

CoV and SARS-CoV-2. Both viruses share a 76% amino acid identity across the genome that could help leverage the previous research on protective immune responses to SAR-CoV to aid in vaccine development for SARS-CoV-2

[0005] Given the high morbidity and mortality rate of these infections, there have been various reports investigating the immune responses to such infections. Both innate as well as adaptive immune responses have been shown to be important. Studies in mice infected with SARS-CoV demonstrated that the severity of SARS correlated with the ability to develop a virus specific immune response. In another study, it was demonstrated that dysregulation of the type I interferon and inflammatory monocyte macrophage response led to lethal pneumonia in SARS-CoV infected mice. A protective role for both humoral as well as cellular immune responses have been demonstrated in the case on SARS-CoV. Antibody responses generated against the S and the N protein have shown to protect from SARS-CoV infection in mice and have been detected in SARS-CoV infected patients. However, these antibody responses detected against the S protein were short-lived and undetectable 6 years post recovery suggesting that CD4 and CD8 responses may be involved in the control of this virus.

[0006] Both CD4⁺ and CD8⁺ T cell responses have been detected in SARS-CoV infected patients. Virus-specific memory CD8 T cells persisted up to 11 years post-infection in recovered patients and were demonstrated to provide protection against a lethal SARS-CoV infection in aged mice. In addition, studies in mice have shown adoptive transfer of virus specific effector CD4⁺ and CD8⁺ T cells resulted in rapid virus clearance and improvement of clinical disease. These studies point to an important role for T cell responses in controlling the disease severity as well as providing protective immunity to SAR-CoV infection. Given the high degree of genomic homology between SARS-CoV and SARS-CoV-2, it was reasoned that similar immune mechanisms might play a critical role in providing protection against SARS-CoV-2.

[0007] The field of the present ~~invention~~disclosure relates to immunotherapeutic peptides, nucleic acids encoding the peptides, peptide binding agents, and their use, for example, in the immunotherapy of a viral disease. In one aspect, the present disclosure provides a composition comprising: (i) a polynucleotide encoding a polypeptide, wherein the polypeptide comprises at least two of the following (a) a sequence comprising an epitope sequence from ORF1ab, (b) a sequence comprising an epitope sequence from membrane glycoprotein (M) and (c) a sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N); (ii) a polypeptide comprising at least two of the following (a) a sequence comprising an epitope sequence from ORF1ab, (b) a sequence comprising an epitope sequence from membrane glycoprotein (M) and (c) a sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N); (iii) a T cell receptor (TCR) or a T cell comprising the TCR, wherein the TCR binds to an epitope sequence of the polypeptide in complex with a corresponding HLA class I or class II molecule;

(iv) an antigen presenting cell comprising (i) or (ii); or (v) an antibody or B cell comprising the antibody, wherein the antibody binds to an epitope sequence of the polypeptide; and a pharmaceutically acceptable excipient. In another aspect, the present disclosure provides a pharmaceutical composition comprising the composition as disclosed herein. In another aspect, the present disclosure provides a pharmaceutical composition comprising: (i) a polypeptide comprising an epitope sequence of Table 1A, Table 1B, Table 1C, Table 2Ai, Table 2Aii, Table 2B and/or Table 16; (ii) a polynucleotide encoding the polypeptide comprising an epitope sequence of Table 1A, Table 1B, Table 1C, Table 2Ai, Table 2Aii, Table 2B and/or Table 16; (iii) a T cell receptor (TCR) or a T cell comprising the TCR, wherein the TCR binds to the epitope sequence in complex with a corresponding HLA class I or class II molecule; (iv) an antigen presenting cell comprising (i) or (ii); or (v) an antibody or B cell comprising the antibody, wherein the antibody binds to the epitope sequence; and a pharmaceutically acceptable excipient. In another aspect, the present disclosure provides a pharmaceutical composition comprising: a polypeptide having an amino acid sequence with at least 70%, 80%, 90% or 100% sequence identity to a sequence of any one of the sequences depicted in column 2 of Table 11, column 2 of Table 12 or column 3 of Table 15; or a recombinant polynucleotide encoding a polypeptide having an amino acid sequence with at least 70%, 80%, 90% or 100% sequence identity to a sequence of any one of the sequences depicted in column 2 of Table 11, column 2 of Table 12 or column 3 of Table 15. In one ~~aspect~~example, the ~~invention~~disclosure provides viral epitopes expressed in virus infected cells, useful alone or in combination with other anti-viral, or immunomodulatory agents to treat viral infection. The present ~~invention~~disclosure is useful in immunotherapy for a coronavirus infection.

[0008] Provided herein is a composition comprising: (i) a polypeptide comprising at least two of the following (a) a sequence comprising an epitope sequence from ORF1ab, (b) a sequence comprising an epitope sequence from membrane glycoprotein (M) and (c) a sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N); (ii) a polynucleotide encoding a polypeptide, wherein the polypeptide comprises at least two of the following (a) a sequence comprising an epitope sequence from ORF1ab, (b) a sequence comprising an epitope sequence from membrane glycoprotein (M) and (c) a sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N); (iii) a T cell receptor

(TCR) or a T cell comprising the TCR, wherein the TCR binds to an epitope sequence of the polypeptide in complex with a corresponding HLA class I or class II molecule; (iv) an antigen presenting cell comprising (i) or (ii); or (v) an antibody or B cell comprising the antibody, wherein the antibody binds to an epitope sequence of the polypeptide; and a pharmaceutically acceptable excipient.

[0009] In some [embodimentexamples](#), the polypeptide comprises (a) a sequence comprising an epitope sequence from ORF1ab, (b) a sequence comprising an epitope sequence from membrane glycoprotein (M) and (c) a sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N). In some [embodimentexamples](#), the sequence comprising an epitope sequence from ORF1ab is C-terminal to the sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N). In some [embodimentexamples](#), the sequence comprising an epitope sequence from ORF1ab is N-terminal to the sequence comprising an epitope sequence from membrane glycoprotein (M). In some [embodimentexamples](#), the sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N) is N-terminal to the sequence comprising an epitope sequence from membrane glycoprotein (M).

[00010] In some [embodimentexamples](#), the polypeptide comprises at least two of the following (a) a sequence comprising an epitope sequence from ORF1ab, (b) a sequence comprising an epitope sequence from membrane glycoprotein (M) and (c) a sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N)

[00011] In some [embodimentexamples](#), the polypeptide comprises (a) 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more epitope sequence from ORF1ab, (b) a sequence comprising an epitope sequence from membrane glycoprotein (M) and (c) a sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N).

[00012] In some [embodimentexamples](#), the epitope sequence from ORF1ab is an epitope sequence from a non-structural protein. In some [embodimentexamples](#), the non-structural protein is selected from the group consisting of NSP1, NSP2, NSP3, NSP4 and combinations thereof. In some [embodimentexamples](#), the polypeptide comprises a sequence comprising an epitope sequence from NSP1, a sequence comprising an epitope sequence from NSP2, a sequence comprising an epitope sequence from NSP3 and a sequence comprising an epitope sequence from NSP4.

[00013] In some [embodimentexamples](#), the epitope sequence from ORF1ab is selected from the group consisting of YLFDESGEFKL, YLFDESGEF, FGDDTVIEV, QLMCQPILL, TTDPSFLGRY, PTDNYITTY, PSFLGRY, AEAELAKNV, KTIQPRVEK and any combination thereof.

[00014] In some [embodimentexamples](#), the epitope sequence from nucleocapsid glycoprotein (N) is LLLDRLNQL. In some [embodimentexamples](#), the epitope sequence from membrane phosphoprotein (M) is VATSRTLSTY. In some [embodimentexamples](#), the polypeptide comprises an epitope sequence from nucleocapsid glycoprotein (N) that is LLLDRLNQL and an epitope sequence from membrane phosphoprotein (M) that is VATSRTLSTY.

[00015] In some [embedimentexamples](#), the polypeptide comprises (a) each of the following epitope sequences from ORF1ab: YLFDESGEFKL, YLFDESGEF, FGDDTVIEV, QLMCQPILL, TTDP SFLGRY, PTDNYITTY, PSFLGRY, AEAELAKNV, KTIQPRVEK; (b) an epitope sequence from nucleocapsid glycoprotein (N) that is LLLDRLNQL; and (c) an epitope sequence from membrane phosphoprotein (M) that is VATSRTL SY.

[00016] In some [embedimentexamples](#), the sequence comprising an epitope sequence from ORF1ab is selected from the group consisting of the following sequences or fragments thereof:
MVTNNTFTLKVPHVGEIPVAYRKVLLKTIQPRVEKYLFDESGEFKLSEVGPEHSLAEYYIFFASFY
Y; MVTNNTFTLKVPHVGEIPVAYRKVLLKTIQPRVEKYLFDESGEFKLSEVGPEHSLAEY;
APKEIIFLEGETLFGDDTVIEVAIILASFSA ST; APKEIIFLEGETLFGDDTVIEV;
HTTDP SFLGRYMSALFADDLNQLTGYHTDFSSEIIGYQLMCQPILLAEAELAKNVSLILGTVSWN
L;
TTDP SFLGRYMSALFADDLNQLTGYHTDFSSEIIGYQLMCQPILLAEAELAKNVSLILGTVSWNL;
LLSAGIFGAITDV FYKENS YKVPTDNYITTY; and combinations thereof.

[00017] In some [embedimentexamples](#), the sequence comprising an epitope sequence from membrane glycoprotein (M) is selected from the group consisting of the following sequences or fragments thereof:
ADSNGTITVEELKKLLEQWNLVIGFLFTWICLLQFAYANRNRFLYIIKLIFLWLLWPVTLACFVL
AAVYRINWITGGIAIAMACLVGLMWLSYFIASFRLFARTRSMWSFNPETNILLNVPLHGTILTRPL
LESELVIGAVILRGHLRIAGHHLGRCDIKDLPKEITVATSRTL SYKLGASQRVAGDSGFAAYS R
YRIGNYKLNTDHSSSSDNIALLVQ;
FAYANRNRFLYIIKLIFLWLLWPVTLACFVLA A VYRINWITGGIAIAMACLVGLMWLSYFIASFR
LF; LGRCDIKDLPKEITVATSRTL SYKLGASQ R V A; K L L E Q W N L V I G F;
N R N R F L Y I I K L I F L W L L W P V T L A C F V L A A V Y; S E L V I G A V I L R G H L R I A G H H L G R;
V A T S R T L S Y Y K L G A S Q R V; G L M W L S Y F; and combinations thereof.

[00018] In some [embedimentexamples](#), the sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N) is selected from the group consisting of the following sequences or fragments thereof:
KDLSR WYFY YLGTGPEAGLPYGANKDGIWVATEGALNTPKDHIGTRNPANNA A I V L Q L P Q G T
T L P K G F Y A E G S R G G S Q A S S R S S S R N S S R N S T P G S S R G T S P A R M A G N G G D A A L A L L L D R L N Q L
E S K M S G K G Q Q Q Q G T V T K K S A A E A S K K P R Q K R T A T K A Y N V T Q A F G R R G P E Q T Q G N F G D Q E L I
R Q G T D Y K H W P Q I A Q F A P S A S A F F G M S R I G M E V T P S G T W L T Y T G A I K L D D K D P N F K D Q V I L L N K H
I D A Y K T F P P T E P K K D K K K A D E T Q A L P Q R Q K K Q Q T V T L L P A A D L D D F S K Q L Q Q S M S S A D S T Q A;
R M A G N G G D A A L A L L L D R L N Q L E S K M S G K G Q Q Q;
Y K H W P Q I A Q F A P S A S A F F G M S R I G M E V T P S G T W L T Y T G A I K L D D K D P N F K D Q V I L L N K H I D A Y K
T F P;

SPARMAGNGGDAALALLLDRLNQLESMSGKGQQQQGQTVTKKSAAEASKKPRQKRTATKAYN
VTQAFGRRGPEQTQGNFGDQELIRQGT DYKHWPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYTGA
IKLDDKDPNFKDQVILLNKHIDAYKTFPPTPEPKKDK and combinations thereof.

[00019] In some [embodimentexamples](#), the polypeptide comprises one or more linker sequences. In some [embodimentexamples](#), the one or more linker sequences are selected from the group consisting of GGSGGGGSGG, GGS LGGGSG. In some [embodimentexamples](#), the one or more linker sequences comprise cleavage sequences. In some [embodimentexamples](#), the one or more cleavage sequences are selected from the group consisting of FRAC, KRCF, KKRY, ARMA, RRS G, MRAC, KMCG, ARCA, KKQG, YRSY, SFMN, FKA A, KRNG, YNSF, KKNG, RRRG, KRYS, and ARYA.

[00020] In some [embodimentexamples](#), the polypeptide comprises a transmembrane domain sequence. In some [embodimentexamples](#), the transmembrane sequence is C-terminal to the sequence comprising an epitope sequence from ORF1ab, the sequence comprising an epitope sequence from membrane glycoprotein (M) and the sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N). In some [embodimentexamples](#), the transmembrane sequence is EQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCC SCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT.

[00021] In some [embodimentexamples](#), the polypeptide comprises an SEC sequence. In some [embodimentexamples](#), the SEC sequence is N-terminal to the sequence comprising an epitope sequence from ORF1ab, the sequence comprising an epitope sequence from membrane glycoprotein (M) and the sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N). In some [embodimentexamples](#), the SEC sequence is MFVFLVLLPLVSSQCVNLT.

[00022] In some [embodimentexamples](#), the composition comprises the polynucleotide encoding the polypeptide. In some [embodimentexamples](#), the polynucleotide is an mRNA. In some [embodimentexamples](#), the polynucleotide comprises a codon optimized sequence for expression in a human.

[00023] In some [embodimentexamples](#), the polynucleotide comprises a dEarI-hAg sequence. In some [embodimentexamples](#), the dEarI-hAg sequence is ATTCTTCTGGTCCCCACAGACTCAGAGAGAACCC, optionally wherein each T is a U.

[00024] In some [embodimentexamples](#), the polynucleotide comprises a Kozak sequence. In some [embodimentexamples](#), the a Kozak sequences is GCCACC.

[00025] In some [embodimentexamples](#), the polynucleotide comprises an F element sequence. In some [embodimentexamples](#), the F element sequence is a 3 UTR of amino-terminal enhancer of split (AES). In some [embodimentexamples](#), the F element sequence is CTGGTACTGCATGCACGCAATGCTAGCTGCCCTTTCCCGTCCTGGGTACCCCGAGTCTCCCCCG ACCTCGGGTCCCAGGTATGCTCCACCTCCACCTGCCCCACTCACCACCTCTGCTAGTTCCAGAC ACCTCC, optionally wherein each T is a U.

[00026] In some [embodimentexamples](#), the polynucleotide comprises an I element sequence. In some [embodimentexamples](#), the I element sequence is a 3' UTR of mitochondrially encoded 12S rRNA (mtRNR1). In some [embodimentexamples](#), the I element sequence is CAAGCACGCAGCAATGCAGCTCAAAACGCTTAGCCTAGCCACACCCCCACGGGAAACAGCA GTGATTAACCTTTAGCAATAAACGAAAGTTTAACTAAGCTATACTAACCCCAGGGTTGGTCA ATTCGTGCCAGCCACACC, optionally wherein each T is a U.

[00027] In some [embodimentexamples](#), the polynucleotide comprises a poly A sequence. In some [embodimentexamples](#), the poly A sequence is AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCATATGACTAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA, optionally wherein each T is a U.

[00028] In some [embodimentexamples](#), each of the epitope sequences from the ORF1ab, the membrane glycoprotein, and the nucleocapsid phosphoprotein are from 2019 SARS-CoV-2.

[00029] In some [embodimentexamples](#), one or more or each epitope elicits a T cell response.

[00030] In some [embodimentexamples](#), one or more or each epitope has been observed by mass spectrometry as being presented by an HLA molecule.

[00031] In some [embodimentexamples](#), the composition comprises (i) a polypeptide with at least 70%, 80%, 90% or 100% sequence identity to a sequence selected from the group consisting of RS C1p1full, RS C2p1full, RS C3p1full, RS C4p1full, RS C5p1, RS C5p2, RS C5p2full, RS C6p1, RS C6p2, RS C6p2full, RS C7p1, RS C7p2, RS C7p2full, RS C8p1, RS C8p2 and RS C8p2full; (ii) a polynucleotide encoding a polypeptide with at least 70%, 80%, 90% or 100% sequence identity to a sequence selected from the group consisting of RS C1p1full, RS C2p1full, RS C3p1full, RS C4p1full, RS C5p1, RS C5p2, RS C5p2full, RS C6p1, RS C6p2, RS C6p2full, RS C7p1, RS C7p2, RS C7p2full, RS C8p1, RS C8p2 and RS C8p2full; or (iii) a polynucleotide with at least 70%, 80%, 90% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID NOs: RS C1n1, RS C2n1, RS C3n1, RS C4n1, RS C5n1, RS C6n1, RS C7n1, RS C8n1, RS C5n2, RS C6n2, RS C7n2, RS C8n2, RS C5n2full, RS C6n2full, RS C7n2full and RS C8n2full.

[00032] Also provided herein is a pharmaceutical composition comprising any of the compositions described herein.

[00033] Also provided herein is a pharmaceutical composition comprising: (i) a polypeptide comprising an epitope sequence of Table 1A, Table 1B, Table 1C, Table 2Ai, Table 2Aii, Table 2B and/or Table 16; (ii) a polynucleotide encoding the polypeptide; (iii) a T cell receptor (TCR) or a T cell comprising the TCR, wherein the TCR binds to the epitope sequence in complex with a corresponding HLA class I or class II molecule; (iv) an antigen presenting cell comprising (i) or (ii); or (v) an antibody or B cell

comprising the antibody, wherein the antibody binds to the epitope sequence; and a pharmaceutically acceptable excipient.

[00034] In some [embodimentexamples](#), the epitope sequence comprises one or more or each of the following: YLFDESGEFKL, YLFDESGEF, FGDDTVIEV, LLLDRLNQL, QLMCQPILL, TTDPFLGRY, PTDNYITTY, PSFLGRY, AEAELAKNV, VATSRTLSY and KTIQPRVEK. In some [embodimentexamples](#), the epitope sequence comprises one or more or each of the following: SAPPAQYEL, AVASKILGL, EYADVHLY, DEFTPFV, VRIQPGQTF, SFRLFARTR, KFLPFQF, VVQEGVLT, RLDKVEAEV, FGADPIHSL, NYNYLYRLF, KYIKWPWYI, KWPWYIWLGF, LPFNDGVYF, QPTESIVRF, IPFAMQMAY, YLQPRTFLL and RLQSLQTYV.

[00035] In some [embodimentexamples](#), the epitope sequence is from an orf1ab protein. In some [embodimentexamples](#), the epitope sequence is from an orf1a protein. In some [embodimentexamples](#), the epitope sequence is from a surface glycoprotein (S) or a shifted reading frame thereof. In some [embodimentexamples](#), the epitope sequence is from a nucleocapsid phosphoprotein (N). In some [embodimentexamples](#), the epitope sequence is from an ORF3a protein. In some [embodimentexamples](#), the epitope sequence is from a membrane glycoprotein (M). In some [embodimentexamples](#), the epitope sequence is from an ORF7a protein. In some [embodimentexamples](#), the epitope sequence is from an ORF8 protein. In some [embodimentexamples](#), the epitope sequence is from an envelope protein (E). In some [embodimentexamples](#), the epitope sequence is from an ORF6 protein. In some [embodimentexamples](#), the epitope sequence is from an ORF7b protein. In some [embodimentexamples](#), the epitope sequence is from an ORF10 protein. In some [embodimentexamples](#), the epitope sequence is from an ORF9b protein.

[00036] Also provided herein is a pharmaceutical composition comprising: a polypeptide having an amino acid sequence with at least 70%, 80%, 90% or 100% sequence identity to a sequence of any one of the sequences depicted in column 2 of Table 11, column 2 of Table 12 or column 3 of Table 15; or a recombinant polynucleotide encoding a polypeptide having an amino acid sequence with at least 70%, 80%, 90% or 100% sequence identity to a sequence of any one of the sequences depicted in column 2 of Table 11, column 2 of Table 12 or column 3 of Table 15.

[00037] In some [embodimentexamples](#), the pharmaceutical composition comprises a polypeptide with at least 70%, 80%, 90% or 100% sequence identity to a sequence selected from the group consisting of RS C1p1full, RS C2p1full, RS C3p1full, RS C4p1full, RS C5p1, RS C5p2, RS C5p2full, RS C6p1, RS C6p2, RS C6p2full, RS C7p1, RS C7p2, RS C7p2full, RS C8p1, RS C8p2 and RS C8p2full; or a polynucleotide encoding a polypeptide with at least 70%, 80%, 90% or 100% sequence identity to a sequence selected from the group consisting of RS C1p1full, RS C2p1full, RS C3p1full, RS C4p1full, RS C5p1, RS C5p2, RS C5p2full, RS C6p1, RS C6p2, RS C6p2full, RS C7p1, RS C7p2, RS C7p2full, RS C8p1, RS C8p2 and RS C8p2full. In some [embodimentexamples](#), the pharmaceutical composition comprises a polynucleotide with at least 70%, 80%, 90% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID NOs: RS C1n1, RS C2n1, RS C3n1, RS C4n1, RS C5n1, RS C6n1, RS

C7n1, RS C8n1, RS C5n2, RS C6n2, RS C7n2, RS C8n2, RS C5n2full, RS C6n2full, RS C7n2full and RS C8n2full.

[00038] In some [embodimentexamples](#), the polynucleotide is an mRNA.

[00039] In some [embodimentexamples](#), the pharmaceutical composition further comprises one or more lipid components. In some [embodimentexamples](#), the one or more lipids comprise a lipid nanoparticle (LNP). In some [embodimentexamples](#), the LNP encapsulates the recombinant polynucleotide construct.

[00040] In some [embodimentexamples](#), the polypeptide is synthetic. In some [embodimentexamples](#), the polypeptide is recombinant.

[00041] In some [embodimentexamples](#), the polypeptide is from 8-1000 amino acids in length.

[00042] In some [embodimentexamples](#), the epitope sequence binds to or is predicted to bind to an HLA class I or class II molecule with a K_D of 1000 nM or less. In some [embodimentexamples](#), the epitope sequence binds to or is predicted to bind to an HLA class I or class II molecule with a K_D of 500 nM or less.

[00043] In some [embodimentexamples](#), the epitope sequence comprises a sequence of a viral protein expressed by a virus-infected cell of a subject.

[00044] Also provided herein is a method of treating or preventing a infection by a virus or treating a respiratory disease or condition associated with an infection by a virus comprising administering to a subject in need thereof a pharmaceutical composition described herein.

[00045] In some [embodimentexamples](#), the virus is a coronavirus. In some [embodimentexamples](#), the virus is 2019 SARS-CoV 2. In some [embodimentexamples](#), an HLA molecule expressed by the subject is unknown at the time of administration. In some [embodimentexamples](#), the ability of the virus to avoid escape of recognition by an immune system of the subject is less compared to the ability of the virus to avoid escape of recognition by an immune system of a subject administered a pharmaceutical composition containing an epitope from a single protein or epitopes from fewer proteins than in a pharmaceutical composition described herein. In some [embodimentexamples](#), the subject express an HLA molecule encoded by an HLA allele of any one of Table 1A, Table 1B, Table 1C, Table 2Ai or Table 2Aii, Table 2B or Table 16 and the epitope sequence is an HLA allele-matched epitope sequence.

[00046] In some [embodimentexamples](#), the epitope sequence comprises one or more or each of the following: SAPPAQYEL, AVASKILGL, EYADVFLY, DEFTPFDVV, VRIQPGQTF, SFRLFARTR, KFLPFQQF, VVQEGVLTA, RLDKVEAEV and FGADPIHSL.

[00047] Also provided herein is a method of treating or preventing a 2019 SARS-CoV 2 infection in a subject in need thereof, comprising administering to the subject a pharmaceutical composition described herein.

[00048] In some [embodimentexamples](#), the pharmaceutical composition is administered in addition to one or more therapeutics for the 2019 SARS-CoV 2 viral infection in the subject. In some [embodimentexamples](#), the pharmaceutical composition is administered in combination with (a) a polypeptide having an amino acid

sequence of a 2019 SARS-CoV 2 spike protein or fragment thereof; (b) a recombinant polynucleotide encoding a 2019 SARS-CoV 2 spike protein or fragment thereof; or a 2019 SARS-CoV 2 spike protein pharmaceutical composition comprising (a) or (b). In some [embodimentexamples](#), the 2019 SARS-CoV 2 spike protein or fragment thereof is a SARS-CoV-2 spike protein or a fragment thereof.

[00049] In some [embodimentexamples](#), the pharmaceutical composition is administered 1-10 weeks after a first administration of the 2019 SARS-CoV 2 spike protein pharmaceutical composition. In some [embodimentexamples](#), the pharmaceutical composition is administered 1-6 weeks, 1-6 months or 1-2 years or later after a first administration of the 2019 SARS-CoV 2 spike protein pharmaceutical composition. In some [embodimentexamples](#), the pharmaceutical composition is administered on the same day or simultaneously with an administration of the 2019 SARS-CoV 2 spike protein pharmaceutical composition. In some [embodimentexamples](#), the pharmaceutical composition is co-formulated with the polypeptide having an amino acid sequence of a 2019 SARS-CoV 2 spike protein or fragment thereof or the recombinant polynucleotide encoding a 2019 SARS-CoV 2 spike protein or fragment thereof. In some [embodimentexample](#), the pharmaceutical composition is administered before an administration of the 2019 SARS-CoV 2 spike protein pharmaceutical composition, such as 2-10 weeks before an administration of the 2019 SARS-CoV 2 spike protein pharmaceutical composition. In some [embodimentexamples](#), the pharmaceutical composition is administered prophylactically. In some [embodimentexamples](#), the pharmaceutical composition is administered once every 1, 2, 3, 4, 5, 6 or more weeks; or once every 1-7, 7-14, 14-21, 21-28, or 28-35 days; or once every 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, or 35 days.

[00050] Also provided herein is a use of a composition described herein for preparing a therapeutic for treating or preventing a respiratory viral infection caused by 2019 SARS CoV-2 virus.

[00051] Also provided herein is a composition described herein or a pharmaceutical composition described herein for use as a medicament.

[00052] Also provided herein is a composition described herein or a pharmaceutical composition described herein for use in the treatment or prevention of a respiratory viral infection caused by 2019 SARS CoV-2 virus.

[00053] Provided herein is an antigenic peptide comprising an epitope sequence from Table 1A, Table 1B, Table 1C, Table 2Ai, Table 2Aii or Table 2B. Also provided herein is a polynucleotide encoding and antigenic peptide comprising an epitope sequence from Table 1A, Table 1B, Table 1C, Table 2Ai, Table 2Aii or Table 2B. The antigenic peptide and/or polynucleotide may be recombinant. The antigenic peptide and/or polynucleotide may be isolated or purified. The antigenic peptide may be synthetic or expressed from a polynucleotide.

[00062] For example, the method can comprise administering to the subject a TCR or T cell comprising a TCR that can bind to an epitope sequence from column 2 (set 1) of Table 2Ai in complex with a corresponding MHC class II molecule from column 3 (set 1) in the same row of Table 2Ai. For example, the method can comprise administering to a TCR or T cell comprising a TCR that can bind to an epitope sequence from column 2 (set 1) of Table 2Ai in complex with a corresponding MHC class II molecule from column 3 (set 1) in the same row of Table 2Ai to a subject that expresses the corresponding MHC class II molecule from column 3 (set 1). For example, the method can comprise administering to the subject a TCR or T cell comprising a TCR that can bind to an epitope sequence from column 4 (set 2) of Table 2Ai in complex with a corresponding MHC class II molecule from column 5 (set 2) in the same row of Table 2Ai. For example, the method can comprise administering to a TCR or T cell comprising a TCR that can bind to an epitope sequence from column 4 (set 2) of Table 2Ai in complex with a corresponding MHC class II molecule from column 5 (set 2) in the same row of Table 2Ai to a subject that expresses the corresponding MHC class II molecule from column 5 (set 2). For example, the method can comprise administering to the subject a TCR or T cell comprising a TCR that can bind to an epitope sequence from the left column of Table 2Aii in complex with a corresponding MHC class II molecule from the right column in the same row of Table 2Aii.

[00063] In one [embodimentexample](#), the antigenic peptide is a viral antigen. In another [embodimentexample](#), the antigenic peptide is a non-mutated overexpressed antigen. In some [embodimentexamples](#), the viral antigen is derived from publicly disclosed information on the viral genetic information. In some [embodimentexamples](#), the viral antigen is derived from analysis of the viral genome to predict suitable epitopes for T cell activation. In some [embodimentexamples](#), the viral antigen is derived from analysis of the sequence of the viral genome in a MHC-peptide presentation prediction algorithm implemented in a computer processor. In some [embodimentexamples](#), the viral antigen is derived from analysis of the viral sequences in an MHC-peptide presentation prediction algorithm implemented in a computer processor that has been trained by a machine learning software, which predicts the likelihood of binding and presentation of an epitope by an MHC class I or an MHC class II antigen. In some [embodimentexamples](#), the MHC-peptide presentation predictor is *neonmhc2*.

[00064] In some [embodimentexamples](#), the MHC-peptide presentation prediction algorithm or MHC-peptide presentation predictor is NetMHCpan or NetMHCIIpan and in addition, further analyzed in MHC-peptide presentation predictor NetMHCpan or NetMHCIIpan for comparison. In some [embodimentexamples](#), a skilled artisan may use hidden markov model approach for MHC-peptide presentation prediction. In some [embodimentexamples](#), the peptide prediction model MARIA may be utilized. In some [embodimentexamples](#), the MHC-peptide presentation prediction algorithm or MHC-peptide presentation predictor used is not NetMHCpan or NetMHCIIpan. In some [embodimentexamples](#), the viral sequences are analyzed in MHC-peptide presentation prediction algorithm implemented in a computer processor where the MHC-peptide presentation predictor is *neonmhc 1* or *neonmhc2*, that refer respectively to class I and class II binding prediction. In some

embodimentexamples, the MHC-peptide presentation predictor model is RECON, which offers high quality MHC-peptide presentation prediction based on expression, processing and binding capabilities.

[00065] In another aspect, the present disclosure provides the use of the pharmaceutical composition as disclosed herein in the manufacture of a medicament for treating or preventing an infection by a virus or treating a respiratory disease or condition associated with an infection by a virus. In another aspect, the present disclosure refers to the use of the pharmaceutical composition as disclosed herein in the manufacture of a medicament for treating or preventing a 2019 SARS-CoV 2 infection in a subject in need thereof. In another aspect, the present disclosure refers to the use of the composition as disclosed herein in the manufacture of a medicament for treating or preventing a respiratory viral infection caused by 2019 SARS CoV-2 virus. In yet another aspect, the present disclosure provides a composition as disclosed herein or a pharmaceutical composition as disclosed herein for use as a medicament. In one aspectexample, provided herein is a method of treating a viral disease in a subject caused by a coronavirus, comprising: administering to the subject a composition comprising one or more viral peptide antigens, wherein the viral peptide antigens are predicted to bind to an MHC class I or an MHC class II peptide of the subject, and are predicted to be presented by an antigen presenting cell to a T cell of the subject such that an antiviral response is initiated in the subject. In some embodimentexamples, the viral antigen is derived from analysis of the sequence of the viral genome in a MHC-peptide presentation prediction algorithm implemented in a computer processor. In some embodimentexamples, the viral antigen is derived from analysis of the viral sequences in an MHC-peptide presentation prediction algorithm implemented in a computer processor that has been trained by a machine learning software, which predicts the likelihood of binding and presentation of an epitope by an MHC class I or an MHC class II antigen. In some embodimentexamples, the MHC-peptide presentation predictor is *neonmhc2*. In some embodimentexamples, the method further comprises analyzing nucleic acid sequence derived from viral genome in an MHC-peptide presentation prediction model, comprising an algorithm implemented in a computer processor that has been trained by a machine learning software, wherein the MHC-peptide presentation prediction model predicts the likelihood of binding and presentation of an epitope encoded by the viral genome by an MHC class I or an MHC class II antigen. In some embodimentexamples, the method further comprises analyzing a biological sample from a subject for identification of the MHC class I and MHC class II repertoire, wherein the analyzing comprises analyzing by genome or whole exome sequencing or by analysis of proteins encoded by an HLA gene. In some embodimentexamples, the method further comprises matching the epitopes predicted by the MHC-peptide presentation prediction model that have a high affinity for an MHC class I or an MHC class II peptide encoded by an HLA gene of the subject, and selecting one or more peptides that are predicted to bind an MHC peptide encoded by an HLA gene of the subject with a high affinity ranked by the MHC-peptide presentation prediction model. In some embodimentexamples, the one or more peptides that are selected have been predicted to bind an MHC peptide encoded by an HLA gene of the subject with an

affinity of at least 1000 nM. In some embodimentexamples, the one or more peptides that are selected have been predicted to bind an MHC class I peptide encoded by an HLA gene of the subject with an affinity of at least 500 nM. In some embodimentexamples, the one or more peptides that are selected have been predicted to bind an MHC class II peptide encoded by an HLA gene of the subject with an affinity of at least 1000 nM.

[00066] In some embodimentexamples, the MHC-peptide presentation prediction model is programmed to provide a ranking order in decreasing order of a likelihood for a particular epitope or antigenic peptide to bind to an HLA allele that would present the peptide to a T cell receptor. In some embodimentexamples, epitope sequences that have the highest likelihood of binding and being presented by an HLA are selected for preparing a therapeutic. In some embodimentexamples, the selection of the HLA may be restricted by HLA expressed in a

subject. In some [embodimentexamples](#), the selection of the HLA may be based on the prevalence (e.g., higher prevalence) of the allele in a population. In some [embodimentexamples](#) the epitopes may be selected for preparing a therapeutic based on the higher likelihood for the peptide (epitope) of binding to and being presented by an HLA allele, e.g., an HLA allele of interest. In some [embodimentexamples](#), this % rank value may be determined by evaluating the percentile in which a query peptide scores for a specific allele compared to a fixed set of reference peptides (with a different set of reference peptides for class I and class II). In some [embodimentexamples](#) the top 10% of the epitopes that have the highest likelihood of binding to an HLA allele may be selected. In some [embodimentexamples](#) the top 2% of the epitopes that have the highest likelihood of binding to an HLA allele may be selected. In some [embodimentexamples](#) the top 5% of the epitopes that have the highest likelihood of binding to an HLA allele may be selected. In some [embodimentexamples](#) the top 8% of the epitopes that have the highest likelihood of binding to an HLA allele may be selected. In some [embodimentexamples](#) the top 1% of the epitopes that have the highest likelihood of binding to an HLA allele may be selected. In some [embodimentexamples](#) the top 0.5 % of the epitopes that have the highest likelihood of binding to an HLA allele may be selected. In some [embodimentexamples](#) the top 0.1 % of the epitopes that have the highest likelihood of binding to an HLA allele may be selected. In some [embodimentexamples](#) the top 0.01 % of the epitopes that have the highest likelihood of binding to an HLA allele may be selected. In some [embodimentexamples](#) the selection of the cut off may be dependent on the availability and number of epitopes predicted to have a high likelihood of binding to an HLA allele as determined by the prediction model.

[00067] In some [embodimentexamples](#), the subject may be infected by the virus. In some [embodimentexamples](#), the subject may be at risk of infection by the virus. In some [embodimentexamples](#), the virus is a coronavirus. In some [embodimentexamples](#), the coronavirus is selected from a SARS virus, a MERS coronavirus or a 2019 SARS CoV-2 virus. In some [embodimentexamples](#), the one or more viral peptide antigen comprises a peptide comprising at least 8 contiguous amino acids of a sequence in Table 1A, Table 1B, Table 1C, Table 2Ai, Table 2Aii, Table 2B, Table 9, Table 10, Table 11, Table 12, Table 14A, Table 14B, Table 15 or Table 16. In some [embodimentexamples](#), the one or more viral peptide antigen comprises a peptide comprising at least 7 contiguous amino acids of a sequence in Table 1A, Table 1B, Table 1C, Table 2Ai, Table 2Aii, Table 2B, Table 9, Table 10, Table 11, Table 12, Table 14A, Table 14B, Table 15 or Table 16. In some [embodimentexamples](#), the one or more viral peptide antigen comprises a peptide comprising at least 6 contiguous amino acids of a sequence in Table 1A, Table 1B, Table 1C, Table 2Ai, Table 2Aii, Table 2B, Table 9, Table 10, Table 11, Table 12, Table 14A, Table 14B, Table 15 or Table 16.

[00068] In one [embodimentexample](#), the antigenic peptide is between about 5 to about 50 amino acids in length. In another [embodimentexample](#), the antigenic peptide is between about 15 to about 35 amino acids in length. In another [embodimentexample](#), the antigenic peptide is about 15 amino acids or less in length. In another [embodimentexample](#), the antigenic peptide is between about 8 and about 11 amino acids in length. In another [embodimentexample](#), the antigenic peptide is 9 or 10 amino acids in length. In one [embodimentexample](#), the antigenic

peptide binds major histocompatibility complex (MHC) class I. In another [embodimentexample](#), the antigenic peptide binds MHC class I with a binding affinity of less than about 500 nM.

In one [embodimentexample](#), the antigenic peptide is about 30 amino acids or less in length. In another [embodimentexample](#), the antigenic peptide is between about 6 and about 25 amino acids in length. In another [embodimentexample](#), the antigenic peptide is between about 15 and about 24 amino acids in length. In another [embodimentexample](#), the antigenic peptide is between about 9 and about 15 amino acids in length. In one [embodimentexample](#), the antigenic peptide binds MHC class II. In another [embodimentexample](#), the antigenic peptide binds MHC class II with a binding affinity of less than about 1000 nM.

[00069] In one [embodimentexample](#), the antigenic peptide further comprises flanking amino acids. In another [embodimentexample](#), the flanking amino acids are not native flanking amino acids. In one [embodimentexample](#), the antigenic peptide is linked to at least a second antigenic peptide. In another [embodimentexample](#), the peptides are linked using a poly-glycine or poly-serine linker. In another [embodimentexample](#), the second antigenic peptide binds MHC class I or class II with a binding affinity of less than about 1000 nM. In another [embodimentexample](#), the second antigenic peptide binds MHC class I or class II with a binding affinity of less than about 500 nM. In another [embodimentexample](#), both of the epitopes bind to human leukocyte antigen (HLA) -A, -B, -C, -DP, -DQ, or -DR. In another [embodimentexample](#), the antigenic peptide binds a class I HLA and the second antigenic peptide binds a class II HLA. In another [embodimentexample](#), the antigenic peptide binds a class II HLA and the second antigenic peptide binds a class I HLA.

[00070] In one [embodimentexample](#), the antigenic peptide further comprises modifications which increase in vivo half-life, cellular targeting, antigen uptake, antigen processing, MHC affinity, MHC stability, or antigen presentation. In another [embodimentexample](#), the modification is conjugation to a carrier protein, conjugation to a ligand, conjugation to an antibody, PEGylation, polysialylation HESylation, recombinant PEG mimetics, Fc fusion, albumin fusion, nanoparticle attachment, nanoparticulate encapsulation, cholesterol fusion, iron fusion, acylation, amidation, glycosylation, side chain oxidation, phosphorylation, biotinylation, the addition of a surface active material, the addition of amino acid mimetics, or the addition of unnatural amino acids, for example, synthetic amino acids, or f-moc amino acids, D-amino acids N-methyl amino acids. In one [embodimentexample](#), the cells that are targeted are antigen presenting cells. In another [embodimentexample](#), the antigen presenting cells are dendritic cells. In another [embodimentexample](#), the dendritic cells are targeted using DEC205, XCR1, CD197, CD80, CD86, CD123, CD209, CD273, CD283, CD289, CD184, CD85h, CD85j, CD85k, CD85d, CD85g, CD85a, CD141, CD11 c, CD83, TSLP receptor, or CD1a marker. In another [embodimentexample](#), the dendritic cells are targeted using the CD141, DEC205, or XCR1 marker.

[00071] In one [embodimentexample](#), provided herein is an *in vivo* delivery system comprising an antigenic peptide described herein. In another [embodimentexample](#), the delivery system includes cell-penetrating peptides, nanoparticulate encapsulation, virus like particles, or liposomes. In another [embodimentexample](#), the cell-penetrating peptide is TAT peptide, herpes simplex virus VP22, transportan, or Antp.

[00072] In one [embodimentexample](#), provided herein is a cell comprising an antigenic peptide described herein. In another [embodimentexample](#), the cell is an antigen presenting cell. In another [embodimentexample](#), the cell is a dendritic cell.

[00073] In one [embodimentexample](#), provided herein is a composition comprising an antigenic peptide described herein. In another [embodimentexample](#), the composition comprises at least 2, 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 of the antigenic peptides comprising an epitope of Table 1A. In another [embodimentexample](#), the composition comprises at least 2, 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 of the antigenic peptides comprising an epitope of Table 1B. In another [embodimentexample](#), the composition comprises at least 2, 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 of the antigenic peptides comprising an epitope of Table 2B. In another [embodimentexample](#), the composition comprises between 2 and 20 antigenic peptides. In another [embodimentexample](#), the composition further comprises at least 1, at least 2, 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, or at least 25, at least 26, at least 27, at least 28, at least 29, or at least 30 additional antigenic peptides. In another [embodimentexample](#), the composition comprises between about 4 and about 20 additional antigenic peptides. In another [embodimentexample](#), the additional antigenic peptide is specific for coronavirus.

[00074] In one [embodimentexample](#), provided herein is a polynucleotide encoding the antigenic peptide described herein. In another [embodimentexample](#), the polynucleotide is RNA, optionally a self-amplifying RNA. In some [embodimentexamples](#) the polynucleotide is DNA. In another [embodimentexample](#), the RNA is modified to increase stability, increase cellular targeting, increase translation efficiency, adjuvanticity, cytosol accessibility, and/or decrease cytotoxicity. In another [embodimentexample](#), the modification is conjugation to a carrier protein, conjugation to a ligand, conjugation to an antibody, codon optimization, increased GC-content, incorporation of modified nucleosides, incorporation of 5'-cap or cap analog, and/or incorporation of a poly-A sequence e.g., an unmasked poly-A sequence, or a disrupted poly-A sequence in which two segments of contiguous A sequences linked by a linker.

[00075] In one [embodimentexample](#), provided herein is a cell comprising a polynucleotide described herein.

[00076] In one [embodimentexample](#), provided herein is a vector comprising a polynucleotide described herein. In another [embodimentexample](#), the polynucleotide is operably linked to a promoter. In another [embodimentexample](#), the vector is a self-amplifying RNA replicon, plasmid, phage, transposon, cosmid, virus, or virion. In another [embodimentexample](#), the vector is an adeno-associated virus, herpesvirus, lentivirus, or pseudotypes thereof

[00077] In one [embodimentexample](#), provided herein is an in vivo delivery system comprising a polynucleotide described herein. In another [embodimentexample](#), the delivery system includes spherical nucleic acids, viruses, virus-like particles, plasmids, bacterial plasmids, or nanoparticles.

[00078] In one [embodimentexample](#), provided herein is a cell comprising a vector or delivery system described herein. In another [embodimentexample](#), the cell is an antigen presenting cell. In another [embodimentexample](#), the cell is a dendritic cell. In another [embodimentexample](#), the cell is an immature dendritic cell.

[00079] In some [embodimentexamples](#), provided herein is a composition comprising at least one polynucleotide described herein. In some [embodimentexamples](#), provided herein is a composition comprising one or more antigenic peptides described herein in combination with one or more 2019 SARS CoV-2 vaccines (e.g., mRNA-based vaccines, DNA-based vaccines, AAV-based vaccines, protein-based vaccines). In some [embodimentexamples](#), provided herein is a composition comprising one or more polynucleotides encoding at least one antigenic peptide described herein in combination with one or more 2019 SARS CoV-2 vaccines (e.g., mRNA-based vaccines, DNA-based vaccines, AAV-based vaccines, protein-based vaccines). In some [embodimentexamples](#), provided herein is a single polynucleotide encoding more than one antigenic peptide as described herein. In some [embodimentexamples](#), provided herein is a single polynucleotide encoding (i) at least one antigenic peptide as described herein and (ii) a 2019 SARS CoV-2 protein (e.g., S protein) and/or immunogenic fragments thereof (e.g., receptor binding domain (RBD) of S protein). In another [embodimentexample](#), the composition comprises at least 2, 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 of the polynucleotides. In another [embodimentexample](#), the composition comprises between about 2 and about 20 polynucleotides. In another [embodimentexample](#), the composition further comprises at least 1, at least 2, 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 additional antigenic polynucleotides encoding for additional antigenic peptides. In another [embodimentexample](#), the composition comprises between about 4 and about 20 additional antigenic polynucleotides. In another [embodimentexample](#), the polynucleotides and the additional antigenic polynucleotides are linked. In another [embodimentexample](#), the polynucleotides are linked using nucleic acids that encode a poly-glycine or poly-serine linker.

[00080] In one [embodimentexample](#), provided herein is a T cell receptor (TCR) capable of binding at least one antigenic peptide described herein. In another [embodimentexample](#), the TCR is capable of binding the antigenic peptide in the context of MHC class I or class II.

[00081] In one [embodimentexample](#), provided herein is a chimeric antigen receptor comprising: (i) a T cell activation molecule; (ii) a transmembrane region; and (iii) an antigen recognition moiety capable of binding an antigenic peptide described herein. In another [embodimentexample](#), CD3-zeta is the T cell activation molecule. In another [embodimentexample](#), the chimeric antigen receptor further comprises at least one costimulatory signaling domain. In another [embodimentexample](#), the signaling domain is CD28, 4-1BB, ICOS, OX40, ITAM, or Fc epsilon RI-gamma. In another [embodimentexample](#), the antigen recognition moiety is capable of binding the antigenic peptide in the context of MHC class I or class II. In another [embodimentexample](#), the chimeric antigen receptor comprises the CD3-zeta, CD28, CTLA-4, ICOS, BTLA, KIR, LAG3, CD137, OX40, CD27, CD4OL, Tim-3, A2aR, or PD-1 transmembrane region.

[00082] In one [embodimentexample](#), provided herein is a T cell comprising the T cell receptor or chimeric antigen receptor described herein. In one [embodimentexample](#), the T cell is a helper or cytotoxic T cell.

[00083] In one [embodimentexample](#), provided herein is a nucleic acid comprising a promoter operably linked to a polynucleotide encoding a T cell receptor described herein. In another [embodimentexample](#), the TCR is capable of binding the at least one antigenic peptide in the context of major histocompatibility complex (MHC) class I or class II. In one [embodimentexample](#), the nucleic acid comprises a promoter operably linked to a polynucleotide encoding a chimeric antigen receptor described herein. In another [embodimentexample](#), the antigen recognition moiety is capable of binding the at least one antigenic peptide in the context of major histocompatibility complex (MHC) class I or class II.

[00084] In one [embodimentexample](#), provided herein is an antibody capable of binding a peptide comprising an epitope of Table 1A, Table 1B, Table 1C, Table 2Ai, Table 2Aii, Table 2B, Table 9, Table 10, Table 11, Table 12, Table 14A, Table 14B, Table 15 or Table 16. In one [embodimentexample](#), provided herein is an antibody capable of binding a peptide comprising an epitope of Table 1B. In one [embodimentexample](#), provided herein is an antibody capable of binding a peptide comprising an epitope of Table 2Ai or Table 2Aii.

[00085] In one [embodimentexample](#), provided herein is a modified cell transfected or transduced with a nucleic acid described herein. In one [embodimentexample](#), the modified cell is a T cell, tumor infiltrating lymphocyte, NK-T cell, TCR-expressing cell, CD4+ T cell, CD8+ T cell, or NK cell.

[00086] In one [embodimentexample](#), provided herein is a composition comprising a T cell receptor or chimeric antigen receptor described herein. In another [embodimentexample](#), a composition comprises autologous patient T cells containing a T cell receptor or chimeric antigen receptor described herein. In another [embodimentexample](#), the composition further comprises an immune checkpoint inhibitor. In another [embodimentexample](#), the composition further comprises at least two immune checkpoint inhibitors. In another [embodimentexample](#), each of the immune checkpoint inhibitors inhibits a checkpoint protein selected from the group consisting of

CTLA-4, PDL1, PDL2, PD1, B7-H3, B7-H4, BTLA, HVEM, TIM3, GAL9, LAG3, VISTA, KIR, 2B4, CD160, CGEN-15049, CLIK 1, CHK2, A2aR, and B-7 family ligands or a combination thereof. In another [embodimentexample](#), each of the immune checkpoint inhibitors interacts with a ligand of a checkpoint protein selected from the group consisting of CTLA-4, PDL1, PDL2, PD1, B7-H3, B7-H4, BTLA, HVEM, TIM3, GAL9, LAG3, VISTA, KIR, 2B4, CD160, CGEN-15049, CHK 1, CHK2, A2aR, and B-7 family ligands or a combination thereof.

[00087] In one [embodimentexample](#), the composition further comprises an immune modulator or adjuvant. In another [embodimentexample](#), the immune modulator is a co-stimulatory ligand, a TNF ligand, an Ig superfamily ligand, CD28, CD80, CD86, ICOS, CD40L, OX40, CD27, GITR, CD30, DR3, CD69, or 4-1BB. In another [embodimentexample](#), the immune modulator is at least one an infected cell extract. In another [embodimentexample](#), the infected cell is autologous to the subject in need of the composition. In another [embodimentexample](#), the infected cell has undergone lysis or been exposed to UV radiation. In another [embodimentexample](#), the composition further comprises an adjuvant. In another [embodimentexample](#), the adjuvant is selected from the group consisting of: Poly(I:C), Poly-ICLC, STING agonist, 1018 ISS, aluminum 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 VG, Montanide ISA 206 VG, Montanide ISA 50 V2, Montanide ISA 51 VG, OK-432, OM-174, OM-197-MP-EC, ISA-TLR2 agonist, ONTAK, PepTel®, vector system, PLG microparticles, resiquimod, SRL172, virosomes and other virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, Pam3CSK4, acrylic or methacrylic polymers, copolymers of maleic anhydride, and QS21 stimulon. In another [embodimentexample](#), the adjuvant induces a humoral when administered to a subject. In another [embodimentexample](#), the adjuvant induces a T helper cell type 1 when administered to a subject.

[00088] In one [embodimentexample](#), provided herein is a method of inhibiting infection by a virus by administering to a subject who has a likelihood of getting infected by the virus, a vaccine composition comprising one or more peptides comprising at least 8 contiguous amino acids from the epitopes defined in Table 1A, Table 1B, Table 1C, Table 2Ai, Table 2Aii or Table 2B, comprising contacting a cell with a peptide, polynucleotide, delivery system, vector, composition, antibody, or cells of the [inventiondisclosure](#).

[00089] In one [embodimentexample](#), provided herein is a method of treating a viral infection specifically, a coronaviral infection, for example a 2019 SARS CoV-2 infection by enhancing, or prolonging an antiviral response in a subject in need thereof comprising administering to the subject the peptide, polynucleotide, vector, composition, antibody, or cells described herein.

[00090] In one [embodimentexample](#), the subject is a human. In another [embodimentexample](#), the subject has a viral infection. In one [embodimentexample](#), the subject is infected by a respiratory virus, such as an acute respiratory virus, for example, a SARS-like virus or a MERS or MERS-like virus, or more specifically, a coronavirus of the 2019 SARS CoV-2 strain. In some [embodimentexamples](#), the subject is infected with a 2019 SARS CoV-2

coronavirus. In some [embodimentexamples](#), the subject has been detectably infected with the 2019 SARS CoV-2 coronavirus. In some [embodimentexamples](#), the subject is asymptomatic. In some [embodimentexamples](#), the subject is symptomatic. In some [embodimentexamples](#), the subject is not detected to have been infected by a 2019 SARS CoV-2 virus or a related virus, but the subject is in close proximity of an infected person, in an infected area or otherwise at risk of infection.

[00091] In one [embodimentexample](#) of the method, a peptide is administered. In another [embodimentexample](#), the administration is systemic. In another [embodimentexample](#) of the method, a polynucleotide, optionally RNA, is administered. In one [embodimentexample](#), the polynucleotide is administered parenterally. In one [embodimentexample](#), the polynucleotide is administered intravenously. In another [embodimentexample](#), the polynucleotide is administered intradermally or intramuscularly, or subcutaneously. In one [embodimentexample](#), the polynucleotide is administered intramuscularly. In one [embodimentexample](#) of the method, a cell is administered. In another [embodimentexample](#), the cell is a T cell or dendritic cell. In another [embodimentexample](#), the peptide or polynucleotide comprises an antigen presenting cell targeting moiety.

[00092] In one [embodimentexample](#), the peptide, polynucleotide, vector, composition, or cells is administered prior to administering concurrent with another therapy, such as another antiviral therapy. In another [embodimentexample](#), the peptide, polynucleotide, vector, composition, or cells is administered before or after the another antiviral therapy. In another [embodimentexample](#), administration of the another antiviral therapy is continued throughout antigen peptide, polynucleotide, vector, composition, or cell therapy.

[00093] In one [embodimentexample](#) of the method, an additional agent is administered. In another [embodimentexample](#), the agent is a chemotherapeutic agent, an immunomodulatory drug, an immune metabolism modifying drug, a targeted therapy, radiation an anti-angiogenesis agent, or an agent that reduces immune-suppression. In another [embodimentexample](#), the administration of a pharmaceutical composition described herein elicits or promotes a CD4+ T cell immune response. In another [embodimentexample](#), the administration of a pharmaceutical composition described herein elicits or promotes a CD4+ T cell immune response and a CD8+ T cell immune response.

[00094] In another [embodimentexample](#), the patient received a chemotherapeutic agent, an immunomodulatory drug, an immune metabolism modifying drug, targeted therapy or radiation prior to and/or during receipt of the antigen peptide or nucleic acid vaccine. In another [embodimentexample](#), the autologous T cells are obtained from a patient that has already received at least one round of T cell therapy containing an antigen. In another [embodimentexample](#), the method further comprises adoptive T cell therapy. In another [embodimentexample](#), the adoptive T cell therapy comprises autologous T cells. In another [embodimentexample](#), the autologous T cells are targeted against viral antigens. In another [embodimentexample](#), the adoptive T cell therapy further comprises allogenic T cells. In another [embodimentexample](#), the allogenic T cells are targeted against viral antigens.

[00095] In one [embodimentexample](#), provided herein is a method for evaluating the efficacy of treatment comprising: (i) measuring the number or concentration of target cells in a first sample obtained from the

subject before administering the modified cell, (ii) measuring the number or concentration of target cells in a second sample obtained from the subject after administration of the modified cell, and (iii) determining an increase or decrease of the number or concentration of target cells in the second sample compared to the number or concentration of target cells in the first sample. In another [embodimentexample](#), the treatment efficacy is determined by monitoring a clinical outcome; an increase, enhancement or prolongation of antiviral activity by T cells; an increase in the number of antiviral T cells or activated T cells as compared with the number prior to treatment; B cell activity; CD4 T cell activity; or a combination thereof. In another [embodimentexample](#), the treatment efficacy is determined by monitoring a biomarker. In another [embodimentexample](#), the treatment effect is predicted by presence of T cells or by presence of a gene signature indicating T cell inflammation or a combination thereof.

[00096] Provided herein a pharmaceutical composition comprising: one or more polypeptides having an amino acid sequence of any one of the sequences depicted in column 2 of Table 11 and 12; or one or more recombinant polynucleotide constructs each encoding a polypeptide having an amino acid sequence of any one of the sequences depicted in column 2 of Table 11 and 12.

[00097] In some [embodimentexamples](#), the one or more polypeptides comprises at least 2, 3, 4, 5, 6, 7 or 8 different polypeptides having an amino acid sequence of any one of the sequences depicted in column 2 of Table 11 and 12; or wherein the one or more recombinant polynucleotide constructs comprises at least 2, 3, 4, 5, 6, 7 or 8 recombinant polynucleotide constructs each encoding a different polypeptide having an amino acid sequence of any one of the sequences depicted in column 2 of Table 11 and 12. In some [embodimentexample](#)s, the pharmaceutical composition comprises at least 8 recombinant polynucleotide strings. In some [embodimentexamples](#), the one or more recombinant polynucleotide strings encoding a plurality of coronavirus peptide antigens, comprises a sequence selected from a group of sequences depicted in SEQ ID RS C1n, RS C2n, RS C3n, RSC4n, RS C5n, RS C6n, RS C7n, and RS C8n, or a sequence that is at least 70% sequence identity to any one of the above. In some [embodimentexample](#)s, the recombinant polynucleotide construct comprises an mRNA. In some [embodimentexamples](#), the recombinant polynucleotide construct is an mRNA. In some [embodimentexamples](#), the pharmaceutical composition further comprises one or more lipid components. In some [embodimentexamples](#), the one or more lipids comprise a lipid nanoparticle (LNP). In some [embodimentexamples](#), the LNP encapsulates the recombinant polynucleotide construct. In some [embodimentexamples](#), the pharmaceutical composition is administered to a subject in need thereof.

[00098] Provided herein is a method of treating COVID in a subject in need thereof, comprising administering to the subject a pharmaceutical composition described above. In some [embodimentexamples](#), the pharmaceutical composition is administered in addition to one or more therapeutic for COVID. In some [embodimentexamples](#), the pharmaceutical composition is administered in combination with one or more polypeptides having an amino acid sequence of a 2019 SARS CoV-2 spike protein or fragment thereof; or one or more recombinant polynucleotide constructs encoding a 2019 SARS CoV-2 spike protein or

fragment thereof. In some [embodimentexamples](#), the 2019 SARS CoV-2 spike protein or fragment thereof is a SARS-CoV-2 spike protein or a fragment thereof. In some [embodimentexamples](#), the pharmaceutical composition is administered 2-10 weeks after a first administration of the 2019 SARS CoV-2 spike protein or fragment thereof. In some [embodimentexamples](#), the pharmaceutical composition is administered 1-6 months after a first administration of the 2019 SARS CoV-2 spike protein or fragment thereof. In some [embodimentexamples](#), the pharmaceutical composition is administered simultaneously with an administration of the 2019 SARS CoV-2 spike protein or fragment thereof. In some [embodimentexamples](#), the pharmaceutical composition is administered 2-10 weeks before an administration of the 2019 SARS CoV-2 spike protein or fragment thereof. In some [embodimentexamples](#), the pharmaceutical composition is administered 2-10 weeks after the first administration of vaccine comprising a SARS-CoV-2 spike protein or polynucleotide encoding the same. In some [embodimentexamples](#), the pharmaceutical composition is administered 1-6 months after the first administration of a SARS-CoV-2 spike protein or polynucleotide encoding the same. In some [embodimentexamples](#), the pharmaceutical composition is administered simultaneously with the administration of a SARS-CoV-2 spike protein or polynucleotide encoding the same. In some [embodimentexamples](#), the pharmaceutical composition is administered prophylactically. In some [embodimentexamples](#), the pharmaceutical composition is administered once every 1, 2, 3, 4, 5, 6 or more weeks.

[00099] Provided herein is an use of any one of the compositions described herein for preparing a therapeutic for treating or preventing a respiratory viral infection caused by 2019 SARS CoV-2 virus.

[000100] Where aspects or [embodimentexamples](#) of the [inventiondisclosure](#) are described in terms of a Markush group or other grouping of alternatives, the present [inventiondisclosure](#) encompasses not only the entire group listed as a whole, but also each member of the group individually and all possible subgroups of the main group, and also the main group absent one or more of the group members. The present [inventiondisclosure](#) also envisages the explicit exclusion of one or more of any of the group members in the [embodimentexamples](#) of the [inventiondisclosure](#).

BRIEF DESCRIPTION OF THE DRAWINGS

[000101] FIG. 1 depicts an exemplary flow diagram of a method to identify peptides most relevant to the generation of CD8+ T cell responses against the viral epitopes described herein.

[000102] FIG. 2 depicts exemplary graphs of results obtained using a T cell epitope prediction algorithm applied to class I peptide-MHC allele pairs in a validation dataset and comparison of the computed percent-ranks of these pairs with reported MHC-binding assay results. The percent-ranks of peptide-MHC allele pairs which had a binary “Positive” result in the MHC-binding assay were significantly lower than pairs with a “Negative” result. In the more granular positive results, stronger assay results (low < intermediate < high) were associated with significantly lower percent-ranks.

[000103] FIG. 3 depicts experimental validation of HLA-A02:01 predicted epitopes from 2019 SARS CoV-2 in human T cell induction assays. 23 peptides that were predicted to be high binders to HLA-A02:01 (see

CLAIMS

WHAT IS CLAIMED IS:

1. A composition comprising:
 - (i) a polynucleotide encoding a polypeptide, wherein the polypeptide comprises at least two of the following (a) a sequence comprising an epitope sequence from ORF1ab, (b) a sequence comprising an epitope sequence from membrane glycoprotein (M) and (c) a sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N);
 - (ii) a polypeptide comprising at least two of the following (a) a sequence comprising an epitope sequence from ORF1ab, (b) a sequence comprising an epitope sequence from membrane glycoprotein (M) and (c) a sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N);
 - ~~(ii) a polynucleotide encoding a polypeptide, wherein the polypeptide comprises at least two of the following (a) a sequence comprising an epitope sequence from ORF1ab, (b) a sequence comprising an epitope sequence from membrane glycoprotein (M) and (c) a sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N);~~
 - (iii) a T cell receptor (TCR) or a T cell comprising the TCR, wherein the TCR binds to an epitope sequence of the polypeptide in complex with a corresponding HLA class I or class II molecule;
 - (iv) an antigen presenting cell comprising (i) or (ii); or
 - (v) an antibody or B cell comprising the antibody, wherein the antibody binds to an epitope sequence of the polypeptide; anda pharmaceutically acceptable excipient.
2. The composition of claim 1, wherein the polypeptide comprises (a) a sequence comprising an epitope sequence from ORF1ab, (b) a sequence comprising an epitope sequence from membrane glycoprotein (M) and (c) a sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N).
3. The composition of claim 1, wherein the sequence comprising an epitope sequence from ORF1ab is C-terminal to the sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N).
4. The composition of claim 1, wherein the sequence comprising an epitope sequence from ORF1ab is N-terminal to the sequence comprising an epitope sequence from membrane glycoprotein (M).
5. The composition of claim 1, wherein the sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N) is N-terminal to the sequence comprising an epitope sequence from membrane glycoprotein (M).
6. The composition of claim 1, wherein the polypeptide comprises (a) 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more epitope sequences from ORF1ab, (b) a sequence comprising an epitope sequence from

membrane glycoprotein (M) and (c) a sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N).

7. The composition of claim 1, wherein the epitope sequence from ORF1ab is an epitope sequence from a non-structural protein (NSP).
8. The composition of claim 7, wherein the non-structural protein (NSP) is selected from the group consisting of NSP1, NSP2, NSP3, NSP4 and combinations thereof.
9. The composition of claim 1, wherein the polypeptide comprises a sequence comprising an epitope sequence from NSP1, a sequence comprising an epitope sequence from NSP2, a sequence comprising an epitope sequence from NSP3 and a sequence comprising an epitope sequence from NSP4.
10. The composition of claim 1, wherein the epitope sequence from ORF1ab is selected from the group consisting of KTIQPRVEK, YLFDESGEF, YLFDESGEFKL, ~~YLFDESGEF~~, FGDDTVIEV, QLMCQPILL, TTDPFLGRY, PTDNYITTY, PSFLGRY, AEAELAKNV, ~~KTIQPRVEK~~ and any combination thereof.
11. The composition of claim 1, wherein the epitope sequence from nucleocapsid glycoprotein (N) is LLLDRLNQL.
12. The composition of claim 1, wherein the epitope sequence from membrane phosphoprotein (M) is VATSRTLSTY.
13. The composition of claim 1, wherein the polypeptide comprises an epitope sequence from nucleocapsid glycoprotein (N) that is LLLDRLNQL and an epitope sequence from membrane phosphoprotein (M) that is VATSRTLSTY.
14. The composition of claim 1, wherein the polypeptide comprises (a) each of the following epitope sequences from ORF1ab: KTIQPRVEK, YLFDESGEF, YLFDESGEFKL, ~~YLFDESGEF~~, FGDDTVIEV, QLMCQPILL, TTDPFLGRY, PTDNYITTY, PSFLGRY, AEAELAKNV, ~~KTIQPRVEK~~; (b) an epitope sequence from nucleocapsid glycoprotein (N) that is LLLDRLNQL; and (c) an epitope sequence from membrane phosphoprotein (M) that is VATSRTLSTY.
15. The composition of claim 1, wherein the sequence comprising an epitope sequence from ORF1ab is selected from the group consisting of the following sequences or fragments thereof:
MVTNNTFTLKVPHVGEIPVAYRKVLLKTIQPRVEKYLFDESGEFKLSEVGPEHSLAEYYIFF
ASFYY;
MVTNNTFTLKVPHVGEIPVAYRKVLLKTIQPRVEKYLFDESGEFKLSEVGPEHSLAEY;
APKEIIFLEGETLFGDDTVIEVAAILASFSAST;
APKEIIFLEGETLFGDDTVIEV;
HTTDPFLGRYMSALFADDLNQLTGYHTDFSSEIIGYQLMCQPILLAEELAKNVSLILGTV
SWNL;

TTDPSFLGRYMSALFADDLNQLTGYHTDFSSEIIGYQLMCQPILLAEAEAKNVSLILGTVS
WNL;

LLSAGIFGAITDVFYKENSYKVPTDNYITTY; and combinations thereof.

16. The composition of claim 1, wherein the sequence comprising an epitope sequence from membrane glycoprotein (M) is selected from the group consisting of the following sequences or fragments thereof:

ADSNGTITVEELKKLLEQWNLVIGFLFTWICLLQFAYANRNRFLYIIKLIFLWLLWPVTLA
CFVLA AVYRINWITGGIAIAMA CLVGLMWLSYFIASFRLFARTRSMWSFNPETNILLNVPL
HGTILTRP LLESELVIGAVILRGHLRIAGHHLGRCDIKDLPKEITVATSRTLSYYKLGASQRV
AGDSGFAAYSRYRIGNYKLNTDHSSSSDNIALLVQ;

FAYANRNRFLYIIKLIFLWLLWPVTLACFVLA AVYRINWITGGIAIAMA CLVGLMWLSYFI
ASFRLF;

LGRCDIKDLPKEITVATSRTLSYYKLGASQRVA;

KLLEQWNLVIGF;

NRNRFLYIIKLIFLWLLWPVTLACFVLA AVY;

SELVIGAVILRGHLRIAGHHLGR;

VATSRTLSYYKLGASQRV;

GLMWLSYF; and combinations thereof.

17. The composition of claim 1, wherein the sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N) is selected from the group consisting of the following sequences or fragments thereof:

KDLSPRWYFYLLGTGPEAGLPYGANKDGIWVATEGALNTPKDHIGTRNPANNA AIVLQL
PQGTTLPKGFYAEGSRGGSQASSRSSRSRNSSRNSTPGSSRGTS PARMAGNGGDAALALL
LLDRLNQLESKMSGKGQQQQGQTVTKKSAAEASKKPRQKRTATKAYNVTQAFGRRGPE
QTQGNFGDQELIRQGT DYKHWPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYTGAIKLD
DKDPNFKDQVILLNKHIDAYKTFPPTPEPKDKKKKADETQALPQRQKKQQT VTLTPAADL
DDFSKQLQQSMSSADSTQA;

RMAGNGGDAALALLLDRLNQLESKMSGKGQQQ;

YKHWPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYTGAIKLDDKDPNFKDQVILLNKHID
AYKTFP;

SPARMAGNGGDAALALLLDRLNQLESKMSGKGQQQQGQTVTKKSAAEASKKPRQKRT
ATKAYNVTQAFGRRGPEQTQGNFGDQELIRQGT DYKHWPQIAQFAPSASAFFGMSRIGME
VTPSGTWLTYTGAIKLDDKDPNFKDQVILLNKHIDAYKTFPPTPEPKDK and combinations
thereof.

18. The composition of claim 1, wherein the polypeptide comprises one or more linker sequences.

19. The composition of claim 18, wherein the one or more linker sequences are selected from the group consisting of GGSGGGGSGG, GGS LGGGGSG.
20. The composition of claim 18, wherein the one or more linker sequences comprise cleavage sequences.
21. The composition of claim 20, wherein the one or more cleavage sequences are selected from the group consisting of FRAC, KR CF, KKRY, ARMA, RRS G, MRAC, KMCG, ARCA, KKQG, YRSY, SFMN, FKAA, KRNG, YNSF, KKNG, RRRG, KRYS, and ARYA.
22. The composition of claim 1, wherein the polypeptide comprises a transmembrane domain sequence.
23. The composition of claim 22, wherein the transmembrane domain sequence is C-terminal to the sequence comprising an epitope sequence from ORF1ab, the sequence comprising an epitope sequence from membrane glycoprotein (M) and the sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N).
24. The composition of claim 22, wherein the transmembrane domain sequence is
EQYIKWPWYIWLGFIAGLIAIVMTIMLCCMTSCC SCLKGCCSCGSCCKFDEDDSEPVLKG
VKLHYT.
25. The composition of claim 1, wherein the polypeptide comprises an SEC sequence.
26. The composition of claim 25, wherein the SEC sequence is N-terminal to the sequence comprising an epitope sequence from ORF1ab, the sequence comprising an epitope sequence from membrane glycoprotein (M) and the sequence comprising an epitope sequence from nucleocapsid phosphoprotein (N).
27. The composition of claim 25, wherein the SEC sequence is MFVFLVLLPLVSSQCVNLT.
28. The composition of claim 1, wherein the composition comprises the polynucleotide encoding the polypeptide.
29. The composition of claim 28, wherein the polynucleotide is an mRNA.
30. The composition of claim 28, wherein the polynucleotide comprises a codon optimized sequence for expression in a human.
31. The composition of claim 28, wherein the polynucleotide comprises a dEarI-hAg sequence.
32. The composition of claim 31, wherein the dEarI-hAg sequence is
ATTCTTCTGGTCCCCACAGACTCAGAGAGAACCC, optionally wherein each T is a U.
33. The composition of claim 28, wherein the polynucleotide comprises a Kozak sequence.
34. The composition of claim 33, wherein the a Kozak sequences is GCCACC.
35. The composition of claim 28, wherein the polynucleotide comprises an F element sequence.
36. The composition of claim 35, wherein the F element sequence is a 3 UTR of amino-terminal enhancer of split (AES).

37. The composition of claim 35, wherein the F element sequence is
CTGGTACTGCATGCACGCAATGCTAGCTGCCCCCTTTCCCGTCCTGGGTACCCCGAGTCT
CCCCCGACCTCGGGTCCCAGGTATGCTCCACCTCCACCTGCCCCACTCACCACCTCTG
CTAGTTCCAGACACCTCC, optionally wherein each T is a U.
38. The composition of claim 28, wherein the polynucleotide comprises an I element sequence.
39. The composition of claim 38, wherein the I element sequence is a 3' UTR of mitochondrially encoded 12S rRNA (mtRNR1).
40. The composition of claim 38, wherein the I element sequence is
CAAGCACGCAGCAATGCAGCTCAAAACGCTTAGCCTAGCCACACCCCCACGGGAAAC
AGCAGTGATTAACCTTTAGCAATAAACGAAAGTTTAACTAAGCTATACTAACCCCAGG
GTTGGTCAATTTCGTGCCAGCCACACC, optionally wherein each T is a U.
41. The composition of claim 28, wherein the polynucleotide comprises a poly A sequence.
42. The composition of claim 41, wherein the poly A sequence is
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCATATGACTAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA,
optionally wherein each T is a U.
43. The composition of claim 1, wherein each of the epitope sequences from the ORF1ab, the membrane glycoprotein, and the nucleocapsid phosphoprotein are from 2019 SARS-CoV-2.
44. The composition of claim 1, wherein one or more of each epitope elicits a T cell response.
45. The composition of claim 1, wherein one or more of each epitope has been observed by mass spectrometry as being presented by an HLA molecule.
46. The composition of claim 1, wherein the composition comprises (i) a polypeptide with at least 70%, 80%, 90% or 100% sequence identity to a sequence selected from the group consisting of RS C1p1full, RS C2p1full, RS C3p1full, RS C4p1full, RS C5p1, RS C5p2, RS C5p2full, RS C6p1, RS C6p2, RS C6p2full, RS C7p1, RS C7p2, RS C7p2full, RS C8p1, RS C8p2 and RS C8p2full; (ii) a polynucleotide encoding a polypeptide with at least 70%, 80%, 90% or 100% sequence identity to a sequence selected from the group consisting of RS C1p1full, RS C2p1full, RS C3p1full, RS C4p1full, RS C5p1, RS C5p2, RS C5p2full, RS C6p1, RS C6p2, RS C6p2full, RS C7p1, RS C7p2, RS C7p2full, RS C8p1, RS C8p2 and RS C8p2full; or (iii) a polynucleotide with at least 70%, 80%, 90% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID NOs: RS C1n1, RS C2n1, RS C3n1, RS C4n1, RS C5n1, RS C6n1, RS C7n1, RS C8n1, RS C5n2, RS C6n2, RS C7n2, RS C8n2, RS C5n2full, RS C6n2full, RS C7n2full and RS C8n2full.
47. A pharmaceutical composition comprising the composition of any one of claims 1-46.
48. A pharmaceutical composition comprising:

- (i) a polypeptide comprising an epitope sequence of Table 1A, Table 1B, Table 1C, Table 2Ai, Table 2Aii, Table 2B and/or Table 16;
 - (ii) a polynucleotide encoding the polypeptide comprising an epitope sequence of Table 1A, Table 1B, Table 1C, Table 2Ai, Table 2Aii, Table 2B and/or Table 16;
 - (iii) a T cell receptor (TCR) or a T cell comprising the TCR, wherein the TCR binds to the epitope sequence in complex with a corresponding HLA class I or class II molecule;
 - (iv) an antigen presenting cell comprising (i) or (ii); or
 - (v) an antibody or B cell comprising the antibody, wherein the antibody binds to the epitope sequence; and
- a pharmaceutically acceptable excipient.
49. The pharmaceutical composition of claim 48, wherein the epitope sequence comprises one or more or each of the following: KTIQPRVEK, YLFDESGEF, YLFDESGEFKL, ~~YLFDESGEF~~, FGDDTVIEV, LLLDRLNQL, QLMCQPILL, TTDPSFLGRY, PTDNYITTY, PSFLGRY, AEAELAKNV, and VATSRTLSTY ~~and KTIQPRVEK~~.
 50. The pharmaceutical composition of claim 48, wherein the epitope sequence comprises one or more or each of the following: SAPPAQYEL, AVASKILGL, EYADVFLHY, DEFTPFDVV, VRIQPGQTF, SFRLFARTR, KFLPFQQF, VVQEGVLTA, RLDKVEAEV, FGADPIHSL, NYNYLYRLF, KYIKWPWYI, KWPWYIWLGF, LPFNDGVYF, QPTESIVRF, IPFAMQMAY, YLQPRTFLL and RLQSLQTYV.
 51. The pharmaceutical composition of claim 48, wherein the epitope sequence is from an orf1ab protein.
 52. The pharmaceutical composition of claim 48, wherein the epitope sequence is from an orf1a protein
 53. The pharmaceutical composition of claim 48, wherein the epitope sequence is from a surface glycoprotein (S) or a shifted reading frame thereof.
 54. The pharmaceutical composition of claim 48, wherein the epitope sequence is from a nucleocapsid phosphoprotein (N).
 55. The pharmaceutical composition of claim 48, wherein the epitope sequence is from an ORF3a protein.
 56. The pharmaceutical composition of claim 48, wherein the epitope sequence is from a membrane glycoprotein (M).
 57. The pharmaceutical composition of claim 48, wherein the epitope sequence is from an ORF7a protein.
 58. The pharmaceutical composition of claim 48, wherein the epitope sequence is from an ORF8 protein.

59. The pharmaceutical composition of claim 48, wherein the epitope sequence is from an envelope protein (E).
60. The pharmaceutical composition of claim 48, wherein the epitope sequence is from an ORF6 protein.
61. The pharmaceutical composition of claim 48, wherein the epitope sequence is from an ORF7b protein.
62. The pharmaceutical composition of claim 48, wherein the epitope sequence is from an ORF10 protein.
63. The pharmaceutical composition of claim 48, wherein the epitope sequence is from an ORF9b protein.
64. A pharmaceutical composition comprising: a polypeptide having an amino acid sequence with at least 70%, 80%, 90% or 100% sequence identity to a sequence of any one of the sequences depicted in column 2 of Table 11, column 2 of Table 12 or column 3 of Table 15; or a recombinant polynucleotide encoding a polypeptide having an amino acid sequence with at least 70%, 80%, 90% or 100% sequence identity to a sequence of any one of the sequences depicted in column 2 of Table 11, column 2 of Table 12 or column 3 of Table 15.
65. The pharmaceutical composition of claim 64, wherein the pharmaceutical composition comprises a polypeptide with at least 70%, 80%, 90% or 100% sequence identity to a sequence selected from the group consisting of RS C1p1full, RS C2p1full, RS C3p1full, RS C4p1full, RS C5p1, RS C5p2, RS C5p2full, RS C6p1, RS C6p2, RS C6p2full, RS C7p1, RS C7p2, RS C7p2full, RS C8p1, RS C8p2 and RS C8p2full; or a polynucleotide encoding a polypeptide with at least 70%, 80%, 90% or 100% sequence identity to a sequence selected from the group consisting of RS C1p1full, RS C2p1full, RS C3p1full, RS C4p1full, RS C5p1, RS C5p2, RS C5p2full, RS C6p1, RS C6p2, RS C6p2full, RS C7p1, RS C7p2, RS C7p2full, RS C8p1, RS C8p2 and RS C8p2full.
66. The pharmaceutical composition of claim 64, wherein the pharmaceutical composition comprises a polynucleotide with at least 70%, 80%, 90% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID NOs: RS C1n1, RS C2n1, RS C3n1, RS C4n1, RS C5n1, RS C6n1, RS C7n1, RS C8n1, RS C5n2, RS C6n2, RS C7n2, RS C8n2, RS C5n2full, RS C6n2full, RS C7n2full and RS C8n2full.
67. The pharmaceutical composition of any one of the claims 47, 48 or 64, wherein the polynucleotide is an mRNA.
68. The pharmaceutical composition of any one of the claims 47, 48 or 64, further comprising one or more lipid components.
69. The pharmaceutical composition of claim 68, wherein the one or more lipids comprise a lipid nanoparticle (LNP).

70. The pharmaceutical composition of claim 69, wherein the LNP encapsulates the recombinant polynucleotide construct.
71. The pharmaceutical composition of any one of the claims 47, 48 or 64, wherein the polypeptide is synthetic.
72. The pharmaceutical composition of any one of the claims 47, 48 or 64, wherein the polypeptide is recombinant.
73. The pharmaceutical composition of any one of the claims 47, 48 or 64, wherein the polypeptide is from 8-1000 amino acids in length.
74. The pharmaceutical composition of any one of the claims 47, 48 or 64, wherein the epitope sequence binds to or is predicted to bind to an HLA class I or class II molecule with a K_D of 1000 nM or less.
75. The pharmaceutical composition of any one of the claims 47, 48 or 64, wherein the epitope sequence binds to or is predicted to bind to an HLA class I or class II molecule with a K_D of 500 nM or less.
76. The pharmaceutical composition of any one of the claims 47, 48 or 64, wherein the epitope sequence comprises a sequence of a viral protein expressed by a virus-infected cell of a subject.
77. The pharmaceutical composition of claim 76, wherein the virus is 2019 SARS-CoV 2.
78. Use of the pharmaceutical composition of any one of the claims 47, 48 or 64 in the manufacture of a medicament for ~~A method of~~ treating or preventing an infection by a virus or treating a respiratory disease or condition associated with an infection by a virus ~~comprising administering to a subject in need thereof the pharmaceutical composition of any one of the claims 47, 48 or 64.~~
79. The ~~method-use~~ of claim 78, wherein the virus is a coronavirus.
80. The ~~method-use~~ of claim 78, wherein the virus is 2019 SARS-CoV 2.
81. The ~~method-use~~ of claim 78, wherein an HLA molecule expressed by the subject is unknown at the time of administration.
82. The ~~method-use~~ of claim 78, wherein the ability of the virus to avoid escape of recognition by an immune system of the subject is less compared to the ability of the virus to avoid escape of recognition by an immune system of a subject to be administered a pharmaceutical composition containing an epitope from a single protein or epitopes from fewer proteins than in the pharmaceutical composition of any one of the claims 47, 48 or 64.
83. The ~~method-use~~ of claim 78, wherein the subject expresses an HLA molecule encoded by an HLA allele of any one of Table 1A, Table 1B, Table 1C, Table 2Ai, Table 2Aii, Table 2B and Table 16 and the epitope sequence is an HLA allele-matched epitope sequence.

84. The ~~method-use~~ of claim 78, wherein the epitope sequence comprises one or more or each of the following: SAPPAQYEL, AVASKILGL, EYADVHLY, DEFTPFDVV, VRIQPGQTF, SFRLFARTR, KFLPFQQF, VVQEGVLTA, RLDKVEAEV and FGADPIHSL.
85. Use of the pharmaceutical composition of any one of the claims 47, 48 or 64 in the manufacture of a medicament for ~~A method of~~ treating or preventing a 2019 SARS-CoV 2 infection in a subject in need thereof, ~~comprising administering to the subject a pharmaceutical composition of any one of the claims 47, 48 or 64.~~
86. The ~~method-use~~ of claim 85, wherein the pharmaceutical composition is to be administered in addition to one or more therapeutics for the 2019 SARS-CoV 2 viral infection in the subject.
87. The ~~method-use~~ of claim 85, wherein the pharmaceutical composition is to be administered in combination with (a) a polypeptide having an amino acid sequence of a 2019 SARS-CoV 2 spike protein or fragment thereof; (b) a recombinant polynucleotide encoding a 2019 SARS-CoV 2 spike protein or fragment thereof; or a 2019 SARS-CoV 2 spike protein pharmaceutical composition comprising (a) or (b).
88. The ~~method-use~~ of claim 85, wherein the 2019 SARS-CoV 2 spike protein or fragment thereof is a SARS-CoV-2 spike protein or a fragment thereof.
89. The ~~method-use~~ of claim 85, wherein the pharmaceutical composition is to be administered 1-10 weeks after a first administration of the 2019 SARS-CoV 2 spike protein pharmaceutical composition.
90. The ~~method-use~~ of claim 85, wherein the pharmaceutical composition is to be administered 1-6 weeks, 1-6 months or 1-2 years or later after a first administration of the 2019 SARS-CoV 2 spike protein pharmaceutical composition.
91. The ~~method-use~~ of claim 85, wherein the pharmaceutical composition is to be administered on the same day or simultaneously with an administration of the 2019 SARS-CoV 2 spike protein pharmaceutical composition.
92. The ~~method-use~~ of claim 91, wherein the pharmaceutical composition is co-formulated with the polypeptide having an amino acid sequence of a 2019 SARS-CoV 2 spike protein or fragment thereof or the recombinant polynucleotide encoding a 2019 SARS-CoV 2 spike protein or fragment thereof.
93. The ~~method-use~~ of claim 85, wherein the pharmaceutical composition is to be administered before an administration of the 2019 SARS-CoV 2 spike protein pharmaceutical composition, such as 2-10 weeks before an administration of the 2019 SARS-CoV 2 spike protein pharmaceutical composition.
94. The ~~method-use~~ of claim 85, wherein the pharmaceutical composition is to be administered prophylactically.

95. The ~~method-use~~ of claim 85, wherein the pharmaceutical composition is to be administered once every 1, 2, 3, 4, 5, 6 or more weeks; or once every 1-7, 7-14, 14-21, 21-28, or 28-35 days; or once every 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, or 35 days.
96. Use of the composition of any one of the claims 1-46 in the manufacture of a medicament for ~~preparing a therapeutic for~~ treating or preventing a respiratory viral infection caused by 2019 SARS CoV-2 virus.
97. A composition according to any one of claims 1-46 or a pharmaceutical composition according to any one of claims 47, 48 and 64 for use as a medicament.
- ~~98. A composition according to any one of claims 1-46 or a pharmaceutical composition according to any one of claims 47, 48 and 64 for use in the treatment or prevention of a respiratory viral infection caused by 2019 SARS CoV-2 virus.~~