

Stabilized Coronavirus Spike (S) Protein Immunogens and Related Vaccines

CROSS-REFERENCE TO RELATED APPLICATIONS

5 [0001] The subject patent application claims the benefit of priority to US Patent Application No. 17/019,825 (filed September 14, 2020; now pending) and US Provisional Patent Application No. 63/045,557 (filed June 29, 2020; now pending). The full disclosures of the priority applications are incorporated herein by reference in their entirety and for all purposes.

10 STATEMENT OF GOVERNMENT SUPPORT

[0002] This invention was made with government support under grant numbers AI139092 and AI137472 awarded by the National Institutes of Health. The government has certain rights in the invention.

15 BACKGROUND OF THE INVENTION

[0003] Coronaviruses (CoV) are enveloped viruses with a positive-stranded RNA genome. In 2002, there was an outbreak of severe acute respiratory syndrome (SARS) in Asia. In 2003, a novel coronavirus was identified to be the causative agent of SARS and subsequently named SARS-CoV. During the 2002-2003 outbreak, SARS-CoV
20 infected over 8000 people with ~10% fatality rate. In 2012, another coronavirus, Middle East respiratory syndrome coronavirus (MERS-CoV), was identified. Since 2012, MERS-CoV has infected over 2000 people in 27 countries with ~35% fatality rate. In December 2019, a novel coronavirus designated as 2019-nCoV (or SARS-CoV-2) appeared in Wuhan, China. The first reported infected individuals, some of whom
25 showed symptoms as early as December 8, were discovered to be among stallholders from the Wuhan South China Seafood Market. On January 10, 2020, gene sequencing determined that this novel coronavirus, a β -coronavirus, is related to the MERS-CoV and the SARS-CoV. On January 30, 2020, the WHO declares SARS-CoV-2 a public health emergency of international concern (PHEIC), and on March 11, 2020,
30 characterized the situation as a pandemic. On May 24, 2020, the WHO Coronavirus

Disease (COVID-19) Dashboard showed a total of 5,304,772 confirmed cases in 216 countries, areas or territories, including 342,029 deaths. SARS-CoV, MERS-CoV, and SARS-CoV-2 belong to the β -coronavirus genus and are highly pathogenic zoonotic viruses. In addition to these three highly pathogenic β -coronaviruses, four low-

5 pathogenicity β -coronaviruses, HCoV-OC43, HCoVHKU1, HCoV-NL63 and HCoV-229E, are also endemic in humans.

[0004] To date, no therapeutics or vaccines have been approved for treating or preventing any human-infecting coronaviruses. There is a strong and urgent need in the art for effective vaccines against coronaviruses. The present invention is directed to this

10 and other pressing needs in the art.

SUMMARY OF THE INVENTION

[0005] In one aspect, the invention provides engineered immunogen polypeptides that are derived or modified from the spike (S) glycoprotein of coronaviruses including

15 SARS-CoV, MERS-CoV and SARS-CoV-2. Relative to a wildtype soluble S protein sequence of the coronavirus, the immunogen polypeptides of the invention contain an altered soluble S sequence with modifications that stabilize the prefusion S structure. In various embodiments, the modifications include (a) a mutation that inactivates the S1/S2 cleavage site, and (b) a mutation in the turn region between the heptad repeat 1

20 (HR1) region and the central helix (CH) region (see Figure 1) that prevents HR1 and CH to form a straight helix during membrane fusion process. In some embodiments, the immunogen polypeptides of the invention also contain truncation of the heptad repeat 2 region (HR2) in addition to the stabilizing mutations noted above.

[0006] Some soluble S immunogen polypeptides of the invention are derived from

25 SARS-CoV-2. In some of these embodiments, the mutation inactivating S1/S2 cleavage site can contain substitution of ⁶⁸²RRAR⁶⁸⁵ (SEQ ID NO:19) with GSAG (SEQ ID NO:20), and the mutation in the turn region can contain double mutation K986G/V987G, K986P/V987P, K986G/V987P or K986P/V987G, using amino acid numbering based on cryo-EM model PDB ID 6VSB as reference. In some

30 embodiments, the wildtype soluble S sequence contains the sequence shown in SEQ ID NO:14, or a substantially identical or conservatively modified variant thereof. In some embodiments, truncation of HR2 entails deletion of the residues shown in SEQ ID

NO:9 at the C-terminus of the wildtype soluble S sequence. In some of these embodiments, the immunogen polypeptides can further include truncation of residues shown in SEQ ID NO:10 at the C-terminus. In some of these embodiments, the immunogen polypeptides contain substitution of residues shown in SEQ ID NO:10 at the C-terminus of the wildtype soluble S sequence with residues GNS.

[0007] In some embodiments, the SARS-CoV-2 derived immunogen polypeptides of the invention can contain a N-terminal leader sequence shown in SEQ ID NO:15. In some embodiments, the immunogen polypeptide can further include in the region of HR1 that interacts with HR2 (a) one or more proline or glycine substitutions, and/or (b) insertion of one or more amino acid residues. In some of these embodiments, the immunogen polypeptide can have one or more substitutions selected from A942P, S943P, A944P, A942G, S943G and A944G. In some of these embodiments, the insertion can be insertion of G or GS between any residues in A942-A944. In some exemplified embodiments, the SARS-CoV-2 derived immunogen polypeptides of the invention contain the sequence shown in any one of SEQ ID NOs:32-37, or a substantially identical or conservatively modified variant thereof.

[0008] Some soluble S immunogen polypeptides of the invention are derived from SARS-CoV. In some of these embodiments, the mutation inactivating S1/S2 cleavage site can be R667G substitution, and the mutation in the turn region comprises double mutation K968G/V969G, K968P/V969P, K968G/V969P or K968P/V969G, using amino acid numbering based on UniProt ID P59594 as reference. In some embodiments, the wildtype soluble S sequence contains the sequence shown in SEQ ID NO:7, or a substantially identical or conservatively modified variant thereof. In some embodiments, the SARS-CoV derived immunogen polypeptides of the invention contain truncation of HR2 (SEQ ID NO:9) at the C-terminus of the wildtype soluble S sequence. In some of these embodiments, immunogen polypeptides can additionally include truncation of residues shown in SEQ ID NO:10 at the C-terminus. In some of these embodiments, the immunogen polypeptides contain substitution of residues shown in SEQ ID NO:10 at the C-terminus of the wildtype soluble S sequence with residues GNS.

[0009] In some embodiments, the SARS-CoV derived immunogen polypeptides of the invention can contain a N-terminal leader sequence shown in SEQ ID NO:8. In

some embodiments, the immunogen polypeptides can further include in the region of HR1 that interacts with HR2 (a) one or more proline or glycine substitutions, and/or (b) insertion of one or more amino acid residues. In some of these embodiments, the immunogen polypeptide can have one or more substitutions selected from S924P, T925P, A926P, S924G, T925G, and A926G. In some of these embodiments, the insertion can be insertion of G or GS after any residue in S924-A926.

[0010] Some other soluble S immunogen polypeptides of the invention are derived from MERS-CoV. In some of these embodiments, the mutation inactivating S1/S2 cleavage site can contain R748A/R751G double mutation, and the mutation in the turn region comprises double mutation V1060G/L1061G, V1060P/L1061P, V1060G/L1061P or V1060P/L1061G, using amino acid numbering based on UniProt ID R9UQ53 as reference. In some embodiments, the wildtype soluble S sequence contains the sequence shown in SEQ ID NO:11 or a substantially identical or conservatively modified variant thereof. In some embodiments, MERS-CoV derived immunogen polypeptides of the invention contain truncation of HR2 (SEQ ID NO:13) at the C-terminus of the wildtype soluble S sequence.

[0011] In some embodiments, the MERS-CoV derived immunogen polypeptides of the invention can contain a N-terminal leader sequence shown in SEQ ID NO:12. In some embodiments, the immunogen polypeptides can further include in the region of HR1 that interacts with HR2 (a) one or more proline or glycine substitutions in the region of HR1 that interacts with HR2 in the region of HR1 that interacts with HR2, and/or (b) insertion of one or more amino acid residues. In some of these embodiments, the immunogen polypeptide can have one or more substitutions selected from T1013P, T1014P, T1015P, T1013G, T1014G and T1015G. In some of these embodiments, the insertion can be insertion of residue G or GS after any residue in T1013-T1015.

[0012] In some embodiments, the coronavirus S protein derived immunogen polypeptides of the invention can additionally include a trimerization motif at the C-terminus. In some of these embodiments, the trimerization motif is foldon or viral capsid protein SHP. In various embodiments, the employed trimerization motif can contain the foldon sequence shown in SEQ ID NO:26 or the SHP sequence shown in SEQ ID NO:27, or a substantially identical or conservatively modified variant thereof.

In some embodiments, the coronavirus S protein derived immunogen polypeptides of the invention can additionally contain the subunit sequence of a self-assembling nanoparticle that is fused to the altered soluble S sequence. In some of these embodiments, C-terminus of the altered soluble S sequence is fused to N-terminus of the nanoparticle subunit sequence.

5 [0013] In another aspect, the invention provides polynucleotide sequences that encode the coronavirus S protein derived immunogen polypeptides described herein. Some of the polynucleotide sequences encode a fusion polypeptide containing the immunogen polypeptide that is fused at its C-terminus to the N-terminus of the subunit sequence of a self-assembling nanoparticle.

10 [0014] In another aspect, the invention provides coronavirus vaccine compositions that contain an immunogen polypeptide described herein that is displayed on the surface of a self-assembling nanoparticle. In some of these embodiments, the self-assembling nanoparticle contains a trimeric sequence, and C-terminus of the immunogen polypeptide is fused to N-terminus of the subunit sequence of the nanoparticle. In some embodiments, the employed self-assembling nanoparticle is composed of ferritin, E2p or I3-01. Some nanoparticle vaccines of the invention display an engineered SARS-CoV-2 spike protein described herein.

15 [0015] In some embodiments, the nanoparticle vaccine contains (1) a polypeptide sequence containing from N terminus to C terminus (a) an engineered SARS-CoV-2 spike polypeptide, a GS linker sequence, and nanoparticle sequence I3-01v9, (b) an engineered SARS-CoV-2 spike polypeptide, a GS linker sequence, and nanoparticle sequence E2p, or (c) an engineered SARS-CoV-2 spike polypeptide, a GS linker sequence, and nanoparticle sequence ferritin; or (2) a conservatively modified variant of the polypeptide sequence. In some of these embodiments, the displayed SARS-CoV-2 spike immunogen polypeptide contains, relative to the wildtype spike sequence, (a) substitution of the S1/S2 cleavage site ⁶⁸²RRAR⁶⁸⁵ (SEQ ID NO:19) with GSAG (SEQ ID NO:20), (b) double mutations K986G/V987G in the turn region, and (c) truncation of HR2 (SEQ ID NO:9) at the C-terminus.

25 [0016] In some nanoparticle scaffolded SARS-CoV-2 vaccines of the invention, the displayed SARS-CoV-2 spike immunogen polypeptide contains the sequence shown in SEQ ID NO:33 or 34, or a conservatively modified variant thereof. In some of

these embodiments, the scaffolded vaccine is composed of (1) a subunit sequence containing from N terminus to C terminus (a) the engineered SARS-CoV-2 spike polypeptide shown in SEQ ID NO:33, linker sequence (G₄S)₂ (SEQ ID NO:22), nanoparticle sequence shown in SEQ ID NO:23 (I3-01v9), locking domain shown in SEQ ID NO:29 (LD7), and T cell epitope shown in SEQ ID NO:30 (PADRE), (b) the engineered SARS-CoV-2 spike polypeptide shown in SEQ ID NO:33, linker sequence G₄S (SEQ ID NO:21), nanoparticle subunit sequence shown in SEQ ID NO:24 (E2p), locking domain shown in SEQ ID NO:28 (LD4), and T cell epitope shown in SEQ ID NO:30 (PADRE), or (c) the engineered SARS-CoV-2 spike polypeptide shown in SEQ ID NO:33, linker sequence G₄S (SEQ ID NO:21), nanoparticle sequence shown in SEQ ID NO:25 (ferritin); or (2) a conservatively modified variant of the subunit sequence. In some embodiments, the subunit of the nanoparticle scaffolded vaccines contains the sequence shown in any one of SEQ ID NOs:38-40, or a substantially identical or conservatively modified variant thereof.

[0017] In still another aspect, the invention provides pharmaceutical compositions that contain the vaccine composition described herein, and a pharmaceutically acceptable carrier. In another aspect, the invention provides methods for preventing or treating a coronavirus infection in a subject. These methods involve administering to the subject a pharmaceutically effective amount of a vaccine composition or a pharmaceutical composition described herein.

[0018] A further understanding of the nature and advantages of the present invention may be realized by reference to the remaining portions of the specification and claims.

DESCRIPTION OF THE DRAWINGS

[0019] Figure 1 illustrates the organization of different structural motifs of coronaviral spike (S) protein. The scheme shown in the figure reflects the structure of S protein of different coronaviruses encompassed by the invention, e.g., SARS-CoV, MERS-CoV and SARS-CoV-2. The structural domains and motifs of the S protein shown in the figure include RBD, HR1, CH1, and HR2 domains or regions, as well as the S2 cleavage site (aka S1/S2 cleavage site) and the S2' cleavage site. In addition to

the various S structural components indicated in the figure, the amino acid residues between HR1 and CH are denoted “the turn region” herein.

[0020] Figure 2 is a schematic representation of the mouse immunization protocol. Groups of five mice were immunized four times with three-week intervals. All vaccine antigens (50ug/injection) were formulated with AddaVax, an oil-in-water emulsion adjuvant, except for I3-01v9, which was formulated with aluminum phosphate (AP). The injections were done through the intraperitoneal (IP) route. Blood samples were collected two weeks after each injection.

[0021] Figure 3 shows results from SARS-CoV-2 vaccine-induced antibody responses in mice. SARS-CoV-2 spike/spike-NP vaccine-induced binding antibody response. Listed in the figure are a summary of ED₅₀ titers measured for five SARS-CoV-2 spike-based vaccine groups (S2P-5GS-1TD0, S2GΔHR2-5GS-1TD0, S2GΔHR2-5GS-FR, S2GΔHR2-5GS-E2p-L4P, and S2GΔHR2-10GS-I3-01v9-L7P) against three coating antigens in ELISA. ED₅₀ values were calculated in GraphPad Prism 8.4.3. Of note, the ED₅₀ values at w2 were derived by setting the lower/upper constraints of OD₄₅₀ at 0.0/3.2 to achieve greater accuracy.

[0022] Figure 4 shows additional results from SARS-CoV-2 vaccine-induced antibody responses in mice. Listed in the figure are a summary of ID₅₀ titers measured for five SARS-CoV-2 spike-based vaccine groups (S2P-5GS-1TD0, S2GΔHR2-5GS-1TD0, S2GΔHR2-5GS-FR, S2GΔHR2-5GS-E2p-L4P, and S2GΔHR2-10GS-I3-01v9-L7P) against two pseudoviruses, SARS-CoV-1-pp and SARS-CoV-2-pp, in neutralization assays. ID₅₀ values were calculated in GraphPad Prism 8.4.3, with the lower/upper constraints of %neutralization set at 0.0/100.0.

[0023] Figure 5 shows results of SARS-CoV-2 vaccine-induced T-cell responses in mice. (A)-(B): Vaccine-induced CD4⁺ T cell immunity. Splenocytes derived from mice at w11 were cultured in the presence of DC-pulsed with the S2PECTO spike (1x10⁻⁷ mM), E2p SApNP (1x10⁻⁷ mM) and I3-01v9 SApNP (1x10⁻⁷ mM) for 16 hours (A) and 4 hours (B), respectively. (C)&(D): Vaccine-induced CD8⁺ T cell immunity. Splenocytes derived from mice at w11 were cultured in the presence of DC-pulsed with the S2PECTO spike (1x10⁻⁷ mM), E2p SApNP (1x10⁻⁷ mM) and I3-01v9 SApNP (1x10⁻⁷ mM) for 16 hours (C) and 4 hours (D), respectively. Splenocytes from five naïve mice were used as the control samples and cultured with PBS. Plots show the

frequencies of cell fraction. The P values were determined by one-way ANOVA analysis. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

DETAILED DESCRIPTION

5 I. Overview

[0024] For SARS-CoV (aka SARS-CoV-1), MERS-CoV, and SARS-CoV-2, the viral genome encodes spike (S), envelope (E), membrane (M), and nucleocapsid (N) structural proteins, among which the S glycoprotein is responsible for binding the host receptor via the receptor-binding domain (RBD) in its S1 subunit, as well as the subsequent membrane fusion and viral entry driven by its S2 subunit. A possible membrane fusion process has been proposed. The receptor binding may help to keep the RBD in a 'standing' state, which facilitates the dissociation of the S1 subunit from the S2 subunit. When the S1 subunit is dissociated from the S2 subunit, a second S2' cleavage can release the fusion peptide. The connecting region, HR1 region and central
10 helix would form an extremely long helix (≥ 200 Å) to insert the fusion peptide into the host cell membrane. Finally, the HR1 and HR2 regions will form a coiled structure and assemble into a six-helix bundle to merge the viral and host membranes.

[0025] In all the prefusion S structures solved for SARS-CoV, MERS-CoV, and SARS-CoV-2, the viral membrane proximal HR2 region is invisible, indicating high
15 mobility in HR2. The RBD contains a core subdomain and a receptor-binding motif (RBM). While the core subdomains are highly similar between the three coronaviruses, their RBMs are markedly different, leading to different receptor specificity: SARS-CoV and SARS-CoV-2 recognize the angiotensin-converting enzyme 2 (ACE2), whereas MERS-CoV binds the dipeptidyl peptidase 4 (DPP4). As the S glycoprotein is surface-
20 exposed and mediates entry into host cells, it is the main target of neutralizing antibodies (NAbs) upon infection and the focus of vaccine design. S trimers are extensively decorated with N-linked glycans that are important for proper folding and for modulating accessibility to NAbs.

[0026] The present invention is predicated in part on the studies undertaken by the
25 inventors to design nanoparticle vaccines for three highly pathogenic β -coronaviruses, SARS-CoV, MERS-CoV, and SARS-CoV-2 based on two rational strategies. In the first strategy, the inventors aimed to stabilize the S trimer in a prefusion conformation

by eliminating the causes of metastability in various regions of S, particularly HR1 and in HR2, prior to displaying it on nanoparticles. In the second vaccine strategy, the inventors utilized the SpyTag/SpyCatcher protein superglue system to create RBD-presenting nanoparticles. A number of S protein derived immunogen polypeptides and nanoparticle vaccine constructs were generated based on the design and examined for activities.

[0027] As exemplified herein with SARS-CoV-2 (and SARS-CoV-1) spike protein, the engineered spike immunogen polypeptides of the invention are more stable and represent more optimal vaccine design relative to the control polypeptides devoid of the engineering. Their advantageous biochemical and structural properties as described herein indicate that they are amenable for rapid and large-scale vaccine production in the industrial setting. When examined in vivo, it was found that the engineered SARS-CoV-2 spike immunogens (e.g., S2GAHR2) are more effective than the non-engineered control protein to elicit potent anti-SARS-CoV-2 NAb responses, alone or presented on self-assembling nanoparticle platforms (SApNPs). As detailed in the Examples herein, the exemplified nanoparticle vaccines of the invention, e.g., S2GAHR2-presenting I3-01v9 SApNP, can also elicit a strong Th1 response as well as other types of T-cell response needed for protective cellular immunity. Results obtained from the exemplified studies herein on the SARS-CoV-2 spike protein indicate that the engineered spike immunogen polypeptides of the invention provide more effective next-generation vaccine candidates for evaluation in human trials.

[0028] The invention provides coronavirus immunogens and vaccine compositions in accordance with the studies and exemplified designs described herein. Related polynucleotide sequences, expression vectors and pharmaceutical compositions are also provided in the invention. In various embodiments, stabilized S trimers and RBD proteins, in the forms of protein or nucleic acid (DNA/mRNA) carried by a viral vector can be used as coronavirus vaccines. In addition, nanoparticles presenting stabilized S trimers and RBDs can be used as VLP-type coronavirus vaccines.

[0029] The coronavirus S-protein based immunogens and vaccines of the invention have several advantageous properties. The S trimer designs described herein, which present conserved neutralizing epitopes in their native-like conformation, enable S trimers to be used as vaccine antigens or displayed multivalently on nanoparticles.

- Nanoparticle vaccines of the invention allows S trimers derived from the three different coronaviruses to be displayed on well-known nanoparticle platforms, such as ferritin, E2p, and I3-01 with a size ranging from 12.2 to 25.0 nm. In addition, the use of high-stability hollow nanocages (E2p and 1VLW/I3-01 variants allows engineering of
- 5 locking domains (LD), T-cell epitopes (e.g. PADRE), and peptide adjuvants within the nanocage, thus providing an all-in-one vaccine solution. All S trimer-presenting nanoparticles can be produced in ExpiCHO cells with high yield. Since CHO is one of the principal mammalian cell lines used for industrial manufacture of protein therapeutics and vaccines and ExpiCHO is a transient version of this CHO cell line,
- 10 nanoparticles obtained from the ExpiCHO production are expected to have the same properties as those from industrial CHO production. Moreover, the high yield of S-presenting nanoparticles produced in ExpiCHO cells with antibody and SEC purification will enable the development of a simple, robust, and cost-effective manufacturing process for industrial production.
- 15 **[0030]** Unless otherwise specified herein, the vaccine immunogens of the invention, the encoding polynucleotides, expression vectors and host cells, as well as the related therapeutic applications, can all be generated or performed in accordance with the procedures exemplified herein or routinely practiced methods well known in the art. See, e.g., *Methods in Enzymology*, Volume 289: Solid-Phase Peptide
- 20 *Synthesis*, J. N. Abelson, M. I. Simon, G. B. Fields (Editors), Academic Press; 1st edition (1997) (ISBN-13: 978-0121821906); U.S. Pat. Nos. 4,965,343, and 5,849,954; Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, N.Y., (3rd ed., 2000); Brent et al., *Current Protocols in Molecular Biology*, John Wiley & Sons, Inc. (ringbrou ed., 2003); Davis et al., *Basic Methods in Molecular Biology*,
- 25 Elsevier Science Publishing, Inc., New York, USA (1986); or *Methods in Enzymology: Guide to Molecular Cloning Techniques Vol. 152*, S. L. Berger and A. R. Kimmerl Eds., Academic Press Inc., San Diego, USA (1987); *Current Protocols in Protein Science (CPPS)* (John E. Coligan, et. al., ed., John Wiley and Sons, Inc.), *Current Protocols in Cell Biology (CPCB)* (Juan S. Bonifacino et. al. ed., John Wiley and Sons,
- 30 Inc.), and *Culture of Animal Cells: A Manual of Basic Technique* by R. Ian Freshney, Publisher: Wiley-Liss; 5th edition (2005), *Animal Cell Culture Methods (Methods in Cell Biology, Vol. 57*, Jennie P. Mather and David Barnes editors, Academic Press, 1st

edition, 1998). The following sections provide additional guidance for practicing the compositions and methods of the present invention.

[0031] Unless otherwise noted, the expression “at least” or “at least one of” as used herein includes individually each of the recited objects after the expression and the various combinations of two or more of the recited objects unless otherwise understood from the context and use. The expression “and/or” in connection with three or more recited objects should be understood to have the same meaning unless otherwise understood from the context.

[0032] The use of the term “include,” “includes,” “including,” “have,” “has,” “having,” “contain,” “contains,” or “containing,” including grammatical equivalents thereof, should be understood generally as open-ended and non-limiting, for example, not excluding additional unrecited elements or steps, unless otherwise specifically stated or understood from the context.

[0033] Where the use of the term “about” is before a quantitative value, the present invention also includes the specific quantitative value itself, unless specifically stated otherwise. As used herein, the term “about” refers to a $\pm 10\%$ variation from the nominal value unless otherwise indicated or inferred.

[0034] Unless otherwise noted, the order of steps or order for performing certain actions is immaterial so long as the present invention remain operable. Moreover, two or more steps or actions may be conducted simultaneously.

[0035] Unless otherwise noted, the use of any and all examples, or exemplary language herein, for example, “such as” or “including,” is intended merely to illustrate better the present invention and does not pose a limitation on the scope of the invention. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the present invention.

II. Definitions

[0036] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by those of ordinary skill in the art to which this invention pertains. The following references provide one of skill with a general definition of many of the terms used in this invention: *Academic Press Dictionary of Science and Technology*, Morris (Ed.), Academic Press (1st ed., 1992);

Oxford Dictionary of Biochemistry and Molecular Biology, Smith et al. (Eds.), Oxford University Press (revised ed., 2000); *Encyclopaedic Dictionary of Chemistry*, Kumar (Ed.), Anmol Publications Pvt. Ltd. (2002); *Dictionary of Microbiology and Molecular Biology*, Singleton et al. (Eds.), John Wiley & Sons (3rd ed., 2002); *Dictionary of Chemistry*, Hunt (Ed.), Routledge (1st ed., 1999); *Dictionary of Pharmaceutical Medicine*, Nahler (Ed.), Springer-Verlag Telos (1994); *Dictionary of Organic Chemistry*, Kumar and Anandand (Eds.), Anmol Publications Pvt. Ltd. (2002); and *A Dictionary of Biology (Oxford Paperback Reference)*, Martin and Hine (Eds.), Oxford University Press (4th ed., 2000). Further clarifications of some of these terms as they apply specifically to this invention are provided herein.

[0037] As used herein, the terms "antigen" or "immunogen" are used interchangeably to refer to a substance, typically a protein, which is capable of inducing an immune response in a subject. The term also refers to proteins that are immunologically active in the sense that once administered to a subject (either directly or by administering to the subject a nucleotide sequence or vector that encodes the protein) is able to evoke an immune response of the humoral and/or cellular type directed against that protein. Unless otherwise noted, the term "vaccine immunogen" is used interchangeably with "protein antigen" or "immunogen polypeptide".

[0038] The term "conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refer to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For polypeptide sequences, "conservatively modified variants" refer to a variant which has conservative amino acid substitutions, amino acid residues replaced with other amino acid residue having a side chain with a similar charge. Families of amino acid residues having side chains with similar charges have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine,

methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine).

[0039] Epitope refers to an antigenic determinant. These are particular chemical groups or peptide sequences on a molecule that are antigenic, such that they elicit a specific immune response, for example, an epitope is the region of an antigen to which B and/or T cells respond. Epitopes can be formed both from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein.

[0040] Effective amount of a vaccine or other agent that is sufficient to generate a desired response, such as reduce or eliminate a sign or symptom of a condition or disease, such as pneumonia. For instance, this can be the amount necessary to inhibit viral replication or to measurably alter outward symptoms of the viral infection. In general, this amount will be sufficient to measurably inhibit virus (for example, SARS-CoV-2) replication or infectivity. When administered to a subject, a dosage will generally be used that will achieve target tissue concentrations that has been shown to achieve in vitro inhibition of viral replication. In some embodiments, an "effective amount" is one that treats (including prophylaxis) one or more symptoms and/or underlying causes of any of a disorder or disease, for example to treat a coronavirus infection. In some embodiments, an effective amount is a therapeutically effective amount. In some embodiments, an effective amount is an amount that prevents one or more signs or symptoms of a particular disease or condition from developing, such as one or more signs or symptoms associated with coronaviral infections.

[0041] Unless otherwise noted, a fusion protein is a recombinant protein containing amino acid sequence from at least two unrelated proteins that have been joined together, via a peptide bond, to make a single protein. Thus, it does not encompass the naturally existing coronaviruses surface antigen that is termed fusion (F) protein as described herein. The unrelated amino acid sequences can be joined directly to each other or they can be joined using a linker sequence. As used herein, proteins are unrelated, if their amino acid sequences are not normally found joined together via a peptide bond in their natural environment (e.g., inside a cell). For example, the amino acid sequences of bacterial enzymes such as *B. stearothermophilus* dihydrolipoyl acyltransferase (E2p) and the amino acid sequences of a soluble coronavirus S glycoprotein are not normally found joined together via a peptide bond.

[0042] Immunogen is a protein or a portion thereof that is capable of inducing an immune response in a mammal, such as a mammal infected or at risk of infection with a pathogen. Administration of an immunogen can lead to protective immunity and/or proactive immunity against a pathogen of interest.

- 5 [0043] Immunogenic composition refers to a composition comprising an immunogenic polypeptide that induces a measurable CTL response against virus expressing the immunogenic polypeptide, or induces a measurable B cell response (such as production of antibodies) against the immunogenic polypeptide.

- [0044] Sequence identity or similarity between two or more nucleic acid sequences, or two or more amino acid sequences, is expressed in terms of the identity or similarity between the sequences. Sequence identity can be measured in terms of percentage identity; the higher the percentage, the more identical the sequences are. Two sequences are "substantially identical" if two sequences have a specified percentage of amino acid residues or nucleotides that are the same (*i.e.*, 60% identity, 10 optionally 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity over a specified region, or, when not specified, over the entire sequence), when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Optionally, the identity exists over a region that is at 15 least about 50 nucleotides (or 10 amino acids) in length, or more preferably over a region that is 100 to 500 or 1000 or more nucleotides (or 20, 50, 200 or more amino acids) in length.

- [0045] Homologs or orthologs of nucleic acid or amino acid sequences possess a relatively high degree of sequence identity/similarity when aligned using standard 25 methods. Methods of alignment of sequences for comparison are well known in the art. Various programs and alignment algorithms are described in: Smith & Waterman, Adv. Appl. Math. 2:482, 1981; Needleman & Wunsch, J. Mol. Biol. 48:443, 1970; Pearson & Lipman, Proc. Natl. Acad. Sci. USA 85:2444, 1988; Higgins & Sharp, Gene, 73:237-44, 1988; Higgins & Sharp, CABIOS 5:151-3, 1989; Corpet et al., Nuc. Acids Res. 16:10881-90, 1988; Huang et al. Computer Appls. in the Biosciences 8, 155-65, 1992; 30 and Pearson et al., Meth. Mol. Bio. 24:307-31, 1994. Altschul et al., J. Mol. Biol.

215:403-10, 1990, presents a detailed consideration of sequence alignment methods and homology calculations.

[0046] SpyCatcher-SpyTag refers to a protein ligation system that is based on based on the internal isopeptide bond of the CnaB2 domain of FbaB, a fibronectin-binding MSCRAMM and virulence factor of *Streptococcus pyogenes*. See, e.g., Terao et al., *J. Biol. Chem.* 2002;277:47428–47435; and Zakeri et al., *Proc. Natl. Acad. Sci. USA.* 2012;109:E690–E697. It utilizes a modified domain from a *Streptococcus pyogenes* surface protein (SpyCatcher), which recognizes a cognate 13-amino-acid peptide (SpyTag). Upon recognition, the two form a covalent isopeptide bond between the side chains of a lysine in SpyCatcher and an aspartate in SpyTag. This technology has been used, among other applications, to create covalently stabilized multi-protein complexes, for modular vaccine production, and to label proteins (e.g., for microscopy). The SpyTag system is versatile as the tag is a short, unfolded peptide that can be genetically fused to exposed positions in target proteins; similarly, SpyCatcher can be fused to reporter proteins such as GFP, and to epitope or purification tags.

[0047] The term "subject" refers to any animal classified as a mammal, e.g., human and non-human mammals. Examples of non-human animals include dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, and etc. Unless otherwise noted, the terms "patient" or "subject" are used herein interchangeably. Preferably, the subject is human.

[0048] The term "treating" or "alleviating" includes the administration of compounds or agents to a subject to prevent or delay the onset of the symptoms, complications, or biochemical indicia of a disease (e.g., A CORONAVIRUS infection), alleviating the symptoms or arresting or inhibiting further development of the disease, condition, or disorder. Subjects in need of treatment include those already suffering from the disease or disorder as well as those being at risk of developing the disorder. Treatment may be prophylactic (to prevent or delay the onset of the disease, or to prevent the manifestation of clinical or subclinical symptoms thereof) or therapeutic suppression or alleviation of symptoms after the manifestation of the disease.

[0049] Vaccine refers to a pharmaceutical composition that elicits a prophylactic or therapeutic immune response in a subject. In some cases, the immune response is a protective immune response. Typically, a vaccine elicits an antigen-specific immune response to an antigen of a pathogen, for example a viral pathogen, or to a cellular

constituent correlated with a pathological condition. A vaccine may include a polynucleotide (such as a nucleic acid encoding a disclosed antigen), a peptide or polypeptide (such as a disclosed antigen), a virus, a cell or one or more cellular constituents. In some embodiments of the invention, vaccines or vaccine immunogens
5 or vaccine compositions are expressed from fusion constructs and self-assemble into nanoparticles displaying an immunogen polypeptide or protein on the surface.

[0050] Virus-like particle (VLP) refers to a non-replicating, viral shell, derived from any of several viruses. VLPs are generally composed of one or more viral proteins, such as, but not limited to, those proteins referred to as capsid, coat, shell,
10 surface and/or envelope proteins, or particle-forming polypeptides derived from these proteins. VLPs can form spontaneously upon recombinant expression of the protein in an appropriate expression system. Methods for producing particular VLPs are known in the art. The presence of VLPs following recombinant expression of viral proteins can be detected using conventional techniques known in the art, such as by electron
15 microscopy, biophysical characterization, and the like. See, for example, Baker et al. (1991) Biophys. J. 60:1445-1456; and Hagensee et al. (1994) J. Virol. 68:4503-4505. For example, VLPs can be isolated by density gradient centrifugation and/or identified by characteristic density banding. Alternatively, cryoelectron microscopy can be performed on vitrified aqueous samples of the VLP preparation in question, and images
20 recorded under appropriate exposure conditions.

[0051] A self-assembling nanoparticle refers to a ball-shape protein shell with a diameter of tens of nanometers and well-defined surface geometry that is formed by identical copies of a non-viral protein capable of automatically assembling into a nanoparticle with a similar appearance to VLPs. Known examples include ferritin (FR),
25 which is conserved across species and forms a 24-mer, as well as *B. stearothermophilus* dihydrolipoyl acyltransferase (E2p), *Aquifex aeolicus* lumazine synthase (LS), and *Thermotoga maritima* encapsulin, which all form 60-mers. Self-assembling nanoparticles can form spontaneously upon recombinant expression of the protein in an appropriate expression system. Methods for nanoparticle production, detection, and
30 characterization can be conducted using the same techniques developed for VLPs.

III. Redesigned coronavirus soluble S immunogens

[0052] The invention provides redesigned or modified soluble S sequences of coronaviruses that can be employed for generating vaccine compositions. The redesigned soluble S trimer immunogens or proteins are stabilized by introducing modifications into the wildtype soluble S sequences of coronaviruses. Some specific wildtype soluble S sequences of specific SARS-CoV, MERS-CoV and SARS-CoV-2 strains or isolates are exemplified herein, e.g., SE ID NOs: 1-3. Due to functional similarity and sequence homology among different isolates or strains of a given coronavirus, redesigned soluble S immunogens derived from other known coronavirus S protein ortholog sequences can also be generated in accordance with the redesign strategy described herein. There are many known coronavirus S protein sequences that have been described in the literature. See, e.g., James et al., J. Mol. Biol. 432:3309-25, 2020; Andersen et al., Nat. Med. 26:450-452, 2020; Walls et al., Cell 180:281-292, 2020; Zhang et al., J. Proteome Res. 19:1351-1360, 2020; Du et al., Expert Opin. Ther. Targets 21:131-143, 2017; Yang et al., Viral Immunol. 27:543-550, 2014; Wang et al., Antiviral Res. 133:165-177, 2016; Bosch et al., J. Virol. 77:8801-8811, 2003; Lio et al., TRENDS Microbiol. 12:106-111, 2004; Chakraborti et al., Virol. J. 2:73, 2005; and Li, Ann. Rev. Virol. 3:237-261, 2016.

[0053] As detailed herein, some redesigned soluble S immunogen polypeptides of the invention contain mutations that can enhance stability of the prefusion S structure. These include mutations that inactivate the S1/S2 cleavage site, and mutations in HR1 that remove any strain in the turn region between HR1 and CH, i.e., to prevent the formation of a straight helix during fusion. In some embodiments, the redesigned soluble S immunogen polypeptides can additionally contain a truncation of the HR2 motif. Truncation of the HR2 domain leads to disruption of the HR1/HR2 fusion core and stabilizes the prefusion S structure.

[0054] Some engineered soluble S immunogen polypeptides are derived from a SARS-CoV-2 virus which caused COVID-19. Some of these polypeptides contain a modified S1/S2 cleavage site. As exemplification, the wildtype soluble S sequence to be used for engineering the SARS-CoV-2 immunogen polypeptides of the invention is shown in SEQ ID NO:3 or N-terminal leader truncated soluble S sequence (SEQ ID NO:14). In other embodiments, the wildtype S sequence to be used can be a variant of SEQ ID NO:3 or 14, e.g., a substantially identical or conservatively modified variant

thereof. Using amino acid numbering based on cryo-EM model PDB ID 6VSB or GenBank accession number MN908947.3 as reference, the modified cleavage site contains ⁶⁸²GSAGSV⁶⁸⁷ (SEQ ID NO:18). Inactivation of this cleavage site can be achieved by a number of sequence alterations (e.g., deletions or substitutions) within or
5 around the site. One mutation that inactivates the cleavage site without otherwise impacting the structure of the protein is substitution of residues ⁶⁸²RRAR⁶⁸⁵ (SEQ ID NO:19) of the cleavage site with GSAG (SEQ ID NO:20), as exemplified herein. In addition to inactivation of the cleavage site, the soluble SARS-CoV-2 immunogen polypeptides can additionally contain a double mutation in the HR1 region that remove
10 strain in the turn region (between HR1 and CH motifs) during fusion by preventing the formation of a straight helix. In various embodiments, this double mutation can be K986G/V987G, K986P/V987P, K986G/V987P or K986P/V987G.

[0055] Additional or alternative to the above-noted mutations that stabilize prefusion S structure, some SARS-CoV-2 immunogen polypeptides of the invention
15 can contain a deletion of a substantial portion of or the entire HR2 domain. Using the exemplified soluble SARS-CoV-2 S sequence SEQ ID NO:3 to illustrate, this deletion can encompass amino acid residues 1150-1208 (SEQ ID NO:9). In various other embodiments, the deletion can be a truncation of the first 35, 40, 45, 50, 55 or more C-terminal residues of SEQ ID NO:3. In still some other embodiments, the C-terminal
20 truncation of the wildtype soluble S sequence can extend beyond the HR2 domain. In some of these embodiments, one or more residues in the region consisting residues 1139-1149 (SEQ ID NO:10) of SEQ ID NO:3 can also be deleted. In some of these embodiments, the C-terminally truncated soluble S sequence can contain an inserted tripeptide motif, GNS, e.g., by substitution of residues 1139-1149 of SEQ ID NO:3
25 with this motif. As described herein, this tripeptide motif functions to increase protein yield when the immunogen polypeptide is displayed on nanoparticles. In some other embodiments, the soluble S sequence can include the N-terminal leader sequence shown in SEQ ID NO:15.

[0056] In some SARS-CoV-2 immunogen polypeptides of the invention, additional
30 mutations of the wildtype soluble S sequence can be introduced to destabilize the postfusion S structure. In some embodiments, one or more proline and/or glycine substitution can be engineered in the region of HR1 that interacts with HR2 to form the

fusion core. These mutations function to disrupt the six-helix-bundle fusion core. In various embodiments, the mutations can include A942P, S943P, A944P, A942G, S943G and A944G. In some embodiments, one or more extra amino acid residues can be inserted into the region of HR1 that interacts with HR2 to form the fusion core.

- 5 Similarly, these insertions also function to disrupt helical pattern of the fusion core. In various embodiments, the insertions can include insertion of G or GS between any residues in A942-A944.

[0057] As detailed in the Examples herein, several specific engineered SARS-CoV-2 spike immunogen polypeptides have demonstrated enhanced immunogenic properties relative to the wildtype SARS-CoV-2 spike ectodomain polypeptide or a well-known SARS-CoV-2 spike polypeptide containing a double-proline mutation (“S2P”). One of these exemplified SARS-CoV-2 spike polypeptides is S2GΔHR2 shown in SEQ ID NO:32. Relative to the wildtype SARS-CoV-2 spike ectodomain sequence (SEQ ID NO:3), S2GΔHR2 contains substitution of the S1/S2 cleavage site sequence
 15 ⁶⁸²RRARSV⁶⁸⁷ (SEQ ID NO:31) replaced with GSAGSV (SEQ ID NO:18). It also contains a K986G/V987G double mutation in HR1. Additionally, it has the HR2 region (E1150-Q1208) removed. As described herein, this engineered SARS-CoV-2 spike immunogen polypeptide produced high-purity trimers, indicating a substantial reduction of spike metastability. It also displayed higher affinity for representative
 20 mAbs specific for the spike in both ELISA and bio-layer interferometry (BLI) assays. When displayed on self-assembling nanoparticle scaffolds, this engineered protein showed satisfactory yield, purity, stability in production, and structural integrity whereas the wild-type spike and the widely used spike with a double proline mutation failed to express on any NP scaffold. The NP displayed S2GΔHR2 also showed
 25 improved antigenicity when tested against a panel of mAbs/Nabs. When examined in vivo, NP vaccines displaying this engineered spike also elicited neutralizing antibody responses that are up-to-10-folds stronger than the control NPs.

[0058] Sequence of engineered SARS-CoV-2 spike protein “S2GΔHR2” (SEQ ID NO:32) is shown below. In the sequence, the N-terminal leader is italicized, the mutated S1/S2 cleavage site is underlined, and the substituted ⁹⁸⁶GG⁹⁸⁷ residues are underlined and italicized.

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLF
 LPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTL
 DSKTQSLNATNVVIKVECFQFCNDPFLGVYHKNKSWMESEFRVYSSA
 NNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLP
 5 QGFSALEPLVDLPIGINITRFQTLALHRSYLT PGDSSSGWTAGAAAYVGYLQ
 PRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKGIYQTSNFRVQPTESI
 VRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCY
 GVSPTKLNDLCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVI
 AWNNSNLD SKVGGNYNYLRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFN
 10 CYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN
 FNFNGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGV
 SVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAG
 CLIGAEHVNNSECDIPIGAGICASYQTQTNSPGSAGSVASQSIIAYTMSLGAEN
 SVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSF
 15 CTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSK
 RSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLCAQKFNGLTVLPPLLTDE
 MIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQK
 LIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
 VLNDILSRLDGGEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKM
 20 SECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAIC
 HDGKAHFPREGVFSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNT
 VYDPLQPELDSFK

- [0059]** Some engineered soluble S immunogen polypeptides are derived from a SARS-CoV virus. Some of these polypeptides contain a modified S1/S2 cleavage site.
- 25 As exemplification, the wildtype soluble S sequence to be used for engineering the SARS-CoV immunogen polypeptides of the invention is shown in SEQ ID NO:1 or N-terminal leader truncated soluble S sequence (SEQ ID NO:7). In other embodiments, the wildtype S sequence to be used can be a variant of SEQ ID NO:1 or 7, e.g., a substantially identical or conservatively modified variant thereof. Using amino acid
- 30 numbering based on UniProt ID P59594 or GenBank accession number NP_828851 as reference, the modified sequence can contain a R667G substitution, which leads to inactivation of the S1/S2 cleavage site. In addition to inactivation of the cleavage site,

- the soluble SARS-CoV immunogen polypeptides can additionally a double mutation in the HR1 region that remove strain in the turn region by preventing the formation of a straight helix during fusion. In various embodiments, this double mutation can be K968G/V969G, K968P/V969P, K968G/V969P or K968P/V969G.
- 5 **[0060]** Additional or alternative to the above-noted mutations that stabilize prefusion S structure, some SARS-CoV immunogen polypeptides of the invention can contain a deletion of a substantial portion of or the entire HR2 domain. Using the exemplified soluble SARS-CoV S sequence SEQ ID NO:1 to illustrate, this deletion can encompass amino acid residues 1132-1190 (SEQ ID NO:9). In various other
- 10 embodiments, the deletion can be a truncation of the first 35, 40, 45, 50, 55 or more C-terminal residues of SEQ ID NO:1. In still some other embodiments, the C-terminal truncation of the wildtype soluble S sequence can extend beyond the HR2 domain. In some of these embodiments, one or more residues in the region consisting residues 1121-1131 (SEQ ID NO:10) of SEQ ID NO:1 can also be deleted. In some of these
- 15 embodiments, the C-terminally truncated soluble S sequence can contain an inserted tripeptide motif, GNS, e.g., by substitution of residues 1121-1131 of SEQ ID NO:1 with this motif. As described herein, this tripeptide motif functions to increase protein yield when the immunogen polypeptide is displayed on nanoparticles. In some other embodiments, the soluble S sequence can have the N-terminal leader sequence
- 20 truncated.
- [0061]** In some SARS-CoV immunogen polypeptides of the invention, additional mutations of the wildtype soluble S sequence can be introduced to destabilize the postfusion S structure. In some embodiments, one or more proline and/or glycine substitution can be engineered in the region of HR1 that interacts with HR2 to form the
- 25 fusion core. These mutations function to disrupt the six-helix-bundle fusion core. In various embodiments, the mutations can include S924P, T925P, A926P, S924G, T925G, and A926G. In some embodiments, one or more extra amino acid residues can be inserted into the region of HR1 that interacts with HR2 to form the fusion core. Similarly, these insertions also function to disrupt helical pattern of the fusion core. In
- 30 various embodiments, the insertions can include insertion of G or GS between any residues in A924-A926.

[0062] Some engineered soluble S immunogen polypeptides are derived from a MERS-CoV virus. Some of these polypeptides contain a modified S1/S2 cleavage site. As exemplification, the wildtype soluble S sequence to be used for engineering the MERS-CoV immunogen polypeptides of the invention is shown in SEQ ID NO:2 or N-terminal leader truncated soluble S sequence (SEQ ID NO:11). In other embodiments, the wildtype S sequence to be used can be a variant of SEQ ID NO:2 or 11, e.g., a substantially identical or conservatively modified variant thereof. Using amino acid numbering based on UniProt ID R9UQ53 or GenBank accession number JX869059.2 as reference, the modified sequence can contain a R748A/R751G double mutation, which leads to inactivation of the S1/S2 cleavage site. In addition to inactivation of the cleavage site, the soluble MERS-CoV immunogen polypeptides can additionally a double mutation in the HR1 region that remove strain in the turn region by preventing the formation of a straight helix during fusion. In various embodiments, this double mutation can be V1060G/L1061G, V1060P/L1061P, V1060G/L1061P or V1060P/L1061G.

[0063] Additional or alternative to the above-noted mutations that stabilize prefusion S structure, some MERS-CoV immunogen polypeptides of the invention can contain a deletion of a substantial portion of or the entire HR2 domain. Using the exemplified soluble MERS-CoV S sequence SEQ ID NO:2 to illustrate, this deletion can encompass amino acid residues 1229-1291 (SEQ ID NO:13). In various other embodiments, the deletion can be a truncation of the first 35, 40, 45, 50, 55, 60 or more C-terminal residues of SEQ ID NO:2. In some other embodiments, the soluble S sequence can have the N-terminal leader sequence truncated.

[0064] In some MERS-CoV immunogen polypeptides of the invention, additional mutations of the wildtype soluble S sequence can be introduced to destabilize the postfusion S structure. In some embodiments, one or more proline and/or glycine substitution can be engineered in the region of HR1 that interacts with HR2 to form the fusion core. These mutations function to disrupt the six-helix-bundle fusion core. In various embodiments, the mutations can include T1013P, T1014P, T1015P, T1013G, T1014G and T1015G. In some embodiments, one or more extra amino acid residues can be inserted into the region of HR1 that interacts with HR2 to form the fusion core. Similarly, these insertions also function to disrupt helical pattern of the fusion core. In

various embodiments, the insertions can include insertion of G or GS between any residues in T1013-T1015.

[0065] In addition to the various substitutions and deletions noted above, the engineered coronavirus soluble S immunogen polypeptides of the invention can further contain a trimerization motif at the C-terminus. Suitable trimerization motifs for the invention include, e.g., T4 fibrin foldon (PDB ID: 4NCV) and viral capsid protein SHP (PDB: 1TD0). T4 fibrin (foldon) is well known in the art, and constitutes the C-terminal 30 amino acid residues of the trimeric protein fibrin from bacteriophage T4, and functions in promoting folding and trimerization of fibrin. See, e.g., Papanikolopoulou et al., J. Biol. Chem. 279: 8991-8998, 2004; and Guthe et al., J. Mol. Biol. 337: 905-915, 2004. Similarly, the SHP protein and its used as a functional trimerization motifs are also well known in the art. See, e.g., Dreier et al., Proc Natl Acad Sci USA 110: E869-E877, 2013; and Hanzelmann et al., Structure 24: 140-147, 2016. The specific foldon and SHP sequences exemplified herein are GYIPEAPRDGQAYVRKDGWVLLSTFL (foldon; SEQ ID NO:26), and EVRIFAGNDPAHTATGSSGSSPTPLTMLDEATGKLVVWDGQKAGSAVGILVPLEGTETALTYKSGTFATEAIHWPEVDEHKKANAFAGSALSHAA (1TD0; SEQ ID NO:27). In some embodiments, the trimerization motif is linked to the redesigned soluble S immunogen polypeptide via a short GS linker. The inclusion of the linker is intended to stabilize the formed trimer molecule. In various embodiments, the linker can contain 1-6 tandem repeats of GS. In some embodiments, an His6-tag can be added to the C-terminus of the trimerization motif to facilitate protein purification, e.g., by using a Nickel column.

[0066] In addition to S2GΔHR2 described above, other exemplary engineered SARS-CoV-2 spike proteins of the invention are shown in SEQ ID NOs:33-37. SEQ ID NO:33 is the sequence of S2GΔHR2 minus its N-terminal leader. Fusions of this sequence to trimerization motif foldon (SEQ ID NO:26) and 1TD0 (SEQ ID NO:27) are shown in SEQ ID NOs:35 and 36, respectively. In each of these two fusion sequences, a restriction site AS is introduced at the C-terminus of the engineered spike protein, which is then connected to the N-terminus of the trimerization motif via a G4S linker. SEQ ID NO:34 is a variant of SEQ ID NO:33 containing a HR1 swap. Specifically, the HR1 region L922-S943 is replaced by the equivalent region from

SARS-CoV-1 spike protein. As exemplified herein, fusions containing this HR1 swapped SARS-CoV-2 spike protein to a trimerization motif (e.g., 1TD0) also displayed satisfactory immunogenic properties only when the HR2 stalk was removed. One such fusion is shown in SEQ ID NO:37. Any of these exemplified sequences, substantially identical sequences or conservatively modified variants thereof can be used in the invention for developing SARS-CoV-2 vaccines, e.g., nanoparticle scaffolded vaccines.

[0067] Sequence of engineered SARS-CoV-2 spike: S2GΔHR2 (minus N-terminal leader) (SEQ ID NO:33):

10 QCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHA
IHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNN
ATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPF
LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDL
PIGINITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENG
15 TITDAVDCALDPLSETKCTLSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPF
EVFNATRFASVYAWNKRISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLCF
TNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKV
GGNYNYLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQP
TNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGV
20 LTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQ
VAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNS
YECDIPIGAGICASYQTQTNSPGSAGSVASQSIIAYTMSLGAENSVAYSNNIAIP
TNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGI
AVEQDKNTQEVFAQVKQIYKTPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNK
25 VTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLA
GTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDG
GEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRV
DFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHHDGKAHFPREG
30 VFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDS
FK

[0068] Sequence of S2GΔHR2-foldon fusion (SEQ ID NO:35). In the sequence, the introduced restriction site AS is italicized and underlined, the G₄S linker is italicized, and the foldon sequence is underlined.

QCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHA
 5 IHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNN
 ATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPF
 LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDL
 PIGINITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENG
 TITDAVDCALDPLSETKCTLSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPLG
 10 EVFNATRFASVYAWNKRISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLCF
 TNVYADSFVIRGDEVQRAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKV
 GGNVNYLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQP
 TNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGV
 LTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQ
 15 VAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSNVFQTRAGCLIGAEHVNS
 YECDIPIGAGICASYQTQNSPGSAGSVASQSIIAYTMSLGAENSVAYSNNIAIP
 TNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGI
 AVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNK
 VTLADAGFIKQYGDCLGDIAARDLCAQKFNGLTVLPPLLTDEMIAQYTSALLA
 20 GTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
 KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLG
 GEAEVQIDRLITGRLQSLQTYVTQQILIRAAEIRASANLAATKMSECVLGQSKRV
 DFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREG
 VFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDS
 25 FKASGGGGSGYIPEAPRDGQAYVRKDGEWVLLSTFL

[0069] Sequence of S2GΔHR2-1TD0 fusion (SEQ ID NO:36). In the sequence, the introduced restriction site AS is italicized and underlined, the G₄S linker is italicized, and the 1TD0 sequence is underlined.

QCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHA
 30 IHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNN
 ATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPF
 LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDL

PIGINITRFQTLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENG
 TITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCFPG
 EVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCF
 TNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKV
 5 GGNYNLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQP
 TNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGV
 LTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQ
 VAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNS
 YECDIPIGAGICASYQTQTNPSGSAGSVASQSIIAYTMSLGAENSVAYSNNIAIP
 10 TNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGI
 AVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNK
 VTLADAGFIKQYGDCLGDIAARDLCAQKFNGLTVLPPLLTDEMIAQYTSALLA
 GTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
 KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLG
 15 GEAEVQIDRLITGRLQSLQTYVTQQLRAAEIRASANLAATKMSECVLGQSKRV
 DFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREG
 VFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDS
 FKASGGGGSEVRIFAGNDPAHTATGSSGISSPTPALTPLMLDEATGKLVVWDGO
KAGSAVGILVLPLEGTETALTYKSGTFATEAIHWPEVDEHKKANAFAGSALS
 20 HAA

[0070] Sequence of HR1 swapped S2GΔHR2 (SEQ ID NO:34): substituting HR1 region from SARs-CoV-1 is underlined.

QCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHA
 IHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNN
 25 ATNVVIKVCFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPF
 LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDL
 PIGINITRFQTLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENG
 TITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCFPG
 EVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCF
 30 TNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKV
 GGNYNLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQP
 TNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGV

LTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQ
 VAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSNVFQTRAGCLIGAEHVNNS
 YECDIPIGAGICASYQTQTNSPGSAGSVASQSIIAYTMSLGAENSVAYSNNNSIAIP
 TNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGI
 5 AVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNK
 VTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLA
 GTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAIS
QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDG
 GEAEVQIDRLITGRLQSLQTYVTQQILIRAAEIRASANLAATKMSECVLGQSKRV
 10 DFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREG
 VFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDS
 FK

[0071] Sequence of fusion of HR1 swapped S2GΔHR2 to 1TD0 (SEQ ID NO:37).
 In the sequence, the introduced restriction site AS is italicized and underlined, the G4S
 15 linker is italicized, and the 1TD0 sequence is underlined.

QCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHA
 IHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNN
 ATNVVIKVCFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPF
 LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDL
 20 PIGINITRFQTLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENG
 TITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCFPG
 EVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLCF
 TNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKV
 GGNYNLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQP
 25 TNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGV
 LTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQ
 VAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSNVFQTRAGCLIGAEHVNNS
 YECDIPIGAGICASYQTQTNSPGSAGSVASQSIIAYTMSLGAENSVAYSNNNSIAIP
 TNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGI
 30 AVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNK
 VTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLA
 GTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAIS

QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLG
 GEAEVQIDRLITGRLQSLQTYVTQQLRAAEIRASANLAATKMSECVLGQSKRV
 DFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREG
 VFVSNGTHWFTVQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDS
 5 FKASGGGGSEVRIFAGNDPAHTATGSSGSSPTPALTPLMLDEATGKLVVWDGO
KAGSAVGILVLPLEGTETALTYYSKSGTFATEAIHWPEVDEHKKANAFAGSALS
HAA

IV. Nanoparticle displayed coronavirus vaccine compositions

10 **[0072]** The invention provides vaccine compositions that contain a heterologous
 scaffold that display at least one immunogen polypeptide or trimer protein derived from
 coronavirus S proteins. In some embodiments, the employed coronavirus S immunogen
 is a stabilized soluble S polypeptide containing various stabilizing mutations described
 above. In some other embodiments, the employed coronavirus immunogen contains or
 15 is derived from the RBD domain of coronavirus S proteins. In the latter embodiments, a
 SpyTag/SpyCatcher ligation system is used. As detailed in the Examples herein, the
 RBD sequence can be fused to a SpyTag motif, and the nanoparticle subunit sequence
 can be fused to a SpyCatcher motif. Alternatively, the RBD sequence can be fused to a
 SpyCatcher motif, and the nanoparticle subunit sequence can be fused to a SpyTag
 20 motif. In exemplified embodiments, the employed RBD sequence can contain the
 sequence shown in any one of SEQ ID NOs:4-6, or a substantially identical or
 conservatively modified variant there. Upon introducing the two constructs expressing
 the SpyTag fusion and the SpyCatcher fusion into host or producer cells, nanoparticle
 vaccines displaying an array of RBD proteins on the surface will be generated as a
 25 result of SpyTag/SpyCatcher mediated ligation of RBD proteins to the self-assembled
 nanoparticles.

[0073] Any heterologous scaffold can be used to present the immunogen protein or
 polypeptide in the construction of the vaccines of the invention. This includes a virus-
 like particle (VLP) such as bacteriophage Q β VLP and nanoparticles. Various
 30 nanoparticle platforms can be employed in generating the vaccine compositions of the
 invention. In general, the nanoparticles employed in the invention need to be formed by
 multiple copies of a single subunit. The nanoparticles are typically ball-like shaped,

and/or have rotational symmetry (e.g., with 3-fold and 5-fold axis), e.g., with an icosahedral structure exemplified herein. Additionally or alternatively, the amino-terminus of the particle subunit has to be exposed and in close proximity to the 3-fold axis, and the spacing of three amino-termini has to closely match the spacing of the carboxyl-termini of the displayed trimeric stabilized soluble S protein.

5 [0074] In various embodiments, the employed self-assembling nanoparticles have a diameter of about 25nm or less (usually assembled from 12, 24, or 60 subunits) and 3-fold axes on the particle surface. Such nanoparticles provide suitable particle platforms to produce multivalent vaccines. In some preferred embodiments, the coronavirus immunogen protein or polypeptide can be presented on self-assembling nanoparticles such as self-assembling nanoparticles derived from ferritin (FR) or E2p as exemplified herein. Other examples of nanoparticles suitable for the invention include nanoparticles derived from I3-01. Well known and routinely used in the art, ferritin is a globular protein found in all animals, bacteria, and plants. As is well known in the art, it acts

10 primarily to control the rate and location of polynuclear Fe(III)₂O₃ formation through the transportation of hydrated iron ions and protons to and from a mineralized core. The globular form of ferritin is made up of monomeric subunit proteins (also referred to as monomeric ferritin subunits), which are polypeptides having a molecule weight of approximately 17-20 kDa. E2p is a redesigned variant of dihydrolipoyl acyltransferase

15 from *Bacillus stearothermophilus* that has been shown to self-assemble into thermostable 60-meric nanoparticle. See, e.g., He et al., Nat. Commun. 7:12041, 2016. Similarly, I3-01 is an engineered protein that can self-assemble into hyperstable nanoparticles. See, e.g., Hsia et al., Nature 535, 136-139, 2016. Sequences of the subunits of these proteins are known in the art. See, e.g., WO2017/192434. More

20 detailed information on the structural and functional properties of the various nanoparticle scaffolds, as well as their use in presenting trimeric protein immunogens, is provided in the art. See, e.g., WO2017/192434, WO2019/089817 and WO2019/241483. In various embodiments, the coronavirus vaccine compositions of the invention can employ any of these known nanoparticles, as well as their conservatively

25 modified variants or variants with substantially identical (e.g., at least 90%, 95% or 30 99% identical) sequences.

[0075] In addition to the nanoparticle sequences noted above, many other nanoparticles or VLPs known in the art may also be used in the practice of the invention. These include, e.g., Aquifex aeolicus lumazine synthase, Thermotoga Maritima encapsulin, Myxococcus xanthus encapsulin, bacteriophage Qbeta virus particle, Flock House Virus (FHV) particle, ORSAY virus particle, and infectious bursal disease virus (IBDV) particle.

[0076] In some exemplary embodiments, the nanoparticle vaccines of the invention contain a nanoparticle subunit sequence as shown in SEQ ID NO:23 (I3-01v9), SEQ ID NO:24 (E2p), or SEQ ID NO:25 (ferritin), a conservatively modified variant or a substantially identical sequence thereof. Typically, C-terminus of the engineered coronavirus immunogen polypeptide is fused to the N-terminus of subunit of the self-assembling nanoparticle (NP). In some embodiments, C-terminus of the engineered coronavirus polypeptide is fused to the nanoparticle subunit sequence of the self-assembling nanoparticle via a GS linker sequence, e.g., G₄S (GGGGS, SEQ ID NO:21) or (G₄S)₂ (GGGSGGGGS; SEQ ID NO:22).

[0077] I3-01v9 subunit sequence (SEQ ID NO:23)
 MKMEELFKKKHIVAVLRANSVEEAKMKALAVFVGGVHLIEITFTVPDADTVIK
 ELSFLKELGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFYM
 PGVMTPTLVKAMKLGHTILKLFPGEVVGPPQFVKAMKGPPFPNVKFPVPTGGVN
 LDNVCEWFKAGVLAVGVGSALVKGITAEVAAKAAAFVEKIRGCTE

[0078] E2p subunit sequence (SEQ ID NO:24)
 AAKPATTEGEFPETREKMSGIRRAIAKAMVHSKHTAPHVTLMDEADVTKLV
 AHRKKFKAIAAEKGIKLTFLPYVVKALVSALREYPVLNTAIDDETEEIIQKHYY
 NIGIAADTDRGLLPVIKHADRKPIFALAEINELAEKARDGKLTPGEMKGASC
 TITNIGSAGGQWFTPVINHPEVAILGIGRIAEKPIVRDGEIVAAPMLALSLSFDHR
 MIDGATAQKALNHIKRLSDPELLLM

[0079] Ferritin sequence (SEQ ID NO:25)
 DIIKLLNEQVNKEMNSSNLYMSMSSWCYTHSLDGAGLFLFDHAAEEYEHAKK
 LIIFLNENNVPVQLTSISAPEHKFEGLTQIFQKAYEHEQHISESINNIVDHAIKSKD
 HATFNFLQWYVAEQHEEEVLFKDILDKIELIGNENHGLYLADQYVKGIAKSRK

[0080] Other than the displayed soluble S immunogen, the nanoparticle vaccine compositions of the invention can include additional motifs for better biological or

pharmaceutical properties. These additional structural components can function to facilitate the immunogen display on the surface of the nanoparticles, to enhance the stability of the displayed immunogens, and/or to improve yield and purity of the self-assembled protein vaccines. In these embodiments, one or more linkers (linker
5 sequences, motifs or moieties) can be used to connect the various structural components in the constructs.

[0081] In some embodiments, the nanoparticle vaccines of the invention can contain the coding sequence of a protein domain that serves to stabilize the immunogen polypeptide, such as the trimerization motif of T4 fibrin (“foldon”) as noted above, or
10 to elevate the immunogen polypeptide from the nanoparticle surface, such as a three-helix bundle (“neck domain”), or to facilitate immunoaffinity purification, such as a protein domain with known binding antibodies. These sequences can be added between the immunogen polypeptide sequence and the nanoparticle subunit sequence.

[0082] In some of these embodiments, a trimerization motif such as foldon and
15 viral capsid protein SHP (PDB: 1TD0) can be added to the C-terminus of the stabilized soluble S protein as exemplified herein. As described above, the trimerization motif can be inserted with a short GS linker to further stabilize the trimer and also to increase the trimer ratio within the total protein yield. In some embodiments, the coding sequence of a polypeptide fragment or motif that serves as an active site for chemical conjugation
20 can be inserted into the construct at an appropriate position. In some embodiments, additional structural components such as a CD4⁺ T-helper epitope or a CD8⁺ T-cell epitope can also be inserted into the nanoparticle construct at an appropriate position. These include, e.g., the PADRE T-helper epitope (AKFVAAWTLKAAA; SEQ ID NO:30) as exemplified herein. In some exemplary embodiments, the T-helper epitope
25 can be inserted to the C-terminus of a locking domain, which is in turn fused to the C-terminus of the NP subunit sequence described below.

[0083] In some embodiments, the nanoparticle vaccines of the invention can contain a locking domain that stabilizes the nanoparticle. The locking domain coding sequence can be fused directly or indirectly to the C-terminus of the nanoparticle
30 subunit coding sequence. The locking domain stabilizes the nanoparticles from the inside so that the nanoparticles presenting the coronavirus immunogen polypeptide can remain intact during manufacture, vaccine formulation, and immunization. The

nanoparticle vaccine immunogens thus constructed have significantly enhanced stability. In general, the locking domain suitable for the invention is a protein subunit that can naturally form a dimer with another protein subunit in solution through non-covalent interactions at the interface. In some preferred embodiments, the two protein subunits can be identical in sequence and form a homodimer. In some other embodiments, the two protein subunits can be different proteins, or two different domains of a single protein derived through engineering, that can form a heterodimer in solution through non-covalent interactions at the interface. Typically, the locking domain is covalently fused to the nanoparticle subunit to which the immunogen polypeptide is linked. Examples of specific locking domains and guidance on the use of a locking domain in the construction of nanoparticle displayed trimeric immunogens can be found in the art, e.g., WO2019/241483. In some exemplary embodiments, the employed LD contains the sequence shown in SEQ ID NO:28 (LD4) or 29 (LD7), a conservatively modified variant or a substantially identical sequence thereof.

[0084] Locking domain LD4 (SEQ ID NO:28):

FSEEQKKALDLAFYFDRRLTPEWRRYLSQRLGLNEEQIERWFRRKEQQIGWSH
PQFEK

[0085] Locking domain LD7 (SEQ ID NO:29):

SPAVDIGDRLDELEKALEALSAEDGHDDVGQRLESLLRRWNSRRAD

[0086] Nanoparticles displaying any of the stabilized coronavirus soluble S protein immunogens described herein (e.g., stabilized SARS-CoV-2 soluble S trimer immunogens) can be constructed by fusing the immunogen polypeptide or subunit of multimeric immunogen protein (e.g., a trimer immunogen) to the subunit of the nanoparticle (e.g., E2p or I3-01 subunit), as well as the other optional or alternative components described herein (e.g., a locking domain or a trimerization motif). To construct the nanoparticle displayed fusion vaccine immunogens of the invention, one or more linker motifs or moieties may be employed to facilitate connection and maintain structural integrity of the different components. Typically, the linker motifs contain short peptide sequences, e.g., GS-rich peptides. In various embodiments, the linkers or linker motifs can be any flexible peptides that connect two protein domains or motifs without interfering with their functions. For example, the employed linker can be a 5-aa G4S linker (SEQ ID NO:21) or a 10-aa (G4S)₂ linker (SEQ ID NO:22) as

exemplified herein to connect (1) a spike protein and a nanoparticle scaffold sequence, (2) a spike protein and a trimerization motif, and/or (3) a nanoparticle scaffold sequence and a locking domain sequence. In some embodiments, a dipeptide GS linker can be used to connect a locking domain to a T epitope as exemplified herein. Detailed procedures for recombinant production of the vaccine compositions of the invention can be based on the protocols described herein and/or other methods that have been described in the art, e.g., He et al., Nat. Comm. 7, 12041, 2016; Kong et al., Nat. Comm. 7, 12040, 2016; He et al., Sci Adv. 4(11):eaau6769, 2018; He et al., bioRxiv, 2020.2008.2022.262634, 2020; WO2017/192434; WO2019/089817 and WO2019/241483.

[0087] Sequences of several specific nanoparticle displayed SARS-CoV-2 spike proteins of the invention are exemplified in SEQ ID NOs:38-40. SEQ ID NO:38 is the fusion sequence containing the leader-less S2GΔHR2 (SEQ ID NO:33) that is connected to nanoparticle sequence I3-01v9 (SEQ ID NO:23) via a (G₄S)₂ linker. This nanoparticle displayed spike further contains at its C-terminus the locking domain LD7 (SEQ ID NO:29) and the PADRE T-epitope (SEQ ID NO:30). SEQ ID NO:39 is the fusion sequence containing the leader-less S2GΔHR2 (SEQ ID NO:33) that is connected to nanoparticle sequence E2p (SEQ ID NO:24) via a G₄S linker. This nanoparticle displayed spike further contains at its C-terminus the locking domain LD4 (SEQ ID NO:28) and the PADRE T-epitope (SEQ ID NO:30). SEQ ID NO:40 is the fusion sequence containing the leader-less S2GΔHR2 (SEQ ID NO:33) that is connected to nanoparticle sequence ferritin (SEQ ID NO:25) via a G₄S linker. In addition to these specifically exemplified fusion constructs, the invention also encompasses SARS-CoV-2 nanoparticle vaccines that contain a subunit sequence that is a substantially identical to or conservatively modified variant of any of these exemplified nanoparticle vaccine sequences.

[0088] Sequence of 3 exemplary SARS-CoV-2 nanoparticle vaccines are shown in SEQ ID NOs:38-40 below. In these sequences, GS linkers (1) between the spike protein and the nanoparticle subunit sequence, (2) between the nanoparticle subunit sequence and the locking domain and (3) between the locking domain and the T-epitope are bolded, the nanoparticle subunit sequence is underlined, introduced restriction site AS

is italicized and underlined, the locking domain sequence is italicized, and the T-epitope sequence is underlined and bolded.

[0089] Sequence of S2GΔHR2-10GS-I3-01v9-LD7-PADRE (SEQ ID NO:38).

QCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHA
 5 IHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNN
 ATNVVIKVCEFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPF
 LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDL
 PIGINITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENG
 TITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPPG
 10 EVFNATRFASVYAWNRRKISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCF
 TNVYADSFVIRGDEVQRAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKV
 GGNYNLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQP
 TNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGV
 LTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQ
 15 VAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSNVFQTRAGCLIGAEHVNN
 YECDIPIGAGICASYQTQTNPSGSAGSVASQSIIAYTMSLGAENSVAYSNNIAIP
 TNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGI
 AVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNK
 VTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLA
 20 GTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
 KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLG
 GEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRV
 DFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREG
 VFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDS
 25 FKASGGGGSGGGGSMKMEELFKKHKIVAVLRANSVEEAKMKALAVFVGGVH
LIEITFTVPDADTVIKELSFLKELGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLD
EEISQFCKEKGVFYMPGVMTPTLVKAMKLGHTILKLFPGEVVGPQFVKAMK
GPFPNVKFVPTGGVNLDNVCEWFKAGVLAVGVGSALVKGTIAEVAAKAAAFV
EKIRGCTEGGGGSSPAVDIGDRLDELEKALEALSAEDGHDDVGQRLESLLRRWNS
 30 RRADGSAKFVAAWTLKAAA

[0090] Sequence of nanoparticle vaccine S2GΔHR2-5GS-E2p-LD4-PADRE (SEQ ID NO:39):

QCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHA
 IHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNN
 ATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPF
 LMDLEGGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDL
 5 PIGINITRFQTLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENG
 TITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPIFG
 EVFNATRFASVYAWNKRISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLCF
 TNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKV
 GGNVNYLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQP
 10 TNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNENGLTGTGV
 LTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQ
 VAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNS
 YECDIPIGAGICASYQTQTNSPGSAGSVASQSIAYTMSLGAENSVAYSNNIAIP
 TNFTISVTTEILPVSMKTSTVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGI
 15 AVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNK
 VTLADAGFIKQYGDCLGDIAARDLCAQKFNGLTVLPPLLTDEMIAQYTSALLA
 GTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
 KIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLG
 GEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRV
 20 DFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDKAHFPREG
 VFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDS
 FKASGGGGSAAAKPATTEGEFPETREKMSGIRRAIAKAMVHSHKHTAPHVTLM
DEADVTKLV AHRKKFK AIAAEKG IKL TFLPYVVKALVSALREYPVLNTAIDDE
TEEIIQKHYYNIGIAADTD RGLLPVVIKHADRKPIFALAEINELAEKARDGKLT
 25 PGEMKGASCTITNIGSAGGQWFTPVINHPEVAILGIGRIAEKPIVRDGEIVAAPM
LALSLSFDHRMIDGATAQKALNHIKRLSDPELLLMGGGGSFSEEQKKALDLAF
YFDRRLTPEWRRYLSQRLGLNEEQIERWFRRKEQQIGWSHPQFEKGSAKFVAAW
TLKAAA

[0091] Sequence of nanoparticle vaccine S2GAHR2-5GS-ferritin (SEQ ID

30 NO:40):

QCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHA
 IHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNN

ATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPF
 LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDL
 PIGINITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENG
 TITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCFPG
 5 EVFNATRFASVYAWNRRKISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCF
 TENVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKV
 GGNYNLYRLFRKSNLKPFERDISTEYQAGSTPCNGVEGFNCYFPLQSYGFQP
 TNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNENGLTGTGV
 LTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQ
 10 VAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSNVFQTRAGCLIGAEHVNS
 YECDIPIGAGICASYQTQTNSPGSAGSVASQSIHAYTMSLGAENSVAYSNNNSIAIP
 TNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGI
 AVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNK
 VTLADAGFIKQYGDCLGDIAARDLCAQKFNGLTVLPPLLDEMIAQYTSALLA
 15 GTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
 KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLG
 GEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRV
 DFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREG
 VFVSNNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDS
 20 FK4SGGGGSDIIKLLNEQVNKEMQSSNLYMSMSSWCYTHSLDGAGLFLFDHA
AEYEHAHKLIIFLNENNVPVQLTSISAPEHKFEGLTQIFQKAYEHEQHISESINNI
VDHAIKSKDHATFNFLQWYVAEQHEEEVLFKDILDKIELIGNENHGLYLADQY
VKGIASRKS

25 V. Polynucleotides and expression constructs

[0092] The stabilized coronavirus soluble S immunogen proteins and the related
 vaccine compositions of the invention are typically produced by first generating
 expression constructs (i.e., expression vectors) that contain operably linked coding
 sequences of the various structural components described herein. Accordingly, in some
 30 related aspects, the invention provides substantially purified polynucleotides (DNA or
 RNA) that encode the immunogens or nanoparticle displayed immunogens as described
 herein. Some polynucleotides of the invention encode one of the engineered spike

immunogen polypeptides described herein, e.g., stabilized SARS-COV-2 soluble S immunogens shown in SEQ ID NOs:32-37. Some polynucleotides of the invention encode the subunit sequence of one of the nanoparticle scaffolded vaccines described herein, e.g., the fusion protein sequences shown in SEQ ID NOs:38-40. While the
5 expressed spike immunogen polypeptides of the invention typically do not contain the N-terminal leader sequence, some of the polynucleotide sequences of the invention additionally encode the leader sequence of the native spike protein. Thus, for example, polynucleotides encoding engineered SARS-COV-2 spike immunogen polypeptides (e.g., SEQ ID NOs:33-37) or the nanoparticle scaffolded polypeptide sequences (e.g.,
10 SEQ ID NO:38-40) can additionally encode the native leader sequence shown in SEQ ID NO:15, or a substantially identical or conservatively modified variant sequence.

[0093] Also provided in the invention are expression vectors that harbor such polynucleotides (e.g., CMV vectors exemplified herein) and host cells for producing the vaccine immunogens (e.g., HEK293F, ExpiCHO, and CHO-S cell lines exemplified
15 herein). The fusion polypeptides encoded by the polynucleotides or expressed from the vectors are also included in the invention. As described herein, the nanoparticle subunit fused soluble S immunogen polypeptides will self-assemble into nanoparticle vaccines that display the immunogen polypeptides or proteins on its surface.

[0094] The polynucleotides and related vectors can be readily generated with
20 standard molecular biology techniques or the protocols exemplified herein. For example, general protocols for cloning, transfecting, transient gene expression and obtaining stable transfected cell lines are described in the art, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, N.Y., (3rd ed., 2000); and Brent et al., *Current Protocols in Molecular Biology*, John Wiley & Sons,
25 Inc. (ingbrou ed., 2003). Introducing mutations to a polynucleotide sequence by PCR can be performed as described in, e.g., *PCR Technology: Principles and Applications for DNA Amplification*, H.A. Erlich (Ed.), Freeman Press, NY, NY, 1992; *PCR Protocols: A Guide to Methods and Applications*, Innis et al. (Ed.), Academic Press, San Diego, CA, 1990; Mattila et al., *Nucleic Acids Res.* 19:967, 1991; and Eckert et al.,
30 *PCR Methods and Applications* 1:17, 1991.

[0095] The selection of a particular vector depends upon the intended use of the fusion polypeptides. For example, the selected vector must be capable of driving

- expression of the fusion polypeptide in the desired cell type, whether that cell type be prokaryotic or eukaryotic. Many vectors contain sequences allowing both prokaryotic vector replication and eukaryotic expression of operably linked gene sequences. Vectors useful for the invention may be autonomously replicating, that is, the vector
- 5 exists extrachromosomally and its replication is not necessarily directly linked to the replication of the host cell's genome. Alternatively, the replication of the vector may be linked to the replication of the host's chromosomal DNA, for example, the vector may be integrated into the chromosome of the host cell as achieved by retroviral vectors and in stably transfected cell lines. Both viral-based and nonviral expression vectors can be
- 10 used to produce the immunogens in a mammalian host cell. Nonviral vectors and systems include plasmids, episomal vectors, typically with an expression cassette for expressing a protein or RNA, and human artificial chromosomes (see, e.g., Harrington et al., *Nat. Genet.* 15:345, 1997). Useful viral vectors include vectors based on lentiviruses or other retroviruses, adenoviruses, adenoassociated viruses,
- 15 Cytomegalovirus, herpes viruses, vectors based on SV40, papilloma virus, HBP Epstein Barr virus, vaccinia virus vectors and Semliki Forest virus (SFV). See, Brent et al., *supra*; Smith, *Annu. Rev. Microbiol.* 49:807, 1995; and Rosenfeld et al., *Cell* 68:143, 1992.
- [0096]** Depending on the specific vector used for expressing the fusion
- 20 polypeptide, various known cells or cell lines can be employed in the practice of the invention. The host cell can be any cell into which recombinant vectors carrying a fusion of the invention may be introduced and wherein the vectors are permitted to drive the expression of the fusion polypeptide is useful for the invention. It may be prokaryotic, such as any of a number of bacterial strains, or may be eukaryotic, such as
- 25 yeast or other fungal cells, insect or amphibian cells, or mammalian cells including, for example, rodent, simian or human cells. Cells expressing the fusion polypeptides of the invention may be primary cultured cells or may be an established cell line. Thus, in addition to the cell lines exemplified herein (e.g., CHO cells), a number of other host cell lines capable well known in the art may also be used in the practice of the
- 30 invention. These include, e.g., various Cos cell lines, HeLa cells, Sf9 cells, HEK293, AtT20, BV2, and N18 cells, myeloma cell lines, transformed B-cells and hybridomas.

[0097] The use of mammalian tissue cell culture to express polypeptides is discussed generally in, e.g., Winnacker, *From Genes to Clones*, VCH Publishers, N.Y., N.Y., 1987. The fusion polypeptide-expressing vectors may be introduced to the selected host cells by any of a number of suitable methods known to those skilled in the art. For the introduction of fusion polypeptide-encoding vectors to mammalian cells, the method used will depend upon the form of the vector. For plasmid vectors, DNA encoding the fusion polypeptide sequences may be introduced by any of a number of transfection methods, including, for example, lipid-mediated transfection (“lipofection”), DEAE-dextran-mediated transfection, electroporation or calcium phosphate precipitation. These methods are detailed, for example, in Brent et al., supra. Lipofection reagents and methods suitable for transient transfection of a wide variety of transformed and non-transformed or primary cells are widely available, making lipofection an attractive method of introducing constructs to eukaryotic, and particularly mammalian cells in culture. For example, LipofectAMINE™ (Life Technologies) or LipoTaxi™ (Stratagene) kits are available. Other companies offering reagents and methods for lipofection include Bio-Rad Laboratories, CLONTECH, Glen Research, Life Technologies, JBL Scientific, MBI Fermentas, PanVera, Promega, Quantum Biotechnologies, Sigma-Aldrich, and Wako Chemicals USA.

[0098] For long-term, high-yield production of recombinant fusion polypeptides, stable expression is preferred. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with the fusion polypeptide-encoding sequences controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and selectable markers. The selectable marker in the recombinant vector confers resistance to the selection and allows cells to stably integrate the vector into their chromosomes. Commonly used selectable markers include neo, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin, et al., J. Mol. Biol., 150:1, 1981); and hygromycin, which confers resistance to hygromycin (Santerre et al., Gene, 30: 147, 1984). Through appropriate selections, the transfected cells can contain integrated copies of the fusion polypeptide encoding sequence.

VI. Pharmaceutical compositions and therapeutic applications

[0099] In another aspect, the invention provides pharmaceutical compositions and related therapeutic methods of using the redesigned coronavirus S immunogens and nanoparticle vaccine compositions as described herein. In various embodiments, the pharmaceutical compositions can contain the engineered viral spike proteins or RBD polypeptides, nanoparticle scaffolded viral spike immunogens, as well as polynucleotide sequences or vectors encoding the engineered viral spike immunogens or nanoparticle vaccines described herein. In some embodiments, the soluble S trimer immunogen for the different viruses (e.g., SARS-COV-2) can be used for preventing and treating the corresponding viral infections. In various other embodiments, the nanoparticle vaccines containing different viral or non-viral immunogens described herein can be employed to prevent or treat the corresponding diseases, e.g., infections caused by the various coronaviruses. Some embodiments of the invention relate to use of the SARS-COV-2 immunogens or vaccines for preventing or treating SARS-COV-2 infections in human subjects. Some embodiments of the invention relate to use of the SARS-CoV immunogens or vaccines for preventing or treating SARS-CoV infections. Some embodiments of the invention relate to use of the MERS-CoV immunogens or vaccines for preventing or treating MERS-CoV infections.

[00100] In the practice of the various therapeutic methods of the invention, the subjects in need of prevention or treatment of a disease or condition (e.g., SARS-COV-2 infection) is administered with the corresponding nanoparticle vaccine, the immunogen protein or polypeptide, or an encoding polynucleotide described herein. Typically, the nanoparticle vaccine, the immunogen protein or the encoding polynucleotide disclosed herein is included in a pharmaceutical composition. The pharmaceutical composition can be either a therapeutic formulation or a prophylactic formulation. Typically, the composition can additionally include one or more pharmaceutically acceptable vehicles and, optionally, other therapeutic ingredients (for example, antiviral drugs). Various pharmaceutically acceptable additives can also be used in the compositions.

[00101] Thus, some of the pharmaceutical compositions of the invention are vaccine compositions. For vaccine compositions, appropriate adjuvants can be additionally included. Examples of suitable adjuvants include, e.g., aluminum hydroxide, lecithin, Freund's adjuvant, MPLTM and IL-12. In some embodiments, the vaccine

compositions or nanoparticle immunogens disclosed herein (e.g., SARS-COV-2 vaccine composition) can be formulated as a controlled-release or time-release formulation. This can be achieved in a composition that contains a slow release polymer or via a microencapsulated delivery system or bioadhesive gel. The various pharmaceutical compositions can be prepared in accordance with standard procedures well known in the art. See, e.g., Remington's Pharmaceutical Sciences, 19th Ed., Mack Publishing Company, Easton, Pa., 1995; Sustained and Controlled Release Drug Delivery Systems, J. R. Robinson, ed., Marcel Dekker, Inc., New York, 1978); U.S. Pat. Nos. 4,652,441 and 4,917,893; U.S. Pat. Nos. 4,677,191 and 4,728,721; and U.S. Pat. No. 4,675,189.

[00102] The pharmaceutical compositions of the invention can be readily employed in a variety of therapeutic or prophylactic applications, e.g., for treating SARS-COV-2 infection or eliciting an immune response to SARS-COV-2 in a subject. In various embodiments, the vaccine compositions can be used for treating or preventing infections caused by a pathogen from which the displayed immunogen polypeptide in the nanoparticle vaccine is derived. Thus, the vaccine compositions of the invention can be used in diverse clinical settings for treating or preventing infections caused by various viruses. As exemplification, a SARS-COV-2 nanoparticle vaccine composition can be administered to a subject to induce an immune response to SARS-COV-2, e.g., to induce production of broadly neutralizing antibodies to the virus. For subjects at risk of developing an SARS-COV-2 infection, a vaccine composition of the invention can be administered to provide prophylactic protection against viral infection. Therapeutic and prophylactic applications of vaccines derived from the other immunogens described herein can be similarly performed. Depending on the specific subject and conditions, pharmaceutical compositions of the invention can be administered to subjects by a variety of administration modes known to the person of ordinary skill in the art, for example, intramuscular, subcutaneous, intravenous, intra-arterial, intra-articular, intraperitoneal, or parenteral routes.

[00103] In general, the pharmaceutical composition is administered to a subject in need of such treatment for a time and under conditions sufficient to prevent, inhibit, and/or ameliorate a selected disease or condition or one or more symptom(s) thereof. In various embodiments, the therapeutic methods of the invention relate to methods of

blocking the entry of a coronavirus (e.g., SARS-CoV, SARS-CoV-2, or MERS-CoV) into a host cell, *e.g.*, a human host cell, methods of preventing the S protein of a coronavirus from binding the host receptor, and methods of treating acute respiratory distress that is often associated with coronavirus infections. In some embodiments, the therapeutic methods and compositions described herein can be employed in combination with other known therapeutic agents and/or modalities useful for treating or preventing coronavirus infections. The known therapeutic agents and/or modalities include, *e.g.*, a nuclease analog or a protease inhibitor (*e.g.*, remdesivir), monoclonal antibodies directed against one or more coronaviruses, an immunosuppressant or anti-inflammatory drug (*e.g.*, sarilumab or tocilizumab), ACE inhibitors, vasodilators, or any combination thereof.

[00104] For therapeutic applications, the compositions should contain a therapeutically effective amount of the nanoparticle immunogen described herein. For prophylactic applications, the compositions should contain a prophylactically effective amount of the nanoparticle immunogen described herein. The appropriate amount of the immunogen can be determined based on the specific disease or condition to be treated or prevented, severity, age of the subject, and other personal attributes of the specific subject (*e.g.*, the general state of the subject's health and the robustness of the subject's immune system). Determination of effective dosages is additionally guided with animal model studies followed up by human clinical trials and is guided by administration protocols that significantly reduce the occurrence or severity of targeted disease symptoms or conditions in the subject.

[00105] For prophylactic applications, the immunogenic composition is provided in advance of any symptom, for example in advance of infection. The prophylactic administration of the immunogenic compositions serves to prevent or ameliorate any subsequent infection. Thus, in some embodiments, a subject to be treated is one who has, or is at risk for developing, an infection (*e.g.*, SARS-COV-2 infection), for example because of exposure or the possibility of exposure to the virus (*e.g.*, SARS-COV-2). Following administration of a therapeutically effective amount of the disclosed therapeutic compositions, the subject can be monitored for an infection (*e.g.*, SARS-COV-2 infection), symptoms associated with an infection (*e.g.*, SARS-COV-2 infection), or both.

- [00106] For therapeutic applications, the immunogenic composition is provided at or after the onset of a symptom of disease or infection, for example after development of a symptom of infection (e.g., SARS-COV-2 infection), or after diagnosis of the infection. The immunogenic composition can thus be provided prior to the anticipated exposure to the virus so as to attenuate the anticipated severity, duration or extent of an infection and/or associated disease symptoms, after exposure or suspected exposure to the virus, or after the actual initiation of an infection. The pharmaceutical composition of the invention can be combined with other agents known in the art for treating or preventing infections by a relevant pathogen (e.g., SARS-COV-2 infection).
- 5
- [00107] The nanoparticle vaccine compositions containing novel structural components as described in the invention (e.g., SARS-COV-2 vaccine) or pharmaceutical compositions of the invention can be provided as components of a kit. Optionally, such a kit includes additional components including packaging, instructions and various other reagents, such as buffers, substrates, antibodies or ligands, such as control antibodies or ligands, and detection reagents. An optional instruction sheet can be additionally provided in the kits.
- 10
- 15

EXAMPLES

- [00108] The following examples are offered to illustrate, but not to limit the present invention.
- 20

Example 1 S antigen stabilization, production, and purification

- [00109] This Example describes redesigned stable and soluble coronavirus S trimers:
- 25
- I. SARS-CoV:
- [00110] The sequence of SARS-CoV S protein was obtained from GenBank with the ID NP_828851. The numbering is based on the UniProt definition with UniPro ID P59594. The soluble S construct is defined as M1-Q1190. Q1190 is immediately upstream of the predicted transmembrane region that starts with the ¹¹⁹¹YIK¹¹⁹³ motif.
- 30
- A truncated soluble S construct is defined as M1-K1131, which is devoid of HR2. The HR2 deletion will disrupt the HR1/HR2 fusion core and stabilize the prefusion S structure. The S construct can be further truncated at Y1120 with a 3-residue “GNS”

- motif (from MERS-CoV S) added to Y1120. This modification will increase protein yield significantly when displayed on nanoparticles.
- [00111]** Uncleaved, prefusion-optimized (UFO) S constructs can be obtained by (a) adding a R667G mutation and a K968P/V969P (or K968G/V969G) double mutation between the HR1 and the central helix (CH). While the R667G mutation aims to remove the S1/ cleavage site, the K968P/V969P double mutation has been shown to stabilize the prefusion S structure. Instead of rigidifying the HR1-turn-CH, the K968G/V969G double mutation aims to remove any strain in the turn region and as a result to stabilize the prefusion S structure.
- [00112]** The UFO S constructs described above can be further stabilized by introducing a proline mutation (S924P, T925P, or A926P), a glycine mutation (S924G, T925G, or A926G), or their combinations to the HR1 region that interacts with HR2 to form a fusion core. These mutations function to disrupt the six-helix-bundle fusion core and destabilize the postfusion S. Other mutations such as inserting one or two residues (e.g. G or GS) in the region S924-A926 to disrupt the helical pattern can also destabilize the postfusion S and prevent conformational change.
- [00113]** Trimerization motifs such as T4 fibrin foldon (PDB ID: 4NCV) and viral capsid protein SHP (PDB: 1TD0) can be further added to the C-terminus of a redesigned S construct described above with a short GS linker in between to stabilize the trimer. In addition, an His6-tag can be added to the C-terminus of the trimerization motif to facilitate protein purification using a Nickel column.
- [00114]** The C-terminus of the redesigned SARS-CoV UFO S constructs can be fused to the N-terminus of a nanoparticle-forming subunit (ferritin 24-mer and two 60-mers, E2p and I3-01) so that the fusion construct, when expressed in appropriate cell lines, can self-assemble into nanoparticles with prefusion S trimers displayed on the nanoparticle surface.
- [00115]** SARS-CoV soluble S sequence (SEQ ID NO:1):
- MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYL
 TQDLFLPFYSNVTGFHTINHTFGNPVIPFKDGIYFAATEKSNVVRGWVFGSTMN
 NKSQSVIIINNSTNVIRACNFELCDNPFFAVSKPMGTQHTMIFDNAFNCTFEY
 ISDAFSLDVSEKSGNFKHLREFVFKNKDGFYVYKGYQPIDVVRDLPSGFNTLK
 PIFKLPLGINITNFRAILTAFAQDIWGTSAAYFVGYLKPTTFMLKYDENGIT

DAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVRFPNITNLCPFGEV
 FNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLCFSN
 VYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATST
 GNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCPPALNCYWPLNDYGFYTT
 5 TGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTP
 SSKRFQPFQFGRDVSDFDTSVRDPKTSEILDISPCAFGGVSVITPGTNASSEVA
 VLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYEC
 DIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITT
 EVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDR
 10 NTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLAD
 AGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGTAT
 AGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQE
 SLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAE
 VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCG
 15 KGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVFVF
 NGTSWFITQRNFFSPQIITDNTFTVSGNCDVVIGIINNTVYDPLQPELDSFKEELD
 KYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYE
 Q

- [00116] SARS-CoV soluble S sequence minus N-terminal leader (SEQ ID NO:7):
 20 residues 14-1190 of SEQ ID NO:1.
 [00117] Leader sequence (SEQ ID NO:8): MFIFLLFLTLTSG (residues 1-13 of
 SEQ ID NO:1).
 [00118] HR2 sequence (SEQ ID NO:9): residues 1132-1190 of SEQ ID NO:1
 EELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELG
 25 KYEQ
 [00119] Further truncated C-terminal sequence (SEQ ID NO:10):
 DPLQPELDSFK (residues 1121-1131 of SEQ ID NO:1).

- II. MERS-CoV:
 30 [00120] The sequence of MERS-CoV S protein was obtained from GenBank with
 the ID JX869059.2. The amino acid numbering is based on the UniProt definition with
 UniPro ID R9UQ53.

[00121] The soluble S construct is defined as M1-Y1291. Y1291 is immediately upstream of the predicted transmembrane region that starts with the ¹²⁹²YNK¹²⁹⁴ motif. A truncated soluble S construct is defined as M1-S1226, which is devoid of HR2. The HR2 deletion will disrupt the HR1/HR2 fusion core and stabilize the prefusion S structure.

[00122] Uncleaved, prefusion-optimized (UFO) S constructs can be obtained by adding a R748A/R751G double mutation and a V1060P/L1061P (or V1060G/L1061G) double mutation. While the R748A/R751G double mutation aims to remove the S1/S2 cleavage site, the V1060P/L1061P double mutation has been shown to stabilize the prefusion S structure. Instead of rigidifying the HR1-turn-CH, the V1060G/L1061G double mutation aims to remove any strain in the turn region and as a result to stabilize the prefusion S structure.

[00123] The UFO S constructs can be further stabilized by introducing a proline mutation (T1013P, T1014P, or T1015P), a glycine mutation (T1013G, T1014G, or T1015G), or their combinations to the HR1 region that interacts with HR2 to form a fusion core. These mutations will disrupt the six-helix-bundle fusion core and destabilize the postfusion S. Other mutations such as inserting one or two residues (e.g. G or GS) in the region T1013-T1015 to disrupt the helical pattern will also destabilize the postfusion S and prevent conformational change.

[00124] Trimerization motifs such as T4 fibrin foldon (PDB ID: 4NCV) and viral capsid protein SHP (PDB: 1TD0) can be added to the C-terminus of the redesigned UFO S constructs described above with a short GS linker in between to stabilize the trimer. An His6-tag can be added to the C-terminus of the trimerization motif to facilitate protein purification by a Nickel column.

[00125] The C-terminus of the redesigned MERS-CoV UFO S constructs can be fused to the N-terminus of a nanoparticle-forming subunit so that the fusion construct, when expressed in appropriate cell lines, can self-assemble into nanoparticles with prefusion S trimers displayed on the nanoparticle surface.

[00126] MERS-CoV soluble S (SEQ ID NO:2):
 MIHSVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQQTFFDKTWPRPIDVSKAD
 GIYPQGRITYSNITITYQGLFPYQGDHGDYVYSAGHATGTTTPQKLFVANYSQ
 DVKQFANGFVVRIGAAANSTGTVIISPSTSATIRKIYPAFMLGSSVGNFSDGKM

GRFFNHTLVLLPDGCGTLLRAFYCILEPRSGNHCPAGNSYTSFATYHTPATDCS
 DGNYNRNASLNSFKEYFNLRNCTFMYTYNITEDEILEWFGITQTAQGVHLFSSR
 YVDLYGGNMFQFATLPVYDTIKYYSIIPHSIRSIQSDRKAWAAFYVYKLQPLTF
 LLDFSVDGYIRRAIDCGFNDLSQLHCSYESFDVESGVYSVSSFEAKPSGSVVEQ
 5 AEGVECDFSPLLSGTPPQVYNFKRLVFTNCNYNLTKLLSLFSVNDFTCSQISPAA
 IASNCYSSLILDYFSYPLSMKSDLSVSSAGPISQFNYKQSFSNPTCLILATVPHNL
 TTITKPLKYSYINKCSRLLSDDRTEVPQLVNANQYSPCVSIVPSTVWEDGDYR
 KQLSPLEGGGWLVASGSTVAMTEQLQMGFGITVQYGTDTNSVCPKLEFANDT
 KIASQLGNCVEYSLYGVSGRGVFQNCTAVGVRQQRFFVYDAYQNLVGYYSDD
 10 GNYYCLRACVSPVSVIYDKETKTHATLFGSVACEHISSTMSQYSRSTRSMLKR
 RDSTYGPLQTPVGCVLGLVNSSLFVEDCKLPLGQSLCALPDTPTSTLTPRSVRSVP
 GEMRLASIAFNHPIQVDQLNSSFYFKLSIPTNFSFGVTQEYIQTTIQKVTVDCKQY
 VCNGFQKCEQLLREYGQFCSKINQALHGANLRQDDSVRNLFASVKSSQSSPIIP
 GFGGDFNLTLLEPVSISTGSRARSASIEDLLFDKVTIADPGYMQGYDDCMQQGP
 15 ASARDLICAQYVAGYKVLPLMDVNMEAAYTSSLLGSIAGVGWTAGLSSFAAI
 PFAQSIFYRLNGVGITQQVLSSENQKLIANKFNQALGAMQTGFTTTNEAFQKVQ
 DAVNNNAQALSKLASELSNTFGAISASIGDIIQRLDVLEQDAQIDRLINGRLTTL
 NAFVAQQLVRSESAALSAQLAKDKVNECVKAQSKRSGFCGQGTHIVSFVVNA
 PNGLYFMHVGYYPSNHIEVVSAYGLCDAANPTNCIAPVNGYFIKTNNTRIVDE
 20 WSYTGSSFYAPEPITSLNTKYVAPQVTYQNISTNLPPLLGNSTGIDFQDELDEF
 FKNVSTSI PNFGSLTQINTTLLDLTYEMLSLQQVVKALNESYIDLKELGNYTY
[00127] MERS-CoV soluble S sequence minus N-terminal leader (SEQ ID NO:11):
 residues 18-1291 of SEQ ID NO:2.
[00128] Leader sequence (SEQ ID NO:12): MIHSVFLLMFLLTPTES (residues 1-
 25 17 of SEQ ID NO:2).
[00129] HR2 sequence (SEQ ID NO:13): residues 1227-1291 of SEQ ID NO:2
 TGIDFQDELDEFKKNVSTSI PNFGSLTQINTTLLDLTYEMLSLQQVVKALNESYI
 DLKELGNYTY

30 III. SARS-CoV-2:

- [00130] The sequence of SARS-CoV-2 S protein was obtained from GenBank with the ID MN908947.3. The amino acid numbering is based on the cryo-EM model with PDB ID 6VSB.
- [00131] The soluble S construct is defined as M1-Q1208. Q1208 is immediately upstream of the predicted transmembrane region that starts with the ¹²⁰⁹YIK¹²¹¹ motif. A truncated soluble S construct is defined as M1-K1149, which is devoid of HR2. The HR2 deletion will disrupt the HR1/HR2 fusion core and stabilize the prefusion S structure. The S construct can be further truncated at Y1138 with a 3-residue “GNS” motif (from MERS-CoV S) added to Y1138. This modification will increase protein yield significantly when displayed on nanoparticles.
- [00132] The uncleaved, prefusion-optimized (UFO) soluble S construct is defined as M1-Q1208 with the modified S1/S2 cleavage site ⁶⁸²GSAGSV⁶⁸⁷ (SEQ ID NO:18) and a K986P/V987P (or K986G/V987G) double mutation. SARS-CoV-2 has a 4-aa insertion prior to the S1/S2 cleavage site, ⁶⁸¹PRRA⁶⁸⁴, which will enhance the cleavage efficiency. The modification ⁶⁸²GSAGSV⁶⁸⁷ (SEQ ID NO:18) aims to remove the S1/S2 cleavage site, and the K986P/V987P double mutation has been shown to stabilize the prefusion S structure. Instead of rigidifying the HR1-turn-CH, the K986G/V987G double mutation aims to remove any strain in the turn region and as a result to stabilize the prefusion S structure.
- [00133] The SARS-CoV-2 UFO S constructs in (b) can be further stabilized by introducing a proline mutation (A942P, S943P, and A944P), a glycine mutation (A942G, S943G, and A944G), or their combinations to the HR1 region that interacts with HR2 to form a fusion core. These mutations will disrupt the six-helix-bundle fusion core and destabilize the postfusion S. Other mutations such as inserting one or two residues (e.g. G or GS) in the region A942-A944 to disrupt the helical pattern will also destabilize the postfusion S and prevent conformational change.
- [00134] Trimerization motifs such as T4 fibrin foldon (PDB ID: 4NCV) and viral capsid protein SHP (PDB: 1TD0) can be added to the C-terminus of a redesigned S construct in (b) and (c) with a short GS linker in between to stabilize the trimer. An His6-tag can be added to the C-terminus of the trimerization motif to facilitate protein purification by a Nickel column.

[00135] The C-terminus of the redesigned SARS-CoV-2 UFO S construct described above can be fused to the N-terminus of a nanoparticle-forming subunit so that the fusion construct, when expressed in appropriate cell lines, can self-assemble into nanoparticles with prefusion S trimers displayed on the nanoparticle surface.

5 **[00136]** SARS-CoV-2 soluble S (SEQ ID NO:3):

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDL
 FLPPFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTT
 LDSKTQSLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSS
 ANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDL
 10 PQGFSALEPLVDLPIGINITRFQTLALHRSYLT PGDSSSGWTAGAAAYVGYL
 QPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTES
 IVRFPNITNLCPFGEVFNATRFASVYAWNRRKISNCVADYSVLYNSASFSTFKC
 YGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGC
 VIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGF
 15 NCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKC
 NFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSF
 GGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRA
 GCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAE
 NSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGS
 20 FCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPS
 KRSFIEDLLFNKVT LADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDE
 MIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQK
 LIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
 VLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKM
 25 SECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAIC
 HDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNT
 VYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVNIQKEIDRLNEVA
 KNLNESLIDLQELGKYEQ

[00137] SARS-CoV-2 soluble S sequence minus N-terminal leader (SEQ ID
 30 NO:14); residues 14-1208 of SEQ ID NO:3.

[00138] Leader sequence (SEQ ID NO:15): MFVFLVLLPLVSS (residues 1-13 of
 SEQ ID NO:3).

[00139] HR2 sequence (SEQ ID NO:9): residues 1150-1208 of SEQ ID NO:3
EELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELG
KYEQ

[00140] Further truncated C-terminal sequence (SEQ ID NO:10):

5 DPLQPELDSFK (residues 1121-1131 of SEQ ID NO:3)

Example 2 Designed RBD domains of coronaviruses

I. SARS-CoV RBD based vaccines:

[00141] The sequence of SARS-CoV S protein and amino acid numbering are noted
10 above. The SARS-CoV RBD used in RBD-based vaccine design is defined as P317-
D518 (see SEQ ID NO:4). Specifically, a trimerization motif, the viral capsid protein
SHP (PDB: 1TD0), can be added to the C-terminus of SARS-CoV RBD with a short
5GS linker in between to stabilize RBD in a trimeric conformation. A His6-tag can be
added to the C-terminus of the trimerization motif with a 1GS linker to facilitate
15 purification.

[00142] SpyTag and SpyCatcher can be attached to SARS-CoV RBD and a
nanoparticle subunit in different combinations to facilitate the multivalent display of
RBD on nanoparticle. For example, if the C-terminus of RBD is fused to the N-
terminus of SpyTag with a 5GS linker, the C-terminus of SpyCatcher can be fused to
20 the N-terminus of a nanoparticle subunit with a 5GS linker to create a pair. SpyTag and
SpyCatcher can be switched in these two constructs to create a different pair. SpyTag or
SpyCatcher can also be fused to the N-terminus of RBD with a 5GS linker. When the
two constructs are introduced into and expressed in the host cells, a recombinant
vaccine protein will be formed through the binding between the SpyTag and
25 SpyCatcher motifs.

[00143] SARS-CoV RBD (SEQ ID NO:4)

PNITNLCPFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVS
ATKLNLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLA
WNTRNIDATSTGNVYKYRYLRHGKLRPFERDISNVPFSPDGKPCPTPALNCY
30 WPLNDYGFYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTD

[00144] SpyTag: VPTIVMVDAYKRYK (SEQ ID NO:16).

[00145] SpyCatcher: SEQ ID NO:17

AMVTTLSGLSGEQGPSGDMTTEEDSATHIKFSKRDEDGRELAGATMELRDSSG
 KTISTWISDGHVKDFYLYPGKYTFVETAAPDGYEVATAITFTVNEQGQVTVNG
 EATKGDAHTAS

5 II. MERS-CoV RBD based vaccines:

[00146] The sequence of MERS-CoV S protein and amino acid numbering are noted above. The MERS-CoV RBD used in RBD-based vaccine design is defined as E382-K587 (see SEQ ID NO:5). A trimerization motif, the viral capsid protein SHP (PDB: 1TD0), can be added to the C-terminus of MERS-CoV RBD with a short 5GS linker in between to stabilize RBD in a trimeric conformation. A His6-tag can be added to the C-terminus of the trimerization motif with a 1GS linker to facilitate purification.

[00147] SpyTag and SpyCatcher can be attached to MERS-CoV RBD and a nanoparticle subunit in different combinations to facilitate the multivalent display of RBD on nanoparticle. For example, if the C-terminus of RBD is fused to the N-terminus of SpyTag with a 5GS linker, the C-terminus of SpyCatcher can be fused to the N-terminus of a nanoparticle subunit with a 5GS linker to create a pair. SpyTag and SpyCatcher can be switched in these two constructs to create a different pair. SpyTag or SpyCatcher can also be fused to the N-terminus of RBD with a 5GS linker. When the two constructs are introduced into and expressed in the host cells, a recombinant vaccine protein will be formed through the binding between the SpyTag and SpyCatcher motifs.

[00148] MERS-CoV RBD (SEQ ID NO:5)
 ECDFSPLLSGTPPQVYNFKRLVFTNCNYNLTKLLSLFSVNDFTCSQISPAAIASN
 CYSSLILDYFSYPLSMKSDLSVSSAGPISQFNYKQSFSNPTCLILATVPHNLTTIT
 25 KPLKYSYINKCSRLLSDDRTEVPQLVNANQYSPCVSIVPSTVWEDGDYYRKQL
 SPLEGGGWLVASGSTVAMTEQLQMFGITVQYGTDTNSVCPK

[00149] SpyTag: VPTIVMVDAYKRYK (SEQ ID NO:16).

[00150] SpyCatcher: SEQ ID NO:17:
 AMVTTLSGLSGEQGPSGDMTTEEDSATHIKFSKRDEDGRELAGATMELRDSSG
 30 KTISTWISDGHVKDFYLYPGKYTFVETAAPDGYEVATAITFTVNEQGQVTVNG
 EATKGDAHTAS

III. SARS-CoV-2 RBD based vaccines:

[00151] The sequence of SARS-CoV-2 S protein and amino acid numbering are noted above. The SARS-CoV-2 RBD used in RBD-based vaccine design is defined as P330-N532 (see SEQ ID NO:6). A trimerization motif, the viral capsid protein SHP (PDB: 1TD0), can be added to the C-terminus of SARS-CoV-2 RBD with a short 5GS linker in between to stabilize RBD in a trimeric conformation. A His6-tag can be added to the C-terminus of the trimerization motif with a 1GS linker to facilitate purification.

[00152] SpyTag and SpyCatcher can be attached to SARS-CoV-2 RBD and a nanoparticle subunit in different combinations to facilitate the multivalent display of RBD on nanoparticle. For example, if the C-terminus of RBD is fused to the N-terminus of SpyTag with a 5GS linker, the C-terminus of SpyCatcher can be fused to the N-terminus of a nanoparticle subunit with a 5GS linker to create a pair. SpyTag and SpyCatcher can be switched in these two constructs to create a different pair. SpyTag and SpyCatcher can also be fused to the N-terminus of RBD with a 5GS linker. When the two constructs are introduced into and expressed in the host cells, a recombinant vaccine protein will be formed through the binding between the SpyTag and SpyCatcher motifs.

[00153] SARS-CoV-2 RBD (SEQ ID NO:6):

PNITNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLYNSASFSTFKCYGVS
PTKLNLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAW
NSNNLDSKVGGNLYLYRLFRKSNLKPFRDISTEIYQAGSTPCNGVEGFNCYF
PLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTN

[00154] SpyTag: VPTIVMVDAYKRYK (SEQ ID NO:16).

[00155] SpyCatcher: SEQ ID NO:17:

AMVTTLSGLSGEQGPSGDMTTEEDSATHIKFSKRDEDGRELAGATMELRDSSG
KTISTWISDGHVKDFYLYPGKYTFVETAAPDGYEVATAITFTVNEQGQVTVNG
EATKGDAHTAS

Example 3 Production and purification of S trimers and RBD domains

[00156] Cell line: All constructs were expressed in HEK293 F cells and ExpiCHO cells, with ExpiCHO showing significantly higher yield.

[00157] Purification: After transient expression, S antigens were purified from the supernatant using three methods including the His6-tag/nickel column and antigen-

specific antibody column. The S230 and CR3022 antibody columns can be used to purify SARS-CoV S and RBD antigens and nanoparticles. The MCA1 antibody column can be used to purify MERS-CoV S and RBD antigens and nanoparticles; The CR3022 antibody column can be used to purify SARS-CoV-2 S and RBD antigens and nanoparticles.

Example 4 Rational design of scaffolded RBD trimer and RBD-presenting SApNPs
[00158] We hypothesized that RBD attached to a trimeric scaffold can mimic the “RBD-up” spike conformation and elicit NAb to block ACE2 binding. To test this possibility, we designed a fusion construct containing SARS-CoV-1/2 RBD, a short 5-aa G4S linker (with a 2-aa restriction site), and a trimeric viral capsid protein, SHP (PDB: 1TD0). Structural modeling showed that the three tethered RBDs form a triangle of 92 Å (measured for L492), which is 14 and 18 Å wider than the SARS-CoV-1 “two-RBD-up” spike (PDB: 6CRX, measured for L478) and the MERS-CoV “all-RBD-up” spike (PDB: 5X59, measured for L506), respectively, allowing NAb access to each RBD. We then developed an immunoaffinity chromatography (IAC) column to facilitate tag-free vaccine purification. Previously, NAb-derived IAC columns have been used to purify HIV-1 Env trimers/NPs, hepatitis C virus (HCV) E2 cores/NPs, and Ebola virus (EBOV) GP trimers/NPs. It was reported that a SARS-CoV-1 NAb, CR3022, can bind SARS-CoV-2 RBD (Tian et al., *Emerg. Microbes Infect.* 9, 382-385, 2020). The SARS-CoV-2 RBD/CR3022 structure revealed the epitope shared by two SARS-CoVs and alluded to a breathing motion of the spike that enables CR3022 binding to RBD. Here, we examined the utility of CR3022 in IAC columns. The SARS-CoV-1/2 RBD-5GS-1TD0 constructs were transiently expressed in 100-ml ExpiCHO cells and purified on a CR3022 antibody column prior to size-exclusion chromatography (SEC) using a Superdex 200 10/300 GL column. While the SARS-CoV-1 RBD construct showed both aggregate (8.6 ml) and trimer (12.7 ml) peaks in the SEC profile, the SARS-CoV-2 RBD construct produced a single trimer peak at 12.8 ml. In sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE), a monomer band of ~37 kD and a trimer band of ~100 kD were observed under reducing and non-reducing conditions, respectively. Antigenicity was assessed for the two scaffolded RBD trimers in enzyme-linked immunosorbent assay (ELISA) after

- CR3022/SEC purification. RBD-specific NAbs targeting SARS-CoV-1 (CR3022, m396, 80R, and S230) and SARS-CoV-2 (B38, CB6, S309 from a SARS survivor, and P2B-2F6), were tested in ELISA. Overall, similar half maximal effective concentration (EC_{50}) values were observed for the two RBD trimers binding to their respective NAbs.
- 5 The SARS-CoV-1 RBD trimer showed greater binding affinity for CR3002 than its SARS-CoV-2 counterpart with a 1.3-fold difference in the EC_{50} value. Of the SARS-CoV-2 NAbs, B38 yielded a similar EC_{50} value to CR3022. The kinetics of antibody binding was measured using biolayer interferometry (BLI). Overall, all tested antibodies exhibited a fast on-rate but with visible differences in their off-rates. For
- 10 example, B38 showed a faster off-rate than other SARS-CoV-2 NAbs, while CR3022, the antibody used to purify SARS-CoV-1/2 RBD proteins, exhibited comparable kinetic profiles.
- [00159]** We then hypothesized that the SpyTag/SpyCatcher (or simply SPY) system can be used to conjugate RBD to SApNPs to create multivalent RBD vaccines capable
- 15 of eliciting a more potent NAb response. The 13-aa SpyTag spontaneously reacts with the SpyCatcher protein to form an irreversible isopeptide bond. The SPY system has been used to attach antigens to SApNPs and VLPs. Here, SpyTag was fused to the C terminus of RBD, while SpyCatcher was fused to the N terminus of an SApNP subunit, both with a 5-aa G4S linker. This design was first tested for FR. We compared two
- 20 production strategies – co-expression of RBD-5GS-SpyTag and SpyCatcher-5GS-FR versus supernatant mix after separate expression – and performed purification on a CR3022 column. Protein obtained from transient transfection in 50-ml ExpiCHO cells was analyzed by SEC on a Superose 6 10/300 GL column. Both production strategies produced a peak (12 ml) corresponding to SApNPs. While the SARS-CoV-2 construct
- 25 notably outperformed its SARS-CoV-1 counterpart in particle yield (0.6-1.0 mg versus 0.3-0.5 mg after CR3022/SEC), supernatant mix appeared to be superior to co-expression. Nonetheless, the results suggest that both strategies can be used to produce RBD-conjugated SApNPs in Good manufacturing practice (GMP)-compatible Chinese hamster ovary (CHO) cells. Antigenicity was assessed for SEC-purified RBD-5GS-
- 30 SPY-5GS-FR SApNPs. In ELISA, RBD-presenting SApNPs showed slightly improved mAb binding, as indicated by lower EC_{50} values. In BLI, a more pronounced effect of

multivalent display on antigenicity was observed, showing notably increased binding signals and plateaued dissociation.

[00160] Structural integrity of various RBD SApNPs was analyzed by negative stain EM. For SARS-CoV-1, an RBD-10GS-FR construct was included for comparison that produced very few SApNPs. In contrast, the RBD-5GS-SPY-5GS-FR construct produced SApNPs with visible surface decorations. For SARS-CoV-2, the purified RBD-5GS-SPY-5GS-FR SApNPs, irrespective of the production strategy, showed morphologies corresponding to well-formed nanoparticles. Following a similar strategy, SARS-CoV-1/2 RBDs were also attached to a multilayered I3-01v9 SApNP (He et al., *bioRxiv*, 2020.2008.2022.262634, 2020). Despite the modest yield, large SApNPs were observed in EM.

[00161] In summary, we demonstrate the utility of the SPY system for rapid development of RBD-based SApNP vaccines. Compared to the two-component RBD SApNPs, the SPY-linked RBD SApNPs presented here may be more advantageous in terms of stability and manufacturability.

Example 5 Rational design of prefusion spike through minimizing metastability

[00162] It is imperative to understand the SARS-CoV-2 spike metastability, and based on which, to design the optimal spike as a vaccine antigen. We first created the His-tagged, uncleaved spike ectodomain (S_{ECTO}) constructs for SARS-CoV-1/2, both containing the 2P mutation and a trimerization motif (1TD0) fused to the C terminus with a G4S linker. The two constructs were transiently expressed in 50-ml ExpiCHO cells followed by purification on a Nickel column or a CR3022 column. The S2P_{ECTO}-5GS-1TD0-His₆ protein was characterized by SEC on a Superose 6 10/300 GL column. After Nickel column, both S2P_{ECTO} constructs showed a trimer peak (~12 ml) with shoulders to the left and right indicative of aggregate and dimer/monomer species, respectively. CR3022 purification resulted in a consistent trimer peak and less dimer/monomer species. We then tested a pair of S_{ECTO} constructs containing a double glycine mutation (V1060G/L1061G, termed 2G). The 2G mutation had little effect on the SARS-CoV-1 spike but produced an abnormal SEC profile and showed no yield for the SARS-CoV-2 spike after purification by Nickel and CR3022 columns, respectively. Lastly, we tested a pair of S2G variants without the HR2 stalk (E1150-Q1208), termed

S2GΔHR2. Deletion of the HR2 stalk restored the SARS-CoV-2 trimer peak and reduced aggregates for both SARS-CoVs, as shown by the SEC profiles upon CR3022 purification.

[00163] We hypothesized that HR2 may be a key determinant of SARS-CoV spike metastability. It is possible that the interactions between HR1 and HR2 of two neighboring spikes may facilitate the pre-to-post-fusion transition in addition to ACE2 binding and S1 dissociation. Given the extensive mutations in HR1 (9 in total) compared to SARS-CoV-1, we sought to examine the role of HR1 in SARS-CoV-2 spike metastability with two HR1-swapped spike constructs. Interestingly, while HR1 swapping proved ineffective, deletion of the HR2 stalk once again restore the trimer peak. Therefore,, S2GΔHR2 provides a general spike design for SARS-CoV-1/2 and perhaps other CoVs. Four separate production runs of SARS-CoV-2 S2GΔHR2-5GS-1TD0 in 300-ml ExpiCHO cells resulted in nearly identical SEC profiles with a trimer yield of 0.8-1.0 mg. Blue native polyacrylamide gel electrophoresis (BN-PAGE) confirmed the purity of the S2GΔHR2 spike across SEC fractions. Antigenicity was assessed for freshly produced SARS-CoV-2 S2P_{ECTO} and S2GΔHR2 spikes. In ELISA, the S2GΔHR2 spike showed consistently higher affinity for the five representative mAbs than the S2P_{ECTO} spike. When tested against three newly identified NABs, C105 and CC12.1/CC12.3, the two spikes yielded similar EC₅₀ values. In BLI, the S2GΔHR2 spike showed higher binding signals than the S2P_{ECTO} spike at the highest concentration, while exhibiting similar binding kinetics. The use of NAB P2B-2F6 for spike purification resulted in much higher trimer yield with similar purity to the CR3022 column across SEC fractions.

[00164] Together, we demonstrate that deletion of the HR2 stalk may improve spike properties and S2GΔHR2 may provide a better spike antigen that improves on the 2P mutation.

Example 6 Rational design of single-component and multilayered SApNPs

[00165] Although it was proven possible to conjugate trimeric SARS-CoV-2 spikes to an SApNP using the SPY system, the random and irreversible chemical linking will result in irregular display with unoccupied but spatially occluded anchoring sites on the surface. The SPY system is perhaps more suitable for individual antigens such as RBD.

We therefore set out to obtain rational design of single-component, multilayered, self-assembling spike nanoparticles, using the gene fusion approach.

[00166] Native SARS-CoV-2 virions present both pre- and post-fusion spikes on the surface. Our vaccine strategy aims to develop single-component, multilayered SApNPs that each present 8 or 20 stable S2GAHR2 spikes to the immune system. To explore this possibility, we modeled the S2GAHR2 spike on FR with a 5-aa G4S linker, on E2p with a 5-aa G4S linker, and on I3-01v9 with a 10-aa (G4S)₂ linker, resulting in large SApNPs with diameters of 47.9 nm, 55.9 nm, and 59.3 nm, respectively. The three S2GAHR2 SApNP constructs were transiently expressed in 400-ml ExpiCHO cells followed by CR3022 purification and SEC on a Superose 6 10/300 GL column. Three separate production runs generated highly consistent SEC profiles for all three constructs, despite the variation of low-m.w. impurities observed for FR and E2p SApNPs. Following CR3022/SEC purification, we obtained on average 0.3-0.4 mg, 0.15-0.25 mg, and 0.3-0.35 mg SApNP for S2GAHR2-5GS-FR, S2GAHR2-5GS-E2p-LD4-PADRE (or E2p-L4P), and S2GAHR2-10GS-I3-01v9-LD7-PADRE (or I3-01v9-L7P). Overall, S2GAHR2-10GS-I3-01v9-L7P appeared to be the best performer in terms of yield, purity, and stability in production.

[00167] The structural integrity of CR3022/SEC-purified SApNPs was characterized by negative stain EM, which showed well-formed particles in the range of 40-60nm, consistent with the modeling. Spikes could be readily recognized on the SApNP surface. Antigenicity of S2GAHR2-presenting SApNPs was assessed using the same panel of mAbs/NAbs. In ELISA, three SApNPs showed slightly improved binding to some, but not all, of the antibodies compared to the individual spike. In BLI, we observed a clear correlation between peak binding signal and antigen valency, with a ranking of E2p/I3-01v9 > FR > spike. Display on the two 60-mers significantly improved antibody binding compared to the 24-mer, FR.

[00168] In summary, these large VLP-size SApNPs with 8 or 20 spikes on the surface provide promising vaccine candidates for *in vivo* evaluation.

Example 7 SARS-CoV-1/2 vaccine-induced binding antibody response

[00169] Selected SARS-CoV-1/2 RBD- and spike-based immunogens were evaluated in BALB/c mice to evaluate vaccine-induced antibody response (Fig. 2).

Groups of five mice were immunized four times with three-week intervals. All vaccine antigens were formulated with AddaVax, an oil-in-water emulsion adjuvant, except for the I3-01v9 SApNP, which was formulated with aluminum phosphate (AP). We first performed a longitudinal analysis of binding antibody response as measured by half maximal effective dilution (ED₅₀) in the two SARS-CoV-2 RBD vaccine groups. Results from the study are shown in Figure 3. The RBD SApNP (RBD-5GS-SPY-5GS-FR) elicited significantly higher ED₅₀ titers than the scaffolded RBD trimer (RBD-5GS-1TD0) at w2 and w5, irrespective of the coating antigen, and showed a *P* value of 0.0009 at w8 when RBD was coated. Compared to the stabilized spike (S2GΔHR2-5GS-1TD0), the RBD SApNP elicited significantly higher ED₅₀ titers against RBD at w2, w5, and w8, demonstrating a strong “epitope-focusing” effect. Mouse sera bound the SARS-CoV-1 spike with lower ED₅₀ titers than the SARS-CoV-2 spike but with similar patterns). We then performed a longitudinal analysis of binding antibody response induced by two SARS-CoV-2 spikes, S2PECTO-5GS-1TD0 and S2GΔHR2-5GS-1TD0, and three SApNPs each displaying 8 or 20 S2GΔHR2 spikes. The S2GΔHR2 spike elicited 2~3-fold higher average ED₅₀ titers than the S2PECTO spike irrespective of the coating antigen, showing greater immunogenicity (of note, to facilitate a fair comparison, mouse sera from the two spike groups were tested against their respective spikes).

[00170] Three SApNPs exhibited different temporal patterns depending on the coating antigen. When spike was used as the coating antigen, the I3-01v9 group showed a steady increase in average ED₅₀ titer over time. This SApNP yielded the highest average ED₅₀ titer at two time points, w2 and w8, and significantly outperformed the S2PECTO spike at all time points. The smaller FR exhibited a similar temporal pattern with lower average ED₅₀ titers, which are still significantly higher than that of the S2PECTO group. Among the three SApNPs, E2p registered the lowest average ED₅₀ titer at w2 and reached the highest at w5, which decreased slightly at w8. In terms of RBD-specific response, the five groups showed a clear ranking based on their average ED₅₀ titers, which remained consistent across time points. At w2, I3-01v9 elicited an average ED₅₀ titer of 175, whereas all other spike-based vaccine groups showed little RBD-specific response. At w5 and w8, S2GΔHR2 elicited higher ED₅₀ titers (on average by 2-fold) than S2PECTO, while all three SApNPs outperformed the individual S2GΔHR2

spike with a ranking of ED₅₀ titers correlated with their size (FR<E2p<I3-01v9). Sera reacted with the SARS-CoV-1 spike similarly, albeit at a lower level.

- [00171] Lastly, we compared binding antibody responses induced by three SARS-CoV-1 vaccines – the S2P_{ECTO} spike (S2P_{ECTO}-5GS-1TD0), the scaffolded RBD trimer (RBD-5GS-1TD0), and the RBD SApNP (RBD-5GS-SPY-5GS-FR). Based on the ED₅₀ titers, the SARS-CoV-1 S2P_{ECTO} spike appeared to be more immunogenic than the SARS-CoV-2 S2GΔHR2 spike, whereas the SARS-COV-1 RBD SApNP was less advantageous than its SARS-COV-2 counterpart. Serum reactivity with the SARS-CoV-2 S2P_{ECTO} spike was observed for all three SARS-CoV-1 vaccine groups.
- [00172] Our results thus indicate that RBD SApNPs can elicit RBD-specific antibody titers at a similar or higher level compared to the spike. Furthermore, the S2GΔHR2 spike is more immunogenic than the widely used S2P_{ECTO} spike, in addition to its superior in-vitro properties. The large multilayered E2p and I3-01v9 SApNPs are the best performers among all the spike-based vaccines, consistent with the findings in our previous HIV-1, HCV, and Ebola vaccine studies.

Example 8 SARS-CoV-1/2 vaccine-induced NAb response

- [00173] One major goal in COVID-19 vaccine development is to generate a potent NAb response that can protect against SARS-CoV-2 infection. Pseudoparticle (SARS-CoV-1/2-pp) neutralization assays were used to evaluate serum NAb responses elicited by different vaccine candidates. As indicated by the results shown in Figure 4, we first performed a longitudinal analysis of NAb response as measured by half maximal inhibitory dilution (*ID*₅₀) in the two SARS-CoV-2 RBD vaccine groups. The RBD SApNP elicited low titers of NAb response against autologous SARS-CoV-2 at as early as w2 and retained its advantage at the two later time points, suggesting that such RBD SApNP vaccines can elicit a rapid NAb response upon vaccination. The scaffolded RBD trimer group showed the lowest average ID₅₀ titer at w5 but a NAb response comparable to that induced by the stabilized S2GΔHR2 spike at w8. A somewhat different pattern was observed in the SARS-CoV-1-pp assay. At the first time point, w2, no vaccine groups showed any detectable heterologous NAb response. At w5 and w8, the S2GΔHR2 spike elicited a more potent SARS-CoV-1 NAb response than both

RBD-based vaccines, suggesting that non-RBD epitopes may contribute to the cross-neutralization.

[00174] We then performed a longitudinal analysis of NAb responses induced by five spike-based vaccines. In terms of autologous neutralization, no spike-based vaccine elicited any SARS-CoV-2-pp NAb response at w2 after the first injection. But a consistent pattern was observed for serum neutralization at w5 and w8: the S2P_{ECTO} spike used in almost all vaccine candidates currently in human trials showed the lowest average ID₅₀ titers, 879 and 2481 at w5 and w8, respectively; the newly designed S2GΔHR2 spike induced a stronger NAb response than the S2P_{ECTO} spike with 2.8-6.7-fold higher average ID₅₀ titers, confirming the beneficial effect of the 2P-to-2G substitution and deletion of the HR2 stalk; among the three SApNPs, E2p was the best performer at w5, showing an average ID₅₀ titer of 8493 that is 9.7-fold higher than S2P_{ECTO} and 1.4-fold higher than S2GΔHR2, while I3-01v9 showed the most potent NAb response at w8 with an average ID₅₀ titer of 17351 that is 7-fold and 2.5-fold higher than S2P_{ECTO} and S2GΔHR2, respectively. A similar temporal pattern of NAb response was observed in the heterologous SARS-CoV-1-pp assay. It is worth noting that the I3-01v9 SApNP elicited a SARS-CoV-1 NAb response with an average ID₅₀ titer of 351 at w2, whereas all other groups showed no detectable neutralization. Nonetheless, our results suggest that the SARS-CoV-2 S2GΔHR2-based vaccines, particularly SApNPs, may provide protection against both SARS-CoV-1/2. Lastly, we performed a longitudinal analysis of NAb responses induced by three SARS-CoV-1 vaccines. In the autologous SARS-CoV-1-pp assay, the S2P_{ECTO} spike and the RBD SApNP induced significantly more potent NAb responses than the scaffolded RBD trimer at w2 and w5 and all three vaccine groups showed similar ID₅₀ titers at w8. However, heterologous SARS-CoV-2 neutralization was below or at the baseline level for three SARS-CoV-1 vaccines at w2, w5, and w8.

[00175] Our results thus demonstrate the advantage of the S2GΔHR2 spike and S2GΔHR2-presenting SApNPs with respect to the S2P_{ECTO} spike in NAb elicitation. While the SARS-CoV-2 RBD- and S2GΔHR2-presenting SApNPs are comparable in eliciting SARS-CoV-2-specific NAb response, the latter may provide a broader protection against SARS-associated CoVs.

Example 9 T-cell response and vaccine safety

- [00176]** While the humoral immunity is required to block host-virus interaction and prevent viral infection, the cellular immunity is essential for eliminating infected host cells to control viral infection. Emerging evidence indicates that an early T-cell response, as well as T-cell memory, is critical for protection against SARS-CoV-2. However, COVID-19 vaccines must induce a CD4⁺ T helper 1 (Th1), but not Th2-type, T-cell response, as the latter has been linked to vaccine-associated enhancement of respiratory disease (VAERD). In addition, T follicular helper cells (Tfh) play an important role in the maturation and production of NAbs. Therefore, understanding T-cell response is crucial for the development of an effective and safe COVID-19 vaccine.
- [00177]** Interferon (IFN)- γ -producing Th1 cells are important for generating an optimal antibody response and for the induction of cellular immunity to clear viruses. We first examined the impact of various SARS-CoV-2 vaccine formulations on the induction of CD4⁺ Th1 responses specific to the spike protein at w11 – two weeks after the fourth immunization, when memory T cells had already developed in spleen. Mouse splenocytes from the S2P group and two SApNP groups (E2p and I3-01v9) were analyzed by flow cytometry (FC) using naïve samples as a negative control. Results from the studies are shown in Figure 5. I3-01v9 induced approximately 1.5- and 2.3-fold higher frequency of IFN- γ -producing CD4⁺ Th1 cells than S2P and E2p, respectively. Notably, following re-stimulation with the respective antigens for as few as 4 hours, both E2p and I3-01v9 groups produced ~2-fold higher frequency of CD107a-producing cytolytic CD4⁺ T cells than the S2P and naïve control groups. IFN- γ /IL-4 (interleukin-4) double-positive cells are memory CD4⁺ T cells that have acquired the ability to produce IL-4 while still retaining the ability to produce IFN- γ under Th1 conditions. It appeared that I3-01v9 induced 3- and 5-fold more IFN- γ /IL-4 double-positive memory CD4⁺ T cells than S2P and E2p. These results suggest that I3-01v9 can induce both potent CD4⁺ Th1 cells and IFN- γ /IL-4 double-positive memory CD4⁺ T cells.
- [00178]** In addition, I3-01v9 induced more IFN- γ /GM-CSF (granulocyte-macrophage colony-stimulating factor) double-positive CD8⁺ effector T cells than S2P and E2p, as shown in Figure 5. These data suggest that protective CD8⁺ T cell responses were also generated in mice immunized with the I3-01v9 SApNP. Of note,

CD8⁺ T cells derived from mice immunized with I3-01v9, rather than those with S2P and E2p, acquired the ability to rapidly produce IFN- γ upon antigen re-stimulation, suggesting the generation of I3-01v9-responsive effector/memory T cells. Together, our findings indicate that the S2GAHR2 I3-01v9 SApNP can induce potent T-cell responses in mice consisting of CD4⁺ Th1 cells, IFN- γ /IL-4 double-positive memory CD4⁺ T cells, and CD8⁺ T cells, thus providing protective cellular immunity required for an effective vaccine against SARS-CoV-2.

Example 10 Some exemplified methods

10 **[00179]** Design, expression and purification of SARS-CoV-2 RBD and spike antigens: The spike (S) genes of the SARS-CoV-1 isolate Tor2 (GenBank accession #: NC_004718) and the SARS-CoV-2 isolate Wuhan-Hu-1 (GenBank accession #: MN908947) were used to design all the RBD and spike constructs following codon-optimization for expression in mammalian cells. The RBD sequence is defined as P317-15 D518 and P330-N532 for SARS-CoV-1 and 2, respectively. The S_{ECTO} sequence is defined as M1-Q1190 and M1-Q1208 for SARS-CoV-1 and 2, respectively. To remove the S1/S2 cleavage site, an R667G mutation and a ⁶⁸²GSAGSV⁶⁸⁷ (SEQ ID NO:18) modification were introduced in the SARS-CoV-1 and 2 spikes, respectively. The 2P (or 2G) mutation was made to K968/V969 and K986/V987 in the SARS-CoV-1 and 2 spikes, respectively. The SARS-CoV-2 C-terminal region (E1150-Q1208) containing the HR2 stalk was removed from S2G_{ECTO}, resulting in an HR2-deleted spike construct termed S2GAHR2. The viral capsid protein SHP (PDB: 1TD0) was used as a trimerization motif in spike constructs for immunization, whereas the foldon domain from the bacteriophage T4 fibrin (PDB: 1RFO) was used in coating spike antigens for ELISA to mask the 1TD0-derived antibody response. All constructs were transiently expressed in ExpiCHO cells (Thermo Fisher). Briefly, ExpiCHO cells were thawed and incubated with ExpiCHOTM Expression Medium (Thermo Fisher) in a shaker incubator at 37 °C, 135 rpm and 8% CO₂. When the cells reached a density of 10×10⁶ ml⁻¹, ExpiCHOTM Expression Medium was added to reduce cell density to 6×10⁶ ml⁻¹ for transfection. The ExpiFectamineTM CHO/plasmid DNA complexes were prepared for 100-ml transfection in ExpiCHO cells following the manufacturer's instructions. For a given construct, 100 μ g of plasmid and 320 μ l of ExpiFectamineTM CHO reagent were

mixed in 7.7 ml of cold OptiPRO™ medium (Thermo Fisher). After the first feed on day one, ExpiCHO cells were cultured in a shaker incubator at 33 °C, 115 rpm and 8% CO₂ following the Max Titer protocol with an additional feed on day five (Thermo Fisher). Culture supernatants were harvested 13 to 14 days after transfection, clarified by centrifugation at 4000 rpm for 25 min, and filtered using a 0.45 µm filter (Thermo Fisher). The CR3022 antibody column was used to extract SARS-CoV-1/2 antigens from the supernatants, which was followed by SEC on a Superdex 200 10/300 GL column (for scaffolded RBD trimer) or a Superose 6 10/300 GL column (for RBD-SPY-NPs, spikes, and spike-presenting NPs). For comparison, His-tagged S_{ECTO}-5GS-ITD0 spike protein was extracted from the supernatants using an immobilized Ni Sepharose™ Excel column (GE Healthcare) and eluted with 500 mM Imidazole prior to SEC. Protein concentration was determined using UV₂₈₀ absorbance with theoretical extinction coefficients.

[00180] *Blue native* polyacrylamide gel electrophoresis: SARS-CoV-2 spikes and spike-presenting NPs were analyzed by *blue native* polyacrylamide gel electrophoresis (BN-PAGE) and stained with Coomassie blue. The proteins were mixed with sample buffer and G250 loading dye and added to a 4-12% Bis-Tris NativePAGE™ gel (Life Technologies). BN-PAGE gels were run for 2 to 2.5 hours at 150 V using the NativePAGE™ running buffer (Life Technologies) according to the manufacturer's instructions.

[00181] Enzyme-linked immunosorbent assay: Each well of a Costar™ 96-well assay plate (Corning) was first coated with 50 µl PBS containing 0.2 µg of the appropriate antigens. The plates were incubated overnight at 4 °C, and then washed five times with wash buffer containing PBS and 0.05% (v/v) Tween 20. Each well was then coated with 150 µl of a blocking buffer consisting of PBS, 40 mg ml⁻¹ blotting-grade blocker (Bio-Rad), and 5% (v/v) FBS. The plates were incubated with the blocking buffer for 1 hour at room temperature, and then washed five times with wash buffer. For antigen binding, antibodies were diluted in the blocking buffer to a maximum concentration of 5 µg ml⁻¹ followed by a 10-fold dilution series. For each antibody dilution, a total of 50 µl volume was added to the appropriate wells. For mouse sample analysis, serum or plasma was diluted by 20-fold in the blocking buffer and subjected to a 10-fold dilution series. For each sample dilution, a total of 50 µl volume was added

to the wells. Each plate was incubated for 1 hour at room temperature, and then washed 5 times with PBS containing 0.05% Tween 20. For antibody binding, a 1:5000 dilution of goat anti-human IgG antibody (Jackson ImmunoResearch Laboratories, Inc), or for mouse sample analysis, a 1:3000 dilution of horseradish peroxidase (HRP)-labeled goat anti-mouse IgG antibody (Jackson ImmunoResearch Laboratories), was then made in the wash buffer (PBS containing 0.05% Tween 20), with 50 μ l of this diluted secondary antibody added to each well. The plates were incubated with the secondary antibody for 1 hour at room temperature, and then washed 5 times with PBS containing 0.05% Tween 20. Finally, the wells were developed with 50 μ l of TMB (Life Sciences) for 3-5 min before stopping the reaction with 50 μ l of 2 N sulfuric acid. The resulting plate readouts were measured at a wavelength of 450 nm. Of note, the w2 serum binding did not reach the plateau (or saturation) to allow for accurate determination of ED₅₀ titers. Nonetheless, the ED₅₀ values at w2 were derived by setting the lower/upper constraints of OD₄₅₀ at 0.0/3.2 to facilitate the comparison of different vaccine groups at the first time point.

[00182] Bio-layer interferometry: The kinetics of SARS-CoV-1/2 vaccine antigens, RBD versus RBD-presenting NPs as well as spike versus spike-presenting NPs, binding to a panel of known antibodies was measured using an Octet RED96 instrument (FortéBio, Pall Life Sciences). All assays were performed with agitation set to 1000 rpm in FortéBio 1 $\times$ kinetic buffer. The final volume for all the solutions was 200 μ l per well. Assays were performed at 30 °C in solid black 96-well plates (Geiger Bio-One). For all antigens with the exception of S2GΔHR2-NPs, 5 μ g ml⁻¹ of antibody in 1 $\times$ kinetic buffer was loaded onto the surface of anti-human Fc Capture Biosensors (AHC) for 300 s. For S2GΔHR2-NPs, anti-human Fc Quantitation Biosensors (AHQ) were used. A 60 s biosensor baseline step was applied prior to the analysis of the association of the antibody on the biosensor to the antigen in solution for 200 s. A two-fold concentration gradient of antigen, starting at 950 nM for scaffolded RBD trimers, 37 nM for RBD-5GS-SPY-5GS-FR NP, 150 nM for spike trimers, and 9/3.5/3.5 nM for S2GΔHR2 presented on FR/E2p/I3-01v9 NPs, was used in a titration series of six. The dissociation of the interaction was followed for 300 s. Correction of baseline drift was performed by subtracting the mean value of shifts recorded for a sensor loaded with antibody but not incubated with antigen and for a sensor without antibody but incubated

with antigen. Octet data were processed by FortéBio's data acquisition software v.8.1. Experimental data were fitted with the binding equations describing a 2:1 interaction to achieve optimal fitting. Of note, S2GΔHR2 trimer binding was also measured using AHQ to facilitate the comparison of antibody binding with S2GΔHR2-presenting NPs.

- 5 **[00183]** Electron microscopy (EM) assessment of nanoparticle constructs: The initial EM analysis of RBD and S2GΔHR2-presenting NPs was conducted at the Core Microscopy Facility at The Scripps Research Institute. Briefly, NP samples were prepared at the concentration of 0.01 mg/ml. Carbon-coated copper grids (400 mesh) were glow-discharged and 8 µL of each sample was adsorbed for 2 min. Excess sample
10 was wicked away and grids were negatively stained with 2% uranyl formate for 2 min. Excess stain was wicked away and the grids were allowed to dry. Samples were analyzed at 80 kV with a Talos L120C transmission electron microscope (Thermo Fisher) and images were acquired with a CETA 16M CMOS camera.

- [00184]** Animal immunization and sample collection: Similar immunization
15 protocols have been reported in our previous NP vaccine studies. Briefly, the Institutional Animal Care and Use Committee (IACUC) guidelines were followed with animal subjects tested in the immunization study. Eight-week-old BALB/c mice were purchased from The Jackson Laboratory and housed in ventilated cages in environmentally controlled rooms at The Scripps Research Institute, in compliance with
20 an approved IACUC protocol and AAALAC (Association for Assessment and Accreditation of Laboratory Animal Care) International guidelines. Mice were immunized at weeks 0, 3, 6, and 9 with 200 µl of antigen/adjuvant mix containing 50 µg of vaccine antigen and 100 µl of adjuvant, AddaVax or Adju-Phos (InvivoGen), via the intraperitoneal (i.p.) route. Blood was collected two weeks after each immunization.
25 All bleeds were performed through the retro-orbital sinus using heparinized capillary tubes into EDTA-coated tubes. Samples were diluted with an equal volume of PBS and then overlaid on 4.5 ml of Ficoll in a 15 ml SepMate™ tube (STEMCELL Technologies) and spun at 1200 RPM for 10 min at 20 °C to separate plasma and cells. The plasma was heat inactivated at 56 °C for 30 min, spun at 1200 RPM for 10 min,
30 and sterile filtered. The cells were washed once in PBS and then resuspended in 1 ml of ACK Red Blood Cell lysis buffer (Lonza). After washing with PBS, peripheral blood mononuclear cells (PBMCs) were resuspended in 2 ml of Bambanker Freezing Media

(Lymphotec). Spleens were also harvested and ground against a 70- μ m cell strainer (BD Falcon) to release the splenocytes into a cell suspension. Splenocytes were centrifuged, washed in PBS, treated with 5 ml of ACK lysing buffer (Lonza), and frozen with 3ml of Bambanker freezing media. Sera were heat inactivated for ELISA binding and pseudovirus neutralization assays.

[00185] SARS-CoV-1/2 pseudovirus neutralization assay: Pseudoparticle (SARS-CoV-1/2-pp) neutralization assays were utilized to assess the neutralizing activity of previously reported antibodies and vaccine-induced murine antibody response. SARS-CoV-1/2-pps were generated by co-transfection of HEK293T cells with the HIV-1 pNL4-3.lucR-E- plasmid (the NIH AIDS reagent program) and the expression plasmid encoding the S gene of SARS-CoV-1 isolate Tor2 (GenBank accession #: NC_004718) and the SARS-CoV-2 isolate Wuhan-Hu-1 (GenBank accession #: MN908947) at a 4:1 ratio by lipofectamine 3000 (Thermo Fisher Scientific). After 48 to 72 hours, SARS-CoV-1/2-pps were collected from the supernatant by centrifugation at 4000 rpm for 10 min, aliquoted, and stored at -80 °C before use. The mAbs at a starting concentration of 0.1-10 μ g/ml, or mouse serum at a starting dilution of 100-fold, were mixed with the supernatant containing SARS-CoV-1/2-pps and incubated for 1 hour at 37°C in white solid-bottom 96-well plate (Corning). A 3-fold dilution series was used in the assay. The HEK293T-hACE2 cell line (catalogue#: NR-52511) and the vector pcDNA3.1(-) containing the SARS-CoV-2 spike gene (catalogue#: NR52420) were obtained from BEI RESOURCES and used in pseudovirus neutralization assays. Briefly, HEK293T-hACE2 cells at 1×10^4 were added to each well and the plate was incubated at 37°C for 48 hours. After incubation, overlying media was removed, and cells were lysed. The firefly luciferase signal from infected cells was determined using the Bright-Glo Luciferase Assay System (Promega) according to the manufacturer's instructions. Data were retrieved from a BioTek microplate reader with Gen 5 software, the average background luminescence from a series of uninfected wells was subtracted from each well, and neutralization curves were generated using GraphPad Prism 8.4.3, in which values from wells were compared against a well containing SARS-CoV-1/2-pp only.

The same HIV-1 vectors pseudotyped with the murine leukemia virus (MLV) Env gene, termed MLV-pps, were produced in HEK293T cells and included in the neutralization assays as a negative control.

[00186] Dendritic cell (DC) production: Mouse bone marrow (BM) was cultured in RPMI 1640 medium containing 10% fetal bovine serum and recombinant mouse Flt3L (50 ng/mL) and SCF (10 ng/ml) for 9 days. To induce DC activation, immature DCs were incubated with lipopolysaccharide (LPS, 100 ng/mL), R848 (Resiquimod, 100 ng/mL) or CpG (ODN 1585, 1 μ M) overnight, which activated Toll-like receptor (TLR)4, TLR7/8 or TLR9 signaling, respectively. Cells were harvested for experiments. pDCs were sorted to isolate CD11c+B220+ cells using FACS cell sorter and magnetic beads (Miltenyi-Biotech, CA).

[00187] Antibodies (Abs) and flow cytometry analysis: All antibodies used for immunofluorescence staining were purchased from eBioscience (San Diego, CA), BioLegend (San Diego, CA) or BD Biosciences (San Jose, CA). Magnetic microbead-conjugated Abs and streptavidin were purchased from Miltenyi-Biotech (Auburn, CA). Recombinant human IL-2 protein was purchased from R&D Systems (Minneapolis, MN). Recombinant mouse Flt3 ligand (Flt3L) and mouse SCF were purchased from Shenandoah Biotech (Warwick, PA). Cells were stained with appropriate concentrations of mAbs. Dead cells were excluded using Fixable Viability Dye from eBioscience (San Diego, CA). Flow cytometry analyses were performed using LSRII (BD Bioscience, CA) and Canto cytometers (Becton Dickinson, NJ). Cell were sorted on BD FACSAria II (BD Bioscience, CA).

[00188] T cell culture and activation: Splenic mononuclear cells from immunized mice were cultured in the presence of DCs pulsed with or without S2P, E2P and I3-01 in complete IMDM medium containing IL-2 (5.0 ng/ml). Cells were collected 16 hours later for intracellular cytokine staining and flow cytometric analysis.

[00189] Statistics: In antibody titer analysis, comparison of different vaccine groups was performed in GraphPad Prism 8.4.3 using the two-tailed unpaired Student's *t* test. In the T cell analysis, comparison of means was done using the two-tailed unpaired Student's *t* test, ANOVA and then post-hoc *t* test. P values of 0.05 or less were considered significant.

[00190] The invention thus has been disclosed broadly and illustrated in reference to representative embodiments described above. It is understood that various

modifications can be made to the present invention without departing from the spirit and scope thereof.

- [00191]** It is further noted that all publications, sequence accession numbers, patents and patent applications cited herein are hereby expressly incorporated by reference in
- 5 their entirety and for all purposes as if each is individually so denoted. Definitions that are contained in text incorporated by reference are excluded to the extent that they contradict definitions in this disclosure.