga agctgttgct gctgatggcc cagctcgagg ccttgaccca 2700 gcgcctgggc gagctgaccc agcaggtggc tcagctgcag gagcagacgc gggccgcggt 2760 tgccacggtg aaatccaaat aaaaaatgaa tcaataaata aacggagacg gttgttgatt 2820 ttaacacaga gtctgaatct ttatttgatt tttcgcgcgc ggtaggccct ggaccaccgg 2880 tctcgatcat tgagcacccg gtggatcttt tccaggaccc ggtagaggtg ggcttggatg 2940 ttgaggtaca tgggcatgag cccgtcccgg gggtggaggt agctccattg cagggcctcg 3000 tgctcggggg tggtgttgta aatcacccag tcatagcagg ggcgcagggc atggtgttgc 3060 acaatatctt tgaggaggag actgatggcc acgggcagcc ctttggtgta ggtgtttaca 3120 aatctgttga gctgggaggg atgcatgcgg ggggagatga ggtgcatctt ggcctggatc 3180 ttgagattgg cgatgttacc gcccagatcc cgcctggggt tcatgttgtg caggaccacc 3240 agcacggtgt atccggtgca cttggggaat ttatcatgca acttggaagg gaaggcgtga 3300 aagaatttgg cgacgccttt gtgcccgccc aggttttcca tgcactcatc catgatgatg 3360 gcgatgggcc cgtgggcggc ggcctgggca aagacgtttc gggggtcgga cacatcatag 3420 ttgtggtcct gggtgaggtc atcataggcc attttaatga atttggggcg gagggtgccg 3480 gactggggga caaaggtacc ctcgatcccg ggggcgtagt tcccctcaca gatctgcatc 3540 tcccaggctt tgagctcgga ggggggggatc atgtccacct gcggggcgat aaagaacacg 3600 gtttccgggg cgggggagat gagctgggcc gaaagcaagt tccggagcag ctgggacttg 3660 ccgcagccgg tggggccgta gatgaccccg atgaccggct gcaggtggta gttgagggag 3720 agacagctgc cgtcctcccg gaggaggggg gccacctcgt tcatcatctc gcgcacgtgc 3780 atgttctcgc gcaccagttc cgccaggagg cgctctcccc ccagggatag gagctcctgg 3840 agcgaggcga agtttttcag cggcttgagt ccgtcggcca tgggcatttt ggagagggtt 3900 tgttgcaaga gttccaggcg gtcccagagc tcggtgatgt gctctacggc atctcgatcc 3960 agcagacctc ctcgtttcgc gggttgggac ggctgcggga gtagggcacc agacgatggg 4020 cgtccagcgc agccagggtc cggtccttcc agggtcgcag cgtccgcgtc agggtggtct 4080

20262014626 26 Feb 2026

ccgtcacggt gaaggggtgc gcgccgggct gggcgcttgc gagggtgcgc ttcaggctca 4140
tccggctggt cgaaaaccgc tcccgatcgg cgccctgcgc gtcggccagg tagcaattga 4200
ccatgagttc gtagttgagc gcctcggccg cgtggccttt ggcgcggagc ttacctttgg 4260
aagtctgccc gcaggcggga cagaggaggg acttgagggc gtagagcttg ggggcgagga 4320
agacggactc gggggcgtag gcgtccgcgc cgcagtgggc gcagacggtc tcgcactcca 4380
cgagccaggt gaggtcgggc tggtcggggt caaaaaccag tttcccgccg ttctttttga 4440
tgcgtttctt acctttggtc tccatgagct cgtgtccccg ctgggtgaca aagaggctgt 4500
ccgtgtcccc gtagaccgac tttatgggcc ggtcctcgag cggtgtgccg cggtcctcct 4560
cgtagaggaa ccccgcccac tccgagacga aagcccgggt ccaggccagc acgaaggagg 4620
ccacgtggga cgggtagcgg tcgttgtcca ccagcgggtc cacctttcc agggtatgca 4680
aacacatgtc cccctcgtcc acatccagga aggtgattgg cttgtaagtg taggccacgt 4740
gaccgggggt cccggccggg ggggtataaa agggtgcggg tccctgctcg tcctcactgt 4800
cttccggatc gctgtccagg agcgccagct gttggggtag gtattccctc tcgaaggcgg 4860
gcatgacctc ggcactcagg ttgtcagttt ctagaaacga ggaggatttg atattgacgg 4920
tgccggcgga gatgcctttc aagagcccct cgtccatctg gtcagaaaag acgatctttt 4980
tgttgtcgag cttggtggcg aaggagccgt agagggcgtt ggagaggagc ttggcgatgg 5040
agcgcatggt ctggtttttt tccttgtcgg cgcgctcctt ggcggcgatg ttgagctgca 5100
cgtactcgcg cgccacgcac ttccattcgg ggaagacggt ggtcagctcg tcgggcacga 5160
ttctgacctg ccagccccga ttatgcaggg tgatgaggtc cacactggtg gccacctcgc 5220
cgcgcagggg ctcattagtc cagcagaggc gtccgccctt gcgcgagcag aaggggggca 5280
gggggtccag catgacctcg tcgggggggt cggcatcgat ggtgaagatg ccgggcagga 5340
ggtcggggtc aaagtagctg atggaagtgg ccagatcgtc cagggcagct tgccattcgc 5400
gcacggccag cgcgcgctcg tagggactga ggggcgtgcc ccagggcatg ggatgggtaa 5460
gcgcggaggc gtacatgccg cagatgtcgt agacgtagag gggctcctcg aggatgccga 5520
tgtaggtggg gtagcagcgc cccccgcgga tgctggcgcg cacgtagtca tacagctcgt 5580
gcgagggggc gaggagcccc gggcccaggt tggtgcgact gggcttttcg gcgcggtaga 5640
cgatctggcg gaaaatggca tgcgagttgg aggagatggt gggcctttgg aagatgttga 5700
agtgggcgtg gggcagtccg accgagtcgc ggatgaagtg ggcgtaggag tcttgcagct 5760
tggcgacgag ctcggcggtg actaggacgt ccagagcgca gtagtcgagg gtctcctgga 5820
tgatgtcata cttgagctgt ccctttttgtt tccacagctc gcggttgaga aggaactctt 5880
cgcggtcctt ccagtactct tcgaggggga acccgtcctg atctgcacgg taagagccta 5940
gcatgtagaa ctggttgacg gccttgtagg cgcagcagcc cttctccacg gggagggcgt 6000
aggcctgggc ggccttgcgc agggaggtgt gcgtgagggc gaaagtgtcc ctgaccatga 6060
ccttgaggaa ctggtgcttg aagtcgatat cgtcgcagcc cccctgctcc cagagctgga 6120
agtccgtgcg cttcttgtag gcggggttgg gcaaagcgaa agtaacatcg ttgaagagga 6180
tcttgcccgc gcggggcata aagttgcgag tgatgcggaa aggttggggc acctcggccc 6240
ggttgttgat gacctgggcg gcgagcacga tctcgtcgaa gccgttgatg ttgtggccca 6300
cgatgtagag ttccacgaat cgcggacggc ccttgacgtg gggcagtttc ttgagctcct 6360
cgtaggtgag ctcgtcgggg tcgctgagcc cgtgctgctc gagcgcccag tcggcgagat 6420
gggggttggc gcggaggaag gaagtccaga gatccacggc cagggcggtt tgcagacggt 6480
cccggtactg acggaactgc tgcccgacgg ccatttttc gggggtgacg cagtagaagg 6540
tgcgggggtc cccgtgccag cgatcccatt tgagctggag ggcgagatcg agggcgagct 6600
cgacgagccg gtcgtccccg gagagtttca tgaccagcat gaaggggacg agctgcttgc 6660
cgaaggaccc catccaggtg taggtttcca catcgtaggt gaggaagagc ctttcggtgc 6720
gaggatgcga gccgatgggg aagaactgga tctcctgcca ccaattggag gaatggctgt 6780
tgatgtgatg gaagtagaaa tgccgacggc gcgccgaaca ctcgtgcttg tgtttataca 6840
agcggccaca gtgctcgcaa cgctgcacgg gatgcacgtg ctgcacgagc tgtacctgag 6900
ttcctttgac gaggaatttc agtgggaagt ggagtcgtgg cgcctgcatc tcgtgctgta 6960
ctacgtcgtg gtggtcggcc tggccctctt ctgcctcgat ggtggtcatg ctgacgagcc 7020
cgcgcgggag gcaggtccag acctcggcgc gagcgggtcg gagagcgagg acgagggcgc 7080
gcaggccgga gctgtccagg gtcctgagac gctgcggagt caggtcagtg ggcagcggcg 7140
gcgcgcggtt gacttgcagg agtttttcca gggcgcgcgg gaggtccaga tggtacttga 7200
tctccaccgc gccattggtg gcgacgtcga tggcttgcag ggtcccgtgc ccctggggtg 7260
tgaccaccgt cccccgtttc ttcttgggcg gctggggcga cgggggcggt gcctcttcca 7320
tggttagaag cggcggcgag gacgcgcgcc gggcggcagg ggcggctcgg ggcccggagg 7380
caggggcggc aggggcacgt cggcgccgcg cgcgggtagg ttctggtact gcgcccggag 7440
aagactggcg tgagcgacga cgcgacggtt gacgtcctgg atctgacgcc tctgggtgaa 7500
ggccacggga cccgtgagtt tgaacctgaa agagagttcg acagaatcaa tctcggtatc 7560
gttgacggcg gcctgccgca ggatctcttg cacgtcgccc gagttgtcct ggtaggcgat 7620
ctcggtcatg aactgctcga tctcctcctc ttgaaggtct ccgcggccgg cgcgctccac 7680
ggtggccgcg aggtcgttgg agatgcggcc catgagctgc gagaaggcgt tcatgcccgc 7740
ctcgttccag acgcggctgt agaccacgac gccctcggga tcgcgggcgc gcatgaccac 7800
ctgggcgagg ttgagctcca cgtggcgcgt gaagaccgcg tagttgcaga ggcgctggta 7860
gaggtagttg agcgtggtgg cgatgtgctc ggtgacgaag aaatacatga tccagcggcg 7920
gagcggcatc tcgctgacgt cgcccagcgc ctccaaacgt tccatggcct cgtaaaagtc 7980
cacggcgaag ttgaaaaact gggagttgcg cgccgagacg gtcaactcct cctccagaag 8040
acggatgagc tcggcgatgg tggcgcgcac ctcgcgctcg aaggcccccg ggagttcctc 8100
cacttcctct tcttcctcct ccactaacat ctcttctact tcctcctcag gcggcagtgg 8160
tggcgggga gggggcctgc gtcgccggcg gcgcacgggc agacggtcga tgaagcgctc 8220
gatggtctcg ccgcgccggc gtcgcatggt ctcggtgacg gcgcgcccgt cctcgcgggg 8280
ccgcagcgtg aagacgccgc cgcgcatctc caggtggccg ggggggtccc cgttgggcag 8340
ggagagggcg ctgacgatgc atcttatcaa ttgccccgta gggactccgc gcaaggacct 8400
gagcgtctcg agatccacgg gatctgaaaa ccgctgaacg aaggcttcga gccagtcgca 8460
gtcgcaaggt aggctgagca cggtttcttc tggcgggtca tgttggttgg gagcggggcg 8520
ggcgatgctg ctggtgatga agttgaaata ggcggttctg agacggcgga tggtggcgag 8580
gagcaccagg tctttgggcc cggcttgctg gatgcgcaga cggtcggcca tgccccaggc 8640

20262014626 26 Feb 2026

gtggtcctga cacctggcca ggtccttgta gtagtcctgc atgagccgct ccacgggcac 8700
ctcctcctcg cccgcgcggc cgtgcatgcg cgtgagcccg aagccgcgct ggggctggac 8760
gagcgccagg tcggcgacga cgcgctcggc gaggatggct tgctggatct gggtgagggt 8820
ggtctggaag tcatcaaagt cgacgaagcg gtggtaggct ccggtgttga tggtgtagga 8880
gcagttggcc atgacggacc agttgacggt ctggtggccc ggacgcacga gctcgtggta 8940
cttgaggcgc gagtaggcgc gcgtgtcgaa gatgtagtcg ttgcaggtgc gcaccaggta 9000
ctggtagccg atgaggaagt gcggcggcgg ctggcggtag agcggccatc gctcggtggc 9060
gggggcgccg ggcgcgaggt cctcgagcat ggtgcggtgg tagccgtaga tgtacctgga 9120
catccaggtg atgccggcgg cggtggtgga ggcgcgcggg aactcgcgga cgcggttcca 9180
gatgttgcgc agcggcagga agtagttcat ggtgggcacg gtctggcccg tgaggcgcgc 9240
gcagtcgtgg atgctctata cgggcaaaaa cgaaagcggt cagcggctcg actccgtggc 9300
ctggaggcta agcgaacggg ttgggctgcg cgtgtacccc ggttcgaatc tcgaatcagg 9360
ctggagccgc agctaacgtg gtattggcac tcccgtctcg acccaagcct gcaccaaccc 9420
tccaggatac ggaggcgggt cgttttgcaa ctttttttg gaggccggat gagactagta 9480
agcgcggaaa gcggccgacc gcgatggctc gctgccgtag tctggagaag aatcgccagg 9540
gttgcgttgc ggtgtgcccc ggttcgaggc cggccggatt ccgcggctaa cgagggcgtg 9600
gctgccccgt cgtttccaag accccatagc cagccgactt ctccagttac ggagcgagcc 9660
cctcttttgt tttgtttgtt tttgccagat gcatcccgta ctgcggcaga tgcgccccca 9720
ccaccctcca ccgcaacaac agccccctcc acagccggcg cttctgcccc cgccccagca 9780
gcaacttcca gccacgaccg ccgcggccgc cgtgagcggg gctggacaga gttatgatca 9840
ccagctggcc ttggaagagg gcgaggggct ggcgcgcctg ggggcgtcgt cgccggagcg 9900
gcacccgcgc gtgcagatga aaagggacgc tcgcgaggcc tacgtgccca agcagaacct 9960
gttcagagac aggagcggcg aggagcccga ggagatgcgc gcggcccggt tccacgcggg 10020
gcgggagctg cggcgcggcc tggaccgaaa gagggtgctg agggacgagg atttcgaggc 10080
ggacgagctg acggggatca gccccgcgcg cgcgcacgtg gccgcggcca acctggtcac 10140
ggcgtacgag cagaccgtga aggaggagag caacttccaa aaatccttca acaaccacgt 10200
gcgcaccctg atcgcgcgcg aggaggtgac cctgggcctg atgcacctgt gggacctgct 10260
ggaggccatc gtgcagaacc ccaccagcaa gccgctgacg gcgcagctgt tcctggtggt 10320
gcagcatagt cgggacaacg aagcgttcag ggaggcgctg ctgaatatca ccgagcccga 10380
gggccgctgg ctcctggacc tggtgaacat tctgcagagc atcgtggtgc aggagcgcgg 10440
gctgccgctg tccgagaagc tggcggccat caacttctcg gtgctgagtt tgggcaagta 10500
ctacgctagg aagatctaca agaccccgta cgtgcccata gacaaggagg tgaagatcga 10560
cgggttttac atgcgcatga ccctgaaagt gctgaccctg agcgacgatc tgggggtgta 10620
ccgcaacgac aggatgcacc gtgcggtgag cgccagcagg cggcgcgagc tgagcgacca 10680
ggagctgatg catagtctgc agcgggccct gaccggggcc gggaccgagg gggagagcta 10740
ctttgacatg ggcgcggacc tgcactggca gcccagccgc cgggccttgg aggcggcggc 10800
aggaccctac gtagaagagg tggacgatga ggtggacgag gagggcgagt acctggaaga 10860
ctgatggcgc gaccgtattt ttgctagatg caacaacaac agccacctcc tgatcccgcg 10920
atgcgggcgg cgctgcagag ccagccgtcc ggcattaact cctcggacga ttggacccag 10980
gccatgcaac gcatcatggc gctgacgacc cgcaaccccg aagcctttag acagcagccc 11040
caggccaacc ggctctcggc catcctggag gccgtggtgc cctcgcgctc caaccccacg 11100
cacgagaagg tcctggccat cgtgaacgcg ctggtggaga acaaggccat ccgcggcgac 11160
gaggccggcc tggtgtacaa cgcgctgctg gagcgcgtgg cccgctacaa cagcaccaac 11220
gtgcagacca acctggaccg catggtgacc gacgtgcgcg aggccgtggc ccagcgcgag 11280
cggttccacc gcgagtccaa cctgggatcc atggtggcgc tgaacgcctt cctcagcacc 11340
cagcccgcca acgtgccccg gggccaggag gactacacca acttcatcag cgccctgcgc 11400
ctgatggtga ccgaggtgcc ccagagcgag gtgtaccagt ccgggccgga ctacttcttc 11460
cagaccagtc gccagggctt gcagaccgtg aacctgagcc aggctttcaa gaacttgcag 11520
ggcctgtggg gcgtgcaggc cccggtcggg gaccgcgcga cggtgtcgag cctgctgacg 11580
ccgaactcgc gcctgctgct gctgctggtg gccccttca cggacagcgg cagcatcaac 11640
cgcaactcgt acctgggcta cctgattaac ctgtaccgcg aggccatcgg ccaggcgcac 11700
gtggacgagc agacctacca ggagatcacc cacgtgagcc gcgccctggg ccaggacgac 11760
ccgggcaacc tggaagccac cctgaacttt ttgctgacca accggtcgca gaagatcccg 11820
ccccagtacg cgctcagcac cgaggaggag cgcatcctgc gttacgtgca gcagagcgtg 11880
ggcctgttcc tgatgcagga gggggccacc cccagcgccg cgctcgacat gaccgcgcgc 11940
aacatggagc ccagcatgta cgccagcaac cgcccgttca tcaataaact gatggactac 12000
ttgcatcggg cggccgccat gaactctgac tatttcacca acgccatcct gaatccccac 12060
tggctcccgc cgccggggtt ctacacgggc gagtacgaca tgcccgaccc caatgacggg 12120
ttcctgtggg acgatgtgga cagcagcgtg ttctcccccc gaccgggtgc taacgagcgc 12180
cccttgtgga agaaggaagg cagcgaccga cgcccgtcct cggcgctgtc cggccgcgag 12240
ggtgctgccg cggcggtgcc cgaggccgcc agtcctttcc cgagcttgcc cttctcgctg 12300
aacagtatcc gcagcagcga gctgggcagg atcacgcgcc cgcgcttgct gggcgaagag 12360
gagtacttga atgactcgct gttgagaccc gagcgggaga agaacttccc caataacggg 12420
atagaaagcc tggtggacaa gatgagccgc tggaagacgt atgcgcagga gcacagggac 12480
gatccccggg cgtcgcaggg ggccacgagc cggggcagcg ccgcccgtaa acgccggtgg 12540
cacgacaggc agcggggaca gatgtgggac gatgaggact ccgccgacga cagcagcgtg 12600
ttggacttgg gtgggagtgg taacccgttc gctcacctgc gcccccgtat cgggcgcatg 12660
atgtaagaga aaccgaaaat aaatgatact caccaaggcc atggcgacca gcgtgcgttc 12720
gtttcttctc tgttgttgtt gtatctagta tgatgaggcg tgcgtacccg gagggtcctc 12780
ctccctcgta cgagagcgtg atgcagcagg cgatggcggc ggcggcgatg cagcccccgc 12840
tggaggctcc ttacgtgccc ccgcggtacc tggcgcctac ggaggggcgg aacagcattc 12900
gttactcgga gctggcaccc ttgtacgata ccacccggtt gtacctggtg gacaacaagt 12960
cggcggacat cgcctcgctg aactaccaga acgaccacag caacttcctg accaccgtgg 13020
tgcagaacaa tgacttcacc cccacggagg ccagcaccca gaccatcaac tttgacgagc 13080
gctcgcggtg gggcggccag ctgaaaacca tcatgcacac caacatgccc aacgtgaacg 13140
agttcatgta cagcaacaag ttcaaggcgc gggtgatggt ctcccgcaag acccccaatg 13200

20262014626 26 Feb 2026

gggtgacagt gacagaggat tatgatggta gtcaggatga gctgaagtat gaatgggtgg 13260
aatttgagct gcccgaaggc aacttctcgg tgaccatgac catcgacctg atgaacaacg 13320
ccatcatcga caattacttg gcggtggggc ggcagaacgg ggtgctggag agcgacatcg 13380
gcgtgaagtt cgacactagg aacttcaggc tgggctggga ccccgtgacc gagctggtca 13440
tgcccggggt gtacaccaac gaggctttcc atcccgatat tgtcttgctg cccggctgcg 13500
gggtggactt caccgagagc cgcctcagca acctgctggg cattcgcaag aggcagccct 13560
tccaggaagg cttccagatc atgtacgagg atctggaggg gggcaacatc cccgcgctcc 13620
tggatgtcga cgcctatgag aaaagcaagg aggatgcagc agctgaagca actgcagccg 13680
tagctaccgc ctctaccgag gtcaggggcg ataattttgc aagcgccgca gcagtggcag 13740
cggccgaggc ggctgaaacc gaaagtaaga tagtcattca gccggtggag aaggatagca 13800
agaacaggag ctacaacgta ctaccggaca agataaacac cgcctaccgc agctggtacc 13860
tagcctacaa ctatggcgac cccgagaagg gcgtgcgctc ctggacgctg ctcaccacct 13920
cggacgtcac ctgcggcgtg gagcaagtct actggtcgct gcccgacatg atgcaagacc 13980
cggtcacctt ccgctccacg cgtcaagtta gcaactaccc ggtggtgggc gccgagctcc 14040
tgcccgtcta ctccaagagc ttcttcaacg agcaggccgt ctactcgcag cagctgcgcg 14100
ccttcacctc gcttacgcac gtcttcaacc gcttccccga gaaccagatc ctcgtccgcc 14160
cgcccgcgcc caccattacc accgtcagtg aaaacgttcc tgctctcaca gatcacggga 14220
ccctgccgct gcgcagcagt atccggggag tccagcgcgt gaccgttact gacgccagac 14280
gccgcacctg cccctacgtc tacaaggccc tgggcatagt cgcgccgcgc gtcctctcga 14340
gccgcacctt ctaaatgtcc attctcatct cgcccagtaa taacaccggt tggggcctgc 14400
gcgcgcccag caagatgtac ggaggcgctc gccaacgctc cacgcaacac cccgtgcgcg 14460
tgcgcgggca cttccgcgct ccctggggcg ccctcaaggg ccgcgtgcgg tcgcgcacca 14520
ccgtcgacga cgtgatcgac caggtggtgg ccgacgcgcg caactacacc cccgccgccg 14580
cgcccgtctc caccgtggac gccgtcatcg acagcgtggt ggccgacgcg cgccggtacg 14640
cccgcgccaa gagccggcgg cggcgcatcg cccggcggca ccggagcacc cccgccatgc 14700
gcgcggcgcg agccttgctg cgcagggcca ggcgcacggg acgcagggcc atgctcaggg 14760
cggccagacg cgcggcttca ggcgccagcg ccggcaggac ccggagacgc gcggccacgg 14820
cggcggcagc ggccatcgcc agcatgtccc gcccgcggcg agggaacgtg tactgggtgc 14880
gcgacgccgc caccggtgtg cgcgtgcccg tgcgcacccg ccccctcgc acttgaagat 14940
gttcacttcg cgatgttgat gtgtcccagc ggcgaggagg atgtccaagc gcaaattcaa 15000
ggaagagatg ctccaggtca tcgcgcctga gatctacggc cctgcggtgg tgaaggagga 15060
aagaaagccc cgcaaaatca agcgggtcaa aaaggacaaa aaggaagaag aaagtgatgt 15120
ggacggattg gtggagtttg tgcgcgagtt cgccccccgg cggcgcgtgc agtggcgcgg 15180
gcggaaggtg caaccggtgc tgagacccgg caccaccgtg gtcttcacgc ccggcgagcg 15240
ctccggcacc gcttccaagc gctcctacga cgaggtgtac ggggatgatg atattctgga 15300
gcaggcggcc gagcgcctgg gcgagtttgc ttacggcaag cgcagccgtt ccgcaccgaa 15360
ggaagaggcg gtgtccatcc cgctggacca cggcaacccc acgccgagcc tcaagcccgt 15420
gaccttgcag caggtgctgc cgaccgcggc gccgcgccgg gggttcaagc gcgagggcga 15480
ggatctgtac cccaccatgc agctgatggt gcccaagcgc cagaagctgg aagacgtgct 15540
ggagaccatg aaggtggacc cggacgtgca gcccgaggtc aaggtgcggc ccatcaagca 15600
ggtggccccg ggcctgggcg tgcagaccgt ggacatcaag attcccacgg agcccatgga 15660
aacgcagacc gagcccatga tcaagcccag caccagcacc atggaggtgc agacggatcc 15720
ctggatgcca tcggctccta gtcgaagacc ccggcgcaag tacggcgcgg ccagcctgct 15780
gatgcccaac tacgcgctgc atccttccat catccccacg ccgggctacc gcggcacgcg 15840
cttctaccgc ggtcatacca gcagccgccg ccgcaagacc accactcgcc gccgccgtcg 15900
ccgcaccgcc gctgcaacca cccctgccgc cctggtgcgg agagtgtacc gccgcggccg 15960
cgcacctctg accctgccgc gcgcgcgcta ccacccgagc atcgccattt aaactttcgc 16020
ctgctttgca gatcaatggc cctcacatgc cgccttcgcg ttcccattac gggctaccga 16080
ggaagaaaac cgcgccgtag aaggctggcg gggaacggga tgcgtcgcca ccaccaccgg 16140
cggcggcgcg ccatcagcaa gcggttgggg ggaggcttcc tgcccgcgct gatccccatc 16200
atcgccgcgg cgatcggggc gatccccggc attgcttccg tggcggtgca ggcctctcag 16260
cgccactgag acacacttgg aaacatcttg taataaacca atggactctg acgctcctgg 16320
tcctgtgatg tgttttcgta gacagatgga agacatcaat ttttcgtccc tggctccgcg 16380
acacggcacg cggccgttca tgggcacctg gagcgacatc ggcaccagcc aactgaacgg 16440
gggcgccttc aattggagca gtctctggag cgggcttaag aatttcgggt ccacgcttaa 16500
aacctatggc agcaaggcgt ggaacagcac cacagggcag gcgctgaggg ataagctgaa 16560
agagcagaac ttccagcaga aggtggtcga tgggctcgcc tcgggcatca acggggtggt 16620
ggacctggcc aaccaggccg tgcagcggca gatcaacagc cgcctggacc cggtgccgcc 16680
cgccggctcc gtggagatgc cgcaggtgga ggaggagctg cctcccctgg acaagcgggg 16740
cgagaagcga ccccgccccg atgcggagga gacgctgctg acgcacacgg acgagccgcc 16800
cccgtacgag gaggcggtga aactgggtct gcccaccacg cggcccatcg cgcccctggc 16860
caccggggtg ctgaaacccg aaaagcccgc gaccctggac ttgcctcctc cccagccttc 16920
ccgcccctct acagtggcta agcccctgcc gccggtggcc gtggcccgcg cgcgacccgg 16980
gggcaccgcc cgccctcatg cgaactggca gagcactctg aacagcatcg tgggtctggg 17040
agtgcagagt gtgaagcgcc gccgctgcta ttaaacctac cgtagcgctt aacttgcttg 17100
tctgtgtgtg tatgtattat gtcgccgccg ccgctgtcca ccagaaggag gagtgaagag 17160
gcgcgtcgcc gagttgcaag atggccaccc catcgatgct gccccagtgg gcgtacatgc 17220
acatcgccgg acaggacgct tcggagtacc tgagtccggg tctggtgcag tttgcccgcg 17280
ccacagacac ctacttcagt ctggggaaca agtttaggaa ccccacggtg gcgcccacgc 17340
acgatgtgac caccgaccgc agccagcggc tgacgctgcg cttcgtgccc gtggaccgcg 17400
aggacaacac ctactcgtac aaagtgcgct acacgctggc cgtgggcgac aaccgcgtgc 17460
tggacatggc cagcacctac tttgacatcc gcggcgtgct ggatcggggc cctagcttca 17520
aaccctactc cggcaccgcc tacaacagtc tggcccccaa gggagcaccc aacacttgtc 17580
agtggacata taaagccgat ggtgaaactg ccacagaaaa aacctataca tatggaaatg 17640
cacccgtgca gggcattaac atcacaaaag atggtattca acttggaact gacaccgatg 17700
atcagccaat ctacgcagat aaaacctatc agcctgaacc tcaagtgggt gatgctgaat 17760

20262014622 26 Feb 2026

ggcatgacat cactggtact gatgaaaagt atggaggcag agctcttaag cctgatacca 17820
aaatgaagcc ttgttatggt tcttttgcca agcctactaa taaagaagga ggtcaggcaa 17880
atgtgaaaac aggaacaggc actactaaag aatatgacat agacatggct ttctttgaca 17940
acagaagtgc ggctgctgct ggcctagctc cagaaattgt tttgtatact gaaaatgtgg 18000
atttggaaac tccagatacc catattgtat acaaagcagg cacagatgac agcagctctt 18060
ctattaattt gggtcagcaa gccatgccca acagacctaa ctacattggt ttcagagaca 18120
actttatcgg gctcatgtac tacaacagca ctggcaatat gggggtgctg gccggtcagg 18180
cttctcagct gaatgctgtg gttgacttgc aagacagaaa caccgagctg tcctaccagc 18240
tcttgcttga ctctctgggt gacagaaccc ggtatttcag tatgtggaat caggcggtgg 18300
acagctatga tcctgatgtg cgcattattg aaaatcatgg tgtggaggat gaacttccca 18360
actattgttt ccctctggat gctgttggca gaacagatac ttatcaggga attaaggcta 18420
atggaactga tcaaaccaca tggaccaaag atgacagtgt caatgatgct aatgagatag 18480
gcaagggtaa tccattcgcc atggaaatca acatccaagc caacctgtgg aggaacttcc 18540
tctacgccaa cgtggccctg tacctgcccg actcttacaa gtacacgccg gccaatgtta 18600
ccctgcccac caacaccaac acctacgatt acatgaacgg ccgggtggtg gcgccctcgc 18660
tggtggactc ctacatcaac atcggggcgc gctggtcgct ggatcccatg gacaacgtga 18720
acccccttcaa ccaccaccgc aatgcggggc tgcgctaccg ctccatgctc ctgggcaacg 18780
ggcgctacgt gcccttccac atccaggtgc cccagaaatt tttcgccatc aagagcctcc 18840
tgctcctgcc cgggtcctac acctacgagt ggaacttccg caaggacgtc aacatgatcc 18900
tgcagagctc cctcggcaac gacctgcgca cggacggggc ctccatctcc ttcaccagca 18960
tcaacctcta cgccaccttc ttccccatgg cgcacaacac ggcctccacg ctcgaggcca 19020
tgctgcgcaa cgacaccaac gaccagtcct tcaacgacta cctctcggcg gccaacatgc 19080
tctaccccat cccggccaac gccaccaacg tgcccatctc catcccctcg cgcaactggg 19140
ccgccttccg cggctggtcc ttcacgcgtc tcaagaccaa ggagacgccc tcgctgggct 19200
ccgggttcga cccctacttc gtctactcgg gctccatccc ctacctcgac ggcaccttct 19260
acctcaacca caccttcaag aaggtctcca tcaccttcga ctcctccgtc agctggcccg 19320
gcaacgaccg gctcctgacg cccaacgagt tcgaaatcaa gcgcaccgtc gacggcgagg 19380
gctacaacgt ggcccagtgc aacatgacca aggactggtt cctggtccag atgctggccc 19440
actacaacat cggctaccag ggcttctacg tgcccgaggg ctacaaggac cgcatgtact 19500
ccttcttccg caacttccag cccatgagcc gccaggtggt ggacgaggtc aactacaagg 19560
actaccaggc cgtcaccctg gcctaccagc acaacaactc gggcttcgtc ggctacctcg 19620
cgcccaccat gcgccagggc cagccctacc ccgccaacta cccctacccg ctcatcggca 19680
agagcgccgt caccagcgtc acccagaaaa agttcctctg cgacagggtc atgtggcgca 19740
tccccttctc cagcaacttc atgtccatgg gcgcgctcac cgacctcggc cagaacatgc 19800
tctatgccaa ctccgcccac gcgctagaca tgaatttcga agtcgacccc atggatgagt 19860
ccacccttct ctatgttgtc ttcgaagtct tcgacgtcgt ccgagtgcac cagccccacc 19920
gcggcgtcat cgaggccgtc tacctgcgca ccccttctc ggccggtaac gccaccacct 19980
aagctcttgc ttcttgcaag ccatggccgc gggctccggc gagcaggagc tcagggccat 20040
catccgcgac ctgggctgcg ggccctactt cctgggcacc ttcgataagc gcttcccggg 20100
attcatggcc ccgcacaagc tggcctgcgc catcgtcaac acggccggcc gcgagaccgg 20160
gggcgagcac tggctggcct tcgcctggaa cccgcgctcg aacacctgct acctcttcga 20220
ccccttcggg ttctcggacg agcgcctcaa gcagatctac cagttcgagt acgagggcct 20280
gctgcgccgc agcgccctgg ccaccgagga ccgctgcgtc accctggaaa agtccaccca 20340
gaccgtgcag ggtccgcgct cggccgcctg cgggctcttc tgctgcatgt tcctgcacgc 20400
cttcgtgcac tggcccgacc gccccatgga caagaacccc accatgaact tgctgacggg 20460
ggtgcccaac ggcatgctcc agtcgcccca ggtggaaccc accctgcgcc gcaaccagga 20520
ggcgctctac cgcttcctca actcccactc cgcctacttt cgctcccacc gcgcgcgcat 20580
cgagaaggcc accgccttcg accgcatgaa tcaagacatg taaaccgtgt gtgtatgtta 20640
aatgtcttta ataaacagca ctttcatgtt acacatgcat ctgagatgat ttatttagaa 20700
atcgaaaggg ttctgccggg tctcggcatg gcccgcgggc agggacacgt tgcggaactg 20760
gtacttggcc agccacttga actcggggat cagcagtttg ggcagcgggg tgtcggggaa 20820
ggagtcggtc cacagcttcc gcgtcagttg cagggcgccc agcaggtcgg gcgcggagat 20880
cttgaaatcg cagttgggac ccgcgttctg cgcgcgggag ttgcggtaca cggggttgca 20940
gcactggaac accatcaggg ccgggtgctt cacgctcgcc agcaccgtcg cgtcggtgat 21000
gctctccacg tcgaggtcct cggcgttggc catcccgaag ggggtcatct tgcaggtctg 21060
ccttcccatg gtgggcacgc acccgggctt gtggttgcaa tcgcagtgca gggggatcag 21120
catcatctgg gcctggtcgg cgttcatccc cgggtacatg gccttcatga aagcctccaa 21180
ttgcctgaac gcctgctggg ccttggctcc ctcggtgaag aagaccccgc aggacttgct 21240
agagaactgg ttggtggcgc acccggcgtc gtgcacgcag cagcgcgcgt cgttgttggc 21300
cagctgcacc acgctgcgcc cccagcggtt ctgggtgatc ttggcccggt cggggttctc 21360
cttcagcgcg cgctgcccgt tctcgctcgc cacatccatc tcgatcatgt gctccttctg 21420
gatcatggtg gtcccgtgca ggcaccgcag cttgccctcg gcctcggtgc acccgtgcag 21480
ccacagcgcg cacccggtgc actcccagtt cttgtgggcg atctgggaat gcgcgtgcac 21540
gaagccctgc aggaagcggc ccatcatggt ggtcagggtc ttgttgctag tgaaggtcag 21600
cggaatgccg cggtgctcct cgttgatgta caggtggcag atgcggcggt acacctcgcc 21660
ctgctcgggc atcagctgga agttggcttt caggtcggtc tccacgcggt agcggtccat 21720
cagcatagtc atgatttcca tacccttctc ccaggccgag acgatgggca ggctcatagg 21780
gttcttcacc atcatcttag cgctagcagc cgcggccagg gggtcgctct cgtccagggt 21840
ctcaaagctc cgcttgccgt ccttctcggt gatccgcacc ggggggtagc tgaagcccac 21900
ggccgccagc tcctcctcgg cctgtctttc gtcctcgctg tcctggctga cgtcctgcag 21960
gaccacatgc ttggtcttgc ggggtttctt cttgggcggc agcggcggcg gagatgttgg 22020
agatggcgag ggggagcgcg agttctcgct caccactact atctcttcct cttcttggtc 22080
cgaggccacg cggcggtagg tatgtctctt cgggggcaga ggcggaggcg acgggctctc 22140
gccgccgcga cttggcggat ggctggcaga gcccccttcg cgttcggggg tgcgctcccg 22200
gcggcgctct gactgacttc ctccgcggcc ggccattgtg ttctcctagg gaggaacaac 22260
aagcatggag actcagccat cgccaacctc gccatctgcc cccaccgccg acgagaagca 22320

20262014626 26 Feb 2026

gcagcagcag aatgaaagct taaccgcccc gccgcccagc cccgccacct ccgacgcggc 22380
cgtcccagac atgcaagaga tggaggaatc catcgagatt gacctgggct atgtgacgcc 22440
cgcggagcac gaggaggagc tggcagtgcg cttttcacaa gaagagatac accaagaaca 22500
gccagagcag gaagcagaga atgagcagag tcaggctggg ctcgagcatg acggcgacta 22560
cctccacctg agcgggggggg aggacgcgct catcaagcat ctggcccggc aggccaccat 22620
cgtcaaggat gcgctgctcg accgcaccga ggtgcccctc agcgtggagg agctcagccg 22680
cgcctacgag ttgaacctct tctcgccgcg cgtgcccccc aagcgccagc ccaatggcac 22740
ctgcgagccc aacccgcgcc tcaacttcta cccggtcttc gcggtgcccg aggccctggc 22800
cacctaccac atctttttca agaaccaaaa gatccccgtc tcctgccgcg ccaaccgcac 22860
ccgcgccgac gccctttttca acctgggtcc cggcgcccgc ctacctgata tcgcctcctt 22920
ggaagaggtt cccaagatct tcgagggtct gggcagcgac gagactcggg ccgcgaacgc 22980
tctgcaagga gaaggaggag agcatgagca ccacagcgcc ctggtcgagt tggaaggcga 23040
caacgcgcgg ctggcggtgc tcaaacgcac ggtcgagctg acccatttcg cctacccggc 23100
tctgaacctg ccccccaaag tcatgagcgc ggtcatggac caggtgctca tcaagcgcgc 23160
gtcgcccatc tccgaggacg agggcatgca agactccgag gagggcaagc ccgtggtcag 23220
cgacgagcag ctggcccggt ggctgggtcc taatgctagt ccccagagtt tggaagagcg 23280
gcgcaaactc atgatggccg tggtcctggt gaccgtggag ctggagtgcc tgcgccgctt 23340
cttcgccgac gcggagaccc tgcgcaaggt cgaggagaac ctgcactacc tcttcaggca 23400
cgggttcgtg cgccaggcct gcaagatctc caacgtggag ctgaccaacc tggtctccta 23460
catgggcatc ttgcacgaga accgcctggg gcagaacgtg ctgcacacca ccctgcgcgg 23520
ggaggcccgg cgcgactaca tccgcgactg cgtctacctc tacctctgcc acacctggca 23580
gacgggcatg ggcgtgtggc agcagtgtct ggaggagcag aacctgaaag agctctgcaa 23640
gctcctgcag aagaacctca agggtctgtg gaccgggttc gacgagcgca ccaccgcctc 23700
ggacctggcc gacctcattt tccccgagcg cctcaggctg acgctgcgca acggcctgcc 23760
cgactttatg agccaaagca tgttgcaaaa ctttcgctct ttcatcctcg aacgctccgg 23820
aatcctgccc gccacctgct ccgcgctgcc ctcggacttc gtgccgctga ccttccgcga 23880
gtgccccccg ccgctgtgga gccactgcta cctgctgcgc ctggccaact acctggccta 23940
ccactcggac gtgatcgagg acgtcagcgg cgagggcctg ctcgagtgcc actgccgctg 24000
caacctctgc acgccgcacc gctccctggc ctgcaacccc cagctgctga gcgagaccca 24060
gatcatcggc accttcgagt tgcaagggcc cagcgaaggc gagggttcag ccgccaaggg 24120
gggtctgaaa ctcaccccgg ggctgtggac ctcggcctac ttgcgcaagt tcgtgcccga 24180
ggactaccat cccttcgaga tcaggttcta cgaggaccaa tcccatccgc ccaaggccga 24240
gctgtcggcc tgcgtcatca cccagggggc gatcctggcc caattgcaag ccatccagaa 24300
atcccgccaa gaattcttgc tgaaaaaggg ccgcggggtc tacctcgacc cccagaccgg 24360
tgaggagctc aaccccggct tcccccagga tgccccgagg aaacaagaag ctgaaagtgg 24420
agctgccgcc cgtggaggat ttggaggaag actgggagaa cagcagtcag gcagaggagg 24480
aggagatgga ggaagactgg gacagcactc aggcagagga ggacagcctg caagacagtc 24540
tggaggaaga cgaggaggag gcagaggagg aggtggaaga agcagccgcc gccagaccgt 24600
cgtcctcggc gggggagaaa gcaagcagca cggataccat ctccgctccg ggtcggggtc 24660
ccgctcgacc acacagtaga tgggacgaga ccggacgatt cccgaacccc accacccaga 24720
ccggtaagaa ggagcggcag ggatacaagt cctggcgggg gcacaaaaac gccatcgtct 24780
cctgcttgca ggcctgcggg ggcaacatct ccttcacccg gcgctacctg ctcttccacc 24840
gcggggtgaa ctttccccgc aacatcttgc attactaccg tcacctccac agcccctact 24900
acttccaaga agaggcagca gcagcagaaa aagaccagca gaaaaccagc agctagaaaa 24960
tccacagcgg cggcagcagg tggactgagg atcgcggcga acgagccggc gcaaacccgg 25020
gagctgagga accggatctt tcccaccctc tatgccatct tccagcagag tcgggggcag 25080
gagcaggaac tgaaagtcaa gaaccgttct ctgcgctcgc tcacccgcag ttgtctgtat 25140
cacaagagcg aagaccaact tcagcgcact ctcgaggacg ccgaggctct cttcaacaag 25200
tactgcgcgc tcactcttaa agagtagccc gcgcccgccc agtcgcagaa aaaggcggga 25260
attacgtcac ctgtgccctt cgccctagcc gcctccaccc atcatcatga gcaaagagat 25320
tcccacgcct tacatgtgga gctaccagcc ccagatgggc ctggccgccg gtgccgccca 25380
ggactactcc acccgcatga attggctcag cgccgggccc gcgatgatct cacgggtgaa 25440
tgacatccgc gcccaccgaa accagatact cctagaacag tcagcgctca ccgccacgcc 25500
ccgcaatcac ctcaatccgc gtaattggcc cgccgccctg gtgtaccagg aaattcccca 25560
gcccacgacc gtactacttc cgcgagacgc ccaggccgaa gtccagctga ctaactcagg 25620
tgtccagctg gcgggcggcg ccaccctgtg tcgtcaccgc cccgctcagg gtataaagcg 25680
gctggtgatc cggggcagag gcacacagct caacgacgag gtggtgagct cttcgctggg 25740
tctgcgacct gacggagtct tccaactcgc cggatcgggg agatcttcct tcacgcctcg 25800
tcaggccgtc ctgactttgg agagttcgtc ctcgcagccc cgctcgggtg gcatcggcac 25860
tctccagttc gtggaggagt tcactccctc ggtctacttc aacccttct ccggctcccc 25920
cggccactac ccggacgagt tcatcccgaa cttcgacgcc atcagcgagt cggtggacgg 25980
ctacgattga aactaatcac ccccttatcc agtgaaataa agatcatatt gatgatgatt 26040
ttacagaaat aaaaaataat catttgattt gaaataaaga tacaatcata ttgatgattt 26100
gagtttaaca aaaaaataaa gaatcactta cttgaaatct gataccaggt ctctgtccat 26160
gttttctgcc aacaccactt cactcccctc ttcccagctc tggtactgca ggccccggcg 26220
ggctgcaaac ttcctccaca cgctgaaggg gatgtcaaat tcctcctgtc cctcaatctt 26280
cattttatct tctatcagat gtccaaaaag cgcgtccggg tggatgatga cttcgacccc 26340
gtctacccct acgatgcaga caacgcaccg accgtgccct tcatcaaccc ccccttcgtc 26400
tcttcagatg gattccaaga gaagcccctg ggggtgttgt ccctgcgact ggccgacccc 26460
gtcaccacca agaacgggga aatcaccctc aagctgggag agggggtgga cctcgattcc 26520
tcgggaaaac tcatctccaa cacggccacc aaggccgccg cccctctcag tttttccaac 26580
aacaccattt cccttaacat ggatcacccc ttttacacta aagatggaaa attatcctta 26640
caagtttctc caccattaaa tatactgaga acaagcattc taaacacact agctttaggt 26700
tttggatcag gtttaggact ccgtggctct gccttggcag tacagttagt ctctccactt 26760
acatttgata ctgatggaaa cataaagctt accttagaca gaggtttgca tgttacaaca 26820
ggagatgcaa ttgaaagcaa cataagctgg gctaaaggtt taaaatttga agatggagcc 26880

2026201462 26 Feb 2026

		atagcaacca acattggaaa tgggttagag tttggaagca gtagtacaga aacaggtgtt 26940 gatgatgctt acccaatcca agttaaactt ggatctggcc ttagctttga cagtacagga 27000 gccataatgg ctggtaacaa agaagacgat aaactcactt tgtggacaac acctgatcca 27060 tcaccaaact gtcaaatact cgcagaaaat gatgcaaaac taacactttg cttgactaaa 27120 tgtggtagtc aaatactggc cactgtgtca gtcttagttg taggaagtgg aaacctaaac 27180 cccattactg gcaccgtaag cagtgctcag gtgtttctac gttttgatgc aaacggtgtt 27240 cttttaacag aacattctac actaaaaaaa tactgggggt ataggcaggg agatagcata 27300 gatggcactc catataccaa tgctgtagga ttcatgccca atttaaaagc ttatccaaag 27360 tcacaaagtt ctactactaa aaataatata gtagggcaag tatacatgaa tggagatgtt 27420 tcaaaaccta tgcttctcac tataaccctc aatggtactg atgacagcaa cagtacatat 27480 tcaatgtcat tttcatacac ctggactaat ggaagctatg ttggagcaac atttggggct 27540 aactcttata ccttctcata catcgcccaa gaatgaacac tgtatcccac cctgcatgcc 27600 aacccttccc accccactct gtggaacaaa ctctgaaaca caaaataaaa taaagttcaa 27660 gtgttttatt gattcaacag ttttacagga ttcgagcagt tatttttcct ccaccctccc 27720 aggacatgga atacaccacc ctctcccccc gcacagcctt gaacatctga atgccattgg 27780 tgatggacat gcttttggtc tccacgttcc acacagtttc agagcgagcc agtctcgggt 27840 cggtcaggga gatgaaaccc tccgggcact cccgcatctg cacctcacag ctcaacagct 27900 gaggattgtc ctcggtggtc gggatcacgg ttatctggaa gaagcagaag agcggcggtg 27960 ggaatcatag tccgcgaacg ggatcggccg gtggtgtcgc atcaggcccc gcagcagtcg 28020 ctgccgccgc cgctccgtca agctgctgct cagggggtcc gggtccaggg actccctcag 28080 catgatgccc acggccctca gcatcagtcg tctggtgcgg cgggcgcagc agcgcatgcg 28140 gatctcgctc aggtcgctgc agtacgtgca acacagaacc accaggttgt tcaacagtcc 28200 atagttcaac acgctccagc cgaaactcat cgcgggaagg atgctaccca cgtggccgtc 28260 gtaccagatc ctcaggtaaa tcaagtggtg ccccctccag aacacgctgc ccacgtacat 28320 gatctccttg ggcatgtggc ggttcaccac ctcccggtac cacatcaccc tctggttgaa 28380 catgcagccc cggatgatcc tgcggaacca cagggccagc accgccccgc ccgccatgca 28440 gcgaagagac cccgggtccc ggcaatggca atggaggacc caccgctcgt acccgtggat 28500 catctgggag ctgaacaagt ctatgttggc acagcacagg catatgctca tgcatctctt 28560 cagcactctc aactcctcgg gggtcaaaac catatcccag ggcacgggga actcttgcag 28620 gacagcgaac cccgcagaac agggcaatcc tcgcacagaa cttacattgt gcatggacag 28680 ggtatcgcaa tcaggcagca ccgggtgatc ctccaccaga gaagcgcggg tctcggtctc 28740 ctcacagcgt ggtaaggggg ccggccgata cgggtgatgg cgggacgcgg ctgatcgtgt 28800 tcgcgaccgt gtcatgatgc agttgctttc ggacattttc gtacttgctg tagcagaacc 28860 tggtccgggc gctgcacacc gatcgccggc ggcggtctcg gcgcttggaa cgctcggtgt 28920 tgaaattgta aaacagccac tctctcagac cgtgcagcag atctagggcc tcaggagtga 28980 tgaagatccc atcatgcctg atggctctga tcacatcgac caccgtggaa tgggccagac 29040 ccagccagat gatgcaattt tgttgggttt cggtgacggc gggggaggga agaacaggaa 29100 gaaccatgat taacttttaa tccaaacggt ctcggagtac ttcaaaatga agatcgcgga 29160 gatggcacct ctcgcccccg ctgtgttggt ggaaaataac agccaggtca aaggtgatac 29220 ggttctcgag atgttccacg gtggcttcca gcaaagcctc cacgcgcaca tccagaaaca 29280 agacaatagc gaaagcggga gggttctcta attcctcaat catcatgtta cactcctgca 29340 ccatccccag ataattttca tttttccagc cttgaatgat tcgaactagt tcctgaggta 29400 aatccaagcc agccatgata aagagctcgc gcagagcgcc ctccaccggc attcttaagc 29460 acaccctcat aattccaaga tattctgctc ctggttcacc tgcagcagat tgacaagcgg 29520 aatatcaaaa tctctgccgc gatccctgag ctcctccctc agcaataact gtaagtactc 29580 tttcatatcc tctccgaaat ttttagccat aggaccacca ggaataagat tagggcaagc 29640 cacagtacag ataaaccgaa gtcctcccca gtgagcattg ccaaatgcaa gactgctata 29700 agcatgctgg ctagacccgg tgatatcttc cagataactg gacagaaaat cgcccaggca 29760 atttttaaga aaatcaacaa aagaaaaatc ctccaggtgg acgtttagag cctcgggaac 29820 aacgatgaag taaatgcaag cggtgcgttc cagcatggtt agttagctga tctgtagaaa 29880 aaacaaaaat gaacattaaa ccatgctagc ctggcgaaca ggtgggtaaa tcgttctctc 29940 cagcaccagg caggccacgg ggtctccggc gcgaccctcg taaaaattgt cgctatgatt 30000 gaaaaccatc acagagagac gttcccggtg gccggcgtga atgattcgac aagatgaata 30060 caccccccgga acattggcgt ccgcgagtga aaaaaagcgc ccgaggaagc aataaggcac 30120 tacaatgctc agtctcaagt ccagcaaagc gatgccatgc ggatgaagca caaaattctc 30180 aggtgcgtac aaaatgtaat tactcccctc ctgcacaggc agcaaagccc ccgatccctc 30240 caggtacaca tacaaagcct cagcgtccat agcttaccga gcagcagcac acaacaggcg 30300 caagagtcag agaaaggctg agctctaacc tgtccacccg ctctctgctc aatatatagc 30360 ccagatctac actgacgtaa aggccaaagt ctaaaaatac ccgccaaata atcacacacg 30420 cccagcacac gcccagaaac cggtgacaca ctcaaaaaaa tacgcgcact tcctcaaacg 30480 cccaaaactg ccgtcatttc cgggttccca cgctacgtca tcaaaacacg actttcaaat 30540 tccgtcgacc gttaaaaacg tcacccgccc cgcccctaac ggtcgcccgt ctctcagcca 30600 atcagcgccc cgcatcccca aattcaaaca cctcatttgc atattaacgc gcacaaaaag 30660 tttgaggtat attattgatg atgg 30684
3-14	**Sequences**	
3-14-1	Sequence Number [ID]	14
3-14-2	Molecule Type	DNA
3-14-3	Length	8602
3-14-4	Features	**misc_feature 1..8602**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..8602
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-14-5	Residues	atgggcggcg catgagagaa gcccagacca attacctacc caaaatggag aaagttcacg 60

20262014626 26 Feb 2026

ttgacatcga ggaagacagc ccattcctca gagctttgca gcggagcttc ccgcagtttg 120
aggtagaagc caagcaggtc actgataatg accatgctaa tgccagagcg ttttcgcatc 180
tggcttcaaa actgatcgaa acggaggtgg acccatccga cacgatcctt gacattggaa 240
gtgcgcccgc ccgcagaatg tattctaagc acaagtatca ttgtatctgt ccgatgagat 300
gtgcggaaga tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgtaagg 360
aaataactga taaggaattg gacaagaaaa tgaaggagct cgccgccgtc atgagcgacc 420
ctgacctgga aactgagact atgtgcctcc acgacgacga gtcgtgtcgc tacgaagggc 480
aagtcgctgt ttaccaggat gtatacgcgg ttgacggacc gacaagtctc tatcaccaag 540
ccaataaggg agttagagtc gcctactgga taggctttga caccacccct tttatgttta 600
agaacttggc tggagcatat ccatcatact ctaccaactg ggccgacgaa accgtgttaa 660
cggctcgtaa cataggccta tgcagctctg acgttatgga gcggtcacgt agagggatgt 720
ccattcttag aaagaagtat ttgaaaccat ccaacaatgt tctattctct gttggctcga 780
ccatctacca cgagaagagg gacttactga ggagctggca cctgccgtct gtatttcact 840
tacgtggcaa gcaaaattac acatgtcggt gtgagactat agttagttgc gacgggtacg 900
tcgttaaaag aatagctatc agtccaggcc tgtatgggaa gccttcaggc tatgctgcta 960
cgatgcaccg cgagggattc ttgtgctgca aagtgacaga cacattgaac ggggagaggg 1020
tctcttttcc cgtgtgcacg tatgtgccag ctacattgtg tgaccaaatg actggcatac 1080
tggcaacaga tgtcagtgcg gacgacgcgc aaaaactgct ggttgggctc aaccagcgta 1140
tagtcgtcaa cggtcgcacc cagagaaaca ccaataccat gaaaaattac cttttgcccg 1200
tagtggccca ggcatttgct aggtgggcaa aggaatataa ggaagatcaa gaagatgaaa 1260
ggccactagg actacgagat agacagttag tcatggggtg ttgttgggct tttagaaggc 1320
acaagataac atctatttat aagcgcccgg atacccaaac catcatcaaa gtgaacagcg 1380
atttccactc attcgtgctg cccaggatag gcagtaacac attggagatc gggctgagaa 1440
caagaatcag gaaaatgtta gaggagcaca aggagccgtc acctctcatt accgccgagg 1500
acgtacaaga agctaagtgc gcagccgatg aggctaagga ggtgcgtgaa gccgaggagt 1560
tgcgcgcagc tctaccacct ttggcagctg atgttgagga gcccactctg gaagccgatg 1620
tcgacttgat gttacaagag gctggggccg gctcagtgga gacacctcgt ggcttgataa 1680
aggttaccag ctacgctggc gaggacaaga tcggctctta cgctgtgctt tctccgcagg 1740
ctgtactcaa gagtgaaaaa ttatcttgca tccaccctct cgctgaacaa gtcatagtga 1800
taacacactc tggccgaaaa gggcgttatg ccgtggaacc ataccatggt aaagtagtgg 1860
tgccagaggg acatgcaata cccgtccagg actttcaagc tctgagtgaa agtgccacca 1920
ttgtgtacaa cgaacgtgag ttcgtaaaca ggtacctgca ccatattgcc acacatggag 1980
gagcgctgaa cactgatgaa gaatattaca aaactgtcaa gcccagcgag cacgacggcg 2040
aatacctgta cgacatcgac aggaaacagt gcgtcaagaa agaactagtc actgggctag 2100
ggctcacagg cgagctggtg gatcctccct tccatgaatt cgcctacgag agtctgagaa 2160
cacgaccagc cgctccttac caagtaccaa ccataggggt gtatggcgtg ccaggatcag 2220
gcaagtctgg catcattaaa agcgcagtca ccaaaaaaga tctagtggtg agcgccaaga 2280
aagaaaactg tgcagaaatt ataagggacg tcaagaaaat gaaagggctg gacgtcaatg 2340
ccagaactgt ggactcagtg ctcttgaatg gatgcaaaca ccccgtagag accctgtata 2400
ttgacgaagc ttttgcttgt catgcaggta ctctcagagc gctcatagcc attataagac 2460
ctaaaaaggc agtgctctgc ggggatccca aacagtgcgg ttttttaac atgatgtgcc 2520
tgaaagtgca ttttaaccac gagatttgca cacaagtctt ccacaaaagc atctctcgcc 2580
gttgcactaa atctgtgact tcggtcgtct caaccttgtt ttacgacaaa aaaatgagaa 2640
cgacgaatcc gaaagagact aagattgtga ttgacactac cggcagtacc aaacctaagc 2700
aggacgatct cattctcact tgtttcagag ggtgggtgaa gcagttgcaa atagattaca 2760
aaggcaacga aataatgacg gcagctgcct ctcaagggct gacccgtaaa ggtgtgtatg 2820
ccgttcggta caaggtgaat gaaaatcctc tgtacgcacc cacctcagaa catgtgaacg 2880
tcctactgac ccgcacggag gaccgcatcg tgtggaaaac actagccggc gacccatgga 2940
taaaaacact gactgccaag taccctggga atttcactgc cacgatagag gagtggcaag 3000
cagagcatga tgccatcatg aggcacatct tggagagacc ggaccctacc gacgtcttcc 3060
agaataaggc aaacgtgtgt tgggccaagg ctttagtgcc ggtgctgaag accgctggca 3120
tagacatgac cactgaacaa tggaacactg tggattattt tgaaacggac aaagctcact 3180
cagcagagat agtattgaac caactatgcg tgaggttctt tggactcgat ctggactccg 3240
gtctattttc tgcacccact gttccgttat ccattaggaa taatcactgg gataactccc 3300
cgtcgcctaa catgtacggg ctgaataaag aagtggtccg tcagctctct cgcaggtacc 3360
cacaactgcc tcgggcagtt gccactggaa gagtctatga catgaacact ggtacactgc 3420
gcaattatga tccgcgcata aacctagtac ctgtaaacag aagactgcct catgctttag 3480
tcctccacca taatgaacac ccacagagtg acttttcttc attcgtcagc aaattgaagg 3540
gcagaactgt cctggtggtc ggggaaaagt tgtccgtccc aggcaaaatg gttgactggt 3600
tgtcagaccg gcctgaggct accttcagag ctcggctgga tttaggcatc ccaggtgatg 3660
tgcccaaata tgacataata tttgttaatg tgaggacccc atataaatac catcactatc 3720
agcagtgtga agaccatgcc attaagctta gcatgttgac caagaaagct tgtctgcatc 3780
tgaatcccgg cggaacctgt gtcagcatag gttatggtta cgctgacagg gccagcgaaa 3840
gcatcattgg tgctatagcg cggcagttca agttttcccg ggtatgcaaa ccgaaatcct 3900
cacttgaaga gacggaagtt ctgtttgtat tcattgggta cgatcgcaag gcccgtacgc 3960
acaatcctta caagctttca tcaaccttga ccaacattta tacaggttcc agactccacg 4020
aagccggatg tgcaccctca tatcatgtgg tgcgagggga tattgccacg gccaccgaag 4080
gagtgattat aaatgctgct aacagcaaag gacaacctgg cggaggggtg tgcggagcgc 4140
tgtataagaa attcccggaa agcttcgatt tacagccgat cgaagtagga aaagcgcgac 4200
tggtcaaagg tgcagctaaa catatcattc atgccgtagg accaaacttc aacaaagttt 4260
cggaggttga aggtgacaaa cagttggcag aggcttatga gtccatcgct aagattgtca 4320
acgataacaa ttacaagtca gtagcgattc cactgttgtc caccggcatc ttttccggga 4380
acaaagatcg actaacccaa tcattgaacc atttgctgac agctttagac accactgatg 4440
cagatgtagc catatactgc agggacaaga aatgggaaat gactctcaag gaagcagtgg 4500
ctaggagaga agcagtggag gagatatgca tatccgacga ctcttcagtg acagaacctg 4560
atgcagagct ggtgagggtg catccgaaga gttctttggc tggaaggaag ggctacagca 4620

2026201462 26 Feb 2026

		caagcgatgg caaaactttc tcatatttgg aagggaccaa gtttcaccag gcggccaagg 4680 atatagcaga aattaatgcc atgtggcccg ttgcaacgga ggccaatgag caggtatgca 4740 tgtatatcct cggagaaagc atgagcagta ttaggtcgaa atgccccgtc gaagagtcgg 4800 aagcctccac accacctagc acgctgcctt gcttgtgcat ccatgccatg actccagaaa 4860 gagtacagcg cctaaaagcc tcacgtccag aacaaattac tgtgtgctca tcctttccat 4920 tgccgaagta tagaatcact ggtgtgcaga agatccaatg ctcccagcct atattgttct 4980 caccgaaagt gcctgcgtat attcatccaa ggaagtatct cgtggaaaca ccaccggtag 5040 acgagactcc ggagccatcg gcagagaacc aatccacaga ggggacacct gaacaaccac 5100 cacttataac cgaggatgag accaggacta gaacgcctga gccgatcatc atcgaagagg 5160 aagaagagga tagcataagt ttgctgtcag atggcccgac ccaccaggtg ctgcaagtcg 5220 aggcagacat tcacgggccg ccctctgtat ctagctcatc ctggtccatt cctcatgcat 5280 ccgactttga tgtggacagt ttatccatac ttgacaccct ggagggagct agcgtgacca 5340 gcggggcaac gtcagccgag actaactctt acttcgcaaa gagtatggag tttctggcgc 5400 gaccggtgcc tgcgcctcga acagtattca ggaaccctcc acatcccgct ccgcgcacaa 5460 gaacaccgtc acttgcaccc agcagggcct gctcgagaac cagcctagtt tccaccccgc 5520 caggcgtgaa tagggtgatc actagagagg agctcgaggc gcttaccccg tcacgcactc 5580 ctagcaggtc ggtctcgaga accagcctgg tctccaaccc gccaggcgta aatagggtga 5640 ttacaagaga ggagtttgag gcgttcgtag cacaacaaca atgacggttt gatgcgggtg 5700 catacatctt ttcctccgac accggtcaag ggcatttaca acaaaaatca gtaaggcaaa 5760 cggtgctatc cgaagtggtg ttggagagga ccgaattgga gatttcgtat gccccgcgcc 5820 tcgaccaaga aaaagaagaa ttactacgca agaaattaca gttaaatccc acacctgcta 5880 acagaagcag ataccagtcc aggaaggtgg agaacatgaa agccataaca gctagacgta 5940 ttctgcaagg cctagggcat tatttgaagg cagaaggaaa agtggagtgc taccgaaccc 6000 tgcatcctgt tcctttgtat tcatctagtg tgaaccgtgc cttttcaagc cccaaggtcg 6060 cagtggaagc ctgtaacgcc atgttgaaag agaactttcc gactgtggct tcttactgta 6120 ttattccaga gtacgatgcc tatttggaca tggttgacgg agcttcatgc tgcttagaca 6180 ctgccagttt ttgccctgca aagctgcgca gctttccaaa gaaacactcc tatttggaac 6240 ccacaatacg atcggcagtg ccttcagcga tccagaacac gctccagaac gtcctggcag 6300 ctgccacaaa aagaaattgc aatgtcacgc aaatgagaga attgcccgta ttggattcgg 6360 cggcctttaa tgtggaatgc ttcaagaaat atgcgtgtaa taatgaatat tgggaaacgt 6420 ttaaagaaaa ccccatcagg cttactgaag aaaacgtggt aaattacatt accaaattaa 6480 aaggaccaaa agctgctgct ctttttgcga agacacataa tttgaatatg ttgcaggaca 6540 taccaatgga caggtttgta atggacttaa agagagacgt gaaagtgact ccaggaacaa 6600 aacatactga agaacggccc aaggtacagg tgatccaggc tgccgatccg ctagcaacag 6660 cgtatctgtg cggaatccac cgagagctgg ttaggagatt aaatgcggtc ctgcttccga 6720 acattcatac actgtttgat atgtcggctg aagactttga cgctattata gccgagcact 6780 tccagcctgg ggattgtgtt ctggaaactg acatcgcgtc gtttgataaa agtgaggacg 6840 acgccatggc tctgaccgcg ttaatgattc tggaagactt aggtgtggac gcagagctgt 6900 tgacgctgat tgaggcggct ttcggcgaaa tttcatcaat acatttgccc actaaaacta 6960 aatttaaatt cggagccatg atgaaatctg gaatgttcct cacactgttt gtgaacacag 7020 tcattaacat tgtaatcgca agcagagtgt tgagagaacg gctaaccgga tcaccatgtg 7080 cagcattcat tggagatgac aatatcgtga aaggagtcaa atcggacaaa ttaatggcag 7140 acaggtgcgc cacctggttg aatatggaag tcaagattat agatgctgtg gtgggcgaga 7200 aagcgcctta tttctgtgga gggtttattt tgtgtgactc cgtgaccggc acagcgtgcc 7260 gtgtggcaga ccccctaaaa aggctgttta agcttggcaa acctctggca gcagacgatg 7320 aacatgatga tgacaggaga agggcattgc atgaagagtc aacacgctgg aaccgagtgg 7380 gtattctttc agagctgtgc aaggcagtag aatcaaggta tgaaaccgta ggaacttcca 7440 tcatagttat ggccatgact actctagcta gcagtgttaa atcattcagc tacctgagag 7500 gggcccctat aactctctac ggctaacctg aatggactac gactctagaa tagtctttaa 7560 ttaaagtccg ccatatgagg ccaccatgca gatcttcgtg aagaccctga ccggcaagac 7620 catcacccta gaggtggagc ccagtgacac catcgagaac gtgaaggcca agatccagga 7680 taaagagggc atccccccctg accagcagag gctgatcttt gccggcaagc agctggaaga 7740 tggccgcacc ctctctgatt acaacatcca gaaggagtca accctgcacc tggtccttcg 7800 cctgagaggt ggcgctgctt acagtataat caactttgaa aaactggctg cttacggcat 7860 cctgggcttt gtgtttacac tggctgccta cctgctgttt ggctatcctg tgtacgtggc 7920 cgcttatgga ctgtgtaccc tggtggccat gctggctgct tacaatctgg tgcctatggt 7980 ggccacagtg gccgcctatt gtcttggcgg actgctgaca atggtggcag cctacagccc 8040 gagctatgcg tatcatcagt ttgcagccta cggcccagga ccaggcgcta aatttgtggc 8100 tgcctggaca ctgaaagccg ccgctggacc aggtcctgga cagtacatca aggccaacag 8160 caagttcatc ggcatcaccg aactcggccc aggaccaggc tatccctacg atgtgcctga 8220 ttacgcctga tagtgatgat tcgaacggcc gtatcacgcc caaacattta cagccgcggt 8280 gtcaaaaacc gcgtggacgt ggttaacatc cctgctggga ggatcagccg taattattat 8340 aattggcttg gtgctggcta ctattgtggc catgtacgtg ctgaccaacc agaaacataa 8400 ttgaatacag cagcaattgg caagctgctt acatagaact cgcggcgatt ggcatgccgc 8460 cttaaaattt ttattttatt ttttcttttc ttttccgaat cggattttgt ttttaatatt 8520 tcaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 8580 aaaaaaaaaa aaaaaaaaaa aa 8602
3-15	**Sequences**	
3-15-1	Sequence Number [ID]	15
3-15-2	Molecule Type	DNA
3-15-3	Length	9595
3-15-4	Features	**misc_feature 1..9595**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..9595
		mol_type=other DNA

2026201462 26 Feb 2026

		organism=synthetic construct
	NonEnglishQualifier Value	
3-15-5	Residues	atgggcggcg catgagagaa gcccagacca attacctacc caaaatggag aaagttcacg 60 ttgacatcga ggaagacagc ccattcctca gagctttgca gcggagcttc ccgcagtttg 120 aggtagaagc caagcaggtc actgataatg accatgctaa tgccagagcg ttttcgcatc 180 tggcttcaaa actgatcgaa acggaggtgg acccatccga cacgatcctt gacattggaa 240 gtgcgcccgc ccgcagaatg tattctaagc acaagtatca ttgtatctgt ccgatgagat 300 gtgcggaaga tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgtaagg 360 aaataactga taaggaattg gacaagaaaa tgaaggagct cgccgccgtc atgagcgacc 420 ctgacctgga aactgagact atgtgcctcc acgacgacga gtcgtgtcgc tacgaagggc 480 aagtcgctgt ttaccaggat gtatacgcgg ttgacggacc gacaagtctc tatcaccaag 540 ccaataaggg agttagagtc gcctactgga taggctttga caccacccct tttatgttta 600 agaacttggc tggagcatat ccatcatact ctaccaactg ggccgacgaa accgtgttaa 660 cggctcgtaa cataggccta tgcagctctg acgttatgga gcggtcacgt agagggatgt 720 ccattcttag aaagaagtat ttgaaaccat ccaacaatgt tctattctct gttggctcga 780 ccatctacca cgagaagagg gacttactga ggagctggca cctgccgtct gtatttcact 840 tacgtggcaa gcaaaattac acatgtcggt gtgagactat agttagttgc gacgggtacg 900 tcgttaaaag aatagctatc agtccaggcc tgtatgggaa gccttcaggc tatgctgcta 960 cgatgcaccg cgagggattc ttgtgctgca aagtgacaga cacattgaac ggggagaggg 1020 tctcttttcc cgtgtgcacg tatgtgccag ctacattgtg tgaccaaatg actggcatac 1080 tggcaacaga tgtcagtgcg gacgacgcgc aaaaactgct ggttgggctc aaccagcgta 1140 tagtcgtcaa cggtcgcacc cagagaaaca ccaataccat gaaaaattac cttttgcccg 1200 tagtggccca ggcatttgct aggtgggcaa aggaatataa ggaagatcaa gaagatgaaa 1260 ggccactagg actacgagat agacagttag tcatggggtg ttgttgggct tttagaaggc 1320 acaagataac atctatttat aagcgcccgg atacccaaac catcatcaaa gtgaacagcg 1380 atttccactc attcgtgctg cccaggatag gcagtaacac attggagatc gggctgagaa 1440 caagaatcag gaaaatgtta gaggagcaca aggagccgtc acctctcatt accgccgagg 1500 acgtacaaga agctaagtgc gcagccgatg aggctaagga ggtgcgtgaa gccgaggagt 1560 tgcgcgcagc tctaccacct ttggcagctg atgttgagga gcccactctg gaagccgatg 1620 tcgacttgat gttacaagag gctggggccg gctcagtgga gacacctcgt ggcttgataa 1680 aggttaccag ctacgctggc gaggacaaga tcggctctta cgctgtgctt tctccgcagg 1740 ctgtactcaa gagtgaaaaa ttatcttgca tccaccctct cgctgaacaa gtcatagtga 1800 taacacactc tggccgaaaa gggcgttatg ccgtggaacc ataccatggt aaagtagtgg 1860 tgccagaggg acatgcaata cccgtccagg actttcaagc tctgagtgaa agtgccacca 1920 ttgtgtacaa cgaacgtgag ttcgtaaaca ggtacctgca ccatattgcc acacatggag 1980 gagcgctgaa cactgatgaa gaatattaca aaactgtcaa gcccagcgag cacgacggcg 2040 aatacctgta cgacatcgac aggaaacagt gcgtcaagaa agaactagtc actgggctag 2100 ggctcacagg cgagctggtg gatcctccct tccatgaatt cgcctacgag agtctgagaa 2160 cacgaccagc cgctccttac caagtaccaa ccataggggt gtatggcgtg ccaggatcag 2220 gcaagtctgg catcattaaa agcgcagtca ccaaaaaaga tctagtggtg agcgccaaga 2280 aagaaaactg tgcagaaatt ataagggacg tcaagaaaat gaaagggctg gacgtcaatg 2340 ccagaactgt ggactcagtg ctcttgaatg gatgcaaaca ccccgtagag accctgtata 2400 ttgacgaagc ttttgcttgt catgcaggta ctctcagagc gctcatagcc attataagac 2460 ctaaaaaggc agtgctctgc ggggatccca aacagtgcgg ttttttaac atgatgtgcc 2520 tgaaagtgca ttttaaccac gagatttgca cacaagtctt ccacaaaagc atctctcgcc 2580 gttgcactaa atctgtgact tcggtcgtct caaccttgtt ttacgacaaa aaaatgagaa 2640 cgacgaatcc gaaagagact aagattgtga ttgacactac cggcagtacc aaacctaagc 2700 aggacgatct cattctcact tgtttcagag ggtgggtgaa gcagttgcaa atagattaca 2760 aaggcaacga aataatgacg gcagctgcct ctcaagggct gacccgtaaa ggtgtgtatg 2820 ccgttcggta caaggtgaat gaaaatcctc tgtacgcacc cacctcagaa catgtgaacg 2880 tcctactgac ccgcacggag gaccgcatcg tgtggaaaac actagccggc gacccatgga 2940 taaaaacact gactgccaag taccctggga atttcactgc cacgatagag gagtggcaag 3000 cagagcatga tgccatcatg aggcacatct tggagagacc ggaccctacc gacgtcttcc 3060 agaataaggc aaacgtgtgt tgggccaagg ctttagtgcc ggtgctgaag accgctggca 3120 tagacatgac cactgaacaa tggaacactg tggattattt tgaaacggac aaagctcact 3180 cagcagagat agtattgaac caactatgcg tgaggttctt tggactcgat ctggactccg 3240 gtctattttc tgcacccact gttccgttat ccattaggaa taatcactgg gataactccc 3300 cgtcgcctaa catgtacggg ctgaataaag aagtggtccg tcagctctct cgcaggtacc 3360 cacaactgcc tcgggcagtt gccactggaa gagtctatga catgaacact ggtacactgc 3420 gcaattatga tccgcgcata aacctagtac ctgtaaacag aagactgcct catgctttag 3480 tcctccacca taatgaacac ccacagagtg acttttcttc attcgtcagc aaattgaagg 3540 gcagaactgt cctggtggtc ggggaaaagt tgtccgtccc aggcaaaatg gttgactggt 3600 tgtcagaccg gcctgaggct accttcagag ctcggctgga tttaggcatc ccaggtgatg 3660 tgcccaaata tgacataata tttgttaatg tgaggacccc atataaatac catcactatc 3720 agcagtgtga agaccatgcc attaagctta gcatgttgac caagaaagct tgtctgcatc 3780 tgaatcccgg cggaacctgt gtcagcatag gttatggtta cgctgacagg gccagcgaaa 3840 gcatcattgg tgctatagcg cggcagttca agttttcccg ggtatgcaaa ccgaaatcct 3900 cacttgaaga gacggaagtt ctgtttgtat tcattgggta cgatcgcaag gcccgtacgc 3960 acaatcctta caagctttca tcaaccttga ccaacattta tacaggttcc agactccacg 4020 aagccggatg tgcaccctca tatcatgtgg tgcgagggga tattgccacg gccaccgaag 4080 gagtgattat aaatgctgct aacagcaaag gacaacctgg cggaggggtg tgcggagcgc 4140 tgtataagaa attcccggaa agcttcgatt tacagccgat cgaagtagga aaagcgcgac 4200 tggtcaaagg tgcagctaaa catatcattc atgccgtagg accaaacttc aacaaagttt 4260 cggaggttga aggtgacaaa cagttggcag aggcttatga gtccatcgct aagattgtca 4320 acgataacaa ttacaagtca gtagcgattc cactgttgtc caccggcatc ttttccggga 4380

20262014626 26 Feb 2026

acaaagatcg actaacccaa tcattgaacc atttgctgac agctttagac accactgatg 4440
cagatgtagc catatactgc agggacaaga aatgggaaat gactctcaag gaagcagtgg 4500
ctaggagaga agcagtggag gagatatgca tatccgacga ctcttcagtg acagaacctg 4560
atgcagagct ggtgagggtg catccgaaga gttctttggc tggaaggaag ggctacagca 4620
caagcgatgg caaaactttc tcatatttgg aagggaccaa gtttcaccag gcggccaagg 4680
atatagcaga aattaatgcc atgtggcccg ttgcaacgga ggccaatgag caggtatgca 4740
tgtatatcct cggagaaagc atgagcagta ttaggtcgaa atgccccgtc gaagagtcgg 4800
aagcctccac accacctagc acgctgcctt gcttgtgcat ccatgccatg actccagaaa 4860
gagtacagcg cctaaaagcc tcacgtccag aacaaattac tgtgtgctca tcctttccat 4920
tgccgaagta tagaatcact ggtgtgcaga agatccaatg ctcccagcct atattgttct 4980
caccgaaagt gcctgcgtat attcatccaa ggaagtatct cgtggaaaca ccaccggtag 5040
acgagactcc ggagccatcg gcagagaacc aatccacaga ggggacacct gaacaaccac 5100
cacttataac cgaggatgag accaggacta gaacgcctga gccgatcatc atcgaagagg 5160
aagaagagga tagcataagt ttgctgtcag atggcccgac ccaccaggtg ctgcaagtcg 5220
aggcagacat tcacgggccg ccctctgtat ctagctcatc ctggtccatt cctcatgcat 5280
ccgactttga tgtggacagt ttatccatac ttgacaccct ggagggagct agcgtgacca 5340
gcggggcaac gtcagccgag actaactctt acttcgcaaa gagtatggag tttctggcgc 5400
gaccggtgcc tgcgcctcga acagtattca ggaaccctcc acatcccgct ccgcgcacaa 5460
gaacaccgtc acttgcaccc agcagggcct gctcgagaac cagcctagtt tccaccccgc 5520
caggcgtgaa tagggtgatc actagagagg agctcgaggc gcttaccccg tcacgcactc 5580
ctagcaggtc ggtctcgaga accagcctgg tctccaaccc gccaggcgta aatagggtga 5640
ttacaagaga ggagtttgag gcgttcgtag cacaacaaca atgacggttt gatgcgggtg 5700
catacatctt ttcctccgac accggtcaag ggcatttaca acaaaaatca gtaaggcaaa 5760
cggtgctatc cgaagtggtg ttggagagga ccgaattgga gatttcgtat gccccgcgcc 5820
tcgaccaaga aaaagaagaa ttactacgca agaaattaca gttaaatccc acacctgcta 5880
acagaagcag ataccagtcc aggaaggtgg agaacatgaa agccataaca gctagacgta 5940
ttctgcaagg cctagggcat tatttgaagg cagaaggaaa agtggagtgc taccgaaccc 6000
tgcatcctgt tcctttgtat tcatctagtg tgaaccgtgc cttttcaagc cccaaggtcg 6060
cagtggaagc ctgtaacgcc atgttgaaag agaactttcc gactgtggct tcttactgta 6120
ttattccaga gtacgatgcc tatttggaca tggttgacgg agcttcatgc tgcttagaca 6180
ctgccagttt ttgccctgca aagctgcgca gctttccaaa gaaacactcc tatttggaac 6240
ccacaatacg atcggcagtg ccttcagcga tccagaacac gctccagaac gtcctggcag 6300
ctgccacaaa aagaaattgc aatgtcacgc aaatgagaga attgcccgta ttggattcgg 6360
cggcctttaa tgtggaatgc ttcaagaaat atgcgtgtaa taatgaatat tgggaaacgt 6420
ttaaagaaaa ccccatcagg cttactgaag aaaacgtggt aaattacatt accaaattaa 6480
aaggaccaaa agctgctgct ctttttgcga agacacataa tttgaatatg ttgcaggaca 6540
taccaatgga caggtttgta atggacttaa agagagacgt gaaagtgact ccaggaacaa 6600
aacatactga agaacggccc aaggtacagg tgatccaggc tgccgatccg ctagcaacag 6660
cgtatctgtg cggaatccac cgagagctgg ttaggagatt aaatgcggtc ctgcttccga 6720
acattcatac actgtttgat atgtcggctg aagactttga cgctattata gccgagcact 6780
tccagcctgg ggattgtgtt ctggaaactg acatcgcgtc gtttgataaa agtgaggacg 6840
acgccatggc tctgaccgcg ttaatgattc tggaagactt aggtgtggac gcagagctgt 6900
tgacgctgat tgaggcggct ttcggcgaaa tttcatcaat acatttgccc actaaaacta 6960
aatttaaatt cggagccatg atgaaatctg gaatgttcct cacactgttt gtgaacacag 7020
tcattaacat tgtaatcgca agcagagtgt tgagagaacg gctaaccgga tcaccatgtg 7080
cagcattcat tggagatgac aatatcgtga aaggagtcaa atcggacaaa ttaatggcag 7140
acaggtgcgc cacctggttg aatatggaag tcaagattat agatgctgtg gtgggcgaga 7200
aagcgcctta tttctgtgga gggtttattt tgtgtgactc cgtgaccggc acagcgtgcc 7260
gtgtggcaga ccccctaaaa aggctgttta agcttggcaa acctctggca gcagacgatg 7320
aacatgatga tgacaggaga agggcattgc atgaagagtc aacacgctgg aaccgagtgg 7380
gtattctttc agagctgtgc aaggcagtag aatcaaggta tgaaaccgta ggaacttcca 7440
tcatagttat ggccatgact actctagcta gcagtgttaa atcattcagc tacctgagag 7500
gggcccctat aactctctac ggctaacctg aatggactac gactctagaa tagtctttaa 7560
ttaaagtccg ccatatgaga tggaagatgc caaaaacatt aagaagggcc cagcgccatt 7620
ctacccactc gaagacggga ccgccggcga gcagctgcac aaagccatga agcgctacgc 7680
cctggtgccc ggcaccatcg cctttaccga cgcacatatc gaggtggaca ttacctacgc 7740
cgagtacttc gagatgagcg ttcggctggc agaagctatg aagcgctatg ggctgaatac 7800
aaaccatcgg atcgtggtgt gcagcgagaa tagcttgcag ttcttcatgc ccgtgttggg 7860
tgccctgttc atcggtgtgg ctgtggcccc agctaacgac atctacaacg agcgcgagct 7920
gctgaacagc atgggcatca gccagcccac cgtcgtattc gtgagcaaga aagggctgca 7980
aaagatcctc aacgtgcaaa agaagctacc gatcatacaa aagatcatca tcatggatag 8040
caagaccgac taccagggct tccaaagcat gtacaccttc gtgacttccc atttgccacc 8100
cggcttcaac gagtacgact tcgtgcccga gagcttcgac cgggacaaaa ccatcgccct 8160
gatcatgaac agtagtggca gtaccggatt gcccaagggc gtagccctac cgcaccgcac 8220
cgcttgtgtc cgattcagtc atgcccgcga ccccatcttc ggcaaccaga tcatccccga 8280
caccgctatc ctcagcgtgg tgccatttca ccacggcttc ggcatgttca ccacgctggg 8340
ctacttgatc tgcggctttc gggtcgtgct catgtaccgc ttcgaggagg agctattctt 8400
gcgcagcttg caagactata agattcaatc tgccctgctg gtgcccacac tatttagctt 8460
cttcgctaag agcactctca tcgacaagta cgacctaagc aacttgcacg agatcgccag 8520
cggcggggcg ccgctcagca aggaggtagg tgaggccgtg gccaaacgct tccacctacc 8580
aggcatccgc cagggctacg gcctgacaga aacaaccagc gccattctga tcacccccga 8640
aggggacgac aagcctggcg cagtaggcaa ggtggtgccc ttcttcgagg ctaaggtggt 8700
ggacttggac accggtaaga cactgggtgt gaaccagcgc ggcgagctgt gcgtccgtgg 8760
ccccatgatc atgagcggct acgttaacaa ccccgaggct acaaacgctc tcatcgacaa 8820
ggacggctgg ctgcacagcg gcgacatcgc ctactgggac gaggacgagc acttcttcat 8880
cgtggaccgg ctgaagagcc tgatcaaata caagggctac caggtagccc cagccgaact 8940

2026201462 26 Feb 2026

		ggagagcatc ctgctgcaac accccaacat cttcgacgcc ggggtcgccg gcctgcccga 9000 cgacgatgcc ggcgagctgc ccgccgcagt cgtcgtgctg gaacacggta aaaccatgac 9060 cgagaaggag atcgtggact atgtggccag ccaggttaca accgccaaga agctgcgcgg 9120 tggtgttgtg ttcgtggacg aggtgcctaa aggactgacc ggcaagttgg acgcccgcaa 9180 gatccgcgag attctcatta aggccaagaa gggcggcaag atcgccgtgt aattcgaacg 9240 gccgtatcac gcccaaacat ttacagccgc ggtgtcaaaa accgcgtgga cgtggttaac 9300 atccctgctg ggaggatcag ccgtaattat tataattggc ttggtgctgg ctactattgt 9360 ggccatgtac gtgctgacca accagaaaca taattgaata cagcagcaat tggcaagctg 9420 cttacataga actcgcggcg attggcatgc cgccttaaaa tttttatttt atttttctt 9480 ttcttttccg aatcggattt tgtttttaat atttcaaaaa aaaaaaaaaa aaaaaaaaaa 9540 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 9595
3-16	**Sequences**	
3-16-1	Sequence Number [ID]	16
3-16-2	Molecule Type	AA
3-16-3	Length	139
3-16-4	Features	**REGION 1..139**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..139
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-16-5	Residues	PSSLSASVGD RVTITCRASQ SINSYLDWYQ QKPGKAPKLL IYAASSLQSG VPSRFSGSGS 60 GTDFTLTISS LQPEDFATYY CQQYYSTPFT FGPGTKVEIK RTVAAPSVFI FPPSDEQLKS 120 GTASVVCLLN NFYPREAKV 139
3-17	**Sequences**	
3-17-1	Sequence Number [ID]	17
3-17-2	Molecule Type	AA
3-17-3	Length	167
3-17-4	Features	**REGION 1..167**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..167
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-17-5	Residues	GVVQPGRSLR LSCAASGFTF SSYGMHWVRQ APGKGLEWVA VIWYDGSNKY YADSVKGRFT 60 ISRDNSKNTL YLQMNSLRAE DTAVYYCARD PRGATLYYYY YGMDVWGQGT TVTVSSASTK 120 GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPVTVSWNSG ALTSGVH 167
3-18	**Sequences**	
3-18-1	Sequence Number [ID]	18
3-18-2	Molecule Type	AA
3-18-3	Length	10
3-18-4	Features	**REGION 1..10**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide
		source 1..10
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-18-5	Residues	GFTFSSYGMH 10
3-19	**Sequences**	
3-19-1	Sequence Number [ID]	19
3-19-2	Molecule Type	AA
3-19-3	Length	15
3-19-4	Features	**REGION 1..15**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide
		source 1..15
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-19-5	Residues	VIWYDGSNKY YADSV 15
3-20	**Sequences**	
3-20-1	Sequence Number [ID]	20
3-20-2	Molecule Type	AA
3-20-3	Length	16
3-20-4	Features	**REGION 1..16**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide
		source 1..16
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-20-5	Residues	DPRGATLYYY YYGMDV 16

2026201462 26 Feb 2026

3-21	**Sequences**		
3-21-1	Sequence Number [ID]	21	
3-21-2	Molecule Type	AA	
3-21-3	Length	11	
3-21-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-21-5	Residues	RASQSINSYL D	11
3-22	**Sequences**		
3-22-1	Sequence Number [ID]	22	
3-22-2	Molecule Type	AA	
3-22-3	Length	7	
3-22-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-22-5	Residues	AASSLQS	7
3-23	**Sequences**		
3-23-1	Sequence Number [ID]	23	
3-23-2	Molecule Type	AA	
3-23-3	Length	9	
3-23-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-23-5	Residues	QQYYSTPFT	9
3-24	**Sequences**		
3-24-1	Sequence Number [ID]	24	
3-24-2	Molecule Type	AA	
3-24-3	Length	108	
3-24-4	Features	**REGION 1..108**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide	
		source 1..108	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-24-5	Residues	EIVLTQSPGT LSLSPGERAT LSCRASQRVS SSYLAWYQQK PGQAPRLLIY DASSRATGIP	60
		DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSLPWTFG QGTKVEIK	108
3-25	**Sequences**		
3-25-1	Sequence Number [ID]	25	
3-25-2	Molecule Type	AA	
3-25-3	Length	121	
3-25-4	Features	**REGION 1..121**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide	
		source 1..121	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-25-5	Residues	EVQLVESGGG LVQPGGSLRL SCAASGFTFS RYWMSWVRQA PGKGLEWVAN IKQDGSEKYY	60
		VDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCAREG GWFGELAFDY WGQGTLVTVS	120
		S	121
3-26	**Sequences**		
3-26-1	Sequence Number [ID]	26	
3-26-2	Molecule Type	AA	
3-26-3	Length	5	
3-26-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		

2026201462 26 Feb 2026

3-26-5	Residues	RYWMS	5
3-27	**Sequences**		
3-27-1	Sequence Number [ID]	27	
3-27-2	Molecule Type	AA	
3-27-3	Length	17	
3-27-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-27-5	Residues	NIKQDGSEKY YVDSVKG	17
3-28	**Sequences**		
3-28-1	Sequence Number [ID]	28	
3-28-2	Molecule Type	AA	
3-28-3	Length	12	
3-28-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-28-5	Residues	EGGWFGELAF DY	12
3-29	**Sequences**		
3-29-1	Sequence Number [ID]	29	
3-29-2	Molecule Type	AA	
3-29-3	Length	12	
3-29-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-29-5	Residues	RASQRVSSSY LA	12
3-30	**Sequences**		
3-30-1	Sequence Number [ID]	30	
3-30-2	Molecule Type	AA	
3-30-3	Length	7	
3-30-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-30-5	Residues	DASSRAT	7
3-31	**Sequences**		
3-31-1	Sequence Number [ID]	31	
3-31-2	Molecule Type	AA	
3-31-3	Length	9	
3-31-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-31-5	Residues	QQYGSLPWT	9
3-32	**Sequences**		
3-32-1	Sequence Number [ID]	32	
3-32-2	Molecule Type	DNA	
3-32-3	Length	2019	
3-32-4	Features	**misc_feature 1..2019**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide	
		source 1..2019	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-32-5	Residues	gcccgggcat ttaaatgcga tcgcatcgat tacgactcta gaatagtcta gtccgcaggc 60 caccatgcag atcttcgtga agaccctgac cggcaagacc atcaccctag aggtggagcc 120	

2026201462 26 Feb 2026

		cagtgacacc atcgagaacg tgaaggccaa gatccaggat aaagagggca tccccccctga 180 ccagcagagg ctgatctttg ccggcaagca gctggaagat ggccgcaccc tctctgatta 240 caacatccag aaggagtcaa ccctgcacct ggtccttcgc ctgagaggtg ccatgtttca 300 ggcgctgagc gaaggctgca ccccgtatga tattaaccag atgctgaacg tgctgggcga 360 tcatcaggtc tcaggccttg agcagcttga gagtataatc aactttgaaa aactgactga 420 atggaccagt tctaatgtta tgcctatcct gtctcctctg acaaagggca tcctgggctt 480 cgtgtttacc ctgaccgtgc cttctgagag aggacttagc tgcattagcg aagcggatgc 540 gaccaccccg gaaagcgcga acctgggcga agaaattctg agccagctgt atctttggcc 600 aagggtgacc taccattccc ctagttatgc ttaccaccaa tttgaaagac gagccaaata 660 taaaagacac ttccccggct ttggccagag cctgctgttt ggctaccctg tgtacgtgtt 720 cggcgattgc gtgcagggcg attgggatgc gattcgcttt cgctattgcg cgccgccggg 780 ctatgcgctg ctgcgctgca acgataccaa ctatagcgct ctgctggctg tgggggccct 840 agaaggaccc aggaatcagg actggcttgg tgtcccaaga caacttgtaa ctcggatgca 900 ggctattcag aatgccggcc tgtgtaccct ggtggccatg ctggaagaga caatcttctg 960 gctgcaagcg tttctgatgg cgctgaccga tagcggcccg aaaaccaaca ttattgtgga 1020 tagccagtat gtgatgggca ttagcaaacc gagctttcag gaatttgtgg attgggaaaa 1080 cgtgagcccg gaactgaaca gcaccgatca gccgttttgg caagccggaa tcctggccag 1140 aaatctggtg cctatggtgg ccacagtgca gggccagaac ctgaagtacc agggtcagtc 1200 actagtcatc tctgcttcta tcattgtctt caacctgctg gaactggaag gtgattatcg 1260 agatgatggc aacgtgtggg tgcatacccc gctgagcccg cgcaccctga acgcgtgggt 1320 gaaagcggtg gaagaaaaaa aaggtattcc agttcaccta gagctggcca gtatgaccaa 1380 catggagctc atgagcagta ttgtgcatca gcaggtcaga acatacggcc ccgtgttcat 1440 gtgtctcggc ggactgctta caatggtggc tggtgctgtg tggctgacag tgcgagtgct 1500 cgagctgttc cgggccgcgc agctggccaa cgacgtggtc ctccagatca tggagctttg 1560 tggtgcagcg tttcgccagg tgtgccatac caccgtgccg tggccgaacg cgagcctgac 1620 cccgaaatgg aacaacgaaa ccacccagcc ccagatcgcc aactgcagcg tgtatgactt 1680 ttttgtgtgg ctccattatt attctgttcg agacacactt tggccaaggg tgacctacca 1740 tatgaacaaa tatgcgtatc atatgctgga aagacgagcc aaatataaaa gaggaccagg 1800 acctggcgct aaatttgtgg ccgcctggac actgaaagcc gctgctggtc ctggacctgg 1860 ccagtacatc aaggccaaca gcaagttcat cggcatcacc gaactcggac ccggaccagg 1920 ctgatgattt cgaaatttaa ataagcttgc ggccgctagg gataacaggg taattatcac 1980 gcccaaacat ttacagccgc ggtgtcaaaa accgcgtgg 2019
3-33	**Sequences**	
3-33-1	Sequence Number [ID]	33
3-33-2	Molecule Type	AA
3-33-3	Length	619
3-33-4	Features	**REGION 1..619**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide **source 1..619** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-33-5	Residues	MQIFVKTLTG KTITLEVEPS DTIENVKAKI QDKEGIPPDQ QRLIFAGKQL EDGRTLSDYN 60 IQKESTLHLV LRLRGAMFQA LSEGCTPYDI NQMLNVLGDH QVSGLEQLES IINFEKLTEW 120 TSSNVMPILS PLTKGILGFV FTLTVPSERG LSCISEADAT TPESANLGEE ILSQLYLWPR 180 VTYHSPSYAY HQFERRAKYK RHFPGFGQSL LFGYPVYVFG DCVQGDWDAI RFRYCAPPGY 240 ALLRCNDTNY SALLAVGALE GPRNQDWLGV PRQLVTRMQA IQNAGLCTLV AMLEETIFWL 300 QAFLMALTDS GPKTNIIVDS QYVMGISKPS FQEFVDWENV SPELNSTDQP FWQAGILARN 360 LVPMVATVQG QNLKYQGQSL VISASIIVFN LLELEGDYRD DGNVWVHTPL SPRTLNAWVK 420 AVEEKKGIPV HLELASMTNM ELMSSIVHQQ VRTYGPVFMC LGGLLTMVAG AVWLTVRVLE 480 LFRAAQLAND VVLQIMELCG AAFRQVCHTT VPWPNASLTP KWNNETTQPQ IANCSVYDFF 540 VWLHYYSVRD TLWPRVTYHM NKYAYHMLER RAKYKRGPGP GAKFVAAWTL KAAAGPGPGQ 600 YIKANSKFIG ITELGPGPG 619
3-34	**Sequences**	
3-34-1	Sequence Number [ID]	34
3-34-2	Molecule Type	DNA
3-34-3	Length	1638
3-34-4	Features	**misc_feature 1..1638**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide **source 1..1638** mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-34-5	Residues	atggccggga tgttccaggc actgtccgaa ggctgcacac cctatgatat taaccagatg 60 ctgaatgtcc tgggagacca ccaggtctct ggcctggagc agctggagag catcatcaac 120 ttcgagaagc tgaccgagtg gacaagctcc aatgtgatgc ctatcctgtc cccactgacc 180 aagggcatcc tgggcttcgt gtttaccctg acagtgcctt ctgagcgggg cctgtcttgc 240 atcagcgagg cagacgcaac cacaccagag tccgccaatc tgggcgagga gatcctgtct 300 cagctgtacc tgtggccccg ggtgacatat cactcccctt cttacgccta tcaccagttc 360 gagcggagag ccaagtacaa gagacacttc ccaggctttg gccagtctct gctgttcggc 420 taccccgtgt acgtgttcgg cgattgcgtg cagggcgact gggatgccat ccggtttaga 480 tactgcgcac cacctggata tgcactgctg aggtgtaacg acaccaatta ttccgccctg 540 ctggcagtgg gcgccctgga gggccctcgc aatcaggatt ggctgggcgt gccaaggcag 600

2026201462 26 Feb 2026

		ctggtgacac gcatgcaggc catccagaac gcaggcctgt gcaccctggt ggcaatgctg 660 gaggagacaa tcttctggct gcaggccttt ctgatggccc tgaccgacag cggccccaag 720 acaaacatca tcgtggattc ccagtacgtg atgggcatct ccaagccttc tttccaggag 780 tttgtggact gggagaacgt gagcccagag ctgaattcca ccgatcagcc attctggcag 840 gcaggaatcc tggcaaggaa cctggtgcct atggtggcca cagtgcaggg ccagaatctg 900 aagtaccagg gccagagcct ggtcatcagc gcctccatca tcgtgtttaa cctgctggag 960 ctggagggcg actatcggga cgatggcaac gtgtgggtgc acaccccact gagccccaga 1020 acactgaacg cctgggtgaa ggccgtggag gagaagaagg gcatcccagt gcacctggag 1080 ctggcctcca tgaccaatat ggagctgatg tctagcatcg tgcaccagca ggtgaggaca 1140 tacggacccg tgttcatgtg cctgggaggc ctgctgacca tggtggcagg agccgtgtgg 1200 ctgacagtgc gggtgctgga gctgttcaga gccgcccagc tggccaacga tgtggtgctg 1260 cagatcatgg agctgtgcgg agcagccttt cgccaggtgt gccacaccac agtgccatgg 1320 cccaatgcct ccctgacccc caagtggaac aatgagacaa cacagcctca gatcgccaac 1380 tgtagcgtgt acgacttctt cgtgtggctg cactactata gcgtgaggga taccctgtgg 1440 ccccgcgtga cataccacat gaataagtac gcctatcaca tgctggagag gcgcgccaag 1500 tataagagag gccctggccc aggcgcaaag tttgtggcag catggaccct gaaggccgcc 1560 gccggccccg gccccggcca gtatatcaag gctaacagta agttcattgg aatcacagag 1620 ctgggacccg gacctgga 1638
3-35	**Sequences**	
3-35-1	Sequence Number [ID]	35
3-35-2	Molecule Type	AA
3-35-3	Length	546
3-35-4	Features	**REGION 1..546**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide **source 1..546** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-35-5	Residues	MAGMFQALSE GCTPYDINQM LNVLGDHQVS GLEQLESIIN FEKLTEWTSS NVMPILSPLT 60 KGILGFVFTL TVPSERGLSC ISEADATTPE SANLGEEILS QLYLWPRVTY HSPSYAYHQF 120 ERRAKYKRHF PGFGQSLLFG YPVYVFGDCV QGDWDAIRFR YCAPPGYALL RCNDTNYSAL 180 LAVGALEGPR NQDWLGVPRQ LVTRMQAIQN AGLCTLVAML EETIFWLQAF LMALTDSGPK 240 TNIIVDSQYV MGISKPSFQE FVDWENVSPE LNSTDQPFWQ AGILARNLVP MVATVQGQNL 300 KYQGQSLVIS ASIIVFNLLE LEGDYRDDGN VWVHTPLSPR TLNAWVKAVE EKKGIPVHLE 360 LASMTNMELM SSIVHQQVRT YGPVFMCLGG LLTMVAGAVW LTVRVLELFR AAQLANDVVL 420 QIMELCGAAF RQVCHTTVPW PNASLTPKWN NETTQPQIAN CSVYDFFVWL HYYSVRDTLW 480 PRVTYHMNKY AYHMLERRAK YKRGPGPGAK FVAAWTLKAA AGPGPGQYIK ANSKFIGITE 540 LGPGPG 546
3-36	**Sequences**	
3-36-1	Sequence Number [ID]	36
3-36-2	Molecule Type	DNA
3-36-3	Length	2019
3-36-4	Features	**misc_feature 1..2019**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide **source 1..2019** mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-36-5	Residues	gcccgggcat ttaaatgcga tcgcatcgat tacgactcta gaatagtcta gtccgcaggc 60 caccatgcag atcttcgtga agaccctgac cggcaagacc atcaccctag aggtggagcc 120 cagtgacacc atcgagaacg tgaaggccaa gatccaggat aaagagggca tccccccctga 180 ccagcagagg ctgatctttg ccggcaagca gctggaagat ggccgcaccc tctctgatta 240 caacatccag aaggagtcaa ccctgcacct ggtccttcgc ctgagaggtg ccatgtttca 300 ggcgctgagc gaaggctgca ccccgtatga tattaaccag atgctgaacg tgctgggcga 360 tcatcagttt aagcacatca aagcctttga ccggacattt gctaacaacc caggtcccat 420 ggttgtgttt gccacacctg ggcctatcct gtctcctctg acaaagggca tcctgggctt 480 cgtgtttacc ctgaccgtgc cttctgagag aggacttagc tgcattagcg aagcggatgc 540 gaccaccccg gaaagcgcga acctgggcga agaaattctg agccagctgt atctttggcc 600 aagggtgacc taccattccc ctagttatgc ttaccaccaa tttgaaagac gagccaaata 660 taaaagacac ttccccggct ttggccagag cctgctgttt ggctaccctg tgtacgtgtt 720 cggcgattgc gtgcagggcg attgggatgc gattcgcttt cgctattgcg cgccgccggg 780 ctatgcgctg ctgcgctgca acgataccaa ctatagcgct ctgctggctg tgggggccct 840 agaaggaccc aggaatcagg actggcttgg tgtcccaaga caacttgtaa ctcggatgca 900 ggctattcag aatgccggcc tgtgtaccct ggtggccatg ctggaagaga caatcttctg 960 gctgcaagcg tttctgatgg cgctgaccga tagcggcccg aaaaccaaca ttattgtgga 1020 tagccagtat gtgatgggca ttagcaaacc gagctttcag gaatttgtgg attgggaaaa 1080 cgtgagcccg gaactgaaca gcaccgatca gccgttttgg caagccggaa tcctggccag 1140 aaatctggtg cctatggtgg ccacagtgca gggccagaac ctgaagtacc agggtcagtc 1200 actagtcatc tctgcttcta tcattgtctt caacctgctg gaactggaag gtgattatcg 1260 agatgatggc aacgtgtggg tgcatacccc gctgagcccg cgcaccctga acgcgtgggt 1320 gaaagcggtg gaagaaaaaa aaggtattcc agttcaccta gagctggcca gtatgaccaa 1380 catggagctc atgagcagta ttgtgcatca gcaggtcaga acatacggcc ccgtgttcat 1440 gtgtctcggc ggactgctta caatggtggc tggtgctgtg tggctgacag tgcgagtgct 1500

20262014 62 26 Feb 2026

		cgagctgttc cgggccgcgc agctggccaa cgacgtggtc ctccagatca tggagctttg 1560 tggtgcagcg tttcgccagg tgtgccatac caccgtgccg tggccgaacg cgagcctgac 1620 cccgaaatgg aacaacgaaa ccacccagcc ccagatcgcc aactgcagcg tgtatgactt 1680 ttttgtgtgg ctccattatt attctgttcg agacacactt tggccaaggg tgacctacca 1740 tatgaacaaa tatgcgtatc atatgctgga aagacgagcc aaatataaaa gaggaccagg 1800 acctggcgct aaatttgtgg ccgcctggac actgaaagcc gctgctggtc ctggacctgg 1860 ccagtacatc aaggccaaca gcaagttcat cggcatcacc gaactcggac ccggaccagg 1920 ctgatgattt cgaaatttaa ataagcttgc ggccgctagg gataacaggg taattatcac 1980 gcccaaacat ttacagccgc ggtgtcaaaa accgcgtgg 2019
3-37	**Sequences**	
3-37-1	Sequence Number [ID]	37
3-37-2	Molecule Type	AA
3-37-3	Length	619
3-37-4	Features	**REGION 1..619**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..619
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-37-5	Residues	MQIFVKTLTG KTITLEVEPS DTIENVKAKI QDKEGIPPDQ QRLIFAGKQL EDGRTLSDYN 60 IQKESTLHLV LRLRGAMFQA LSEGCTPYDI NQMLNVLGDH QFKHIKAFDR TFANNPGPMV 120 VFATPGPILS PLTKGILGFV FTLTVPSERG LSCISEADAT TPESANLGEE ILSQLYLWPR 180 VTYHSPSYAY HQFERRAKYK RHFPGFGQSL LFGYPVYVFG DCVQGDWDAI RFRYCAPPGY 240 ALLRCNDTNY SALLAVGALE GPRNQDWLGV PRQLVTRMQA IQNAGLCTLV AMLEETIFWL 300 QAFLMALTDS GPKTNIIVDS QYVMGISKPS FQEFVDWENV SPELNSTDQP FWQAGILARN 360 LVPMVATVQG QNLKYQGQSL VISASIIVFN LLELEGDYRD DGNVWVHTPL SPRTLNAWVK 420 AVEEKKGIPV HLELASMTNM ELMSSIVHQQ VRTYGPVFMC LGGLLTMVAG AVWLTVRVLE 480 LFRAAQLAND VVLQIMELCG AAFRQVCHTT VPWPNASLTP KWNNETTQPQ IANCSVYDFF 540 VWLHYYSVRD TLWPRVTYHM NKYAYHMLER RAKYKRGPGP GAKFVAAWTL KAAAGPGPGQ 600 YIKANSKFIG ITELGPGPG 619
3-38	**Sequences**	
3-38-1	Sequence Number [ID]	38
3-38-2	Molecule Type	DNA
3-38-3	Length	228
3-38-4	Features	**misc_feature 1..228**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..228
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-38-5	Residues	atgcagatct tcgtgaagac cctgaccggc aagaccatca ccctagaggt ggagcccagt 60 gacaccatcg agaacgtgaa ggccaagatc caggataaag agggcatccc ccctgaccag 120 cagaggctga tctttgccgg caagcagctg gaagatggcc gcaccctctc tgattacaac 180 atccagaagg agtcaaccct gcacctggtc cttcgcctga gaggtggc 228
3-39	**Sequences**	
3-39-1	Sequence Number [ID]	39
3-39-2	Molecule Type	DNA
3-39-3	Length	228
3-39-4	Features	**misc_feature 1..228**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..228
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-39-5	Residues	atgcagatct tcgtgaagac cctgaccggc aagaccatca ccctagaggt ggagcccagt 60 gacaccatcg agaacgtgaa ggccaagatc caggataaag agggcatccc ccctgaccag 120 cagaggctga tctttgccgg caagcagctg gaagatggcc gcaccctctc tgattacaac 180 atccagaagg agtcaaccct gcacctggtc cttcgcctga gaggtgcc 228
3-40	**Sequences**	
3-40-1	Sequence Number [ID]	40
3-40-2	Molecule Type	DNA
3-40-3	Length	78
3-40-4	Features	**source 1..78**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-40-5	Residues	atggccgtca tggcgccccg aaccctcgtc ctgctactct cgggggctct ggccctgacc 60 cagacctggg cgggctct 78
3-41	**Sequences**	
3-41-1	Sequence Number [ID]	41
3-41-2	Molecule Type	DNA

2026201462 26 Feb 2026

3-41-3	Length	201
3-41-4	Features	**source 1..201**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-41-5	Residues	ccgtcttccc agcccaccat ccccatcgtg ggcatcattg ctggcctggt tctctttgga 60 gctgtgatca ctggagctgt ggtcgctgct gtgatgtgga ggaggaagag ctcagataga 120 aaaggaggga gctactctca ggctgcaagc agtgacagtg cccagggctc tgatgtgtct 180 ctcacagctt gtaaagtgtg a 201
3-42	**Sequences**	
3-42-1	Sequence Number [ID]	42
3-42-2	Molecule Type	DNA
3-42-3	Length	60
3-42-4	Features	**misc_feature 1..60**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic oligonucleotide
		source 1..60
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-42-5	Residues	atggagaccg atacactgct gctgtgggtg ctgctcctgt gggtgccagg aagcacaggc 60
3-43	**Sequences**	
3-43-1	Sequence Number [ID]	43
3-43-2	Molecule Type	DNA
3-43-3	Length	3178
3-43-4	Features	**source 1..3178**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-43-5	Residues	ggcaccgatt cggggcctgc ccggacttcg ccgcacgctg cagaacctcg cccagcgccc 60 accatgcccc ggcagctcag cgcggcggcc gcgctcttcg cgtccctggc cgtaattttg 120 cacgatggca gtcaaatgag agcaaaagca tttccagaaa ccagagatta ttctcaacct 180 actgcagcag caacagtaca ggacataaaa aaacctgtcc agcaaccagc taagcaagca 240 cctcaccaaa ctttagcagc aagattcatg gatggtcata tcacctttca aacagcggcc 300 acagtaaaaa ttccaacaac taccccagca actacaaaaa acactgcaac caccagccca 360 attacctaca ccctggtcac aacccaggcc acacccaaca actcacacac agctcctcca 420 gttactgaag ttacagtcgg ccctagctta gccccttatt cactgccacc caccatcacc 480 ccaccagctc atacagctgg aaccagttca tcaaccgtca gccacacaac tgggaacacc 540 actcaaccca gtaaccagac cacccttcca gcaactttat cgatagcact gcacaaaagc 600 acaaccggtc agaagcctga tcaacccacc catgccccag gaacaacggc agctgcccac 660 aataccaccc gcacagctgc acctgcctcc acggttcctg ggcccaccct tgcacctcag 720 ccatcgtcag tcaagactgg aatttatcag gttctaaacg gaagcagact ctgtataaaa 780 gcagagatgg ggatacagct gattgttcaa gacaaggagt cggttttttc acctcggaga 840 tacttcaaca tcgaccccaa cgcaacgcaa gcctctggga actgtggcac ccgaaaatcc 900 aaccttctgt tgaattttca gggcggattt gtgaatctca catttaccaa ggatgaagaa 960 tcatattata tcagtgaagt gggagcctat ttgaccgtct cagatccaga gacagtttac 1020 caaggaatca aacatgcggt ggtgatgttc cagacagcag tcgggcattc cttcaagtgc 1080 gtgagtgaac agagcctcca gttgtcagcc cacctgcagg tgaaaacaac cgatgtccaa 1140 cttcaagcct ttgattttga agatgaccac tttggaaatg tggatgagtg ctcgtctgac 1200 tacacaattg tgcttcctgt gattggggcc atcgtggttg gtctctgcct tatgggtatg 1260 ggtgtctata aaatccgcct aaggtgtcaa tcatctggat accagagaat ctaattgttg 1320 cccgggggga atgaaaataa tggaatttag agaactcttt catcccttcc aggatggatg 1380 ttgggaaatt ccctcagagt gtgggtcctt caaacaatgt aaaccaccat cttctattca 1440 aatgaagtga gtcatgtgtg atttaagttc aggcagcaca tcaatttcta aatacttttt 1500 gtttatttta tgaaagatat agtgagctgt ttattttcta gtttccttta gaatatttta 1560 gccactcaaa gtcaacattt gagatatgtt gaattaacat aatatatgta aagtagaata 1620 agccttcaaa ttataaacca agggtcaatt gtaactaata ctactgtgtg tgcattgaag 1680 attttatttt acccttgatc ttaacaaagc ctttgctttg ttatcaaatg gactttcagt 1740 gcttttacta tctgtgtttt atggtttcat gtaacataca tattcctggt gtagcactta 1800 actccttttc cactttaaat ttgtttttgt tttttgagac ggagtttcac tcttgtcacc 1860 caggctggag tacagtggca cgatctcggc ttatggcaac ctccgcctcc cgggttcaag 1920 tgattctcct gcttcagctt cccgagtagc tgggattaca ggcacacact accacgcctg 1980 gctaattttt gtatttttat tatagacggg tttcaccatg ttggccagac tggtcttgaa 2040 ctcttgacct caggtgatcc acccacctca gcctcccaaa gtgctgggat tacaggcatg 2100 agccattgcg cccggcctta aatgtttttt ttaatcatca aaaagaacaa catatctcag 2160 gttgtctaag tgtttttatg taaaaccaac aaaaagaaca aatcagctta tatttttat 2220 cttgatgact cctgctccag aattgctaga ctaagaatta ggtggctaca gatggtagaa 2280 ctaaacaata agcaagagac aataataatg gcccttaatt attaacaaag tgccagagtc 2340 taggctaagc actttatcta tatctcattt cattctcaca acttataagt gaatgagtaa 2400 actgagactt aagggaactg aatcacttaa atgtcacctg gctaactgat ggcagagcca 2460 gagcttgaat tcatgttggt ctgacatcaa ggtctttggt cttctcccta caccaagtta 2520 cctacaagaa caatgacacc acactctgcc tgaaggctca cacctcatac cagcatacgc 2580 tcaccttaca gggaaatggg tttatccagg atcatgagac attagggtag atgaaaggag 2640 agctttgcag ataacaaaat agcctatcct taataaatcc tccactctct ggaaggagac 2700

2026201462 26 Feb 2026

		tgaggggctt tgtaaaacat tagtcagttg ctcattttta tgggattgct tagctgggct 2760 gtaaagatga aggcatcaaa taaactcaaa gtatttttaa attttttttga taatagagaa 2820 acttcgctaa ccaactgttc tttcttgagt gtatagcccc atcttgtggt aacttgctgc 2880 ttctgcactt catatccata tttcctattg ttcactttat tctgtagagc agcctgccaa 2940 gaattttatt tctgctgttt tttttgctgc taaagaaagg aactaagtca ggatgttaac 3000 agaaaagtcc acataaccct agaattctta gtcaaggaat aattcaagtc agcctagaga 3060 ccatgttgac tttcctcatg tgtttcctta tgactcagta agttggcaag gtcctgactt 3120 tagtcttaat aaaacattga attgtagtaa aggtttttgc aataaaaact tactttgg 3178
3-44	**Sequences**	
3-44-1	Sequence Number [ID]	44
3-44-2	Molecule Type	DNA
3-44-3	Length	1858
3-44-4	Features	**source 1..1858**
	Location/Qualifiers	mol_type=genomic DNA organism=Mus sp.
	NonEnglishQualifier Value	
3-44-5	Residues	attccggagg tgaaaaacaa tggcacaacg tgtataatgg ccagcttctc tgcctccttt 60 ctgaccacct acgagactgc gaatggttct cagatcgtga acatttccct gccagcctct 120 gcagaagtac tgaaaaatgg cagttcttgt ggtaaagaaa atgtttctga ccccagcctc 180 acaattactt ttggaagagg atatttactg acactcaact tcacaaaaaa tacaacacgt 240 tacagtgtcc agcatatgta ttttacatat aacttgtcag atacagaaca ttttcccaat 300 gccatcagca aagagatcta caccatggat tccacaactg acatcaaggc agacatcaac 360 aaagcatacc ggtgtgtcag tgatatccgg gtctacatga agaatgtgac cgttgtgctc 420 cgggatgcca ctatccaggc ctacctgtcg agtggcaact tcagcaagga agagacacac 480 tgcacacagg atggaccttc cccaaccact gggccaccca gcccctcacc accacttgtg 540 cccacaaacc ccactgtatc caagtacaat gttactggta acaacggaac ctgcctgctg 600 gcctctatgg cactgcaact gaatatcacc tacctgaaaa aggacaacaa gacggtgacc 660 agagcgttca acatcagccc aaatgacaca tctagtggga gttgcggtat caacttggtg 720 accctgaaag tggagaacaa gaacagagcc ctggaattgc agtttgggat gaatgccagc 780 tctagcctgt ttttcttgca aggagtgcgc ttgaatatga ctcttcctga tgccctagtg 840 cccacattca gcatctccaa ccattcactg aaagctcttc aggccactgt gggaaactca 900 tacaagtgca acactgagga acacatcttt gtcagcaaga tgctctccct caatgtcttc 960 agtgtgcagg tccaggcttt caaggtggac agtgacaggt ttgggtctgt ggaagagtgt 1020 gttcaggatg gtaacaacat gttgatcccc attgctgtgg gcggtgccct ggcagggctg 1080 atcctcatcg tcctcattgc ctacctcatt ggcaggaaga ggagtcacgc cggctatcag 1140 accatctagc ctggtgggca ggtgcaccag agatgcacag gggcctgttc tcacatcccc 1200 aagcttagat aggtgtggaa gggaggcaca ctttctggca aactgtttta aaatctgctt 1260 tatcaaatgt gaagttcatc ttgcaacatt tactatgcac aaaggaataa ctattgaaat 1320 gacggtgtta attttgctaa ctgggttaaa tattgatgag aaggctccac tgatttgact 1380 tttaagactt ggtgtttggt tcttcattct tttactcaga tttaagccta tcaaagggat 1440 actctggtcc agaccttggc ctggcaaggg tggctgatgg ttaggctgca cacacttaag 1500 aagcaacggg agcagggaag gcttgcacac aggcacgcac agggtcaacc tctggacact 1560 tggcttgggc tacctggcct tgggggggct gaactctggc atctggctgg gtacacaccc 1620 ccccaatttc tgtgctctgc cacccgtgag ctgccacttt cctaaataga aaatggcatt 1680 atttttattt actttttttgt aaagtgattt ccagtcttgt gttggcgttc agggtggccc 1740 tgtctctgca ctgtgtacaa taatagattc acactgctga cgtgtcttgc agcgtaggtg 1800 ggttgtacac tgggcatcag ctcacgtaat gcattgcctg taacgatgct aataaaaa 1858
3-45	**Sequences**	
3-45-1	Sequence Number [ID]	45
3-45-2	Molecule Type	DNA
3-45-3	Length	2339
3-45-4	Features	**source 1..2339**
	Location/Qualifiers	mol_type=genomic DNA organism=Homo sapiens
	NonEnglishQualifier Value	
3-45-5	Residues	ggcccaaccg ccgcccgcgc ccccgctctc cgcaccgtac ccggccgcct cgcgccatgg 60 cggcccccgg cagcgcccgg cgacccctgc tgctgctact gctgttgctg ctgctcggcc 120 tcatgcattg tgcgtcagca gcaatgttta tggtgaaaaa tggcaacggg accgcgtgca 180 taatggccaa cttctctgct gccttctcag tgaactacga caccaagagt ggccctaaga 240 acatgacctt tgacctgcca tcagatgcca cagtggtgct caaccgcagc tcctgtggaa 300 aagagaacac ttctgacccc agtctcgtga ttgcttttgg aagaggacat acactcactc 360 tcaatttcac gagaaatgca acacgttaca gcgtccagct catgagtttt gtttataact 420 tgtcagacac acacctttc cccaatgcga gctccaaaga aatcaagact gtggaatcta 480 taactgacat cagggcagat atagataaaa aatacagatg tgttagtggc acccaggtcc 540 acatgaacaa cgtgaccgta acgctccatg atgccaccat ccaggcgtac ctttccaaca 600 gcagcttcag caggggagag acacgctgtg aacaagacag gccttcccca accacagcgc 660 cccctgcgcc acccagcccc tcgccctcac ccgtgcccaa gagcccctct gtggacaagt 720 acaacgtgag cggcaccaac gggacctgcc tgctggccag catggggctg cagctgaacc 780 tcacctatga gaggaaggac aacacgacgg tgacaaggct tctcaacatc aaccccaaca 840 agacctcggc cagcgggagc tgcggcgccc acctggtgac tctggagctg cacagcgagg 900 gcaccaccgt cctgctcttc cagttcggga tgaatgcaag ttctagccgg tttttcctac 960 aaggaatcca gttgaataca attcttcctg acgccagaga ccctgccttt aaagctgcca 1020 acggctccct gcgagcgctg caggccacag tcggcaattc ctacaagtgc aacgcggagg 1080 agcacgtccg tgtcacgaag gcgttttcag tcaatatatt caaagtgtgg gtccaggctt 1140

2026201462 26 Feb 2026

		tcaaggtgga aggtggccag tttggctctg tggaggagtg tctgctggac gagaacagca	1200
		tgctgatccc catcgctgtg ggtggtgccc tggcggggct ggtcctcatc gtcctcatcg	1260
		cctacctcgt cggcaggaag aggagtcacg caggctacca gactatctag cctggtgcac	1320
		gcaggcacag cagctgcagg ggcctctgtt cctttctctg ggcttagggt cctgtcgaag	1380
		gggaggcaca ctttctggca aacgtttctc aaatctgctt catccaatgt gaagttcatc	1440
		ttgcagcatt tactatgcac aacagagtaa ctatcgaaat gacggtgtta attttgctaa	1500
		ctgggttaaa tattttgcta actggttaaa cattaatatt taccaaagta ggattttgag	1560
		ggtgggggtg ctctctctga gggggtgggg gtgccgctgt ctctgagggg tgggggtgcc	1620
		gctgtctctg aggggtgggg gtgccgctct ctctgagggg gtgggggtgc cgctttctct	1680
		gaggggggtgg gggtgccgct ctctctgagg gggtgggggt gctgctctct ccgaggggtg	1740
		gaatgccgct gtctctgagg ggtgggggtg ccgctctaaa ttggctccat atcatttgag	1800
		tttagggttc tggtgtttgg tttcttcatt ctttactgca ctcagattta agccttacaa	1860
		agggaaagcc tctggccgtc acacgtagga cgcatgaagg tcactcgtgg tgaggctgac	1920
		atgctcacac attacaacag tagagaggga aaatcctaag acagaggaac tccagagatg	1980
		agtgtctgga gcgcttcagt tcagctttaa aggccaggac gggccacacg tggctggcgg	2040
		cctcgttcca gtggcggcac gtccttgggc gtctctaatg tctgcagctc aagggctggc	2100
		acttttttaa atataaaaat gggtgttatt tttatttttt tttgtaaagt gatttttggt	2160
		cttctgttga cattcggggt gatcctgttc tgcgctgtgt acaatgtgag atcggtgcgt	2220
		tctcctgatg ttttgccgtg gcttggggat tgtacacggg accagctcac gtaatgcatt	2280
		gcctgtaaca atgtaataaa aagcctcttt cttttaaaaa aaaaaaaaaa aaaaaaaaa	2339
3-46	**Sequences**		
3-46-1	Sequence Number [ID]	46	
3-46-2	Molecule Type	DNA	
3-46-3	Length	45	
3-46-4	Features	**misc_feature 1..45**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic oligonucleotide	
		source 1..45	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-46-5	Residues	cagtacatca aggccaacag caagttcatc ggcatcaccg aactc	45
3-47	**Sequences**		
3-47-1	Sequence Number [ID]	47	
3-47-2	Molecule Type	AA	
3-47-3	Length	15	
3-47-4	Features	**REGION 1..15**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..15	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-47-5	Residues	QYIKANSKFI GITEL	15
3-48	**Sequences**		
3-48-1	Sequence Number [ID]	48	
3-48-2	Molecule Type	DNA	
3-48-3	Length	39	
3-48-4	Features	**misc_feature 1..39**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic oligonucleotide	
		source 1..39	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-48-5	Residues	gctaaatttg tggctgcctg gacactgaaa gccgccgct	39
3-49	**Sequences**		
3-49-1	Sequence Number [ID]	49	
3-49-2	Molecule Type	AA	
3-49-3	Length	13	
3-49-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-49-5	Residues	AKFVAAWTLK AAA	13
3-50	**Sequences**		
3-50-1	Sequence Number [ID]	50	
3-50-2	Molecule Type	DNA	
3-50-3	Length	593	
3-50-4	Features	**source 1..593**	
	Location/Qualifiers	mol_type=genomic DNA	

2026201462 26 Feb 2026

		organism=Woodchuck hepatitis virus
	NonEnglishQualifier Value	
3-50-5	Residues	aatcaacctc tggattacaa aatttgtgaa agattgactg gtattcttaa ctatgttgct 60 ccttttacgc tatgtggata cgctgcttta atgcctttgt atcatgctat tgcttcccgt 120 atggctttca ttttctcctc cttgtataaa tcctggttgc tgtctcttta tgaggagttg 180 tggcccgttg tcaggcaacg tggcgtggtg tgcactgtgt ttgctgacgc aacccccact 240 ggttggggca ttgccaccac ctgtcagctc ctttccggga ctttcgcttt ccccctccct 300 attgccacgg cggaactcat cgccgcctgc cttgcccgct gctggacagg ggctcggctg 360 ttgggcactg acaattccgt ggtgttgtcg gggaagctga cgtcctttcc atggctgctc 420 gcctgtgttg ccacctggat tctgcgcggg acgtccttct gctacgtccc ttcggccctc 480 aatccagcgg accttccttc ccgcggcctg ctgccggctc tgcggcctct tccgcgtctt 540 cgccttcgcc ctcagacgag tcggatctcc ctttgggccg cctccccgcc tgt 593
3-51	**Sequences**	
3-51-1	Sequence Number [ID]	51
3-51-2	Molecule Type	DNA
3-51-3	Length	589
3-51-4	Features	**misc_feature 1..589**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..589
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-51-5	Residues	tctccccccc ccccctctcc ctcccccccc cctaacgtta ctggccgaag ccgcttggaa 60 taaggccggt gtgcgtttgt ctatatgtta ttttccacca tattgccgtc ttttggcaat 120 gtgagggccc ggaaacctgg ccctgtcttc ttgacgagca ttcctagggg tctttccccct 180 ctcgccaaag gaatgcaagg tctgttgaat gtcgtgaagg aagcagttcc tctggaagct 240 tcttgaagac aaacaacgtc tgtagcgacc ctttgcaggc agcggaaccc cccacctggc 300 gacaggtgcc tctgcggcca aaagccacgt gtataagata cacctgcaaa ggcggcacaa 360 ccccagtgcc acgttgtgag ttggatagtt gtggaaagag tcaaatggct ctcctcaagc 420 gtattcaaca aggggctgaa ggatgcccag aaggtacccc attgtatggg atctgatctg 480 gggcctcggt gcacatgctt tacatgtgtt tagtcgaggt taaaaaaacg tctaggcccc 540 ccgaaccacg gggacgtggt tttcctttga aaaacacgat gataatatg 589
3-52	**Sequences**	
3-52-1	Sequence Number [ID]	52
3-52-2	Molecule Type	DNA
3-52-3	Length	720
3-52-4	Features	**misc_feature 1..720**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..720
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-52-5	Residues	atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac 60 ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac 120 ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180 ctcgtgacca ccctgaccta cggcgtgcag tgcttcagcc gctaccccga ccacatgaag 240 cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc 300 ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg 360 gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420 aagctggagt acaactacaa cagccacaac gtctatatca tggccgacaa gcagaagaac 480 ggcatcaagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540 gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac 600 tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc 660 ctgctggagt tcgtgaccgc cgccgggatc actctcggca tggacgagct gtacaagtag 720
3-53	**Sequences**	
3-53-1	Sequence Number [ID]	53
3-53-2	Molecule Type	DNA
3-53-3	Length	1563
3-53-4	Features	**misc_feature 1..1563**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..1563
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-53-5	Residues	atgctgctgc tgctgctgct gctgggcctg aggctacagc tctccctggg catcatccca 60 gttgaggagg agaacccgga cttctggaac cgcgaggcag ccgaggccct gggtgccgcc 120 aagaagctgc agcctgcaca gacagccgcc aagaacctca tcatcttcct gggcgatggg 180 atgggggtgt ctacggtgac agctgccagg atcctaaaag ggcagaagaa ggacaaactg 240 gggcctgaga taccctggc catggaccgc ttcccatatg tggctctgtc caagacatac 300 aatgtagaca aacatgtgcc agacagtgga gccacagcca cggcctacct gtgcggggtc 360 aagggcaact tccagaccat tggcttgagt gcagccgccc gctttaacca gtgcaacacg 420 acacgcggca acgaggtcat ctccgtgatg aatcgggcca agaaagcagg gaagtcagtg 480

2026201462 26 Feb 2026

		ggagtggtaa ccaccacacg agtgcagcac gcctcgccag ccggcaccta cgcccacacg 540 gtgaaccgca actggtactc ggacgccgac gtgcctgcct cggcccgcca ggaggggtgc 600 caggacatcg ctacgcagct catctccaac atggacattg acgtgatcct aggtggaggc 660 cgaaagtaca tgtttcgcat gggaacccca gaccctgagt acccagatga ctacagccaa 720 ggtgggacca ggctggacgg gaagaatctg gtgcaggaat ggctggcgaa gcgccagggt 780 gcccggtatg tgtggaaccg cactgagctc atgcaggctt ccctggaccc gtctgtgacc 840 catctcatgg gtctctttga gcctggagac atgaaatacg agatccaccg agactccaca 900 ctggacccct ccctgatgga gatgacagag gctgccctgc gcctgctgag caggaacccc 960 cgcggcttct tcctcttcgt ggagggtggt cgcatcgacc atggtcatca tgaaagcagg 1020 gcttaccggg cactgactga gacgatcatg ttcgacgacg ccattgagag ggcgggccag 1080 ctcaccagcg aggaggacac gctgagcctc gtcactgccg accactccca cgtcttctcc 1140 ttcggaggct acccccctgcg agggagctcc atcttcgggc tggcccctgg caaggcccgg 1200 gacaggaagg cctacacggt cctcctatac ggaaacggtc caggctatgt gctcaaggac 1260 ggcgcccggc cggatgttac cgagagcgag agcgggagcc ccgagtatcg gcagcagtca 1320 gcagtgcccc tggacgaaga gacccacgca ggcgaggacg tggcggtgtt cgcgcgcggc 1380 ccgcaggcgc acctggttca cggcgtgcag gagcagacct tcatagcgca cgtcatggcc 1440 ttcgccgcct gcctggagcc ctacaccgcc tgcgacctgg cgccccccgc cggcaccacc 1500 gacgccgcgc acccgggtta ctctagagtc ggggcggccg gccgcttcga gcagacatga 1560 taa 1563
3-54	**Sequences**	
3-54-1	Sequence Number [ID]	54
3-54-2	Molecule Type	DNA
3-54-3	Length	1653
3-54-4	Features	**misc_feature 1..1653**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polynucleotide
		source 1..1653
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-54-5	Residues	atggaagatg ccaaaaacat taagaagggc ccagcgccat tctacccact cgaagacggg 60 accgccggcg agcagctgca caaagccatg aagcgctacg ccctggtgcc cggcaccatc 120 gcctttaccg acgcacatat cgaggtggac attacctacg ccgagtactt cgagatgagc 180 gttcggctgg cagaagctat gaagcgctat gggctgaata caaaccatcg gatcgtggtg 240 tgcagcgaga atagcttgca gttcttcatg cccgtgttgg gtgccctgtt catcggtgtg 300 gctgtggccc cagctaacga catctacaac gagcgcgagc tgctgaacag catgggcatc 360 agccagccca ccgtcgtatt cgtgagcaag aaagggctgc aaaagatcct caacgtgcaa 420 aagaagctac cgatcataca aaagatcatc atcatggata gcaagaccga ctaccagggc 480 ttccaaagca tgtacacctt cgtgacttcc catttgccac ccggcttcaa cgagtacgac 540 ttcgtgcccg agagcttcga ccgggacaaa accatcgccc tgatcatgaa cagtagtggc 600 agtaccggat tgcccaaggg cgtagcccta ccgcaccgca ccgcttgtgt ccgattcagt 660 catgcccgcg accccatctt cggcaaccag atcatccccg acaccgctat cctcagcgtg 720 gtgccatttc accacggctt cggcatgttc accacgctgg gctacttgat ctgcggcttt 780 cgggtcgtgc tcatgtaccg cttcgaggag gagctattct tgcgcagctt gcaagactat 840 aagattcaat ctgccctgct ggtgcccaca ctatttagct tcttcgctaa gagcactctc 900 atcgacaagt acgacctaag caacttgcac gagatcgcca gcggcggggc gccgctcagc 960 aaggaggtag gtgaggccgt ggccaaacgc ttccacctac caggcatccg ccagggctac 1020 ggcctgacag aaacaaccag cgccattctg atcacccccg aaggggacga caagcctggc 1080 gcagtaggca aggtggtgcc cttcttcgag gctaaggtgg tggacttgga caccggtaag 1140 acactgggtg tgaaccagcg cggcgagctg tgcgtccgtg gccccatgat catgagcggc 1200 tacgttaaca accccgaggc tacaaacgct ctcatcgaca aggacggctg gctgcacagc 1260 ggcgacatcg cctactggga cgaggacgag cacttcttca tcgtggaccg gctgaagagc 1320 ctgatcaaat acaagggcta ccaggtagcc ccagccgaac tggagagcat cctgctgcaa 1380 caccccaaca tcttcgacgc cggggtcgcc ggcctgcccg acgacgatgc cggcgagctg 1440 cccgccgcag tcgtcgtgct ggaacacggt aaaaccatga ccgagaagga gatcgtggac 1500 tatgtggcca gccaggttac aaccgccaag aagctgcgcg gtggtgttgt gttcgtggac 1560 gaggtgccta aaggactgac cggcaagttg gacgcccgca agatccgcga gattctcatt 1620 aaggccaaga agggcggcaa gatcgccgtg taa 1653
3-55	**Sequences**	
3-55-1	Sequence Number [ID]	55
3-55-2	Molecule Type	DNA
3-55-3	Length	66
3-55-4	Features	**source 1..66**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Foot-and-mouth disease virus
	NonEnglishQualifier Value	
3-55-5	Residues	gtaaagcaaa cactgaactt tgaccttctc aagttggctg gagacgttga gtccaatcct 60 gggccc 66
3-56	**Sequences**	
3-56-1	Sequence Number [ID]	56
3-56-2	Molecule Type	AA
3-56-3	Length	5
3-56-4	Features	**REGION 1..5**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide

2026201462 26 Feb 2026

		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-56-5	Residues	GPGPG	5
3-57	**Sequences**		
3-57-1	Sequence Number [ID]	57	
3-57-2	Molecule Type	AA	
3-57-3	Length	8	
3-57-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-57-5	Residues	SIINFEKL	8
3-58	**Sequences**		
3-58-1	Sequence Number [ID]	58	
3-58-2	Molecule Type	AA	
3-58-3	Length	9	
3-58-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-58-5	Residues	SPSYAYHQF	9
3-59	**Sequences**		
3-59-1	Sequence Number [ID]	59	
3-59-2	Molecule Type	AA	
3-59-3	Length	10	
3-59-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-59-5	Residues	YVYVADVAAK	10
3-60	**Sequences**		
3-60-1	Sequence Number [ID]	60	
3-60-2	Molecule Type	AA	
3-60-3	Length	8	
3-60-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-60-5	Residues	YEMFNDKS	8
3-61	**Sequences**		
3-61-1	Sequence Number [ID]	61	
3-61-2	Molecule Type	AA	
3-61-3	Length	17	
3-61-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-61-5	Residues	YEMFNDKSQR APDDKMF	17
3-62	**Sequences**		
3-62-1	Sequence Number [ID]	62	
3-62-2	Molecule Type	AA	
3-62-3	Length	9	
3-62-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	

20262014621 26 Feb 2026

		organism=synthetic construct	
	NonEnglishQualifier Value		
3-62-5	Residues	YEMFNDKSF	9
3-63	**Sequences**		
3-63-1	Sequence Number [ID]	63	
3-63-2	Molecule Type	AA	
3-63-3	Length	11	
3-63-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 3	
		note=Pyrrolysine	
		MOD_RES 11	
		note=Ile or Leu	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-63-5	Residues	HRXEIFSHDF X	11
3-64	**Sequences**		
3-64-1	Sequence Number [ID]	64	
3-64-2	Molecule Type	AA	
3-64-3	Length	10	
3-64-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 2	
		note=Ile or Leu	
		MOD_RES 5	
		note=Ile or Leu	
		MOD_RES 7	
		note=Pyrrolysine	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-64-5	Residues	FXIEXFXESS	10
3-65	**Sequences**		
3-65-1	Sequence Number [ID]	65	
3-65-2	Molecule Type	AA	
3-65-3	Length	10	
3-65-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 4	
		note=Pyrrolysine	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-65-5	Residues	NEIXREIREI	10
3-66	**Sequences**		
3-66-1	Sequence Number [ID]	66	
3-66-2	Molecule Type	AA	
3-66-3	Length	15	
3-66-4	Features	**REGION 1..15**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 1	
		note=Ile or Leu	
		MOD_RES 11	
		note=Ile or Leu	
		MOD_RES 15	
		note=Selenocysteine	
		source 1..15	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-66-5	Residues	XFKSIFEMMS XDSSX	15
3-67	**Sequences**		
3-67-1	Sequence Number [ID]	67	
3-67-2	Molecule Type	AA	

2026201462 26 Feb 2026

3-67-3	Length	13	
3-67-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 11	
		note=Pyrrolysine	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-67-5	Residues	KNFLENFIES XFI	13
3-68	**Sequences**		
3-68-1	Sequence Number [ID]	68	
3-68-2	Molecule Type	AA	
3-68-3	Length	27	
3-68-4	Features	**REGION 1..27**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 1	
		note=Ile or Leu	
		MOD_RES 11	
		note=Ile or Leu	
		MOD_RES 15	
		note=Selenocysteine	
		MOD_RES 21	
		note=Ile or Leu	
		MOD_RES 27	
		note=Ile or Leu	
		source 1..27	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-68-5	Residues	XFKSIFEMMS XDSSXIFLKS XFIEIFX	27
3-69	**Sequences**		
3-69-1	Sequence Number [ID]	69	
3-69-2	Molecule Type	AA	
3-69-3	Length	15	
3-69-4	Features	**REGION 1..15**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 2	
		note=Pyrrolysine	
		MOD_RES 14	
		note=Ile or Leu	
		source 1..15	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-69-5	Residues	FXEIFNDKSL DKFXI	15
3-70	**Sequences**		
3-70-1	Sequence Number [ID]	70	
3-70-2	Molecule Type	AA	
3-70-3	Length	9	
3-70-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 5	
		note=Pyrrolysine	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-70-5	Residues	QCEIXWARE	9
3-71	**Sequences**		
3-71-1	Sequence Number [ID]	71	
3-71-2	Molecule Type	AA	
3-71-3	Length	8	
3-71-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 4	
		note=Selenocysteine	
		source 1..8	

2026201462 26 Feb 2026

		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-71-5	Residues	FIEXHFWI	8
3-72	**Sequences**		
3-72-1	Sequence Number [ID]	72	
3-72-2	Molecule Type	AA	
3-72-3	Length	12	
3-72-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 7	
		note=Ile or Leu	
		MOD_RES 10	
		note=Selenocysteine	
		MOD_RES 11	
		note=Ile or Leu	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-72-5	Residues	FEWRHRXTRX XR	12
3-73	**Sequences**		
3-73-1	Sequence Number [ID]	73	
3-73-2	Molecule Type	AA	
3-73-3	Length	9	
3-73-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 4	
		note=Ile or Leu	
		MOD_RES 5	
		note=Pyrrolysine	
		MOD_RES 8	
		note=Ile or Leu	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-73-5	Residues	QIEXXEIXE	9
3-74	**Sequences**		
3-74-1	Sequence Number [ID]	74	
3-74-2	Molecule Type	AA	
3-74-3	Length	14	
3-74-4	Features	**REGION 1..14**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 2	
		note=Ile or Leu	
		MOD_RES 9	
		note=Pyrrolysine	
		MOD_RES 11	
		note=Ile or Leu	
		source 1..14	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-74-5	Residues	FXELFISBXS XFIE	14
3-75	**Sequences**		
3-75-1	Sequence Number [ID]	75	
3-75-2	Molecule Type	AA	
3-75-3	Length	16	
3-75-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 5	
		note=Pyrrolysine	
		MOD_RES 16	
		note=Ile or Leu	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	

20262014621 26 Feb 2026

	NonEnglishQualifier Value		
3-75-5	Residues	QCEIXWAREF LKEIGX	16
3-76	**Sequences**		
3-76-1	Sequence Number [ID]	76	
3-76-2	Molecule Type	AA	
3-76-3	Length	11	
3-76-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 5	
		note=Pyrrolysine	
		MOD_RES 9	
		note=Ile or Leu	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-76-5	Residues	IEFRXEIFXE F	11
3-77	**Sequences**		
3-77-1	Sequence Number [ID]	77	
3-77-2	Molecule Type	AA	
3-77-3	Length	9	
3-77-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 5	
		note=Pyrrolysine	
		MOD_RES 9	
		note=Ile or Leu	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-77-5	Residues	IEFRXEIFX	9
3-78	**Sequences**		
3-78-1	Sequence Number [ID]	78	
3-78-2	Molecule Type	AA	
3-78-3	Length	9	
3-78-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 4	
		note=Pyrrolysine	
		MOD_RES 8	
		note=Ile or Leu	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-78-5	Residues	EFRXEIFXE	9
3-79	**Sequences**		
3-79-1	Sequence Number [ID]	79	
3-79-2	Molecule Type	AA	
3-79-3	Length	9	
3-79-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 3	
		note=Pyrrolysine	
		MOD_RES 7	
		note=Ile or Leu	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-79-5	Residues	FRXEIFXEF	9
3-80	**Sequences**		
3-80-1	Sequence Number [ID]	80	
3-80-2	Molecule Type	AA	
3-80-3	Length	7	
3-80-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	

2026201462 26 Feb 2026

		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-80-5	Residues	SINFEKL	7
3-81	**Sequences**		
3-81-1	Sequence Number [ID]	81	
3-81-2	Molecule Type	AA	
3-81-3	Length	9	
3-81-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-81-5	Residues	LLLLLVVVV	9
3-82	**Sequences**		
3-82-1	Sequence Number [ID]	82	
3-82-2	Molecule Type	AA	
3-82-3	Length	9	
3-82-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-82-5	Residues	EKLAAYLLL	9
3-83	**Sequences**		
3-83-1	Sequence Number [ID]	83	
3-83-2	Molecule Type	AA	
3-83-3	Length	10	
3-83-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-83-5	Residues	KLAAYLLLLL	10
3-84	**Sequences**		
3-84-1	Sequence Number [ID]	84	
3-84-2	Molecule Type	AA	
3-84-3	Length	8	
3-84-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-84-5	Residues	FEKLAAYL	8
3-85	**Sequences**		
3-85-1	Sequence Number [ID]	85	
3-85-2	Molecule Type	AA	
3-85-3	Length	8	
3-85-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-85-5	Residues	AAYLLLLL	8
3-86	**Sequences**		
3-86-1	Sequence Number [ID]	86	
3-86-2	Molecule Type	AA	
3-86-3	Length	9	
3-86-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	

20262014622 26 Feb 2026

		organism=synthetic construct	
	NonEnglishQualifier Value		
3-86-5	Residues	YLLLLLVVV	9
3-87	**Sequences**		
3-87-1	Sequence Number [ID]	87	
3-87-2	Molecule Type	AA	
3-87-3	Length	10	
3-87-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-87-5	Residues	VVVVAAYSIN	10
3-88	**Sequences**		
3-88-1	Sequence Number [ID]	88	
3-88-2	Molecule Type	AA	
3-88-3	Length	7	
3-88-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-88-5	Residues	VVVVAAY	7
3-89	**Sequences**		
3-89-1	Sequence Number [ID]	89	
3-89-2	Molecule Type	AA	
3-89-3	Length	8	
3-89-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-89-5	Residues	AYSINFEK	8
3-90	**Sequences**		
3-90-1	Sequence Number [ID]	90	
3-90-2	Molecule Type	AA	
3-90-3	Length	25	
3-90-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-90-5	Residues	YNYSYWISIF AHTMWYNIWH VQWNK	25
3-91	**Sequences**		
3-91-1	Sequence Number [ID]	91	
3-91-2	Molecule Type	AA	
3-91-3	Length	25	
3-91-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-91-5	Residues	IEALPYVFLQ DQFELRLLKG EQGNN	25
3-92	**Sequences**		
3-92-1	Sequence Number [ID]	92	
3-92-2	Molecule Type	AA	
3-92-3	Length	25	
3-92-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		

20262014462 26 Feb 2026

3-92-5	Residues	DSEETNTNYL HYCHFHWTWA QQTTV	25
3-93	**Sequences**		
3-93-1	Sequence Number [ID]	93	
3-93-2	Molecule Type	AA	
3-93-3	Length	25	
3-93-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-93-5	Residues	GMLSQYELKD CSLGFSWNDP AKYLR	25
3-94	**Sequences**		
3-94-1	Sequence Number [ID]	94	
3-94-2	Molecule Type	AA	
3-94-3	Length	25	
3-94-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-94-5	Residues	VRIDKFLMYV WYSAPFSAYP LYQDA	25
3-95	**Sequences**		
3-95-1	Sequence Number [ID]	95	
3-95-2	Molecule Type	AA	
3-95-3	Length	25	
3-95-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-95-5	Residues	CVHIYNNYPR MLGIPFSVMV SGFAM	25
3-96	**Sequences**		
3-96-1	Sequence Number [ID]	96	
3-96-2	Molecule Type	AA	
3-96-3	Length	25	
3-96-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-96-5	Residues	FTFKGNIWIE MAGQFERTWN YPLSL	25
3-97	**Sequences**		
3-97-1	Sequence Number [ID]	97	
3-97-2	Molecule Type	AA	
3-97-3	Length	25	
3-97-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-97-5	Residues	ANDDTPDFRK CYIEDHSFRF SQTMN	25
3-98	**Sequences**		
3-98-1	Sequence Number [ID]	98	
3-98-2	Molecule Type	AA	
3-98-3	Length	25	
3-98-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-98-5	Residues	AAQYIACMVN RQMTIVYHLT RWGMK	25
3-99	**Sequences**		

2026201462 26 Feb 2026

3-99-1	Sequence Number [ID]	99	
3-99-2	Molecule Type	AA	
3-99-3	Length	25	
3-99-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-99-5	Residues	KYLKEFTQLL TFVDCYMWIT FCGPD	25
3-100	**Sequences**		
3-100-1	Sequence Number [ID]	100	
3-100-2	Molecule Type	AA	
3-100-3	Length	25	
3-100-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-100-5	Residues	AMHYRTDIHG YWIEYRQVDN QMWNT	25
3-101	**Sequences**		
3-101-1	Sequence Number [ID]	101	
3-101-2	Molecule Type	AA	
3-101-3	Length	25	
3-101-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-101-5	Residues	THVNEHQLEA VYRFHQVHCR FPYEN	25
3-102	**Sequences**		
3-102-1	Sequence Number [ID]	102	
3-102-2	Molecule Type	AA	
3-102-3	Length	25	
3-102-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-102-5	Residues	QTFSECLFFH CLKVWNNVKY AKSLK	25
3-103	**Sequences**		
3-103-1	Sequence Number [ID]	103	
3-103-2	Molecule Type	AA	
3-103-3	Length	25	
3-103-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-103-5	Residues	SFSSWHYKES HIALLMSPKK NHNNT	25
3-104	**Sequences**		
3-104-1	Sequence Number [ID]	104	
3-104-2	Molecule Type	AA	
3-104-3	Length	25	
3-104-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-104-5	Residues	ILDGIMSRWE KVCTRQTRYS YCQCA	25
3-105	**Sequences**		
3-105-1	Sequence Number [ID]	105	
3-105-2	Molecule Type	AA	

2026201462 26 Feb 2026

3-105-3	Length	25	
3-105-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-105-5	Residues	YRAAQMSKWP NKYFDFPEFM AYMPI	25
3-106	**Sequences**		
3-106-1	Sequence Number [ID]	106	
3-106-2	Molecule Type	AA	
3-106-3	Length	25	
3-106-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-106-5	Residues	PRPGMPCQHH NTHGLNDRQA FDDFV	25
3-107	**Sequences**		
3-107-1	Sequence Number [ID]	107	
3-107-2	Molecule Type	AA	
3-107-3	Length	25	
3-107-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-107-5	Residues	HNIISDETEV WEQAPHITWV YMWCR	25
3-108	**Sequences**		
3-108-1	Sequence Number [ID]	108	
3-108-2	Molecule Type	AA	
3-108-3	Length	25	
3-108-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-108-5	Residues	AYSWPVVPMK WIPYRALCAN HPPGT	25
3-109	**Sequences**		
3-109-1	Sequence Number [ID]	109	
3-109-2	Molecule Type	AA	
3-109-3	Length	25	
3-109-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-109-5	Residues	HVMPHVAMNI CNWYEFLYRI SHIGR	25
3-110	**Sequences**		
3-110-1	Sequence Number [ID]	110	
3-110-2	Molecule Type	AA	
3-110-3	Length	484	
3-110-4	Features	**REGION 1..484**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide	
		source 1..484	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-110-5	Residues	THVNEHQLEA VYRFHQVHCR FPYENAMHYQ MWNTYRAAQM SKWPNKYFDF PEFMAYMPIC 60 VHIYNNYPRM LGIPFSVMVS GFAMAYSWPV VPMKWIPYRA LCANHPPGTA NDDTPDFRKC 120 YIEDHSFRFS QTMNIEALPY VFLQDQFELR LLKGEQGNND SEETNTNYLH YCHFHWTWAQ 180 QTTVILDGIM SRWEKVCTRQ TRYSYCQCAF TFKGNIWIEM AGQFERTWNY PLSLSFSSWH 240 YKESHIALLM SPKKNHNNTQ TFSECLFFHC LKVWNNVKYA KSLKHVMPHV AMNICNWYEF 300 LYRISHIGRH NIISDETEVW EQAPHITWVY MWCRVRIDKF LMYVWYSAPF SAYPLYQDAK 360 YLKEFTQLLT FVDCYMWITF CGPDAAQYIA CMVNRQMTIV YHLTRWGMKY NYSYWISIFA 420	

2026201462 26 Feb 2026

		HTMWYNIWHV QWNKGMLSQY ELKDCSLGFS WNDPAKYLRP RPGMPCQHHN THGLNDRQAF 480 DDFV 484
3-111	**Sequences**	
3-111-1	Sequence Number [ID]	111
3-111-2	Molecule Type	AA
3-111-3	Length	484
3-111-4	Features	**REGION 1..484**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide **source 1..484** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-111-5	Residues	IEALPYVFLQ DQFELRLLKG EQGNNILDGI MSRWEKVCTR QTRYSYCQCA HVMPHVAMNI 60 CNWYEFLYRI SHIGRTHVNE HQLEAVYRFH QVHCRFPYEN FTFKGNIWIE MAGQFERTWN 120 YPLSLAMHYQ MWNTSFSSWH YKESHIALLM SPKKNHNNTV RIDKFLMYVW YSAPFSAYPL 180 YQDAQTFSEC LFFHCLKVWN NVKYAKSLKY RAAQMSKWPN KYFDFPEFMA YMPIAYSWPV 240 VPMKWIPYRA LCANHPPGTC VHIYNNYPRM LGIPFSVMVS GFAMHNIISD ETEVWEQAPH 300 ITWVYMWCRA AQYIACMVNR QMTIVYHLTR WGMKYNYSYW ISIFAHTMWY NIWHVQWNKG 360 MLSQYELKDC SLGFSWNDPA KYLRKYLKEF TQLLTFVDCY MWITFCGPDA NDDTPDFRKC 420 YIEDHSFRFS QTMNDSEETN TNYLHYCHFH WTWAQQTTVP RPGMPCQHHN THGLNDRQAF 480 DDFV 484
3-112	**Sequences**	
3-112-1	Sequence Number [ID]	112
3-112-2	Molecule Type	AA
3-112-3	Length	25
3-112-4	Features	**REGION 1..25**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide **source 1..25** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-112-5	Residues	SSTPYLYYGT SSVSYQFPMV PGGDR 25
3-113	**Sequences**	
3-113-1	Sequence Number [ID]	113
3-113-2	Molecule Type	AA
3-113-3	Length	25
3-113-4	Features	**REGION 1..25**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide **source 1..25** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-113-5	Residues	EMAGKIDLLR DSYIFQLFWR EAAEP 25
3-114	**Sequences**	
3-114-1	Sequence Number [ID]	114
3-114-2	Molecule Type	AA
3-114-3	Length	25
3-114-4	Features	**REGION 1..25**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide **source 1..25** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-114-5	Residues	ALKQRTWQAL AHKYNSQPSV SLRDF 25
3-115	**Sequences**	
3-115-1	Sequence Number [ID]	115
3-115-2	Molecule Type	AA
3-115-3	Length	25
3-115-4	Features	**REGION 1..25**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide **source 1..25** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-115-5	Residues	VSSHSSQATK DSAVGLKYSA STPVR 25
3-116	**Sequences**	
3-116-1	Sequence Number [ID]	116
3-116-2	Molecule Type	AA
3-116-3	Length	25

2026201462 26 Feb 2026

3-116-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-116-5	Residues	KEAIDAWAPY LPEYIDHVIS PGVTS	25
3-117	**Sequences**		
3-117-1	Sequence Number [ID]	117	
3-117-2	Molecule Type	AA	
3-117-3	Length	25	
3-117-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-117-5	Residues	SPVITAPPSS PVFDTSDIRK EPMNI	25
3-118	**Sequences**		
3-118-1	Sequence Number [ID]	118	
3-118-2	Molecule Type	AA	
3-118-3	Length	25	
3-118-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-118-5	Residues	PAEVAEQYSE KLVYMPHTFF IGDHA	25
3-119	**Sequences**		
3-119-1	Sequence Number [ID]	119	
3-119-2	Molecule Type	AA	
3-119-3	Length	22	
3-119-4	Features	**REGION 1..22**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..22	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-119-5	Residues	MADLDKLNIH SIIQRLLEVR GS	22
3-120	**Sequences**		
3-120-1	Sequence Number [ID]	120	
3-120-2	Molecule Type	AA	
3-120-3	Length	25	
3-120-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-120-5	Residues	AAAYNEKSGR ITLLSLLFQK VFAQI	25
3-121	**Sequences**		
3-121-1	Sequence Number [ID]	121	
3-121-2	Molecule Type	AA	
3-121-3	Length	25	
3-121-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-121-5	Residues	KIEEVRDAME NEIRTQLRRQ AAAHT	25
3-122	**Sequences**		
3-122-1	Sequence Number [ID]	122	
3-122-2	Molecule Type	AA	
3-122-3	Length	25	
3-122-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	

2026201462 26 Feb 2026

		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-122-5	Residues	DRGHYVLCDF GSTTNKFQNP QTEGV	25
3-123	**Sequences**		
3-123-1	Sequence Number [ID]	123	
3-123-2	Molecule Type	AA	
3-123-3	Length	25	
3-123-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-123-5	Residues	QVDNRKAEAE EAIKRLSYIS QKVSD	25
3-124	**Sequences**		
3-124-1	Sequence Number [ID]	124	
3-124-2	Molecule Type	AA	
3-124-3	Length	25	
3-124-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-124-5	Residues	CLSDAGVRKM TAAVRVMKRG LENLT	25
3-125	**Sequences**		
3-125-1	Sequence Number [ID]	125	
3-125-2	Molecule Type	AA	
3-125-3	Length	25	
3-125-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-125-5	Residues	LPPRSLPSDP FSQVPASPQS QSSSQ	25
3-126	**Sequences**		
3-126-1	Sequence Number [ID]	126	
3-126-2	Molecule Type	AA	
3-126-3	Length	25	
3-126-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-126-5	Residues	ELVLEDLQDG DVKMGGSFRG AFSNS	25
3-127	**Sequences**		
3-127-1	Sequence Number [ID]	127	
3-127-2	Molecule Type	AA	
3-127-3	Length	25	
3-127-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-127-5	Residues	VTMDGVREED LASFSLRKRW ESEPH	25
3-128	**Sequences**		
3-128-1	Sequence Number [ID]	128	
3-128-2	Molecule Type	AA	
3-128-3	Length	25	
3-128-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	

20262014462 26 Feb 2026

		organism=synthetic construct	
	NonEnglishQualifier Value		
3-128-5	Residues	IVGVMFFERA FDEGADAIYD HINEG	25
3-129	**Sequences**		
3-129-1	Sequence Number [ID]	129	
3-129-2	Molecule Type	AA	
3-129-3	Length	25	
3-129-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-129-5	Residues	TVTPTPTPTG TQSPTPTPIT TTTTV	25
3-130	**Sequences**		
3-130-1	Sequence Number [ID]	130	
3-130-2	Molecule Type	AA	
3-130-3	Length	25	
3-130-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-130-5	Residues	QEEMPPRPCG GHTSSSLPKS HLEPS	25
3-131	**Sequences**		
3-131-1	Sequence Number [ID]	131	
3-131-2	Molecule Type	AA	
3-131-3	Length	21	
3-131-4	Features	**REGION 1..21**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..21	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-131-5	Residues	PNIQAVLLPK KTDSHHKAKG K	21
3-132	**Sequences**		
3-132-1	Sequence Number [ID]	132	
3-132-2	Molecule Type	AA	
3-132-3	Length	9	
3-132-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-132-5	Residues	NLVPMVATV	9
3-133	**Sequences**		
3-133-1	Sequence Number [ID]	133	
3-133-2	Molecule Type	AA	
3-133-3	Length	9	
3-133-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-133-5	Residues	CLGGLLTMV	9
3-134	**Sequences**		
3-134-1	Sequence Number [ID]	134	
3-134-2	Molecule Type	AA	
3-134-3	Length	9	
3-134-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		

20262014622 26 Feb 2026

3-134-5	Residues	GILGFVFTL	9
3-135	**Sequences**		
3-135-1	Sequence Number [ID]	135	
3-135-2	Molecule Type	AA	
3-135-3	Length	9	
3-135-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-135-5	Residues	LLFGYPVYV	9
3-136	**Sequences**		
3-136-1	Sequence Number [ID]	136	
3-136-2	Molecule Type	AA	
3-136-3	Length	9	
3-136-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-136-5	Residues	GLCTLVAML	9
3-137	**Sequences**		
3-137-1	Sequence Number [ID]	137	
3-137-2	Molecule Type	AA	
3-137-3	Length	9	
3-137-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-137-5	Residues	WLSLLVPFV	9
3-138	**Sequences**		
3-138-1	Sequence Number [ID]	138	
3-138-2	Molecule Type	AA	
3-138-3	Length	8	
3-138-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-138-5	Residues	FLLTRICT	8
3-139	**Sequences**		
3-139-1	Sequence Number [ID]	139	
3-139-2	Molecule Type	AA	
3-139-3	Length	8	
3-139-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-139-5	Residues	WQAGILAR	8
3-140	**Sequences**		
3-140-1	Sequence Number [ID]	140	
3-140-2	Molecule Type	AA	
3-140-3	Length	8	
3-140-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-140-5	Residues	QGQNLKYQ	8
3-141	**Sequences**		

2026201462 26 Feb 2026

3-141-1	Sequence Number [ID]	141	
3-141-2	Molecule Type	AA	
3-141-3	Length	25	
3-141-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-141-5	Residues	WQAGILARNL VPMVATVQGQ NLKYQ	25
3-142	**Sequences**		
3-142-1	Sequence Number [ID]	142	
3-142-2	Molecule Type	DNA	
3-142-3	Length	20	
3-142-4	Features	**misc_feature 1..20**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic primer	
		source 1..20	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-142-5	Residues	gtggtgtgca gcgagaatag	20
3-143	**Sequences**		
3-143-1	Sequence Number [ID]	143	
3-143-2	Molecule Type	DNA	
3-143-3	Length	22	
3-143-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic primer	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-143-5	Residues	cgctcgttgt agatgtcgtt ag	22
3-144	**Sequences**		
3-144-1	Sequence Number [ID]	144	
3-144-2	Molecule Type	DNA	
3-144-3	Length	15	
3-144-4	Features	**misc_feature 1..15**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic probe	
		source 1..15	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-144-5	Residues	ttcatgcccg tgttg	15
3-145	**Sequences**		
3-145-1	Sequence Number [ID]	145	
3-145-2	Molecule Type	DNA	
3-145-3	Length	22	
3-145-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic primer	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-145-5	Residues	gtttttgatc cagacccaga tg	22
3-146	**Sequences**		
3-146-1	Sequence Number [ID]	146	
3-146-2	Molecule Type	DNA	
3-146-3	Length	21	
3-146-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic primer	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-146-5	Residues	gcccattatt cagagcgagt a	21
3-147	**Sequences**		
3-147-1	Sequence Number [ID]	147	
3-147-2	Molecule Type	DNA	

20262014462 26 Feb 2026

3-147-3	Length	14	
3-147-4	Features	**misc_feature 1..14**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic probe	
		source 1..14	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-147-5	Residues	tcaccaggat ccac	14
3-148	**Sequences**		
3-148-1	Sequence Number [ID]	148	
3-148-2	Molecule Type	DNA	
3-148-3	Length	17	
3-148-4	Features	**misc_feature 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic primer	
		source 1..17	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-148-5	Residues	ccttgcacat gccggag	17
3-149	**Sequences**		
3-149-1	Sequence Number [ID]	149	
3-149-2	Molecule Type	DNA	
3-149-3	Length	17	
3-149-4	Features	**misc_feature 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic primer	
		source 1..17	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-149-5	Residues	acagagcctc gcctttg	17
3-150	**Sequences**		
3-150-1	Sequence Number [ID]	150	
3-150-2	Molecule Type	DNA	
3-150-3	Length	12	
3-150-4	Features	**misc_feature 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic probe	
		source 1..12	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-150-5	Residues	gtgagctggc gg	12
3-151	**Sequences**		
3-151-1	Sequence Number [ID]	151	
3-151-2	Molecule Type	DNA	
3-151-3	Length	22	
3-151-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic primer	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-151-5	Residues	ctgaaagctc ggtttgctaa tg	22
3-152	**Sequences**		
3-152-1	Sequence Number [ID]	152	
3-152-2	Molecule Type	DNA	
3-152-3	Length	21	
3-152-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic primer	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-152-5	Residues	ccatgctgga agagacaatc t	21
3-153	**Sequences**		
3-153-1	Sequence Number [ID]	153	
3-153-2	Molecule Type	DNA	
3-153-3	Length	15	
3-153-4	Features	**misc_feature 1..15**	

2026201462 26 Feb 2026

	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic probe	
		source 1..15	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-153-5	Residues	tggcgctgac cgata	15
3-154	**Sequences**		
3-154-1	Sequence Number [ID]	154	
3-154-2	Molecule Type	DNA	
3-154-3	Length	22	
3-154-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic primer	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-154-5	Residues	tatgcctatc ctgtctcctc tg	22
3-155	**Sequences**		
3-155-1	Sequence Number [ID]	155	
3-155-2	Molecule Type	DNA	
3-155-3	Length	22	
3-155-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic primer	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-155-5	Residues	gctaatgcag ctaagtcctc tc	22
3-156	**Sequences**		
3-156-1	Sequence Number [ID]	156	
3-156-2	Molecule Type	DNA	
3-156-3	Length	15	
3-156-4	Features	**misc_feature 1..15**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic probe	
		source 1..15	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-156-5	Residues	tgaccgtgcc ttctg	15
3-157	**Sequences**		
3-157-1	Sequence Number [ID]	157	
3-157-2	Molecule Type	AA	
3-157-3	Length	18	
3-157-4	Features	**REGION 1..18**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..18	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-157-5	Residues	YEMFNDKSFQ RAPDDKMF	18
3-158	**Sequences**		
3-158-1	Sequence Number [ID]	158	
3-158-2	Molecule Type	AA	
3-158-3	Length	9	
3-158-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 6	
		note=Selenocysteine	
		MOD_RES 7..8	
		note=Pyrrolysine	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-158-5	Residues	FEGRKXXXI	9
3-159	**Sequences**		
3-159-1	Sequence Number [ID]	159	
3-159-2	Molecule Type	AA	

2026201462 26 Feb 2026

3-159-3	Length	14	
3-159-4	Features	**REGION 1..14**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		MOD_RES 2	
		note=Ile or Leu	
		MOD_RES 5	
		note=Pyrrolysine	
		MOD_RES 7	
		note=Ile or Leu	
		MOD_RES 8	
		note=Pyrrolysine	
		MOD_RES 10	
		note=Ile or Leu	
		MOD_RES 14	
		note=Pyrrolysine	
		source 1..14	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-159-5	Residues	PXFIXEXXIX GEIX	14
3-160	**Sequences**		
3-160-1	Sequence Number [ID]	160	
3-160-2	Molecule Type	AA	
3-160-3	Length	13	
3-160-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-160-5	Residues	AKFVAAWTLK AAA	13
3-161	**Sequences**		
3-161-1	Sequence Number [ID]	161	
3-161-2	Molecule Type	AA	
3-161-3	Length	14	
3-161-4	Features	**REGION 1..14**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..14	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-161-5	Residues	QYIKANSKFI GITE	14
3-162	**Sequences**		
3-162-1	Sequence Number [ID]	162	
3-162-2	Molecule Type	AA	
3-162-3	Length	9	
3-162-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-162-5	Residues	DLMGYIPAV	9
3-163	**Sequences**		
3-163-1	Sequence Number [ID]	163	
3-163-2	Molecule Type	AA	
3-163-3	Length	10	
3-163-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-163-5	Residues	FLPSDFFPSV	10
3-164	**Sequences**		
3-164-1	Sequence Number [ID]	164	
3-164-2	Molecule Type	AA	
3-164-3	Length	9	

20262014462 26 Feb 2026

3-164-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-164-5	Residues	FLLTRILTI	9
3-165	**Sequences**		
3-165-1	Sequence Number [ID]	165	
3-165-2	Molecule Type	AA	
3-165-3	Length	9	
3-165-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-165-5	Residues	FLLSLGIHL	9
3-166	**Sequences**		
3-166-1	Sequence Number [ID]	166	
3-166-2	Molecule Type	AA	
3-166-3	Length	9	
3-166-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-166-5	Residues	ILKEPVHGV	9
3-167	**Sequences**		
3-167-1	Sequence Number [ID]	167	
3-167-2	Molecule Type	AA	
3-167-3	Length	10	
3-167-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-167-5	Residues	YMLDLQPETT	10
3-168	**Sequences**		
3-168-1	Sequence Number [ID]	168	
3-168-2	Molecule Type	AA	
3-168-3	Length	9	
3-168-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-168-5	Residues	CINGVCWTV	9
3-169	**Sequences**		
3-169-1	Sequence Number [ID]	169	
3-169-2	Molecule Type	AA	
3-169-3	Length	10	
3-169-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-169-5	Residues	YLLPRRGPRL	10
3-170	**Sequences**		
3-170-1	Sequence Number [ID]	170	
3-170-2	Molecule Type	AA	
3-170-3	Length	9	
3-170-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	

2026201462 26 Feb 2026

		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-170-5	Residues	FLYALALLL	9
3-171	**Sequences**		
3-171-1	Sequence Number [ID]	171	
3-171-2	Molecule Type	AA	
3-171-3	Length	9	
3-171-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-171-5	Residues	AAGIGILTV	9
3-172	**Sequences**		
3-172-1	Sequence Number [ID]	172	
3-172-2	Molecule Type	AA	
3-172-3	Length	9	
3-172-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-172-5	Residues	SLLMWITQV	9
3-173	**Sequences**		
3-173-1	Sequence Number [ID]	173	
3-173-2	Molecule Type	AA	
3-173-3	Length	9	
3-173-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-173-5	Residues	KLGGALQAK	9
3-174	**Sequences**		
3-174-1	Sequence Number [ID]	174	
3-174-2	Molecule Type	AA	
3-174-3	Length	9	
3-174-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-174-5	Residues	RLRAEAQVK	9
3-175	**Sequences**		
3-175-1	Sequence Number [ID]	175	
3-175-2	Molecule Type	AA	
3-175-3	Length	10	
3-175-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-175-5	Residues	EENLLDFVRF	10
3-176	**Sequences**		
3-176-1	Sequence Number [ID]	176	
3-176-2	Molecule Type	AA	
3-176-3	Length	9	
3-176-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	

20262014621 26 Feb 2026

		organism=synthetic construct	
	NonEnglishQualifier Value		
3-176-5	Residues	EEYLQAFTY	9
3-177	**Sequences**		
3-177-1	Sequence Number [ID]	177	
3-177-2	Molecule Type	AA	
3-177-3	Length	9	
3-177-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-177-5	Residues	CTPYDINQM	9
3-178	**Sequences**		
3-178-1	Sequence Number [ID]	178	
3-178-2	Molecule Type	AA	
3-178-3	Length	8	
3-178-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-178-5	Residues	TTPESANL	8
3-179	**Sequences**		
3-179-1	Sequence Number [ID]	179	
3-179-2	Molecule Type	AA	
3-179-3	Length	9	
3-179-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-179-5	Residues	CAPPGYALL	9
3-180	**Sequences**		
3-180-1	Sequence Number [ID]	180	
3-180-2	Molecule Type	AA	
3-180-3	Length	9	
3-180-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-180-5	Residues	SGPKTNIIV	9
3-181	**Sequences**		
3-181-1	Sequence Number [ID]	181	
3-181-2	Molecule Type	AA	
3-181-3	Length	9	
3-181-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-181-5	Residues	LSPRTLNAW	9
3-182	**Sequences**		
3-182-1	Sequence Number [ID]	182	
3-182-2	Molecule Type	AA	
3-182-3	Length	9	
3-182-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		

20262014462 26 Feb 2026

3-182-5	Residues	TVPWPNASL	9
3-183	**Sequences**		
3-183-1	Sequence Number [ID]	183	
3-183-2	Molecule Type	AA	
3-183-3	Length	9	
3-183-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-183-5	Residues	EGPRNQDWL	9
3-184	**Sequences**		
3-184-1	Sequence Number [ID]	184	
3-184-2	Molecule Type	AA	
3-184-3	Length	9	
3-184-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-184-5	Residues	DWENVSPEL	9
3-185	**Sequences**		
3-185-1	Sequence Number [ID]	185	
3-185-2	Molecule Type	AA	
3-185-3	Length	8	
3-185-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-185-5	Residues	SIIVFNLL	8
3-186	**Sequences**		
3-186-1	Sequence Number [ID]	186	
3-186-2	Molecule Type	AA	
3-186-3	Length	9	
3-186-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-186-5	Residues	ASMTNMELM	9
3-187	**Sequences**		
3-187-1	Sequence Number [ID]	187	
3-187-2	Molecule Type	AA	
3-187-3	Length	9	
3-187-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-187-5	Residues	AQLANDVVL	9
3-188	**Sequences**		
3-188-1	Sequence Number [ID]	188	
3-188-2	Molecule Type	AA	
3-188-3	Length	9	
3-188-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-188-5	Residues	SVYDFFVWL	9
3-189	**Sequences**		

20262014462 26 Feb 2026

3-189-1	Sequence Number [ID]	189	
3-189-2	Molecule Type	AA	
3-189-3	Length	9	
3-189-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-189-5	Residues	MNKYAYHML	9
3-190	**Sequences**		
3-190-1	Sequence Number [ID]	190	
3-190-2	Molecule Type	AA	
3-190-3	Length	15	
3-190-4	Features	**REGION 1..15**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..15	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-190-5	Residues	QYIKANSKFI GITEL	15
3-191	**Sequences**		
3-191-1	Sequence Number [ID]	191	
3-191-2	Molecule Type	AA	
3-191-3	Length	19	
3-191-4	Features	**REGION 1..19**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..19	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-191-5	Residues	SINFEKLAAY LLLLLVVVV	19
3-192	**Sequences**		
3-192-1	Sequence Number [ID]	192	
3-192-2	Molecule Type	AA	
3-192-3	Length	19	
3-192-4	Features	**REGION 1..19**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..19	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-192-5	Residues	LLLLLVVVVA AYSINFEKL	19
3-193	**Sequences**		
3-193-1	Sequence Number [ID]	193	
3-193-2	Molecule Type	AA	
3-193-3	Length	9	
3-193-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-193-5	Residues	SPSYVYHQF	9