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(54) Title: HEPATITIS C VIRUS IMMUNOGENIC COMPOSITIONS COMPRISING AS AN ADJUVANT A CYCLIC DINUCLEOTIDE OR AN ARCHAEOsome AND METHODS OF USE THEREOF

(57) Abstract: The present disclosure provides immunogenic compositions comprising: a) hepatitis C virus (HCV) E1E2 heterodimers, HCV E2, or HCV E1; and b) an adjuvant, where the adjuvant is a cyclic dinucleotide or an archaeosome. The present disclosure provides methods of inducing an immune response in an individual to HCV, the methods comprising administering to an individual an effective amount of an immunogenic composition of the present disclosure.



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HEPATITIS C VIRUS IMMUNOGENIC COMPOSITIONS COMPRISING AS AN ADJUVANT A CYCLIC DINUCLEOTIDE OR AN ARCHAEOSOME AND METHODS OF USE THEREOF

CROSS-REFERENCE

- [0001] This application claims the benefit of U.S. Provisional Patent Application No. 62/406,770, filed October 11, 2016, which application is incorporated herein by reference in its entirety.

INTRODUCTION

- [0002] Hepatitis C virus (HCV) is a blood-borne pathogen that is estimated to infect 150-200 million people worldwide. Infection by HCV may be non-symptomatic, and can be cleared by patients, sometimes without medical intervention. However, the majority of patients develop a chronic HCV infection, which may lead to liver inflammation, scarring, and even to liver failure or liver cancer. In the United States alone, over 3 million people have a chronic infection.
- [0003] The HCV virion contains a positive-sense single stranded RNA genome of about 9.5 kb. The genome encodes a single polyprotein of 3,010 to 3,030 amino acids. The structural proteins comprise a core protein forming the viral nucleocapsid and two envelope glycoproteins, E1 and E2.
- [0004] A vaccine based on the recombinant envelope glycoproteins (rE1E2) from a single genotype 1a strain (HCV-1) protected chimpanzees from chronic infection following homologous and heterologous genotype 1a (gt1a) viral challenge (reviewed in Houghton, M Immunol Rev 2011). Antisera from the immunized chimpanzees were shown to exhibit *in vitro* cross-neutralizing activity (Meunier et al. (2011) *J. Infect. Dis.* 204:1186). A phase I clinical trial was conducted in human volunteers with a similar antigen (Frey et al. (2010) *Vaccine* 28:6367). Antisera from selected vaccinated individuals were similarly capable of neutralizing chimeric cell culture-derived viruses (HCVcc) expressing the structural proteins of strains representing all 7 major HCV genotypes *in vitro* (Law et al. (2013) *PLoS One* 8:e59776) and to be able to compete with the binding of numerous discrete monoclonal antibodies with broad cross-neutralizing activities (Wong et al. (2014) *J. Virol.* 88:14278).
- [0005] There is a need in the art for compositions and methods for inducing immune responses to HCV.

SUMMARY

- [0006] The present disclosure provides immunogenic compositions comprising: a) hepatitis C virus (HCV) E1E2 heterodimers, HCV E2, or HCV E1; and b) an adjuvant, where the adjuvant

is a cyclic dinucleotide or an archaeosome. The present disclosure provides methods of inducing an immune response in an individual to HCV, the methods comprising administering to an individual an effective amount of an immunogenic composition of the present disclosure.

BRIEF DESCRIPTION OF THE DRAWINGS

- [0007]** FIG. 1A-1C provide an amino acid sequence alignment of examples of the core-E1-E2 coding regions of a HCV genotype 1 virus, specifically representative HCV 1A, 1B and 1C genotypes. Genbank database sequences for the coding region core-E1-E2 were aligned using Geneious software v5.6.4. Numbering of amino acids is according to strain NP_671941 (H77). Consensus: SEQ ID NO:1; AVI1a129: SEQ ID NO:2; NP_671491 (H77): SEQ ID NO:3; EU155269: SEQ ID NO:4; EU781810: SEQ ID NO:5; EU781771: SEQ ID NO:6; AB250610: SEQ ID NO:7; EU781752: SEQ ID NO:8; EU781759: SEQ ID NO:9; EF407439: SEQ ID NO:10; EF407427: SEQ ID NO:11; EU362905: SEQ ID NO:12; EF407413: SEQ ID NO:13; EU781808: SEQ ID NO:14; EU78170: SEQ ID NO:15; AJ238799 (Con1): SEQ ID NO:16; AAK97744: SEQ ID NO:17; AF139594: SEQ ID NO:18; AF176573: SEQ ID NO:19; BAA19625: SEQ ID NO:20; BAA25076: SEQ ID NO:21; BAC54896: SEQ ID NO:22; BAD91386: SEQ ID NO:23; BAF46764: SEQ ID NO:24; BAG30950: SEQ ID NO:25; CAB41951: SEQ ID NO:26; AAK95832: SEQ ID NO:27; AAT69968: SEQ ID NO:28; and BAA03581: SEQ ID NO:29.
- [0008]** FIG. 2A-2C provide an alignment of amino acid sequences of the core-E1-E2 coding region of representative HCV 2A and HCV2B subtypes. Genbank database sequences for the coding region core-E1-E2 were aligned using Geneious software v5.6.4. The amino acid numbering depicted is in accordance to the common HCV strains: ABO47639 (JFH1) and HPCJ8G-J8 (J8) for HCV2A and HCV2B, respectively. AB047639 (JFH1): SEQ ID NO:30; AB047645: SEQ ID NO:31; AF169003: SEQ ID NO:32; AF169005: SEQ ID NO:33; AF238482: SEQ ID NO:34; AY746460: SEQ ID NO:35; HPCPOLP: SEQ ID NO:36; NC_009823: SEQ ID NO:37; HPCJ8G HC-J8: SEQ ID NO:38; AB030907: SEQ ID NO:39; AY232730: SEQ ID NO:40; AY232747: SEQ ID NO:41; and DQ430817: SEQ ID NO:42.
- [0009]** FIG. 3A-3C provide an amino acid sequence alignment of the core-E1-E2 coding region for representative HCV 3A, 3B and 3K genotypes. Genbank database sequences for the coding region core-E1-E2 were aligned using Geneious software v5.6.4. Consensus: SEQ ID NO:43; AVI3a177: SEQ ID NO:44; YP_0014696: SEQ ID NO:45; CAA54244: SEQ ID NO:46; AAC03058: SEQ ID NO:47; AAY29642: SEQ ID NO:48; ABD85062: SEQ ID NO:49; ABD85063: SEQ ID NO:50; ABD97104: SEQ ID NO:51; BAA06044: SEQ ID NO:52; BAA08372: SEQ ID NO:53; and BAA09890: SEQ ID NO:54.

- [0010] FIG. 4A-4B provide an amino acid sequence of the core-E1-E2 coding region for HCV genotype 7a. Amino acid sequence for the coding region core-E1-E2 of genotype 7a (isolate QC69; Genbank: ABN05226.1; SEQ ID NO:55) is shown according to the numbering scheme of the reference strain, NP_671941 (H77).
- [0011] FIG. 5A-5C provide amino acid sequences of immunoglobulin Fc regions for GenBank 3S7G_A *Homo sapiens* IgG1 Fc: SEQ ID NO:56; GenBank AAN76044 *Homo sapiens* IgG2 Fc: SEQ ID NO: 57; GenBank AAW65947 *Homo sapiens* IgG3 Fc: SEQ ID NO:58; GenBank AAA52770 *Homo sapiens* IgD Fc: SEQ ID NO:59; GenBank 0308221A *Homo sapiens* IgM Fc: SEQ ID NO:60; GenBank P01876 *Homo sapiens* IgA Fc: SEQ ID NO:61; GenBank IF6A_B *Homo sapiens* IgE Fc: SEQ ID NO:62; and GenBank P01861 *Homo sapiens* IgG4 Fc: SEQ ID NO:63.
- [0012] FIG. 6 presents Table 1, which provides conserved regions based on conserved CD4 epitopes (CD4⁺ T cell epitopes) conserved among HCV genotypes. Top to Bottom: SEQ ID NOs.:64-74.
- [0013] FIG. 7 presents Table 2, which provides the number of located HCV CD8⁺ T cell epitopes and anchor positions for common human leukocyte antigen (HLA)-I Alleles in the United States.
- [0014] FIG. 8 presents Table 3, which provides conserved regions based on CD8 epitopes (CD8⁺ T cell epitopes) conserved among HCV genotypes. Top to Bottom: SEQ ID NOs.:75-84.
- [0015] FIG. 9A-9B provide a list of CD4 and CD8 epitopes that are conserved among HCV genotypes 1a, 1b, 2a, 2b, and 3.
- [0016] FIG. 10A-10D provide amino acid sequences of examples of polypeptides comprising multiple T-cell epitopes (TP29: SEQ ID NO:85; TP50: SEQ ID NO:86; TP52: SEQ ID NO:87; TP70: SEQ ID NO:88; TP100: SEQ ID NO:89; TP171: SEQ ID NO:90; TP228: SEQ ID NO:91; TP553: SEQ ID NO:92; TP778: SEQ ID NO:93; and TP1985: SEQ ID NO:94). The start and end amino acids are based on the sequence designated "Consensus" in FIG. 12A-12L. The T-cell epitopes contained within each polypeptide are provided; the T-cell epitope designations correspond to those presented in FIG. 11A-11N.
- [0017] FIG. 11A-11N provide consensus amino acid sequences of HCV polypeptides; and depict the locations of T-cell epitopes (SEQ ID NO:95).
- [0018] FIG. 12A-12L provide consensus amino acid sequences of HCV polypeptides (SEQ ID NOs.96-107).
- [0019] FIG. 13 depicts the experimental protocol.
- [0020] FIG. 14 depicts neutralization activity of recombinant E1E2 (rE1E2), in combination with adjuvant, in mice.
- [0021] FIG. 15 depicts differential detection of T cell immune responses in mice.

DEFINITIONS

- [0022]** The term “hepatitis C virus” (“HCV”), as used herein, refers to any one of a number of different genotypes and isolates of hepatitis C virus. Thus, “HCV” encompasses any of a number of genotypes, subtypes, or quasispecies, of HCV, including, e.g., genotype 1, 2, 3, 4, 6, 7, etc. and subtypes (e.g., 1a, 1b, 2a, 2b, 3a, 4a, 4c, etc.), and quasispecies. Representative HCV genotypes and isolates include: the “Chiron” isolate HCV-1, H77, J6, Con1, isolate 1, BK, EC1, EC10, HC-J2, HC-J5; HC-J6, HC-J7, HC-J8, HC-JT, HCT18, HCT27, HCV-476, HCV-KF, “Hunan”, “Japanese”, “Taiwan”, TH, type 1, type 1a, H77 type 1b, type 1c, type 1d, type 1e, type 1f, type 10, type 2, type 2a, type 2b, type 2c, type 2d, type 2f, type 3, type 3a, type 3b, type 3g, type 4, type 4a, type 4c, type 4d, type 4f, type 4h, type 4k, type 5, type 5a, type 6 and type 6a.
- [0023]** The terms "individual," "host," "subject," and "patient" are used interchangeably herein, and refer to a mammal, including, but not limited to, non-human primates (e.g., simians), equines (e.g., horses), rodents (e.g., rats; mice), and humans.
- [0024]** As used herein, the term “isolated,” in reference to a polypeptide, refers to a polypeptide that is in an environment different from that in which the polypeptide naturally occurs. An isolated polypeptide can be purified. By “purified” is meant a compound of interest (e.g., a polypeptide) has been separated from components that accompany it in nature. “Purified” can also be used to refer to a polypeptide separated from components that can accompany it during production of the polypeptide (e.g., during synthesis in vitro, etc.). In some embodiments, a polypeptide (or a mixture of polypeptides) is substantially pure when the polypeptide (or mixture of polypeptides) is at least 60% or at least 75% by weight free from organic molecules with which it is naturally associated or with which it is associated during production. In some embodiments, the polypeptide is from 30% to 60% pure. In some embodiments, the polypeptide (or mixture of polypeptides) is at least 60%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99%, by weight, pure. For example, in some embodiments, an E1 or an E2 polypeptide (or a mixture of E1 and E2 polypeptides, e.g., an E1/E2 heterodimer) is substantially pure when the E1 or E2 polypeptide (or mixture of E1 and E2 polypeptides) is at least 60% or at least 75% by weight free from organic molecules with which the polypeptide(s) is naturally associated or with which it is associated during production. In some embodiments, the E1 or E2 polypeptide (or mixture of E1 and E2 polypeptides) is at least 60%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99%, by weight, pure. In some embodiments, where a composition comprises an E2 polypeptide, the E2 polypeptide is at least 60%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99%, by weight, pure. In some

embodiments, where a composition comprises an E1/E2 heterodimeric complex polypeptide, the E1/E2 heterodimeric complex polypeptide is at least 60%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99%, by weight, pure. In some embodiments, where a composition comprises a T-cell epitope polypeptide, the T-cell epitope polypeptide is at least 60%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99%, by weight, pure.

- [0025]** The terms “polynucleotide” and “nucleic acid,” used interchangeably herein, refer to a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. Thus, this term includes, but is not limited to, single-, double-, or multi-stranded DNA or RNA, genomic DNA, cDNA, DNA-RNA hybrids, or a polymer comprising purine and pyrimidine bases or other natural, chemically or biochemically modified, non-natural, or derivatized nucleotide bases. In some cases, a polynucleotide is RNA. In some cases, a polynucleotide is DNA. A “polynucleotide” includes a nucleic acid that is incorporated into a viral vector or a bacterial vector.
- [0026]** The terms “peptide,” “polypeptide,” and “protein” are used interchangeably herein, and refer to a polymeric form of amino acids of any length, which can include coded and non-coded amino acids, chemically or biochemically modified or derivatized amino acids, and polypeptides having modified peptide backbones. The term “polypeptide” includes glycosylated polypeptides.
- [0027]** The term “heterologous” refers to two components that are defined by structures derived from different sources. For example, where “heterologous” is used in the context of a polypeptide, where the polypeptide includes operably linked amino acid sequences that can be derived from one or more different polypeptides, e.g., amino acid sequences that are not operably linked to the polypeptide in nature. As another example, where a composition comprises an HCV E1/E2 heterodimer and a “heterologous” polypeptide, the “heterologous polypeptide is a polypeptide other than HCV E1 or HCV E2. As another example, where a composition comprises an HCV E1 polypeptide and a “heterologous” polypeptide, the “heterologous polypeptide is a polypeptide other than HCV E1. As another example, where a composition comprises an HCV E2 polypeptide and a “heterologous” polypeptide, the “heterologous polypeptide is a polypeptide other than HCV E2.
- [0028]** The term “archaeal lipid” refer to a polar lipid common to the Domain Archaea typified by isoprenoid chains in ether linkage to the sn-2,3 carbons of the glycerol backbone.
- [0029]** Archaeal core lipids are most commonly 2,3-di-O-sn-diphytanylglycerol (archaeol), and 2,2',3,3'-tetra-O-dibiphytanyl-sn-diglycerol (caldarchaeol).

- [0030] Synthetic archaeal lipids or polar synthetic lipids refer to core lipid precursors either derived from Archaeal lipids by hydrolysis or made by chemical synthesis, conjugated to at least one new head group.
- [0031] Archaeol phospholipids are referred herein to using archaetidyl, for example, AG, archaetidylglycerol; AS, archaetidylserine.
- [0032] The term “conventional lipids” refers to the lipids common to the Domains Bacteria and Eukarya. This includes polar lipids typified by fatty acyl chains in ester linkage to the sn-1,2 carbons of the glycerol backbone, and neutral lipids such as cholesterol. Conventional phospholipids are referred to in the usual way, for example, DPPG, dipalmitoylphosphatidylglycerol; DPPS, dipalmitoylphosphatidylserine.
- [0033] The term “archaeosome” refers to a closed lipid vesicle that contains any amount of synthetic archaeal lipid(s).
- [0034] Before the present invention is further described, it is to be understood that this invention is not limited to particular embodiments described, as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.
- [0035] Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range and any other stated or intervening value in that stated range, is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.
- [0036] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the present invention, the preferred methods and materials are now described. All publications mentioned herein are incorporated herein by reference to disclose and describe the methods and/or materials in connection with which the publications are cited.
- [0037] It must be noted that as used herein and in the appended claims, the singular forms “a,” “an,” and “the” include plural referents unless the context clearly dictates otherwise. Thus, for

example, reference to “an HCV E1E2 heterodimer” includes a plurality of such heterodimer and reference to “the cyclic dinucleotide” includes reference to one or more cyclic dinucleotides and equivalents thereof known to those skilled in the art, and so forth. It is further noted that the claims may be drafted to exclude any optional element. As such, this statement is intended to serve as antecedent basis for use of such exclusive terminology as “solely,” “only” and the like in connection with the recitation of claim elements, or use of a “negative” limitation.

[0038] It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable sub-combination. All combinations of the embodiments pertaining to the invention are specifically embraced by the present invention and are disclosed herein just as if each and every combination was individually and explicitly disclosed. In addition, all sub-combinations of the various embodiments and elements thereof are also specifically embraced by the present invention and are disclosed herein just as if each and every such sub-combination was individually and explicitly disclosed herein.

[0039] The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. Further, the dates of publication provided may be different from the actual publication dates which may need to be independently confirmed.

DETAILED DESCRIPTION

[0040] The present disclosure provides immunogenic compositions comprising: a) hepatitis C virus (HCV) E1E2 heterodimers, HCV E2, or HCV E1; and b) an adjuvant, where the adjuvant is a cyclic dinucleotide or an archaeosome. The present disclosure provides methods of inducing an immune response in an individual to HCV, the methods comprising administering to an individual an effective amount of an immunogenic composition of the present disclosure.

IMMUNOGENIC COMPOSITIONS COMPRISING HCV E1E2, E2, OR E1 POLYPEPTIDE + CYCLIC DINUCLEOTIDE

[0041] The present disclosure provides an immunogenic composition comprising: a) an HCV E1E2 heterodimer; and b) a cyclic dinucleotide (CDN). The present disclosure provides an immunogenic composition comprising: a) an HCV E2 polypeptide; and b) a CDN. The present disclosure provides an immunogenic composition comprising: a) an HCV E1 polypeptide; and b) a CDN.

- [0042]** In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to one or more HCV genotypes. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to one or more HCV genotypes, where the immune response is greater than the immune response induced by administration of a control composition comprising the HCV E1/E2 heterodimer (or E1 polypeptide, or E2 polypeptide) but lacking the CDN.
- [0043]** In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces CD8⁺ CTLs specific for HCV, where the number of HCV-specific CD8⁺ CTLs induced is at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% (or 2-fold), at least 2.5-fold, at least 5-fold, at least 7.5-fold, at least 10-fold, at least 20-fold, at least 50-fold, or at least 100-fold, or more than 100-fold, higher than the number of HCV-specific CD8⁺ CTLs induced by administration of a control composition (e.g., a composition comprising the HCV E1/E2 heterodimer but lacking the CDN; a composition comprising an E1 polypeptide but lacking the CDN; a composition comprising an E2 polypeptide but lacking the CDN).
- [0044]** In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces CD4⁺ T cells specific for HCV, where the number of HCV-specific CD4⁺ T cells induced is at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% (or 2-fold), at least 2.5-fold, at least 5-fold, at least 7.5-fold, at least 10-fold, at least 20-fold, at least 50-fold, or at least 100-fold, or more than 100-fold, higher than the number of HCV-specific CD4⁺ T cells induced by administration of a control composition (e.g., a composition comprising the HCV E1/E2 heterodimer but lacking the CDN; a composition comprising an E1 polypeptide but lacking the CDN; a composition comprising an E2 polypeptide but lacking the CDN).
- [0045]** In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces production of HCV-specific CD4⁺ T cells and CD8⁺ T cells in the individual, where the number of HCV-specific CD4⁺ T cells and/or CD8⁺ T cells is increased, such that the percent of total peripheral CD4⁺ and/or CD8⁺ T cells that is HCV-specific is from 0.01% to 0.05%, from 0.05% to 0.10%, from 0.10% to 0.125%, from 0.125% to 0.25%, from 0.25% to from 0.50%, or 0.5% to 10% (e.g., from 0.5% to 1%, from 1% to 2%, from 2% to 5%, or from 5% to 10%). The number of HCV-specific CD4⁺ T cells and CD8⁺ T cells in a control individual (e.g., an individual not infected with HCV) not treated with the immunogenic composition would be undetectable.

- [0046]** In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, increases the number of HCV E1/E2-specific CD4⁺ T cells and CD8⁺ T cells in the individual by at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% (or 2-fold), at least 2.5-fold, at least 5-fold, at least 7.5-fold, at least 10-fold, at least 20-fold, at least 50-fold, or at least 100-fold, or more than 100-fold, compared to the number of HCV E1/E2-specific CD4⁺ T cells and CD8⁺ T cells in the individual induced by administration of a control composition comprising the HCV E1/E2 heterodimer (or HCV E2 polypeptide, or HCV E1 polypeptide) but lacking the CDN, or compared to the number of HCV E1/E2-specific CD4⁺ T cells and CD8⁺ T cells in the individual before administration of the immunogenic composition.
- [0047]** In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces helper T lymphocytes (e.g., CD4⁺ T cells) specific for HCV, where the number of HCV-specific helper T lymphocytes induced is at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% (or 2-fold), at least 2.5-fold, at least 5-fold, at least 7.5-fold, at least 10-fold, at least 20-fold, at least 50-fold, or at least 100-fold, or more than 100-fold, higher than the number of HCV-specific helper T cells induced by administration of a control composition comprising the HCV E1/E2 heterodimer (or HCV E2 polypeptide, or HCV E1 polypeptide) but lacking the CDN, or compared to the number of HCV-specific CD4⁺ T cells in the individual before administration of the immunogenic composition.
- [0048]** In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces antibody specific for HCV, where the level of HCV-specific antibody induced is at least as high as the level of HCV-specific antibody induced by administration of a control composition comprising the HCV E1/E2 heterodimer (or HCV E2 polypeptide, or HCV E1 polypeptide) but lacking the CDN.
- [0049]** In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces antibody specific for HCV, where the level of HCV-specific antibody induced is at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% (or 2-fold), at least 2.5-fold, at least 5-fold, at least 7.5-fold, at least 10-fold, at least 20-fold, at least 50-fold, or at least 100-fold, or more than 100-fold, higher than the level of HCV-specific antibody induced by administration of a control composition comprising the HCV E1/E2 heterodimer (or HCV E2 polypeptide, or HCV E1 polypeptide) but lacking the CDN, or compared the level of HCV-specific antibody in the individual before administration of the immunogenic composition.

[0050] An immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response (e.g., a cellular immune response) in the individual to one or more HCV genotypes. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to HCV genotype 1. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to HCV genotype 2. In some cases, an immunogenic composition of the present disclosure when administered to an individual in need thereof, induces an immune response in the individual to HCV genotype 3. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to HCV genotype 1 and HCV genotype 3. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to HCV genotype 1, HCV genotype 2, and HCV genotype 3. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to HCV genotype 1, HCV genotype 2, HCV genotype 3, and HCV genotype 7. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to HCV genotype 1, HCV genotype 2, HCV genotype 3, HCV genotype 4, HCV genotype 5, HCV genotype 6, and HCV genotype 7.

HCV E1/E2 heterodimers; HCV E2 polypeptides; HCV E1 polypeptides

[0051] HCV E1/E2 heterodimers suitable for use in an immunogenic composition of the present disclosure include HCV E1/E2 heterodimers comprising wild-type HCV E1 polypeptides; HCV E1/E2 heterodimers comprising wild-type HCV E2 polypeptides; HCV E1/E2 heterodimers comprising variant HCV E1 polypeptides; and HCV E1/E2 heterodimers comprising variant HCV E2 polypeptides. HCV E2 polypeptides suitable for use in an immunogenic composition of the present disclosure include wild-type E2 polypeptides and variant E2 polypeptides. HCV E1 polypeptides suitable for use in an immunogenic composition of the present disclosure include wild-type E1 polypeptides and variant E1 polypeptides.

E2 polypeptides

[0052] An E2 polypeptide suitable for inclusion in an E1/E2 heterodimer for inclusion in an immunogenic composition of the present disclosure, or for inclusion by itself in an immunogenic composition of the present disclosure, can have a length of from about 200 amino acids (aa) to about 250 aa, from about 250 aa to about 275 aa, from about 275 aa to about 300 aa, from about 300 aa to about 325 aa, from about 325 aa to about 350 aa, or from about 350 aa to about 365 aa. In some cases, an HCV E2 polypeptide suitable for inclusion in an immunogenic composition of

the present disclosure is an HCV E2 ectodomain polypeptide. In some cases, an HCV E2 polypeptide suitable for inclusion in an immunogenic composition of the present disclosure is a full-length HCV E2 polypeptide.

- [0053]** In FIG. 1A-AC, the amino acid sequence of E2 is amino acid 384 to amino acid 746. In FIG. 2A-2B, the amino acid sequence of E2 is amino acid 384 to amino acid 751. In FIG. 3A-3C, the amino acid sequence of E2 is amino acid 385 to amino acid 754. In FIG. 4A-4B, the amino acid sequence of E2 is amino acid 384 to amino acid 750. As used herein, an "E2 polypeptide" includes a precursor E2 protein, including the signal sequence; includes a mature E2 polypeptide which lacks this sequence; and includes an E2 polypeptide with a heterologous signal sequence. An E2 polypeptide can include a C-terminal membrane anchor sequence which occurs at approximately amino acid positions 715-730 and may extend as far as approximately amino acid residue 746 (see, Lin et al., J. Virol. (1994) 68:5063-5073).
- [0054]** In some cases, a E2 polypeptide suitable for inclusion in an immunogenic composition of the present disclosure lacks a portion of its C-terminal region, e.g., from about amino acid 715 to the C-terminus; from about amino acid 625 to the C-terminus; from about amino acid 661 to the C-terminus; from about amino acid 655 to the C-terminus; from about amino acid 500 to the C-terminus, where the amino acid numbering is with reference to the numbering in FIG. 1A-1C. See, e.g., U.S. Patent No. 6,521,423.
- [0055]** An E2 polypeptide suitable for inclusion in an immunogenic composition of the present disclosure can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to an amino acid sequence of an E2 polypeptide depicted in FIG. 1A-1C, FIG. 2A-2C, FIG. 3A-3C, or FIG. 4A-4B. An E2 polypeptide suitable for inclusion in an immunogenic composition of the present disclosure can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, or at least about 75%, amino acid sequence identity to an amino acid sequence of an E2 polypeptide depicted in FIG. 1A-1C, FIG. 2A-2C, FIG. 3A-3C, or FIG. 4A-4B.
- [0056]** An E2 polypeptide suitable for inclusion in an immunogenic composition of the present disclosure can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%,

amino acid sequence identity to an amino acid sequence of an E2 polypeptide depicted in FIG. 1A-1C. For example, an E2 polypeptide of genotype 1 can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 384-746 of an amino acid sequence depicted in FIG. 1A-1C. For example, an E2 polypeptide of genotype 1A can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 384-746 of an amino acid sequence identified as 1A and depicted in FIG. 1A-1C. For example, an E2 polypeptide of genotype 1B can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 384-746 of an amino acid sequence identified as 1B and depicted in FIG. 1A-1C. For example, an E2 polypeptide of genotype 1C can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 384-746 of an amino acid sequence identified as 1C and depicted in FIG. 1A-1C.

[0057] An E2 polypeptide suitable for inclusion in an immunogenic composition of the present disclosure can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to an amino acid sequence of an E2 polypeptide depicted in FIG. 2A-2C. For example, an E2 polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 384-751 of an amino

acid sequence depicted in FIG. 2A-2C. For example, an E2 polypeptide of genotype 2A can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 384-751 of the “consensus” amino acid sequence depicted in FIG. 2A-2C. For example, an E2 polypeptide of genotype 2B can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 384-751 of the “consensus” amino acid sequence depicted in FIG. 2A-2C.

[0058] An E2 polypeptide suitable for inclusion in an immunogenic composition of the present disclosure can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to an amino acid sequence of an E2 polypeptide depicted in FIG. 3A-3C. For example, an E2 polypeptide of genotype 3 can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 385-754 of an amino acid sequence depicted in FIG. 3A-3C. For example, an E2 polypeptide of genotype 3A can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 385-754 of an amino acid sequence identified as 3A and depicted in FIG. 3A-3C. For example, an E2 polypeptide of genotype 3B can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 385-754 of the amino acid sequence identified as 3B and

depicted in FIG. 3A-3C. For example, an E2 polypeptide of genotype 3K can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 385-754 of the amino acid sequence identified as 3K and depicted in FIG. 3A-3C.

- [0059]** An E2 polypeptide suitable for inclusion in an immunogenic composition of the present disclosure can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence of the E2 polypeptide depicted in FIG. 4A-4B. For example, an E2 polypeptide of genotype 7A can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 384-750 of the amino acid sequence depicted in FIG. 4A-4B.

E1 polypeptides

- [0060]** An HCV E1 polypeptide suitable for inclusion in an E1/E2 heterodimer for inclusion in an immunogenic composition of the present disclosure, or for inclusion by itself in an immunogenic composition of the present disclosure, can have a length of from about 100 amino acids (aa) to about 150 aa, from about 150 aa to about 175 aa, from about 175 aa to about 195 aa, from about 131 aa to about 175 aa, or from about 175 aa to about 193 aa. In some cases, an HCV E1 polypeptide suitable for inclusion in an E1/E2 heterodimer present in an immunogenic composition of the present disclosure is an HCV E1 ectodomain polypeptide. In some cases, an HCV E1 polypeptide suitable for inclusion in an E1/E2 heterodimer present in an immunogenic composition of the present disclosure is a full-length HCV E1 polypeptide.
- [0061]** In FIG. 1A-1C, the amino acid sequence of E1 is amino acid 192 to amino acid 383. In FIG. 2A-2C, the amino acid sequence of E1 is amino acid 192 to amino acid 383. In FIG. 3A-3C, the amino acid sequence of E1 is amino acid 192 to amino acid 384. In FIG. 4A-4B, the amino acid sequence of E1 is amino acid 192 to amino acid 383. Amino acids at around 170 through approximately 191 serve as a signal sequence for E1. As used herein, "E1 polypeptide" includes a precursor E1 protein, including the signal sequence; includes a mature E1 polypeptide which lacks this sequence; and includes an E1 polypeptide with a heterologous signal sequence. An E1

polypeptide can include a C-terminal membrane anchor sequence which occurs at approximately amino acid positions 360-383 (see, e.g., WO 96/04301). In some cases, a suitable E1 polypeptide lacks a C-terminal portion that includes a transmembrane region. For example, in some cases, a suitable E1 polypeptide lacks the C-terminal portion from amino acid 330 to amino acid 384, or from amino acid 360 to amino acid 384. E1 polypeptides can be an E1 polypeptide of any genotype, subtype or isolate of HCV. E1 polypeptides of genotype 1 and E1 polypeptides of genotype 3 are included in an E1/E2 heterodimer of the present disclosure.

[0062] An E1 polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to an amino acid sequence of an E1 polypeptide depicted in FIG. 1A-1C, FIG. 2A-2C, FIG. 3A-3C, or FIG. 4A-4B.

[0063] An E1 polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to an amino acid sequence of an E1 polypeptide depicted in FIG. 1A-1C. For example, an E1 polypeptide of genotype 1A can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 192-383 of an amino acid sequence identified as 1A and depicted in FIG. 1A-1C. For example, an E1 polypeptide of genotype 1B can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 192-383 of an amino acid sequence identified as 1B and depicted in FIG. 1A-1C. For example, an E1 polypeptide of genotype 1C can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or

100%, amino acid sequence identity to amino acids 192-383 of an amino acid sequence identified as 1C and depicted in FIG. 1A-1C.

- [0064]** An E1 polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to an amino acid sequence of an E1 polypeptide depicted in FIG. 2A-2C. For example, an E1 polypeptide of genotype 2A can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 192-383 of an amino acid sequence identified as 2A and depicted in FIG. 2A-2C. For example, an E1 polypeptide of genotype 2B can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 192-383 of an amino acid sequence identified as 2B and depicted in FIG. 2A-2C.
- [0065]** An E1 polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the consensus E1 polypeptide amino acid sequence depicted in FIG. 3A-3C.
- [0066]** An E1 polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to an amino acid sequence of an E1 polypeptide depicted in FIG. 4A-4B. For example, an E1 polypeptide of genotype 7A can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about

95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 192-383 of the amino acid sequence depicted in FIG. 4A-4B.

HCV E1 and E2 polypeptides comprising amino acids from a proteolytically cleavable linker

[0067] As described in more detail below, an HCV E1/E2 heterodimer can be generated using a method that involves an HCV E1 or an HCV E2 polypeptide comprising a heterologous proteolytically cleavable linker. Following enzymatic cleavage of the proteolytically cleavable linker, from 1 to 6 (e.g., 1, 2, 3, 4, 5, or 6) heterologous amino acids can remain on the HCV E1 or E2 polypeptide. For example, from 1 to 6 (e.g., 1, 2, 3, 4, 5, or 6) heterologous amino acids can remain at the N-terminus of an HCV E2 polypeptide. As another example, from 1 to 6 (e.g., 1, 2, 3, 4, 5, or 6) heterologous amino acids can remain at the C-terminus of an HCV E2 polypeptide. As another example, from 1 to 6 (e.g., 1, 2, 3, 4, 5, or 6) heterologous amino acids can remain at the N-terminus of an HCV E1 polypeptide. As another example, from 1 to 6 (e.g., 1, 2, 3, 4, 5, or 6) heterologous amino acids can remain at the C-terminus of an HCV E1 polypeptide.

[0068] In some cases, amino acids C-terminal to the proteolytic cleavage site in a proteolytically cleavable linker are Gly-Pro, Ser, Gly, or Gly-Ser. Thus, in some cases, a modified HCV E1 polypeptide comprises, appended to the N-terminus of an HCV E1 polypeptide: Gly-Pro, Ser, Gly, or Gly-Ser. In other words, in some cases, a modified HCV E1 polypeptide comprises, in order from N-terminus to C-terminus: a) Gly-Pro, Ser, Gly, or Gly-Ser; and b) an HCV E1 polypeptide.

[0069] In some cases, amino acids C-terminal to the proteolytic cleavage site in a proteolytically cleavable linker are Gly-Pro, Ser, Gly, or Gly-Ser. Thus, in some cases, a modified HCV E2 polypeptide comprises, appended to the N-terminus of an HCV E2 polypeptide: Gly-Pro, Ser, Gly, or Gly-Ser. In other words, in some cases, a modified HCV E2 polypeptide comprises, in order from N-terminus to C-terminus: a) Gly-Pro, Ser, Gly, or Gly-Ser; and b) an HCV E2 polypeptide.

[0070] In some cases, amino acids N-terminal to the proteolytic cleavage site in a proteolytically cleavable linker are LEVLFQ (SEQ ID NO:122), ENLYYFQ (SEQ ID NO:150), LVPR (SEQ ID NO:124), I(E/D)GR (SEQ ID NO:125), or DDDDK (SEQ ID NO:123). Thus, in some cases, a modified HCV E1 polypeptide comprises, appended to the C-terminus of an HCV E1 polypeptide: LEVLFQ (SEQ ID NO:122), ENLYYFQ (SEQ ID NO:150), LVPR (SEQ ID NO:124), I(E/D)GR (SEQ ID NO:125), or DDDDK (SEQ ID NO:123). In other words, in some cases, a modified HCV E1 polypeptide comprises, in order from N-terminus to C-terminus: a) an HCV E1 polypeptide; and b) LEVLFQ (SEQ ID NO:122), ENLYYFQ (SEQ ID NO:150), LVPR (SEQ ID NO:124), I(E/D)GR (SEQ ID NO:125), or DDDDK (SEQ ID NO:123).

- [0071]** In some cases, amino acids N-terminal to the proteolytic cleavage site in a proteolytically cleavable linker are LEVLFQ (SEQ ID NO:122), ENLYYFQ (SEQ ID NO:150), LVPR (SEQ ID NO:124), I(E/D)GR (SEQ ID NO:125), or DDDDK (SEQ ID NO:123). Thus, in some cases, a modified HCV E2 polypeptide comprises, appended to the C-terminus of an HCV E2 polypeptide: LEVLFQ (SEQ ID NO:122), ENLYYFQ (SEQ ID NO:150), LVPR (SEQ ID NO:124), I(E/D)GR (SEQ ID NO:125), or DDDDK (SEQ ID NO:123). In other words, in some cases, a modified HCV E2 polypeptide comprises, in order from N-terminus to C-terminus: a) an HCV E2 polypeptide; and b) LEVLFQ (SEQ ID NO:122), ENLYYFQ (SEQ ID NO:150), LVPR (SEQ ID NO:124), I(E/D)GR (SEQ ID NO:125), or DDDDK (SEQ ID NO:123).
- [0072]** In some cases, a flexible linker of from 1 to 10 amino acids is interposed between the proteolytically cleavable linker and the HCV E1 or E2 polypeptide. Flexible linkers are intrinsically disordered flexible linker domains or loops that vary in length and can be rich in polar uncharged amino acids. Flexible linkers include, e.g., glycine polymers (G)_n, glycine-serine polymers (including, for example, (GS)_n, GSGGS_n (SEQ ID NO:108), GSGGS_n (SEQ ID NO:109), and GGS_n (SEQ ID NO:110), where n is an integer of at least one, e.g., where n is 1, 2, 3, 4, 5, or 6); glycine-alanine polymers, such as GAGAGAGA and the like; and alanine-serine polymers, e.g., SASASASA and the like. Exemplary linkers can comprise amino acid sequences including, but not limited to, GGSG (SEQ ID NO:111), GGSGG (SEQ ID NO:112), GSGSG (SEQ ID NO:113), GSGGG (SEQ ID NO:114), GGGSG (SEQ ID NO:115), GSSSG (SEQ ID NO:116), and the like.
- [0073]** For example, in some cases, a modified E1 polypeptide comprises, in order from N-terminus to C-terminus: a) Gly-Pro, Ser, Gly, or Gly-Ser; b) a flexible linker of from 1 to 10 amino acids; and c) an HCV E1 polypeptide.
- [0074]** As another example, in some cases, a modified E2 polypeptide comprises, in order from N-terminus to C-terminus: a) Gly-Pro, Ser, Gly, or Gly-Ser; b) a flexible linker of from 1 to 10 amino acids; and c) an HCV E2 polypeptide.
- [0075]** As another in some cases, a modified E1 polypeptide comprises, from N-terminus to C-terminus: a) an HCV E1 polypeptide; b) a flexible linker of from 1 to 10 amino acids; and c) LEVLFQ (SEQ ID NO:122), ENLYYFQ (SEQ ID NO:150), LVPR (SEQ ID NO:124), I(E/D)GR (SEQ ID NO:125), or DDDDK (SEQ ID NO:123).
- [0076]** As another in some cases, a modified E2 polypeptide comprises, from N-terminus to C-terminus: a) an HCV E2 polypeptide; b) a flexible linker of from 1 to 10 amino acids; and c) LEVLFQ (SEQ ID NO:122), ENLYYFQ (SEQ ID NO:150), LVPR (SEQ ID NO:124), I(E/D)GR (SEQ ID NO:125), or DDDDK (SEQ ID NO:123).

E2 with N-terminal heterologous amino acids

- [0077]** In some cases, an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises a modified HCV E2 polypeptide with from 1 to 6 amino acids from the proteolytically cleavable linker on the N-terminus of the E2 polypeptide. In some cases, an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises: a) an HCV E1 polypeptide; and b) a modified E2 polypeptide comprising, in order from N-terminus to C-terminus: i) from 1 to 6 heterologous amino acids wherein the from 1 to 6 heterologous amino acids are C-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; and ii) an HCV E2 polypeptide.
- [0078]** Proteolytically cleavable linkers are described elsewhere herein. Following proteolytic cleavage of a precursor polypeptide, as described herein, a modified E2 polypeptide is generated, which modified E2 polypeptide comprises, at its N-terminus, amino acids C-terminal to the protease cleavage site within the proteolytically cleavable linker.
- [0079]** For example, where the proteolytically cleavable linker comprises a PreScission cleavage site (LEVLFQGP; SEQ ID NO:117), where cleavage occurs between the glutamine and the glycine, a modified E2 polypeptide present in a heterodimeric E1/E2 polypeptide suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) Gly-Pro; and b) an HCV E2 polypeptide. As another example, where the proteolytically cleavable linker comprises a TEV cleavage site (ENLYFQS; SEQ ID NO:118), where cleavage occurs between the glutamine and the serine, a modified E2 polypeptide present in a heterodimeric E1/E2 polypeptide suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) Ser; and b) an HCV E2 polypeptide.
- [0080]** As another example, where the proteolytically cleavable linker comprises a TEV cleavage site (ENLYFQG; SEQ ID NO:119), where cleavage occurs between the glutamine and the glycine, a modified E2 polypeptide present in a heterodimeric E1/E2 polypeptide suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) Gly; and b) an HCV E2 polypeptide.
- [0081]** As another example, where the proteolytically cleavable linker comprises a thrombin cleavage site (LVPRGS; SEQ ID NO:120), where cleavage occurs between the arginine and the glycine, a modified E2 polypeptide present in a heterodimeric E1/E2 polypeptide suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) Gly-Ser; and an HCV E2 polypeptide.

[0082] As another example, where the proteolytically cleavable linker comprises a Factor Xa cleavage site (I(E/D)GRX, where X is any amino acid except arginine or proline; SEQ ID NO:121), where cleavage occurs between the arginine and the X, a modified E2 polypeptide present in a heterodimeric E1/E2 polypeptide suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) X (where X is any amino acid except arginine or proline); and an HCV E2 polypeptide.

[0083] Thus, for example, in some cases, an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises: a) an HCV E1 polypeptide; and b) a modified E2 polypeptide comprising, in order from N-terminus to C-terminus: i) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 (e.g., 1, 2, 3, 4, 5, or 6) heterologous amino acids are C-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; and ii) an HCV E2 polypeptide. In some cases, the 1 to 6 heterologous amino acids are Gly-Pro. In some cases, the 1 to 6 heterologous amino acids is Ser. In some cases, the 1 to 6 heterologous amino acids is Gly. In some cases, the 1 to 6 heterologous amino acids are Gly-Ser.

[0084] As another example, in some cases, an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises: a) an HCV E2 polypeptide; and b) a modified E1 polypeptide comprising, in order from N-terminus to C-terminus: i) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 (e.g., 1, 2, 3, 4, 5, or 6) heterologous amino acids are C-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; and ii) an HCV E1 polypeptide. In some cases, the 1 to 6 heterologous amino acids are Gly-Pro. In some cases, the 1 to 6 heterologous amino acids is Ser. In some cases, the 1 to 6 heterologous amino acids is Gly. In some cases, the 1 to 6 heterologous amino acids are Gly-Ser.

E1 with N-terminal heterologous amino acids

[0085] In some cases, an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises a modified HCV E1 polypeptide with from 1 to 6 amino acids from a proteolytically cleavable linker on the N-terminus of the E1 polypeptide. In some cases, an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises: a) an HCV E2 polypeptide; and b) a modified E1 polypeptide comprising, in order from N-terminus to C-terminus: i) from 1 to 6 heterologous amino acids wherein the from 1 to 6 heterologous amino acids are C-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; and ii) an HCV E1 polypeptide.

[0086] Proteolytically cleavable linkers are described elsewhere herein. Following proteolytic cleavage of a precursor polypeptide (e.g., a precursor polypeptide comprising, in order from N-terminus to C-terminus: a) an Fc polypeptide or an HCV E2 polypeptide; b) a proteolytically

cleavable linker; and c) an HCV E1 polypeptide), a modified E1 polypeptide is generated, which modified E1 polypeptide comprises, at its N-terminus, amino acids C-terminal to the protease cleavage site within the proteolytically cleavable linker.

[0087] For example, where the proteolytically cleavable linker comprises a PreScission cleavage site (LEVLFQGP; SEQ ID NO:117), where cleavage occurs between the glutamine and the glycine, a modified E1 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) Gly-Pro; and b) an HCV E1 polypeptide.

[0088] As another example, where the proteolytically cleavable linker comprises a TEV cleavage site (ENLYFQS; SEQ ID NO:118), where cleavage occurs between the glutamine and the serine, a modified E1 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) Ser; and b) an HCV E1 polypeptide.

[0089] As another example, where the proteolytically cleavable linker comprises a TEV cleavage site (ENLYFQG; SEQ ID NO:119), where cleavage occurs between the glutamine and the glycine, a modified E1 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) Gly; and b) an HCV E1 polypeptide.

[0090] As another example, where the proteolytically cleavable linker comprises a thrombin cleavage site (LVPRGS; SEQ ID NO:120), where cleavage occurs between the arginine and the glycine, a modified E1 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) Gly-Ser; and an HCV E1 polypeptide.

[0091] As another example, where the proteolytically cleavable linker comprises a Factor Xa cleavage site (I(E/D)GRX, where X is any amino acid except arginine or proline; SEQ ID NO:121), where cleavage occurs between the arginine and the X, a modified E1 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) X (where X is any amino acid except arginine or proline); and an HCV E1 polypeptide.

E2 with C-terminal heterologous amino acids

[0092] In some cases, an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises a modified HCV E2 polypeptide with from 1 to 6 amino acids from a proteolytically cleavable linker on the C-terminus of the E2 polypeptide. In some cases, an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition

of the present disclosure comprises: a) an HCV E1 polypeptide; and b) a modified E2 polypeptide comprising, in order from N-terminus to C-terminus: i) an HCV E2 polypeptide; and ii) from 1 to 6 heterologous amino acids wherein the from 1 to 6 heterologous amino acids are N-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker.

[0093] Proteolytically cleavable linkers are described elsewhere herein. Following proteolytic cleavage of a precursor polypeptide (e.g., a precursor polypeptide comprising, in order from N-terminus to C-terminus: a) HCV E2 polypeptide; b) a proteolytically cleavable linker; and c) an Fc polypeptide or an HCV E1 polypeptide), a modified E2 polypeptide is generated, which modified E2 polypeptide comprises, at its C-terminus, amino acids N-terminal to the protease cleavage site within the proteolytically cleavable linker.

[0094] For example, where the proteolytically cleavable linker comprises a PreScission cleavage site (LEVLFQGP; SEQ ID NO:117), where cleavage occurs between the glutamine and the glycine, a modified E2 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) an HCV E2 polypeptide; and b) LEVLFQ (SEQ ID NO:122).

[0095] As another example, where the proteolytically cleavable linker comprises an enterokinase cleavage site (DDDDK; SEQ ID NO:123), where cleavage occurs C-terminal to the Lys, a modified E2 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) an HCV E2 polypeptide; and b) DDDDK (SEQ ID NO:123).

[0096] As another example, where the proteolytically cleavable linker comprises a TEV cleavage site (ENLYFQG; SEQ ID NO:119), where cleavage occurs between the glutamine and the glycine, a modified E2 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) an HCV E2 polypeptide; and b) ENLYFQ (SEQ ID NO:151).

[0097] As another example, where the proteolytically cleavable linker comprises a thrombin cleavage site (LVPRGS; SEQ ID NO:120), where cleavage occurs between the arginine and the glycine, a modified E2 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) an HCV E2 polypeptide; and b) LVPR (SEQ ID NO:124).

[0098] As another example, where the proteolytically cleavable linker comprises a Factor Xa cleavage site (I(E/D)GRX, where X is any amino acid except arginine or proline; SEQ ID NO:121), where cleavage occurs between the arginine and the X, a modified E2 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of

the present disclosure comprises, in order from N-terminus to C-terminus: a) an HCV E2 polypeptide; and I(E/D)GR (SEQ ID NO: 125).

E1 with C-terminal heterologous amino acids

- [0099] In some cases, an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises a modified HCV E1 polypeptide with from 1 to 6 amino acids from a proteolytically cleavable linker on the C-terminus of the E1 polypeptide. In some cases, an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises: a) an HCV E2 polypeptide; and b) a modified E1 polypeptide comprising, in order from N-terminus to C-terminus: i) an HCV E1 polypeptide; and ii) from 1 to 6 heterologous amino acids wherein the from 1 to 6 heterologous amino acids are N-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker.
- [00100] Proteolytically cleavable linkers are described elsewhere herein. Following proteolytic cleavage of a precursor polypeptide (e.g., a precursor polypeptide comprising, in order from N-terminus to C-terminus: a) HCV E1 polypeptide; b) a proteolytically cleavable linker; and c) an Fc polypeptide or an HCV E2 polypeptide), a modified E1 polypeptide is generated, which modified E1 polypeptide comprises, at its C-terminus, amino acids N-terminal to the protease cleavage site within the proteolytically cleavable linker.
- [00101] For example, where the proteolytically cleavable linker comprises a PreScission cleavage site (LEVLFQGP; SEQ ID NO:117), where cleavage occurs between the glutamine and the glycine, a modified E1 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) an HCV E1 polypeptide; and b) LEVLFQ (SEQ ID NO:122).
- [00102] As another example, where the proteolytically cleavable linker comprises an enterokinase cleavage site (DDDDK; SEQ ID NO:123), where cleavage occurs C-terminal to the Lys, a modified E1 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) an HCV E1 polypeptide; and b) DDDDK (SEQ ID NO:123).
- [00103] As another example, where the proteolytically cleavable linker comprises a TEV cleavage site (ENLYFQG; SEQ ID NO:119), where cleavage occurs between the glutamine and the glycine, a modified E1 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) an HCV E1 polypeptide; and b) ENLYFQ (SEQ ID NO:151).
- [00104] As another example, where the proteolytically cleavable linker comprises a thrombin cleavage site (LVPRGS; SEQ ID NO:120), where cleavage occurs between the arginine and the

glycine, a modified E1 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) an HCV E1 polypeptide; and LVPR (SEQ ID NO:124).

[00105] As another example, where the proteolytically cleavable linker comprises a Factor Xa cleavage site (I(E/D)GRX, where X is any amino acid except arginine or proline; SEQ ID NO:121), where cleavage occurs between the arginine and the X, a modified E1 polypeptide present in an HCV E1/E2 heterodimer suitable for inclusion in an immunogenic composition of the present disclosure comprises, in order from N-terminus to C-terminus: a) an HCV E1 polypeptide; and I(E/D)GR (SEQ ID NO:125).

Additional polypeptides

[00106] In any of the above-described embodiments, one or both of the polypeptide chains of the E1/E2 heterodimer can include one or more additional polypeptides. For example, the E1 polypeptide, the E2 polypeptide, or both the E1 and the E2 polypeptide, can include an affinity tag. Suitable affinity tags include, e.g., immunoglobulin Fc polypeptides, a poly(histidine) tag (e.g., His₆), a maltose binding protein (MBP), a glutathione-S-transferase (GST) polypeptide, calmodulin-binding peptide (CBP), Streptavidin-binding peptide (SBP), Strep-tag II, FLAG (e.g., DYKDDDDK (SEQ ID NO:126), hemagglutinin (HA) (e.g., YPYDVPDYA (SEQ ID NO:127), c-myc T7 ((e.g., EQKLISEEDL; SEQ ID NO:128), Glu-Glu, starch-binding domain (SBD), and Flag-Acidic-Target Tag (FATT), and the like.

[00107] In some cases, an E1/E2 heterodimer included in a composition of the present disclosure includes a variant E2 polypeptide. In some cases, the E1 polypeptide or the variant E2 polypeptide can include an Ig Fc polypeptide at the C-terminus of the E1 polypeptide or the variant E2 polypeptide. As another example, in some cases, the E1 polypeptide or the variant E2 polypeptide can include an Ig Fc polypeptide at the N-terminus of the E1 polypeptide or the variant E2 polypeptide. Ig Fc polypeptides are known in the art, and are described elsewhere herein.

T-cell epitope polypeptides

[00108] In some cases, one or both of the polypeptide chains of the E1/E2 heterodimer present in an immunogenic composition of the present disclosure can include a T-cell epitope polypeptide. In some cases, an E2 polypeptide present in an E1/E2 heterodimer present in an immunogenic composition of the present disclosure includes a T-cell epitope polypeptide. In some cases, an E1 polypeptide present in an E1/E2 heterodimer present in an immunogenic composition of the present disclosure includes a T-cell epitope polypeptide. In some cases, an HCV E2 polypeptide present in an immunogenic composition of the present disclosure includes a T-cell epitope polypeptide. In some cases, an HCV E1 polypeptide present in an immunogenic composition of

the present disclosure includes a T-cell epitope polypeptide. In these embodiments, the T-cell epitope is covalently linked to the E1 and/or E2 polypeptide. For example, in some cases, the T-cell epitope is covalently linked to the amino terminus (N-terminus) of the HCV E1 polypeptide. In some cases, the T-cell epitope is covalently linked to the carboxyl terminus (C-terminus) of the HCV E1 polypeptide. Thus, e.g., in some cases, an immunogenic composition of the present disclosure comprises: a) a fusion polypeptide comprising, in order from N-terminus to C-terminus: i) an HCV E1 polypeptide; and ii) a T-cell epitope polypeptide; and b) a CDN. In some cases, an immunogenic composition of the present disclosure comprises: a) a fusion polypeptide comprising, in order from N-terminus to C-terminus: i) an HCV E2 polypeptide; and ii) a T-cell epitope polypeptide; and b) a CDN. In some cases, an immunogenic composition of the present disclosure comprises: a) a fusion polypeptide comprising, in order from N-terminus to C-terminus: i) a T-cell epitope polypeptide; and ii) an HCV E1 polypeptide; and b) a CDN. In some cases, an immunogenic composition of the present disclosure comprises: a) a fusion polypeptide comprising, in order from N-terminus to C-terminus: i) a T-cell epitope polypeptide; and ii) an HCV E2 polypeptide; and b) a CDN. In some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E1E2 heterodimer comprising i) a fusion polypeptide comprising, in order from N-terminus to C-terminus: an HCV E1 polypeptide; and a T-cell epitope polypeptide; and ii) an HCV E2 polypeptide; and b) a CDN. In some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E1E2 heterodimer comprising i) a fusion polypeptide comprising, in order from N-terminus to C-terminus: an HCV E2 polypeptide; and a T-cell epitope polypeptide; and ii) an HCV E2 polypeptide; and b) a CDN. In some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E1E2 heterodimer comprising i) a fusion polypeptide comprising, in order from N-terminus to C-terminus: a T-cell epitope polypeptide; and an HCV E1 polypeptide; and ii) an HCV E2 polypeptide; and b) a CDN. In some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E1E2 heterodimer comprising i) a fusion polypeptide comprising, in order from N-terminus to C-terminus: a T-cell epitope polypeptide; and an HCV E2 polypeptide; and ii) an HCV E1 polypeptide; and b) a CDN.

[00109] In some cases, an immunogenic composition of the present disclosure comprises a T-cell epitope polypeptide, where the T-cell epitope polypeptide is not covalently linked to the HCV E1/E2 heterodimer, the HCV E1 polypeptide or the HCV E2 polypeptide. For example, in some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E1/E2 heterodimer; b) a CDN; and c) a T-cell epitope polypeptide. In some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E2 polypeptide; b) a CDN; and c) a

T-cell epitope polypeptide. In some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E1 polypeptide; b) a CDN; and c) a T-cell epitope polypeptide.

[00110] A T-cell epitope polypeptide suitable for inclusion in an immunogenic composition of the present disclosure comprises a T-cell epitope present in an HCV protein other than E1 and E2. T-cell epitope polypeptides suitable for inclusion in an immunogenic composition of the present disclosure comprise T cell epitopes that are conserved among different HCV genotypes leading to cross-reactive cellular immune responses. In some cases, the T-cell epitope polypeptide does not include a neotope; for example, in some cases, the T-cell epitope polypeptide does not include a junction formed by amino acid sequences that do not naturally occur adjacent to one another in a naturally-occurring HCV polypeptide.

[00111] In some cases, the T-cell epitope polypeptide comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, or more than 10 (e.g., from 10 to 15, from 15 to 20, from 20 to 25, or from 25 to 30, or more than 30), T cell epitopes. T-cell epitopes are epitopes that, when presented with a major histocompatibility complex (MHC) (e.g., a human leukocyte antigen (HLA)) Class I or MHC Class II molecule, are recognized and bound by a T-cell receptor (TCR) present on a T cell surface. T-cell epitopes include epitopes recognized by cytotoxic T cells (e.g., CD8⁺ T cells), and epitopes recognized by helper T cells (e.g., CD4⁺ T cells).

[00112] The one or more T-cell epitopes can include one or more T-cell epitopes present in: a) an HCV NS3 polypeptide; b) an HCV NS2 polypeptide; c) an HCV NS4A polypeptide; d) an HCV NS4B polypeptide; e) an HCV NS5A polypeptide; f) an HCV NS5B polypeptide; g) an HCV core polypeptide; or h) an HCV p7 polypeptide. In some cases, the one or more T-cell epitopes are T-cell epitopes present in an HCV NS3 polypeptide. In some cases, the T-cell epitope polypeptide further comprises one or more T cell epitopes present in: a) cholera toxin or toxoid; and/or b) tetanus toxin or toxoid; and/or c) diphtheria toxin or toxoid; and/or d) a meningococcal outer membrane protein. A suitable source of T-cell epitopes includes non-toxic mutants of toxins, where the mutants are referred to as “cross-reactive material (CRM).” Other examples of strong T helper epitopes are diphtheria toxoid, tetanus toxoid, meningococcal outer membrane protein, or mutant diphtheria protein CRM197 (see, e.g.: [http://www\(dot\)medscape\(dot\)com/viewarticle/431127](http://www(dot)medscape(dot)com/viewarticle/431127)).

[00113] In some cases, the T-cell epitope polypeptide comprises a single T-cell epitope. In some cases, the heterologous polypeptide comprises a single HCV-NS3 T-cell epitope. In some cases, the T-cell epitope polypeptide comprises 2 or more T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises 2 or more HCV-NS3 T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises 3 or more HCV-NS3 T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises 4 or more HCV-NS3 T-cell epitopes. In some cases, the T-cell

epitope polypeptide comprises a single HCV-NS3 CD4⁺ T-cell epitope. In some cases, the T-cell epitope polypeptide comprises 2 or more HCV-NS3 CD4⁺ T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises one or more HCV CD8⁺ T cell epitopes. In some cases, the T-cell epitope polypeptide comprises a single HCV-NS3 CD8⁺ T-cell epitope. In some cases, the T-cell epitope polypeptide comprises 2 or more HCV-NS3 CD8⁺ T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises at least one HCV CD4⁺ T cell epitope and at least one HCV CD8⁺ T cell epitope. In some cases, the T-cell epitope polypeptide comprises at least one HCV-NS3 CD4⁺ T cell epitope and at least one HCV-NS3 CD8⁺ T cell epitope. In some cases, T-cell epitope polypeptide comprises 2 or more HCV-NS3 CD4⁺ T-cell epitopes and 2 or more HCV-NS3 CD8⁺ T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises 2, 3, 4, or 5 HCV-NS3 CD4⁺ T-cell epitopes and 2, 3, 4, or 5 HCV-NS3 CD8⁺ T-cell epitopes.

[00114] In some cases, the T-cell epitope polypeptide comprises a single T-cell epitope. In some cases, the T-cell epitope polypeptide comprises a single HCV-NS2 T-cell epitope. In some cases, the T-cell epitope polypeptide comprises 2 or more T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises 2 or more HCV-NS2 T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises 3 or more HCV-NS2 T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises 4 or more HCV-NS2 T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises a single HCV-NS2 CD4⁺ T-cell epitope. In some cases, the T-cell epitope polypeptide comprises 2 or more HCV-NS2 CD4⁺ T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises one or more HCV CD8⁺ T cell epitopes. In some cases, the T-cell epitope polypeptide comprises a single HCV-NS2 CD8⁺ T-cell epitope. In some cases, the T-cell epitope polypeptide comprises 2 or more HCV-NS2 CD8⁺ T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises at least one HCV CD4⁺ T cell epitope and at least one HCV CD8⁺ T cell epitope. In some cases, the T-cell epitope polypeptide comprises at least one HCV-NS2 CD4⁺ T cell epitope and at least one HCV-NS2 CD8⁺ T cell epitope. In some cases, T-cell epitope polypeptide comprises 2 or more HCV-NS2 CD4⁺ T-cell epitopes and 2 or more HCV-NS2 CD8⁺ T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises 2, 3, 4, or 5 HCV-NS2 CD4⁺ T-cell epitopes and 2, 3, 4, or 5 HCV-NS2 CD8⁺ T-cell epitopes.

[00115] In some cases, the T cell epitope polypeptide comprises a single T-cell epitope. In some cases, the T cell epitope polypeptide comprises a single HCV-NS4A T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-NS4A T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 3 or more HCV-NS4A T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 4 or more HCV-NS4A T-cell epitopes. In some cases, the T cell epitope polypeptide comprises a single HCV-NS4A CD4⁺ T-cell epitope. In some cases, the

T cell epitope polypeptide comprises 2 or more HCV-NS4A CD4⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises one or more HCV CD8⁺ T cell epitopes. In some cases, the T cell epitope polypeptide comprises a single HCV-NS4A CD8⁺ T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-NS4A CD8⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises at least one HCV CD4⁺ T cell epitope and at least one HCV CD8⁺ T cell epitope. In some cases, the T cell epitope polypeptide comprises at least one HCV-NS4A CD4⁺ T cell epitope and at least one HCV-NS4A CD8⁺ T cell epitope. In some cases, T cell epitope polypeptide comprises 2 or more HCV-NS4A CD4⁺ T-cell epitopes and 2 or more HCV-NS4A CD8⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 2, 3, 4, or 5 HCV-NS4A CD4⁺ T-cell epitopes and 2, 3, 4, or 5 HCV-NS4A CD8⁺ T-cell epitopes.

[00116] In some cases, the T cell epitope polypeptide comprises a single T-cell epitope. In some cases, the T cell epitope polypeptide comprises a single HCV-NS5A T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-NS5A T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 3 or more HCV-NS5A T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 4 or more HCV-NS5A T-cell epitopes. In some cases, the T cell epitope polypeptide comprises a single HCV-NS5A CD4⁺ T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-NS5A CD4⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises one or more HCV CD8⁺ T cell epitopes. In some cases, the T cell epitope polypeptide comprises a single HCV-NS5A CD8⁺ T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-NS5A CD8⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises at least one HCV CD4⁺ T cell epitope and at least one HCV CD8⁺ T cell epitope. In some cases, the T cell epitope polypeptide comprises at least one HCV-NS5A CD4⁺ T cell epitope and at least one HCV-NS5A CD8⁺ T cell epitope. In some cases, T cell epitope polypeptide comprises 2 or more HCV-NS5A CD4⁺ T-cell epitopes and 2 or more HCV-NS5A CD8⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 2, 3, 4, or 5 HCV-NS5A CD4⁺ T-cell epitopes and 2, 3, 4, or 5 HCV-NS5A CD8⁺ T-cell epitopes.

[00117] In some cases, the T cell epitope polypeptide comprises a single T-cell epitope. In some cases, the T cell epitope polypeptide comprises a single HCV-NS5B T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-NS5B T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 3 or more HCV-NS5B T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 4 or more HCV-NS5B T-cell epitopes. In some cases, the T

cell epitope polypeptide comprises a single HCV-NS5B CD4⁺ T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-NS5B CD4⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises one or more HCV CD8⁺ T cell epitopes. In some cases, the T cell epitope polypeptide comprises a single HCV-NS5B CD8⁺ T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-NS5B CD8⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises at least one HCV CD4⁺ T cell epitope and at least one HCV CD8⁺ T cell epitope. In some cases, the T cell epitope polypeptide comprises at least one HCV-NS5B CD4⁺ T cell epitope and at least one HCV-NS5B CD8⁺ T cell epitope. In some cases, T cell epitope polypeptide comprises 2 or more HCV-NS5B CD4⁺ T-cell epitopes and 2 or more HCV-NS5B CD8⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 2, 3, 4, or 5 HCV-NS5B CD4⁺ T-cell epitopes and 2, 3, 4, or 5 HCV-NS5B CD8⁺ T-cell epitopes.

[00118] In some cases, the T cell epitope polypeptide comprises a single T-cell epitope. In some cases, the T cell epitope polypeptide comprises a single HCV-core T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-core T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 3 or more HCV-core T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 4 or more HCV-core T-cell epitopes. In some cases, the T cell epitope polypeptide comprises a single HCV-core CD4⁺ T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-core CD4⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises one or more HCV CD8⁺ T cell epitopes. In some cases, the T cell epitope polypeptide comprises a single HCV-core CD8⁺ T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-core CD8⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises at least one HCV CD4⁺ T cell epitope and at least one HCV CD8⁺ T cell epitope. In some cases, the T cell epitope polypeptide comprises at least one HCV-core CD4⁺ T cell epitope and at least one HCV-core CD8⁺ T cell epitope. In some cases, T cell epitope polypeptide comprises 2 or more HCV-core CD4⁺ T-cell epitopes and 2 or more HCV-core CD8⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 2, 3, 4, or 5 HCV-core CD4⁺ T-cell epitopes and 2, 3, 4, or 5 HCV-core CD8⁺ T-cell epitopes.

[00119] In some cases, the T cell epitope polypeptide comprises a single T-cell epitope. In some cases, the T cell epitope polypeptide comprises a single HCV-p7 T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-p7 T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 3 or more HCV-p7 T-cell epitopes. In some cases, the T cell epitope polypeptide comprises 4 or more HCV-p7 T-cell epitopes. In some cases, the T cell

epitope polypeptide comprises a single HCV-p7 CD4⁺ T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-core CD4⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises one or more HCV CD8⁺ T cell epitopes. In some cases, the T cell epitope polypeptide comprises a single HCV-p7 CD8⁺ T-cell epitope. In some cases, the T cell epitope polypeptide comprises 2 or more HCV-p7 CD8⁺ T-cell epitopes. In some cases, the T cell epitope polypeptide comprises at least one HCV CD4⁺ T cell epitope and at least one HCV CD8⁺ T cell epitope. In some cases, the T cell epitope polypeptide comprises at least one HCV-p7 CD4⁺ T cell epitope and at least one HCV-p7 CD8⁺ T cell epitope. In some cases, T cell epitope polypeptide comprises 2 or more HCV-p7 CD4⁺ T-cell epitopes and 2 or more HCV-p7 CD8⁺ T-cell epitopes. In some cases, the T-cell epitope polypeptide comprises 2, 3, 4, or 5 HCV-p7 CD4⁺ T-cell epitopes and 2, 3, 4, or 5 HCV-p7 CD8⁺ T-cell epitopes.

[00120] In some cases, the T cell epitope polypeptide comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, or 63, of the T-cell epitopes set out in FIG. 9A-9B. In some cases, the T cell epitope polypeptide comprises from 1 to 3, from 3 to 5, from 5 to 10, from 10 to 15, from 15 to 20, from 20 to 25, or from 25 to 30 of the T-cell epitopes set out in FIG. 9A-9B. For example, in some cases, the T cell epitope polypeptide comprises the T-cell epitopes designated NS3-3, NS3-4, and NS3-11 in FIG. 9A-9B and FIG. 11A-11N. As another example, in some cases, the T cell epitope polypeptide comprises the T-cell epitopes designated NS2-1, NS2-2, NS2-3, NS2-7, and NS2-8 in FIG. 9A-9B and FIG. 11A-11N. As another example, in some cases, the T cell epitope polypeptide comprises the T-cell epitopes designated NS3-3, NS3-4, NS3-5, and NS3-11 in FIG. 9A-9B and FIG. 11A-11N. As another example, in some cases, the T cell epitope polypeptide comprises the T-cell epitopes designated NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-11, NS3-12, and NS3-13 in FIG. 9A-9B and FIG. 11A-11N. As another example, in some cases, the T cell epitope polypeptide comprises the T-cell epitopes designated NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-10, NS3-11, NS3-12, and NS3-13 in FIG. 9A-9B and FIG. 11A-11N. As another example, in some cases, the T cell epitope polypeptide comprises the T-cell epitopes designated Core-1, Core-2, Core-3, Core-4, Core-5, Core-6, Core-7, Core-8, Core-9, Core-10, Core-11, Core-12, Core-13, Core-14, Core-16, Core-17, Core-18, Core-19, Core-20, Core-21, and Core-22 in FIG. 9A-9B and FIG. 11A-11N. As another example, in some cases, the T cell epitope polypeptide comprises the T-cell epitopes designated NS3-1, NS3-2, NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-9, NS3-10, NS3-11, NS3-12, and NS3-13 in FIG. 9A-9B and FIG. 11A-11N. As another example, in some cases, the T cell epitope polypeptide comprises the T-cell epitopes designated NS2-1, NS2-2, NS2-3, NS2-4, NS2-5, NS2-6, NS2-7, NS2-8, NS3-1, NS3-

2, NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-9, NS3-10, NS3-11, NS3-12, and NS3-13 in FIG. 9A-9B and FIG. 11A-11N. As another example, in some cases, the T cell epitope polypeptide comprises the T-cell epitopes designated NS3-1, NS3-2, NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-8, NS3-9, NS3-10, NS3-11, NS3-12, NS3-13, NS3-14, NS4a-1, NS4b-1, NS4b-2, NS4b-3, NS4b-4, NS4b-5, NS4b-6, NS4b-7, NS4b-8, NS4b-9, and NS4b-10 in FIG. 9A-9B and FIG. 11A-11N. As another example, in some cases, the T cell epitope polypeptide comprises the T-cell epitopes designated NS3-1, NS3-2, NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-8, NS3-9, NS3-10, NS3-11, NS3-12, NS3-13, NS3-14, NS4a-1, NS4b-1, NS4b-2, NS4b-3, NS4b-4, NS4b-5, NS4b-6, NS4b-7, NS4b-8, NS4b-9, NS4b-10, NS5a-1, NS5a-2, NS5b-1, and NS5b-2 in FIG. 9A-9B and FIG. 11A-11N. In some cases, the T-cell epitopes are contiguous. In some cases, any two T-cell epitopes are separated by linkers (e.g., a linker having a length of from 1 amino acid to about 50 amino acids, e.g., from 1 amino acid to 5 amino acids (aa), from 5 aa to 10 aa, from 10 aa to 15 aa, from 15 aa to 20 aa, from 20 aa to 25 aa, from 25 aa to 30 aa, from 30 aa to 40 aa, or from 40 aa to 50 aa).

[00121] In some cases, the T cell epitope polypeptide comprises at least one HCV CD4⁺ T cell epitope and at least one HCV CD8⁺ T cell epitope, where epitopes are conserved among HCV genotypes 1 and 2. In some cases, the T cell epitope polypeptide comprises at least one HCV CD4⁺ T cell epitope and at least one HCV CD8⁺ T cell epitope, where epitopes are conserved among HCV genotypes 1 and 3. In some cases, the T cell epitope polypeptide comprises at least one HCV CD4⁺ T cell epitope and at least one HCV CD8⁺ T cell epitope, where epitopes are conserved among HCV genotypes 1, 2, and 3. In some cases, the T cell epitope polypeptide comprises at least one HCV CD4⁺ T cell epitope and at least one HCV CD8⁺ T cell epitope, where epitopes are conserved among HCV genotypes 1, 2, 3, and 7. In some cases, the T cell epitope polypeptide comprises at least one HCV CD4⁺ T cell epitope and at least one HCV CD8⁺ T cell epitope, where epitopes are conserved among HCV genotypes 1-7.

[00122] The T cell epitope polypeptide can have a length of from about 10 amino acids to about 2000 amino acids; e.g., the T cell epitope polypeptide can have a length of from 10 amino acids (aa) to 15 aa, from 15 aa to 20 aa, from 20 aa to 25 aa, from 25 aa to 50 aa, from 50 aa to 75 aa, from 75 aa to 100 aa, from 100 aa to 150 aa, from 150 aa to 200 aa, from 200 aa to 250 aa, from 250 aa to 300 aa, from 300 aa to 350 aa, from 350 aa to 400 aa, from 450 aa to 500 aa, from 500 aa to 550 aa, from 550 aa to 600 aa, from 600 aa to 650 aa, from 650 aa to 700 aa, from 700 aa to 750 aa, or from 750 aa to 800 aa. The T-cell epitope polypeptide can have a length of from about 25 amino acids to about 2000 amino acids, e.g., from about 25 amino acids (aa) to 50 aa, from 50 aa to 75 aa, from 75 aa to 100 aa, from 100 aa to 150 aa, from 150 aa to 200 aa, from 200 aa to 250 aa, from 250 aa to 300 aa, from 300 aa to 350 aa, from 350 aa to 400 aa, from 400 aa to 500

aa, from 500 aa to 600 aa, from 600 aa to 700 aa, from 700 aa to 800 aa, from 800 aa to 900 aa, from 900 aa to 1000 aa, from 1000 aa to 1100 aa, from 1100 aa to 1200 aa, from 1200 aa to 1300 aa, from 1300 aa to 1400 aa, from 1400 aa to 1500 aa, from 1500 aa to 1600 aa, from 1600 aa to 1700 aa, from 1700 aa to 1800 aa, from 1800 aa to 1900 aa, or from 1900 aa to 2000 aa. The T-cell epitope polypeptide can have a length of from about 25 amino acids to about 3000 amino acids, e.g., from about 25 amino acids (aa) to 50 aa, from 50 aa to 75 aa, from 75 aa to 100 aa, from 100 aa to 150 aa, from 150 aa to 200 aa, from 200 aa to 250 aa, from 250 aa to 300 aa, from 300 aa to 350 aa, from 350 aa to 400 aa, from 400 aa to 500 aa, from 500 aa to 600 aa, from 600 aa to 700 aa, from 700 aa to 800 aa, from 800 aa to 900 aa, from 900 aa to 1000 aa, from 1000 aa to 1100 aa, from 1100 aa to 1200 aa, from 1200 aa to 1300 aa, from 1300 aa to 1400 aa, from 1400 aa to 1500 aa, from 1500 aa to 1600 aa, from 1600 aa to 1700 aa, from 1700 aa to 1800 aa, from 1800 aa to 1900 aa, from 1900 aa to 2000 aa, from 2000 aa to 2250 aa, from 2250 aa to 2500 aa, from 2500 aa to 2750 aa, or from 2750 aa to 3000 aa.

[00123] The T cell epitope polypeptide can have a length of from about 25 amino acids to about 800 amino acids, e.g., from about 25 amino acids (aa) to 50 aa, from 50 aa to 75 aa, from 75 aa to 100 aa, from 100 aa to 150 aa, from 150 aa to 200 aa, from 200 aa to 250 aa, from 250 aa to 300 aa, from 300 aa to 350 aa, from 350 aa to 400 aa, from 450 aa to 500 aa, from 500 aa to 550 aa, from 550 aa to 600 aa, from 600 aa to 650 aa, from 650 aa to 700 aa, from 700 aa to 750 aa, or from 750 aa to 800 aa. The T-cell epitope polypeptide can have a length of from about 25 amino acids to about 400 amino acids, e.g., from about 25 amino acids (aa) to 50 aa, from 50 aa to 75 aa, from 75 aa to 100 aa, from 100 aa to 150 aa, from 150 aa to 200 aa, from 200 aa to 250 aa, from 250 aa to 300 aa, from 300 aa to 350 aa, or from 350 aa to 400 aa. The T-cell epitope polypeptide can have a length of 25 amino acids (aa), 26 aa, 27 aa, 28 aa, 29 aa, 30 aa, 31 aa, 32 aa, 33 aa, 34 aa, 35 aa, 36 aa, 37 aa, 38 aa, 39 aa, 40 aa, 41 aa, 42 aa, 43 aa, 44 aa, 45 aa, 46 aa, 47 aa, 48 aa, 49 aa, or 50 aa. The T cell epitope polypeptide can have a length of from about 100 amino acids (aa) to 800 aa, e.g., from 100 aa to 150 aa, from 150 aa to 200 aa, from 200 aa to 250 aa, from 250 aa to 300 aa, from 300 aa to 350 aa, from 350 aa to 400 aa, from 450 aa to 500 aa, from 500 aa to 550 aa, from 550 aa to 600 aa, from 600 aa to 650 aa, from 650 aa to 700 aa, from 700 aa to 750 aa, or from 750 aa to 800 aa. The T cell epitope polypeptide can have a length of from 25 aa to 30 aa. The T cell epitope polypeptide can have a length of from 30 aa to 40 aa. The T cell epitope polypeptide can have a length of from 40 aa to 50 aa. The T-cell epitope polypeptide can have a length of from 50 aa to 60 aa (e.g., 50 aa, 51 aa, 52, aa, 53 aa, 54 aa, 55 aa, 56 aa, 57 aa, 58 aa, 59 aa, or 60 aa). The T cell epitope polypeptide can have a length of from 60 aa to 70 aa. The T cell epitope polypeptide can have a length of from 65 aa to 75 aa (e.g., 65, 66, 67, 68, 69, 70, 71, 72, 7, 74, or 75 aa). The T cell epitope polypeptide can have a

length of 70 aa. The T cell epitope polypeptide can have a length of from 70 aa to 80 aa. The T cell epitope polypeptide can have a length of from 80 aa to 90 aa. The T cell epitope polypeptide can have a length of from 90 aa to 100 aa. The T cell epitope polypeptide can have a length of from 100 aa to 105 aa (e.g., 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, or 110 aa). The T cell epitope polypeptide can have a length of 100 aa. The T cell epitope polypeptide can have a length of from 10 amino acids (aa) to 50 aa; e.g., from 10 aa to 15 aa, from 15 aa to 20 aa, from 20 aa to 25 aa, from 25 aa to 30 aa, from 30 aa to 35 aa, from 35 aa to 40 aa, from 40 aa to 45 aa, or from 45 aa to 50 aa. The T cell epitope polypeptide can have a length of from 10 amino acids (aa) to 20 aa, e.g., 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 aa.

HCV NS3 T-cell epitopes

[00124] In some cases, the T cell epitope polypeptide present in an immunogenic composition of the present disclosure includes one or more T-cell epitopes present in an HCV NS3 polypeptide. Examples of T-cell epitopes present in NS3 polypeptides are depicted in FIG. 11A-11N, FIG. 9B, and FIG. 10A-10B.

[00125] The T cell epitope polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: AIPLEVIKGGRHLIFCHSKKKCDELA AKL (SEQ ID NO:85).

AIPLEVIKGGRHLIFCHSKKKCDELA AKL (SEQ ID NO:85) is referred to in FIG. 10A as "TP29." In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: AIPLEVIKGGRHLIFCHSKKKCDELA AKL (SEQ ID NO:85); and has a length of from 25 aa to 35 aa (e.g., 25 aa, 26 aa, 27 aa, 28 aa, 29 aa, 30 aa, 31 aa, 32 aa, 33 aa, 34 aa, or 35 aa). In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: AIPLEVIKGGRHLIFCHSKKKCDELA AKL (SEQ ID NO:85); and has a length

of 29 amino acids. Such a polypeptide can include NS3 T-cell epitopes designated NS3-3, NS3-4, and NS3-11 in FIG. 9B and FIG. 11A-11N.

[00126] The T cell epitope polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: AIPLEVIKGGRLIFCHSKKKCDELA AKLV ALGINAVAYYRGLDVSVIPTSG (SEQ ID NO:87). AIPLEVIKGGRLIFCHSKKKCDELA AKLV ALGINAVAYYRGLDVSVIPTSG (SEQ ID NO:87) is referred to in FIG. 10A as "TP52." In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: AIPLEVIKGGRLIFCHSKKKCDELA AKLV ALGINAVAYYRGLDVSVIPTSG (SEQ ID NO:87); and has a length of from 45 amino acids to 60 amino acids (e.g., 45 aa, 46 aa, 47 aa, 48 aa, 49 aa, 50 aa, 51 aa, 52 aa, 53 aa, 54 aa, 55 aa, 56 aa, 57 aa, 58 aa, 59 aa, or 60 aa). In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: AIPLEVIKGGRLIFCHSKKKCDELA AKLV ALGINAVAYYRGLDVSVIPTSG (SEQ ID NO:87); and has a length of 52 amino acids. Such a polypeptide can include NS3 T-cell epitopes designated NS3-3, NS3-4, NS3-5, and NS3-11 in FIG. 9B and FIG. 11A-11N.

[00127] The T cell epitope polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: KGGRHLIFCHSKKKCDELA AKLV ALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTG FTGDFDSVIDCN (SEQ ID NO:88); and has a length of from 65 amino acids to 80 amino acids (e.g., 65 aa, 66 aa, 67 aa, 68 aa, 69 aa, 70 aa, 71 aa, 72 aa, 73 aa, 74 aa, 75 aa, 76 aa, 77 aa, 78 aa, 79 aa, or 80 aa).

KGGRHLIFCHSKKKCELA AAKLVALGINAVAYYRGLDVS VIPTSGDVVVVATDALMTGFTGDFDSVIDCN (SEQ ID NO:88) is referred to in FIG. 10A as “TP70.”

[00128] In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence:

KGGRHLIFCHSKKKCELA AAKLVALGINAVAYYRGLDVS VIPTSGDVVVVATDALMTGFTGDFDSVIDCN (SEQ ID NO:88); and has a length of 70 amino acids. Such a polypeptide can include NS3 T-cell epitopes designated NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-11, NS3-12, and NS3-13 in FIG. 9B and FIG. 11A-11N.

[00129] The T cell epitope polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence:

VALSTTGEIPFYGKAIPLEVIKGG RHLIFCHSKKKCELA AAKLVALGINAVAYYRGLDVS VIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVTQTVDF (SEQ ID NO:89); and has a length of from 95 amino acids (aa) to 105 aa (e.g., 95 aa, 96 aa, 97 aa, 98 aa, 99 aa, 100 aa, 101 aa, 102 aa, 103 aa, 104 aa, or 105 aa).

VALSTTGEIPFYGKAIPLEVIKGG RHLIFCHSKKKCELA AAKLVALGINAVAYYRGLDVS VIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVTQTVDF (SEQ ID NO:89) is referred to in FIG. 10A as “TP100.”

[00130] In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence:

VALSTTGEIPFYGKAIPLEVIKGG RHLIFCHSKKKCELA AAKLVALGINAVAYYRGLDVS VIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVTQTVDF (SEQ ID NO:89); and has a length of 100 amino acids. Such a polypeptide can include NS3 T-cell epitopes designated NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-10, NS3-11, NS3-12, and NS3-13 in FIG. 9B and FIG. 11A-11N.

[00131] The T cell epitope polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQP RGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRS RNLGKVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPG (SEQ ID NO:90); and has a length of from 171 amino acids (aa) to 180 aa (e.g., 171 aa, 172 aa, 173 aa, 174 aa, 175 aa, 176 aa, 177 aa, 178 aa, 179 aa, or 180 aa. MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQP RGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRS RNLGKVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPG (SEQ ID NO:90) is referred to in FIG. 10A as “TP171.”

[00132] In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQP RGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRS RNLGKVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPG (SEQ ID NO:90); and has a length of 171 amino acids.

[00133] The T cell epitope polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQP RGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRS RNLGKVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSF SIFLLALLSCLTVPASA (SEQ ID NO:129); and has a length of from 190 amino acids (aa) to 200 aa (e.g., 190 aa, 191 aa, 192 aa, 193 aa, 194 aa, 195 aa, 196 aa, 197 aa, 198 aa, 199 aa, or 200 aa.

[00134] In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence:

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQP
RGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRS
RNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSF
SIFLLALLSCLTVPASA (SEQ ID NO:129); and has a length of 191 amino acids.

[00135] The T cell epitope polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence:

LHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTIT
TGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLA
TATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRH LIFCHSKKKCDELA AKLV
ALGINAVAYYRGLDVS VIPTSGDVVVVATDALMTGFTGDFDSVIDCN (SEQ ID NO:91);
and has a length of from 215 amino acids (aa) to 235 aa (e.g., 215 aa, 216 aa, 217 aa, 218 aa, 219 aa, 220 aa, 221 aa, 222 aa, 223 aa, 224 aa, 225 aa, 226 aa, 227 aa, 228 aa, 229 aa, 230 aa, 231 aa, 232 aa, 233 aa, 234 aa, or 235 aa).

LHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTIT
TGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLA
TATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRH LIFCHSKKKCDELA AKLV
ALGINAVAYYRGLDVS VIPTSGDVVVVATDALMTGFTGDFDSVIDCN (SEQ ID NO:91)
is referred to in FIG. 10A as “TP228.”

[00136] In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence:

LHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTIT
TGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLA

TATPPGSVTVPHPNIEEVALSTTGEPFYGKAIPLEVIKGGRRHLIFCHSKKKCDELA AKLV
 ALGINAVAYYRGLDVSIVIPTSGD VVVVATDALMTGFTGDFDSVIDCN (SEQ ID NO:91);
 and has a length of 228 amino acids. Such a polypeptide can include NS3 T-cell epitopes
 designated NS3-1, NS3-2, NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-9, NS3-10, NS3-11, NS3-
 12, and NS3-13 in FIG. 9B and FIG. 11A-11N.

[00137] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1265-1279 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 15 amino acids (aa) to 20 amino acids (e.g., 15 aa, 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

[00138] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1309-1323 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 15 amino acids (aa) to 20 amino acids (e.g., 15 aa, 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

[00139] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1401-1415 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 15 amino acids (aa) to 20 amino acids (e.g., 15 aa, 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

[00140] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at

least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1402-1412 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 11 amino acids (aa) to 16 amino acids (e.g., 11 aa, 12 aa, 13 aa, 14 aa, 15 aa, or 16 aa).

[00141] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1429-1439 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 11 amino acids (aa) to 16 amino acids (e.g., 11 aa, 12 aa, 13 aa, 14 aa, 15 aa, or 16 aa).

[00142] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1450-1464 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 15 amino acids (aa) to 20 amino acids (e.g., 15 aa, 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

[00143] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1453-1467 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 15 amino acids (aa) to 20 amino acids (e.g., 15 aa, 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

[00144] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at

least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1577-1591 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 15 amino acids (aa) to 20 amino acids (e.g., 15 aa, 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

[00145] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1306-1314 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00146] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1387-1394 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 1 amino acids (aa) to 15 amino acids (e.g., 8 aa, 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00147] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1405-1413 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00148] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1450-1458 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00149] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1457-1465 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00150] As another example, the T cell epitope polypeptide can comprise an HCV NS3 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1610-1618 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS3 amino acid sequence of any HCV genotype; and the HCV NS3 T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

HCV NS2 T-cell epitopes

[00151] In some cases, the T cell epitope polypeptide present in an immunogenic composition of the present disclosure includes one or more T-cell epitopes present in an HCV NS2 polypeptide. Examples of T-cell epitopes present in NS2 polypeptides are depicted in FIG. 11A-11N, and FIG. 9A.

[00152] For example, the T cell epitope polypeptide can comprise an NS2 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about

30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 955-974 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS2 amino acid sequence of any HCV genotype; and the NS2 T cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00153] As another example, the T cell epitope polypeptide can comprise an NS2 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 975-994 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS2 amino acid sequence of any HCV genotype; and the NS2 T cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00154] As another example, the T cell epitope polypeptide can comprise an NS2 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 985-1004 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS2 amino acid sequence of any HCV genotype; and the NS2 T cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00155] As another example, the T cell epitope polypeptide can comprise an NS2 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1015-1034 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS2 amino acid sequence of any HCV genotype; and the NS2 T cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

- [00156]** As another example, the T cell epitope polypeptide can comprise an NS2 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1035-1054 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS2 amino acid sequence of any HCV genotype; and the NS2 T cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).
- [00157]** As another example, the T cell epitope polypeptide can comprise an NS2 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 924-933 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS2 amino acid sequence of any HCV genotype; and the NS2 T cell epitope can have a length of from 10 amino acids (aa) to 15 amino acids (e.g., 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).
- [00158]** As another example, the T cell epitope polypeptide can comprise an NS2 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 961-970 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS2 amino acid sequence of any HCV genotype; and the NS2 T cell epitope can have a length of from 10 amino acids (aa) to 15 amino acids (e.g., 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).
- [00159]** As another example, the T cell epitope polypeptide can comprise an NS2 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 989-997 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS2 amino acid sequence of any HCV genotype; and

the NS2 T cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00160] In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to a contiguous stretch of from 10 amino acids (aa) to 50 aa (e.g., from 10 aa to 25 aa, or from 25 aa to 50 aa) of amino acids 955-1004 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS2 amino acid sequence of any HCV genotype; and has a length of from 10 amino acids (aa) to 25 aa, or from 25 aa to 50 aa. In some cases, the T-cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 955-1004 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS2 amino acid sequence of any HCV genotype; and has a length of about 50 amino acids.

[00161] In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to a contiguous stretch of from 10 amino acids (aa) to 553 aa (e.g., from 10 aa to 25 aa, from 25 aa to 50 aa, from 50 aa to 100 aa, from 100 aa to 200 aa, from 200 aa to 300 aa, from 300 aa to 400 aa, from 400 aa to 500 aa, or from 500 aa to 553 aa) of amino acids 917-1469 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS2 and NS3 amino acid sequence of any HCV genotype; and has a length of from 10 amino acids (aa) to 25 aa, from 25 aa to 50 aa, from 50 aa to 100 aa, from 100 aa to 200 aa, from 200 aa to 300 aa, from 300 aa to 400 aa, from 400 aa to 500 aa, or from 500 aa to 553 aa. In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 917-1469 of the amino acid sequence designated “Consensus”

in FIG. 12A-12L, or a corresponding HCV NS2 and NS3 amino acid sequence of any HCV genotype; and has a length of about 553 amino acids.

[00162] The T cell epitope polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: LGALTGTYVYNHLTPLRDWAHNGLRDLAVAVEPVVFSQMETKLITWGADT (SEQ ID NO:86). LGALTGTYVYNHLTPLRDWAHNGLRDLAVAVEPVVFSQMETKLITWGADT (SEQ ID NO:86) is referred to in FIG. 10A as "TP50." In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: LGALTGTYVYNHLTPLRDWAHNGLRDLAVAVEPVVFSQMETKLITWGADT (SEQ ID NO:86); and has a length of from 50 amino acids to 60 amino acids (e.g., 50 aa, 51 aa, 52 aa, 53 aa, 54 aa, 55 aa, 56 aa, 57 aa, 58 aa, 59 aa, or 60 aa). In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: LGALTGTYVYNHLTPLRDWAHNGLRDLAVAVEPVVFSQMETKLITWGADT (SEQ ID NO:86); and has a length of 50 amino acids. Such a polypeptide can include NS2 T-cell epitopes designated NS2-1, NS2-2, NS2-3, NS2-7, and NS2-8 in FIG. 9A and FIG. 11A-11N.

HCV NS4A T-cell epitopes

[00163] In some cases, the T cell epitope polypeptide present in an immunogenic composition of the present disclosure includes one or more T-cell epitopes present in an HCV NS4A polypeptide. Examples of T-cell epitopes present in NS4A polypeptides are depicted in FIG. 11A-11N and FIG. 9B.

[00164] The T cell epitope polypeptide can comprise an NS4A T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%,

at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1683-1692 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS4A amino acid sequence of any HCV genotype; and the NS4A T-cell epitope can have a length of from 10 amino acids (aa) to 15 amino acids (e.g., 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

HCV NS4B T-cell epitopes

[00165] In some cases, the T cell epitope polypeptide present in an immunogenic composition of the present disclosure includes one or more T-cell epitopes present in an HCV NS4B polypeptide. Examples of T-cell epitopes present in NS4B polypeptides are depicted in FIG. 11A-11N and FIG. 9B.

[00166] As one example, the T cell epitope polypeptide can comprise an NS4B T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1790-1801 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS4B amino acid sequence of any HCV genotype; and the NS4B T-cell epitope can have a length of from 12 amino acids (aa) to 20 amino acids (e.g., 12 aa, 13 aa, 14 aa, 15 aa, 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

[00167] As another example, the T cell epitope polypeptide can comprise an NS4B T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1792-1802 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS4B amino acid sequence of any HCV genotype; and the NS4B T-cell epitope can have a length of from 11 amino acids (aa) to 20 amino acids (e.g., 11 aa, 12 aa, 13 aa, 14 aa, 15 aa, 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

[00168] As another example, the T cell epitope polypeptide can comprise an NS4B T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1898-1905 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS4B amino acid sequence of any HCV genotype;

and the NS4B T-cell epitope can have a length of from 8 amino acids (aa) to 15 amino acids (e.g., 8 aa, 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00169] As another example, the T cell epitope polypeptide can comprise an NS4B T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1921-1935 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS4B amino acid sequence of any HCV genotype; and the NS4B T-cell epitope can have a length of from 15 amino acids (aa) to 20 amino acids (e.g., 15 aa, 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

[00170] As another example, the T cell epitope polypeptide can comprise an NS4B T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1922-1941 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS4B amino acid sequence of any HCV genotype; and the NS4B T-cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00171] As another example, the T cell epitope polypeptide can comprise an NS4B T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1928-1947 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV NS4B amino acid sequence of any HCV genotype; and the NS4B T-cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00172] As another example, the T cell epitope polypeptide can comprise an NS4B T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1868-1876 of the amino acid sequence designated "Consensus"

in FIG. 12A-12L, or a corresponding HCV NS4B amino acid sequence of any HCV genotype; and the NS4B T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00173] As another example, the T cell epitope polypeptide can comprise an NS4B T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1927-1942 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS4B amino acid sequence of any HCV genotype; and the NS4B T-cell epitope can have a length of from 16 amino acids (aa) to 20 amino acids (e.g., 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

[00174] As another example, the T cell epitope polypeptide can comprise an NS4B T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1932-1940 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS4B amino acid sequence of any HCV genotype; and the NS4B T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00175] As another example, the T cell epitope polypeptide can comprise an NS4B T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1948-1962 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS4B amino acid sequence of any HCV genotype; and the NS4B T-cell epitope can have a length of from 15 amino acids (aa) to 20 amino acids (e.g., 15 aa, 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

HCV NS5A T-cell epitopes

[00176] In some cases, the T cell epitope polypeptide present in an immunogenic composition of the present disclosure includes one or more T-cell epitopes present in an HCV NS5A polypeptide. Examples of T-cell epitopes present in NS5A polypeptides are depicted in **FIG. 11A-11N** and **FIG. 9B**.

[00177] As one example, the T cell epitope polypeptide can comprise an NS5A T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 2218-2232 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS5A amino acid sequence of any HCV genotype; and the NS5A T-cell epitope can have a length of from 15 amino acids (aa) to 20 amino acids (e.g., 15 aa, 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

[00178] As another example, the T cell epitope polypeptide can comprise an NS5A T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 2309-2317 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS5A amino acid sequence of any HCV genotype; and the NS5A T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

HCV NS5B T-cell epitopes

[00179] In some cases, the T cell epitope polypeptide present in an immunogenic composition of the present disclosure includes one or more T-cell epitopes present in an HCV NS5B polypeptide. Examples of T-cell epitopes present in NS5B polypeptides are depicted in **FIG. 11A-11N** and **FIG. 9B**.

[00180] As one example, the T cell epitope polypeptide can comprise an NS5B T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 2847-2851 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS5B amino acid sequence of any HCV genotype; and the NS5B T-cell epitope can have a length of from 5 amino acids (aa) to 10 amino acids (e.g., 5 aa, 6 aa, 7 aa, 8 aa, 9 aa, or 10 aa).

[00181] As another example, the T cell epitope polypeptide can comprise an NS5B T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about

30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 2602-2610 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV NS5B amino acid sequence of any HCV genotype; and the NS5B T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

HCV core T-cell epitopes

[00182] In some cases, the T cell epitope polypeptide present in an immunogenic composition of the present disclosure includes one or more T-cell epitopes present in an HCV core polypeptide. Examples of T-cell epitopes present in HCV Core polypeptides are depicted in **FIG. 11A-11N** and **FIG. 9A**.

[00183] As one example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1-20 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00184] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 11-30 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00185] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino

acid sequence identity to amino acids 21-40 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00186] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 39-63 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 23 amino acids (aa) to 28 amino acids (e.g., 23 aa, 24 aa, 25 aa, 26 aa, 27 aa, or 28 aa).

[00187] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 47-70 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 24 amino acids (aa) to 29 amino acids (e.g., 24 aa, 25 aa, 26 aa, 27 aa, 28 aa, or 29 aa).

[00188] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 61-80 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00189] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%,

at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 71-90 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00190] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 81-100 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00191] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 91-110 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00192] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 101-115 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 15 amino acids (aa) to 20 amino acids (e.g., 15 aa, 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

[00193] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at

least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 111-130 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00194] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 125-139 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 15 amino acids (aa) to 20 amino acids (e.g., 15 aa, 16 aa, 17 aa, 18 aa, 19 aa, or 20 aa).

[00195] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 131-150 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00196] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 151-170 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00197] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at

least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 161-180 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 20 amino acids (aa) to 25 amino acids (e.g., 20 aa, 21 aa, 22 aa, 23 aa, 24 aa, or 25 aa).

[00198] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 35-44 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 10 amino acids (aa) to 15 amino acids (e.g., 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00199] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 43-51 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00200] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 51-59 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

- [00201]** As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 129-137 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).
- [00202]** As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 131-140 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 10 amino acids (aa) to 15 amino acids (e.g., 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).
- [00203]** As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 150-158 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).
- [00204]** As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 154-162 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV

genotype; and the HCV core T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00205] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 168-176 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00206] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 177-187 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 11 amino acids (aa) to 16 amino acids (e.g., 11 aa, 12 aa, 13 aa, 14 aa, 15 aa, or 16 aa).

[00207] As another example, the T cell epitope polypeptide can comprise an HCV core T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 178-187 of the amino acid sequence designated “Consensus” in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and the HCV core T-cell epitope can have a length of from 10 amino acids (aa) to 15 amino acids (e.g., 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

[00208] In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to a contiguous stretch of from 10 amino acids (aa) to 191 aa (e.g., from 10 aa to 25 aa, from 25 aa to 50 aa, from 50 aa to

75 aa, from 75 aa to 100 aa, from 100 aa to 150 aa, or from 150 aa to 191aa) of amino acids 1-191 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and has a length of from 10 amino acids (aa) to 25 aa, from 25 aa to 50 aa, from 50 aa to 100 aa, or from 100 aa to 150 aa, or from 150 aa to 191 aa. In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 1-191 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV core amino acid sequence of any HCV genotype; and has a length of about 191 amino acids.

[00209] The T cell epitope polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQP RGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRS RNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPG (SEQ ID NO:90); and has a length of from 171 amino acids (aa) to 180 aa (e.g., 171 aa, 172 aa, 173 aa, 174 aa, 175 aa, 176 aa, 177 aa, 178 aa, 179 aa, or 180 aa. In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence: MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQP RGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRS RNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPG (SEQ ID NO:90); and has a length of 171 amino acids. Such a polypeptide can include core T-cell epitopes designated Core-1, Core-2, Core-3, Core-4, Core-5, Core-6, Core-7, Core-8, Core-9, Core-10, Core-11, Core-12, Core-13, Core-14, Core-16, Core-17, Core-18, Core-19, Core-20, Core-21, Core-22 in FIG. 9A and FIG. 11A-11N.

HCV p7 T-cell epitopes

[00210] In some cases, the T cell epitope polypeptide present in an immunogenic composition of the present disclosure includes one or more T-cell epitopes present in an HCV p7 polypeptide. Examples of T-cell epitopes present in HCV p7 polypeptides are depicted in **FIG. 11A-11N** or **FIG. 9A**.

[00211] As another example, the T cell epitope polypeptide can comprise an HCV p7 T cell epitope comprising an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to amino acids 803-811 of the amino acid sequence designated "Consensus" in FIG. 12A-12L, or a corresponding HCV p7 amino acid sequence of any HCV genotype; and the HCV p7 T-cell epitope can have a length of from 9 amino acids (aa) to 15 amino acids (e.g., 9 aa, 10 aa, 11 aa, 12 aa, 13 aa, 14 aa, or 15 aa).

T-cell epitope polypeptides including HCV T-cell epitopes from more than one HCV polypeptide other than E1 and E2

[00212] As noted above, a T-cell epitope polypeptide can include T-cell epitopes from more than one HCV polypeptide other than E1 and E2.

[00213] As one example, a T cell epitope polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence:

QASLLKVPYFVRVQGLLRICALARKMAGGHYVQMAIIKLGALTGTYVYNALTPLRDW
 AHNGLRDLAVAVEPVVFSQMETKLITWGADTAACGDIINGLPVSARRGREILLGPADG
 MVSKGWRL LAPITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCING
 VCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPAPQGARS LTPCTCGSSDLYLVT
 RHADVIPVRRRGDSRGSLLSPRPISYLKGSAGGPLLCPAGHAVGIFRAAVCTRGVAKAV
 DFIPVENLETTMRSPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVL
 VLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDII
 ICDECHSTDATSILGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPF
 YGKAIPLEVIKGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVS VIPTSGDVVV
 VATDALMTGFTGDFDSVIDCN (SEQ ID NO:92); and has a length of from 550 amino acids

(aa) to 560 aa (e.g., 550 aa, 551 aa, 552 aa, 553 aa, 554 aa, 555 aa, 556 aa, 557 aa, 558 aa, 559 aa, or 560 aa).

[00214] QASLLKVPYFVRVQGLLRICALARKMAGGHYVQMAIIKLGALTGTYVYNALTPLRDLWAHNGLRDLAVAVEPVVFSQMETKLITWGADTAACGDIINGLPVSARRGREILLGPADGMVSKGWRL LAPITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPAPQGARS LTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSAGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMRSPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRH LIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCN (SEQ ID NO:92) is referred to in FIG. 10A-10B as “TP553.”

[00215] In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence:

QASLLKVPYFVRVQGLLRICALARKMAGGHYVQMAIIKLGALTGTYVYNALTPLRDLWAHNGLRDLAVAVEPVVFSQMETKLITWGADTAACGDIINGLPVSARRGREILLGPADGMVSKGWRL LAPITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPAPQGARS LTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSAGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMRSPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRH LIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCN (SEQ ID NO:92); and has a length of 553 amino acids. Such a polypeptide can include T-cell epitopes designated NS2-1, NS2-2, NS2-3, NS2-4, NS2-5, NS2-6, NS2-7, NS2-8, NS3-1, NS3-2, NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-9, NS3-10, NS3-11, NS3-12, and NS3-13 in Fig. 9A-9B and Fig. 11A-11N. This polypeptide is also referred to as “TP553” (FIG. 12A-12D). In order to prevent self cleavage of the TP553 polypeptide (amino acids 917-1469) (FIG. 11E-11G) at the NS2-NS3 junction that is mediated by the catalytic domain of the NS2 protease (amino acids 917-1040), the histidine at position 966 (H966), a

critical residue for NS2 protease activity, is mutated to alanine (H966A) (FIG. 11E). See, e.g., Grakoui, A. et al. A second hepatitis C virus-encoded proteinase. *Proc. Natl Acad. Sci. USA* 90, 10583--10587 (1993); Hijikata, M. et al. Two distinct proteinase activities required for the processing of a putative nonstructural precursor protein of hepatitis C virus. *J. Virol.* 67, 4665--4675 (1993); and Lorenz, IC. Structure of the catalytic domain of the hepatitis C virus NS2-3 protease. *Nature*. Aug 17;442(7104):831-5 (2006).

[00216] As another example, the T cell epitope polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to a contiguous stretch of from 25 amino acids (aa) to 778 aa (e.g., from 25 aa to 50 aa, from 50 aa to 75 aa, from 75 aa to 100 aa, from 100 aa to 150 aa, from 150 aa to 200 aa, from 200 aa to 250 aa, from 250 aa to 300 aa, from 300 aa to 350 aa, from 350 aa to 400 aa, from 400 aa to 450 aa, from 450 aa to 500 aa, from 500 aa to 550 aa, from 550 aa to 600 aa, from 600 aa to 650 aa, from 650 aa to 700 aa, from 700 aa to 750 aa, or from 750 aa to 778 aa) the following amino acid sequence:

LHAPTGSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTIT
TGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVLA
TATPPGSVTVPHPNIEVALSTTGEIPFYGKAIPLEVIKGGRHILFCHSKKKCDELA AKLV
ALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVTQTVDFSLD
PTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGERPSGMFDSSVLCECYDAGCA
WYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLTHIDAHFLSQTKQSGENLP
YLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLYRLGAVQNEVTLTHPIT
KYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRIVLSGKPAIIPDREVL
YREFDEMEEC SQHLPYIEQGMMLAEQFKQKALGLLQTASRQAEVIAPAVQTNWQKLEA
FWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAFTAAVTSPLTTSQTLLFNILGGWVAA
QLAAPGAATAFVGAGLAGAAIGSVGLGKVLVDILAGYGAGVAGALVAFKIMSGEVPST
EDLVNLLPAILSPGALVVGVVCAAILRRHVGPGE GAVQWMNRLIAFASRGNHVSPTHY
VPESDAAARVTAILSSLTVTQLLRRLHQWISSECTTPCSGSWLRDIWDWICEVLSDFKTW
LKAKLMPQLPG (SEQ ID NO:93); and has a length of from 778 amino acids (aa) to 790 aa
(e.g., 778 aa, 779 aa, 780 aa, 781 aa, 782 aa, 783 aa, 784 aa, 785 aa, 786 aa, 787 aa, 788 aa, or
790 aa).

[00217] LHAPTGSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGAYMSKAHGIDPNIRT
GVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGA

RLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRHILFCHSKKKCDE
 LAAKLVALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVTQ
 TVDFSOLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGERPSGMFDSSVLCEC
 YDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLTHIDAHFLSQTKQ
 SGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLYRLGAVQNEVT
 LTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRIVLSGKPAIIP
 DREVLRYREFDEMEEC SQHLPYIEQGMMLAEQFKQKALG LLQTASRQAEVIAPAVQTNW
 QKLEAFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAFTAAVTSPLTTSQTLLFNILGG
 WVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLVDILAGYGAGVAGALVAFKIMSG
 EVPSTEDLVNLLPAILSPGALVVG VVCAAILRRHVGPGE GAVQWMNR LIAFASRG NHVS
 PTHYVPESDAAARVTAILSSLTVTQLLRRLHQWISSECTTPCSGSWLRDIWDWICEVLSD
 FKTWLKAKLMPQLPG (SEQ ID NO:93) is referred to in FIG. 10B as “TP778.”

[00218] In some cases, the T cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to a contiguous stretch of from 25 amino acids (aa) to 778 aa (e.g., from 25 aa to 50 aa, from 50 aa to 75 aa, from 75 aa to 100 aa, from 100 aa to 150 aa, from 150 aa to 200 aa, from 200 aa to 250 aa, from 250 aa to 300 aa, from 300 aa to 350 aa, from 350 aa to 400 aa, from 400 aa to 450 aa, from 450 aa to 500 aa, from 500 aa to 550 aa, from 550 aa to 600 aa, from 600 aa to 650 aa, from 650 aa to 700 aa, from 700 aa to 750 aa, or from 750 aa to 778 aa) of the following amino acid sequence:

LHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTIT
 TGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVLA
 TATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRHILFCHSKKKCDELA AKLV
 ALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVTQTVD FSLD
 PTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGERPSGMFDSSVLCECYDAGCA
 WYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLTHIDAHFLSQTKQSGENLP
 YLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLYRLGAVQNEVT LTHPIT
 KYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRIVLSGKPAIIPDREVL
 YREFDEMEEC SQHLPYIEQGMMLAEQFKQKALG LLQTASRQAEVIAPAVQTNWQKLEA
 FWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAFTAAVTSPLTTSQTLLFNILGGWVAA
 QLAAPGAATAFVGAGLAGAAIGSVGLGKVLVDILAGYGAGVAGALVAFKIMSGEVPST
 EDLVNLLPAILSPGALVVG VVCAAILRRHVGPGE GAVQWMNR LIAFASRG NHVSPTHY
 VPESDAAARVTAILSSLTVTQLLRRLHQWISSECTTPCSGSWLRDIWDWICEVLSDFKTW

LKAKLMPQLPG (SEQ ID NO:93); and has a length of from 25 amino acids (aa) to 50 aa, from 50 aa to 100 aa, from 100 aa to 200 aa, from 200 aa to 300 aa, from 300 aa to 400 aa, from 400 aa to 500 aa, from 500 aa to 600 aa, from 600 aa to 700 aa, or from 700 aa to 778 aa. In some cases, the T-cell epitope polypeptide comprises an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence:

LHAPTGSKGSTKVPAAYAAQGYKVLVLNPSVAATLGFGAYMSKAHGIDPNIRTVRTIT
 TGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLA
 TATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRLIFCHSKKKCDELAACL
 ALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVTQTVD
 PTFITETTLTPQDAVSRTQRRGRTGRGKPGIYRFVAPGERPSGMFDSSVLCECYDAGCA
 WYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLTHIDAHFLSQTKQSGENLP
 YLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLYRLGAVQNEVTLTHPIT
 KYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRIVLSGKPAIIPDREVL
 YREFDEMEEC SQHLPYIEQGMMLAEQFKQKALGLLQTASRQAEVIAPAVQTNWQKLEA
 FWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAFTAAVTSPLTTSQTLLFNILGGWVAA
 QLAAPGAATAFVGAGLAGAAIGSVGLGKVLVDILAGYGAGVAGALVAFKIMSGEVPST
 EDLVNLLPAILSPGALVVGVC AAILRRHVGPGE GAVQWMNRLIAFASRGNHVSPTHY
 VPESDAAARVTAILSSLTVTQLLRRLHQWISSECTTPCSGSWLRDIWDWICEVLSDFKTW
 LKAKLMPQLPG (SEQ ID NO:93); and has a length of 778 amino acids. Such a polypeptide can include T-cell epitopes designated NS3-1, NS3-2, NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-8, NS3-9, NS3-10, NS3-11, NS3-12, NS3-13, NS2-14, NS4a-1, NS4b-1, NS4b-2, NS4b-3, NS4b-4, NS4b-5, NS4b-6, NS4b-7, NS4b-8, NS4b-9, and NS4b-10 in FIG. 9B and FIG. 11A-11N.

[00219] As another example, the T cell epitope polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to a contiguous stretch of from 25 amino acids (aa) to 1985 aa (e.g., from 25 aa to 50 aa, from 50 aa to 75 aa, from 75 aa to 100 aa, from 100 aa to 150 aa, from 150 aa to 200 aa, from 200 aa to 250 aa, from 250 aa to 500 aa, from 500 aa to 750 aa, from 750 aa to 1000 aa, from 1000 aa to 1500 aa, or from 1500 aa to 1985 aa) of the following amino acid sequence:

APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGA
 GTRTIASPKGPVIQMYTNVDQDLVGWPAPQGARS LTPCTCGSSDLYLVTRHADVIPVRR
 RGDSRGSLLSPRPISYLKGSAGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETT
 MRSPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLV LNPSVAATL
 GFGAYMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDA
 TSILGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVI
 KGGRHLIFCHSKKKCELA AAKLV ALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTG
 FTGDFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGR TGRGKPGIYRFVAP
 GERPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGV
 FTGLTHIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPSWDQMWKCLIRLKPTLH
 GPTPLLYRLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLST
 GCVVIVGRIVLSGKPAIIPDREVLYREFDEMEECSQHLPYIEQGMMLAEQFKQKALGLLQ
 TASRQAEVIAPAVQTNWQKLEAFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAFTA
 AVTSPLTTSQTLLFNILGGWVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLVDILAG
 YGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVC AAILRRHVGPGE GAV
 QWMNRLIAFASRGNHVSPTHYVPESDAAARVTAILSSLTVTQLLRRLHQWISSECTTPCS
 GSWLRDIWDWICEVLSDFKTWLKAKLMPQLPGIPFVSCQRGYRGVWRGDGIMHTRCH
 CGAEITGHVKNGTMRIVGPRTCRNMWSGTFPINAYTTGPCTPLPAPNYTFALWRVSAEE
 YVEIRQVGDFHYVTGMTTDNLKCPQVPSPEFFTEL DGVRLHRFAPPCKPLLREEVSFR
 VGLHEYPVGSQLPCEPEPDVAVLTSM LTPSHITAEAAGRRLARGSPPSVASSASQLSA
 PSLKATCTANHDS PDAELIEANLLWRQEMGNITRVESENKVILDSFDPLVAEEDEREI
 SVPAEILRKSRRFAPALPIWARPDYNPPLLETWKKPDYEPV VHGCPPLPPQSPVPPPRK
 KRTVVLTTESTVSTALAE LATSFGSSSTSGITGDNTTTSSEPAPSGCPPDSDAESYSSMPP
 LEGEPGDPDLSDGSWSTVSSEADTEDV VCCSMSYSWTGALVTPCAAEEQKLPINALSNS
 LLRHHNLVYSTTSRSACQRQKKVTFDRLQVLD SHYQDVLKEVKAAASKVKANLLSVEE
 ACSLTPPHSAKSKFGYGAKDVRCHARKAVNHINSVWKDLLED SVTPIDTTIMAKNEVFC
 VQPEKGGRKPARLIVFDLGVRVCEKMALYDVVSKLPLAVMGSSYGFQYSPGQRVEFL
 VQAWKSKKTPMGFSYDTRCFDSTVTESDIRTEEAIYQCCDLD PQARVAIKSLTERLYVG
 GPLTNSRGENCYRRCRASGVLT TSCGNTLT CYIKARAACRAAGLQDCTMLVCGNNLV
 VICESAGVQEDAASLRAFTEAMTRYSA PPGDPPQPEYDLELITSCSSNVSV AHDGAGKR
 VYYLTRDPTTPLARA AWETARHTPVNSWLGNII MFAPTLWARMILMTHFFSVLIARDQL
 EQALDCEIYGACYSIEPLDLPPIIQR LHGLSAFSLHSYSPGEINRVA ACLRKLGVPPLRAW
 RHRARSVRARLLSRGGRAAICGKYLFNWA VRTKLKLTPIAAAGQLDLSGWFTAGYSGG
 DIYHSVSHARPRWFWFCLLLLAAGVGIYLLPNR (SEQ ID NO:94); this polypeptide is also
 referred to as “TP1985” and is depicted in FIG. 10C.

[00220] In some cases, the T cell epitope polypeptide can comprise an amino acid sequence having at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the following amino acid sequence:

APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGA
 GTRTIASPKGPVIQMYTNVDQDLVGWPAPQGARS LTPCTCGSSDLYLVTRHADVIPVRR
 RGDSRGSLLSPRPISYLKGSAGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETT
 MRSPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATL
 GFGAYMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDA
 TSILGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVI
 KGGRHLIFCHSKKKKCELA AAKLV ALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTG
 FTGDFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGR TGRGKPGIYRFVAP
 GERPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGV
 FTGLTHIDAHFLSQT KQSGENLPYL VAYQATVCARAQAPPSWDQMWKCLIRLKPTLH
 GPTPLLYRLGAVQNEVT LTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLST
 GCVVIVGRIVLSGKPAIIPDREVL YREFDEMEECSQHLPYIEQGMMLAEQFKQKALGLLQ
 TASRQAEVIAPAVQTNWQKLEAFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAFTA
 AVTSPLTTSQTLLFNILGGWVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLVDILAG
 YGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVC AAILRRHVGPGE GAV
 QWMNRLIAFASRGNHVSPTHYVPESDAAARVTAILSSLT VTTQLLRLHQWISSECTTPCS
 GSWLRDIWDWICEVLSDFKTWLKAKLMPQLPGIPFVSCQRGYRGVWRGDGIMHTRCH
 CGAEITGHVKNGTMRIVGPRTCRNMWSGTFPINAYTTGPCTPLPAPNYTFALWRVSAEE
 YVEIRQVGDFHYVTGMTTDNLKCPCQVPSPEFFTELDGVRLHRFAPPCKPLLREEVSFR
 VGLHEYPVGSQLPCEPEPDVAVLTSM LTPSHITAEAAAGRRLARGSPPSVASSASQLSA
 PSLKATCTANHDS PDAELIEANLLWRQEMGGNITRVESENKVVILDSFDPLVAEEDEREI
 SVPAEILRKSRRFAPALPIWARPDYNPPLLETWKKPDYEPPVVHGCPLPPPQSPVPVPPRK
 KRTVVLTESTVSTALAE LTKSFGSSSTSGITGDNTTTSSEPAPSGCPPDS DAESYSSMPP
 LEGEPGDPDLSDGSWSTVSSEADTEDV VCCSMSYSWTGALVTPCAAEEQKLPINALSNS
 LLRHNLVYSTTSRSACQRQKKVTFDRLQVLD SHYQDVLKEVKAAASKVKANLLSVEE
 ACSLTPPHSAKSKFGYGAKDVRCHARKAVNHINSVWKDLLED SVTPIDTTIMAKNEVFC
 VQPEKGGRKPARLIVFDLGV RVCEKMALYDVVSKLPLAVMGSSYGFQYSPGQRVEFL
 VQAWKSKKTPMGFSYDTRCFDSTVTESDIRTEEAIYQCCDLDPQARVAIKSLTERLYVG
 GPLTNSRGENCYRRCRASGVLT TSCGNTLT CYIKARAACRAAGLQDCTMLVCGNNLLV

VICESAGVQEDAASLRAFTEAMTRYSAAPPDPPQPEYDLELITSCSSNVSAHGDGAGKR
 VYYLTRDPTTPLARAAWETARHTPVNSWLGNIMFAPTLWARMILMTHFFSVLIARDQL
 EQALDCEIYGACYSIEPLDLPPIIQRHLHGLSAFSLHSYSPGEINRVAACLRLKLGVPPLRAW
 RHRARSVRARLLSRGGRAAICGKYLFNWAVRTKLKLTPIAAAGQLDLGWFTAGYSGG
 DIYHSVSHARPRWFWFCLLLAAGVGIYLLPNR (SEQ ID NO:94); and has a length of
 1985 amino acids. Such a polypeptide can include T-cell epitopes designated NS3-1, NS3-2,
 NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-8, NS3-9, NS3-10, NS3-11, NS3-12, NS3-13, NS3-
 14, NS4a-1, NS4b-1, NS4b-2, NS4b-3, NS4b-4, NS4b-5, NS4b-6, NS4b-7, NS4b-8, NS4b-9,
 NS4b-10, NS5a-1, NS5a-2, NS5b-1, NS5b-2 in FIG. 9A-9B and FIG. 11A-11N.

Additional T-cell epitopes

[00221] As discussed above, an immunogenic composition of the present disclosure includes: a) an HCV E1/E2 heterodimer; b) a T cell epitope polypeptide that comprises one or more T-cell epitopes (e.g., one or more T cell epitopes present in an HCV polypeptide other than an HCV E1 polypeptide or an HCV E2 polypeptide); and c) a CDN. The one or more T-cell epitopes can include one or more T-cell epitopes present in: a) an HCV NS3 polypeptide; b) an HCV NS2 polypeptide; c) an HCV NS4A polypeptide; d) an HCV NS4B polypeptide; e) an HCV NS5A polypeptide; f) an HCV NS5B polypeptide; g) an HCV core polypeptide; or h) an HCV p7 polypeptide. In some cases, the one or more T-cell epitopes are T-cell epitopes present in an HCV NS3 polypeptide. In some cases, the T cell epitope polypeptide further comprises one or more T cell epitopes present in: a) cholera toxin or toxoid; and/or b) tetanus toxin or toxoid; and/or c) diphtheria toxin or toxoid; and/or d) a meningococcal outer membrane protein.

[00222] Thus, in some cases, an immunogenic composition of the present disclosure includes: a) an HCV E1/E2 heterodimer; b) a T-cell epitope polypeptide that comprises one or more T-cell epitopes, where the one or more T-cell epitopes are T-cell epitopes present in: i) one or more of an HCV NS3 polypeptide, an HCV NS2 polypeptide, an HCV NS4A polypeptide, an HCV NS4B polypeptide, an HCV NS5A polypeptide, an HCV NS5B polypeptide, an HCV core polypeptide, and an HCV p7 polypeptide; and ii) one or more of cholera toxin or toxoid, tetanus toxin or toxoid, diphtheria toxin or toxoid, and a meningococcal outer membrane protein; and c) a CDN.

[00223] A T helper tetanus toxin epitope or other bacterial T-cell epitope could be fused (e.g., by recombinant expression) or chemically conjugated to the T cell epitope polypeptide, or can be unconjugated (e.g., provided as a separate polypeptide), to further enhance both T and B cell responses to both the T-cell epitopes present in the T cell epitope polypeptide and in the E1/E2 polypeptides. Alternatively, the whole or part of the detoxified toxin ("toxoid") can be used, wherein specific amino acids of the toxins are mutated to render the toxins inactive, thereby

generating toxoids. Methods of generating toxoids are well known in the art. Examples of bacterial epitopes include the use of diphtheria toxoid, meningococcal outer membrane protein, or mutant diphtheria protein CRM197 (see, e.g.: [http://www\(dot\)medscape\(dot\)com/viewarticle/431127](http://www(dot)medscape(dot)com/viewarticle/431127)).

[00224] In some cases, a suitable tetanus toxoid polypeptide comprises the amino acid sequence QYIKANSKFIGIFE (SEQ ID NO:130). In some cases, a suitable tetanus toxoid polypeptide comprises the amino acid sequence QYIKANSKFIGITE (SEQ ID NO:131).

[00225] In some cases, a T cell epitope polypeptide can comprise cholera toxin (or toxoid) epitope. In some cases, a suitable T-cell epitope polypeptide comprising a cholera toxoid epitope comprises a fragment of cholera toxin-B subunit (CT-B), e.g., a fragment of from 5 amino acids to 25 amino acids, or from 25 amino acids to 50 amino acids, of the following amino acid sequence: MIKLKFGVFF TVLLSSAYAH GTPQNITDLC AEYHNTQIHT LNDKIFSYTE SLAGKREMAI ITFKNGATFQ VEVPGSQHID SQKKAIERMK DTLRIAYLTE AKVEKLCVWN NKTPHAIAAI SMAN (SEQ ID NO:132).

[00226] In some cases, a T cell epitope polypeptide can comprise a tetanus toxin (or toxoid) T-cell epitope. In some cases, a suitable T cell epitope polypeptide comprising a tetanus toxin T-cell epitope comprises the amino acid sequence: ILMQYIKANSKFIGI (SEQ ID NO:133); and has a length of from 15 amino acids to 20 amino acids. In some cases, a suitable T cell epitope polypeptide comprising a tetanus toxin T-cell epitope comprises the amino acid sequence: VN NESSE (SEQ ID NO:134). In some cases, a suitable T cell epitope polypeptide comprising a tetanus toxin T-cell epitope comprises the amino acid sequence: PGINGKAIHLVN NESSE (SEQ ID NO:135). In some cases, a suitable T cell epitope polypeptide comprising a tetanus toxin T-cell epitope comprises the amino acid sequence: PNRDIL (SEQ ID NO:136). In some cases, a suitable T cell epitope polypeptide comprising a tetanus toxin T-cell epitope comprises the amino acid sequence: FIGITEL (SEQ ID NO:137). In some cases, a suitable tetanus toxin T-cell epitope comprises the amino acid sequence: SYFPSV (SEQ ID NO:138). In some cases, a suitable T cell epitope polypeptide comprising a tetanus toxin T-cell epitope comprises the amino acid sequence: NSVDDALINSTKIYSYFPSV (SEQ ID NO:139). In some cases, a suitable T cell epitope polypeptide comprising a tetanus toxin T-cell epitope comprises the amino acid sequence: IDKISDVSTIVPYIGPALNI (SEQ ID NO:140).

[00227] In some cases, a T cell epitope polypeptide can comprise a diphtheria toxin T-cell epitope. In some cases, a suitable T-cell epitope polypeptide comprising a diphtheria toxin T-cell epitope comprises the amino acid sequence: QSIALSSLMVAQAIP (SEQ ID NO:141); and has a length of from 15 amino acids to 20 amino acids. In some cases, a suitable T cell epitope polypeptide comprising a diphtheria toxin T-cell epitope comprises the amino acid sequence:

PVFAGANYAAWAVNVAQVI (SEQ ID NO:142). In some cases, a suitable T cell epitope polypeptide comprising a diphtheria toxin T-cell epitope comprises the amino acid sequence: VHHNTEEIQAQSIALLSLMV (SEQ ID NO:143). In some cases, a suitable T cell epitope polypeptide comprising a diphtheria toxin T-cell epitope comprises the amino acid sequence: QSIALLSLMVAAIPLVGEL (SEQ ID NO:144). In some cases, a suitable T cell epitope polypeptide comprising a diphtheria toxin T-cell epitope comprises the amino acid sequence: VDIGFAAYNFVESIINLFQV (SEQ ID NO:145). In some cases, a suitable T cell epitope polypeptide comprising a diphtheria toxin T-cell epitope comprises the amino acid sequence: QGESGHDIKITAENTPLPIA (SEQ ID NO:146). In some cases, a suitable T cell epitope polypeptide comprising a diphtheria toxin T-cell epitope comprises the amino acid sequence: GVLLPTIPGKLDVNKSKTHI (SEQ ID NO:147). In some cases, a suitable T cell epitope polypeptide comprising a diphtheria toxin T-cell epitope comprises the amino acid sequence of CRM197 (see, e.g., Giannini et al. (1984) *Nucl. Acids. Res.* 12:4063).

[00228] The amino acid sequence of CRM197 is as follows:

[00229] laddvvdssksfvmenfssyhgtpgyvdsiqkqkpksgtqgnydddwkefystdnky
daagysvdenplsgkaggvkvtypgltkvlalkvdnaetikkelglslteplmeqvgteefikrfgdgarvvlsfpfaegssveyi
nnweqakalsveinfetrgkrqgdamyeymaacagnrvrrsvgsslsclndwdvirdktktieslkehgpiknkmsspnkt
vseekakqyleefhtalehpelselktvtgtnpvfaganyaawavnvavqvidsetadnlekttaalsilpgigsvmgiaadgavhhnte
eivaqsiasslmvqaipvlvgelvdigfaaynfvesiinfqvvhnsynrpayspghtqpflhdgyavswntvedsiirtgfgesgh
dikitaentplpiagvllptipgkldvnkskthisvngkrirmrcraidgdvtcrpkspvyvgngvhanlhvafhrsssekihsneissd
sigvlglyqktvdhtkvnsklsffeiks (SEQ ID NO:148).

[00230] In some cases, a T cell epitope polypeptide can comprise a tetanus toxin T-cell epitope and a diphtheria toxin T-cell epitope. In some of these cases, the T cell epitope polypeptide can comprise the amino acid sequence: IMQYIKANSKFIGIQSIALLSLMVAAQ (SEQ ID NO:149); and can have a length of from 26 amino acids to 30 amino acids.

Mixtures of T-cell epitope polypeptides (T-cell epitope polypeptides)

[00231] In some cases, an immunogenic composition of the present disclosure comprises two or more different T-cell epitope polypeptides comprising a T-cell epitope present in an HCV protein other than E1 and E2 (e.g., a mixture of two or more different T-cell epitope polypeptides comprising a T-cell epitope present in an HCV protein other than E1 and E2).

[00232] For example, in some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E1/E2 heterodimeric polypeptide; b) two or more different T-cell epitope polypeptides comprising a T-cell epitope present in an HCV protein other than E1 and E2; and c) a CDN. In some cases, an immunogenic composition of the present disclosure comprises: a) an

HCV E2 polypeptide; b) two or more different T-cell epitope polypeptides comprising a T-cell epitope present in an HCV protein other than E1 and E2; and c) a CDNs.

[00233] For example, the two or more different T cell epitope polypeptides can include: i) a first T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP29, and having a length of from 29 amino acids to 35 amino acids; and ii) a second T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP50, and having a length of from 50 amino acids to 55 amino acids.

[00234] As another example, the two or more different T cell epitope polypeptides can include: i) a first T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP29, and having a length of from 29 amino acids to 35 amino acids; and ii) a second T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP52, and having a length of from 52 amino acids to 60 amino acids.

[00235] As another example, the two or more different T cell epitope polypeptides can include: i) a first T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP29, and having a length of from 29 amino acids to 35 amino acids; and ii) a T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP70, and having a length of from 70 amino acids to 75 amino acids.

[00236] As another example, the two or more different T cell epitope polypeptides can include: i) a first T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP29, and having a length of from 29 amino acids to 35 amino acids; and ii) a second T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP100, and having a length of from 100 amino acids to 110 amino acids.

- [00237]** As another example, the two or more different T cell epitope polypeptides can include: i) a first T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP29, and having a length of from 29 amino acids to 35 amino acids; and ii) a second T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP171, and having a length of from 171 amino acids to 180 amino acids.
- [00238]** As another example, the two or more different T cell epitope polypeptides can include: i) a first T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP29, and having a length of from 29 amino acids to 35 amino acids; and ii) a T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP228, and having a length of from 228 amino acids to 235 amino acids.
- [00239]** As another example, the two or more different T cell epitope polypeptides can include: i) a first T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP29, and having a length of from 29 amino acids to 35 amino acids; and ii) a second T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP553, and having a length of from 553 amino acids to 565 amino acids.
- [00240]** As another example, the two or more different T cell epitope polypeptides can include: i) a first T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP29, and having a length of from 29 amino acids to 35 amino acids; and ii) a second T cell epitope polypeptide comprising an amino acid sequence having at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or 100%, amino acid sequence identity to TP778, and having a length of from 778 amino acids to 785 amino acids.

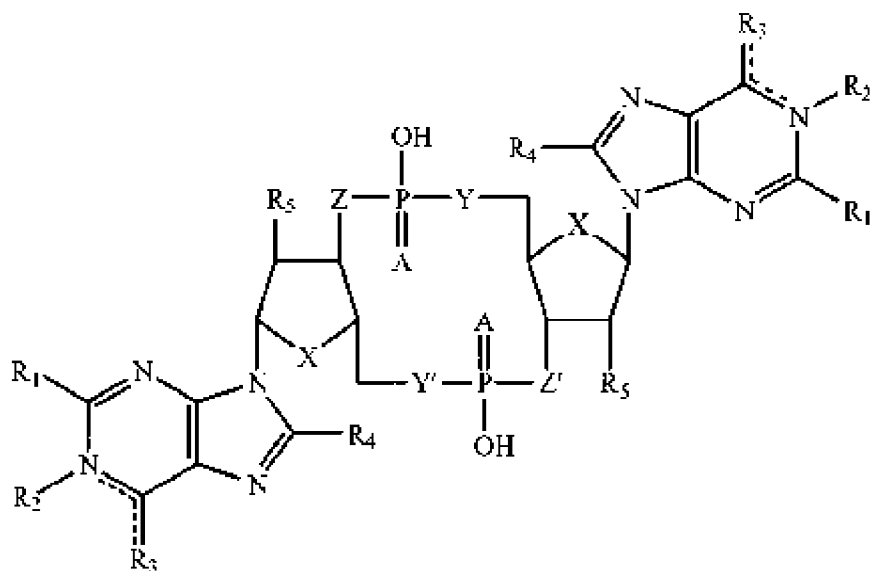
Pharmaceutically acceptable excipients

[00241] An immunogenic composition of the present disclosure can include a pharmaceutically acceptable excipient. A wide variety of pharmaceutically acceptable excipients is known in the art and need not be discussed in detail herein. Pharmaceutically acceptable excipients have been amply described in a variety of publications, including, for example, A. Gennaro (2000) "Remington: The Science and Practice of Pharmacy", 20th edition, Lippincott, Williams, & Wilkins; Pharmaceutical Dosage Forms and Drug Delivery Systems (1999) H. C. Ansel et al., eds 7th ed., Lippincott, Williams, & Wilkins; and Handbook of Pharmaceutical Excipients (2000) A. H. Kibbe et al., eds., 3rd ed. Amer. Pharmaceutical Assoc.

[00242] In some cases, a pharmaceutically acceptable excipient is an aqueous buffer. Thus, an immunogenic composition of the present disclosure can include an aqueous buffer. Suitable aqueous buffers include, but are not limited to, acetate, succinate, citrate, and phosphate buffers varying in strengths from about 5 mM to about 100 mM. In some cases, the aqueous buffer includes reagents that provide for an isotonic solution. Such reagents include, but are not limited to, sodium chloride; and sugars e.g., mannitol, dextrose, sucrose, and the like. In some embodiments, the aqueous buffer further includes a non-ionic surfactant such as polysorbate 20 (TWEEN®20) or polysorbate 80 (TWEEN®80). For example, an immunogenic composition of the present disclosure in an aqueous buffer can include, e.g., from about 0.01% to about 0.05% polysorbate-20 (TWEEN®20) non-ionic detergent. Optionally the formulations may further include a preservative. Suitable preservatives include, but are not limited to, a benzyl alcohol, phenol, chlorobutanol, benzalkonium chloride, and the like. In many cases, the formulation is stored at about 4°C. Formulations may also be lyophilized, in which case they generally include cryoprotectants such as sucrose, trehalose, lactose, maltose, mannitol, and the like. Lyophilized formulations can be stored over extended periods of time, even at ambient temperatures. In some cases, the aqueous buffer further includes a non-ionic surfactant. In some cases, the aqueous buffer includes the non-ionic surfactant Triton™X-100, e.g., 0.1% Triton™X-100.

Cyclic dinucleotides

[00243] In some cases, a CDN suitable for use in an immunogenic composition of the present disclosure is of Formula (I):



[00244] wherein:

[00245] A is S or O;

[00246] X is S, N, O, CH₂;

[00247] Y, Y' is NH, CH₂, O;

[00248] Z, Z' is NH, CH₂, O;

[00249] R1 represents hydrogen or NH₂ which may be substituted;

[00250] R2 is hydrogen or absent;

[00251] R3 represents NH₂, O, OH, H, or a halogen;

[00252] R4 represents hydrogen, halogen, or a straight or branched C₁-C₆ alkyl group which may optionally be substituted;

[00253] R5 represents hydrogen, OH or a straight or branched C₁-C₆ alkyl chain or C₁-C₆ straight or branched alkoxy chain which may optionally be substituted;

[00254]  is a single or double bond;

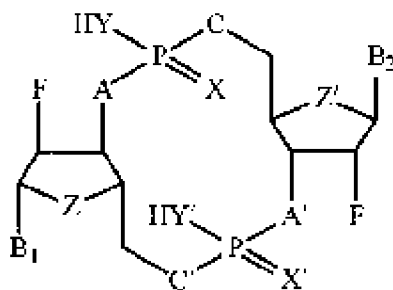
[00255] or conjugates thereof, and salts or solvates thereof. See, e.g., US 2008/0286296.

[00256] In formula (I), the purine residue is in some cases a guanine (G), adenine (A), xanthine or hypoxanthine (X), or inosine (I) residue. The compound can have identical purine residues, e.g. c-diGMP, c-diAMP, c-diIMP, or c-dXMP, or can contain different purine residues, e.g. c-GpAp, c-GpIp, c-GpXp, c-ApIp, c-ApXp, or c-lpXp. Further, R5 is in some cases an OH group. In addition, X is in some cases an oxygen atom. In one embodiment, Y, Y', Z, and Z' are an oxygen atom, O. Thus, in one embodiment, the compound of formula (I) is a cyclic bis(3'-5')diguanilylic acid (c-diGMP) or conjugates thereof or a cyclic bis(3'-5')diadenylylic acid (c-

diAMP) or conjugates thereof, or salts or solvates thereof. In one embodiment, the compound of formula (I) is cyclic Bis(3'-5')adenylic acid, which is also referred to as c-di-AMP; or the pegylated conjugate. With the term "which may be substituted" is meant the substitution with a straight or branched C1-C6 alkyl group or a straight or branched C1-C6 alkoxy group and/or with a halogen, hydroxyl group or carboxyl group.

[00257] In some cases, a CDN suitable for use in an immunogenic composition of the present disclosure is selected from the group consisting of cyclic di-adenosine monophosphate (c-di-AMP), cyclic di-guanosine monophosphate (c-di-GMP), and cyclic guanosine monophosphate-adenosine monophosphate (cGAMP). In some cases, a CDN suitable for use in an immunogenic composition of the present disclosure is cGAMP (2'-3'-cyclic GMP-AMP) or cGAMP (3'-3'-cyclic GMP-AMP). In some cases, a CDN suitable for use in an immunogenic composition of the present disclosure is cGAMP (2'-3'-cyclic GMP-AMP). In some cases, a CDN suitable for use in an immunogenic composition of the present disclosure is cGAMP (3'-3'-cyclic GMP-AMP).

[00258] In some cases, a CDN suitable for use in an immunogenic composition of the present disclosure is of Formula (II):



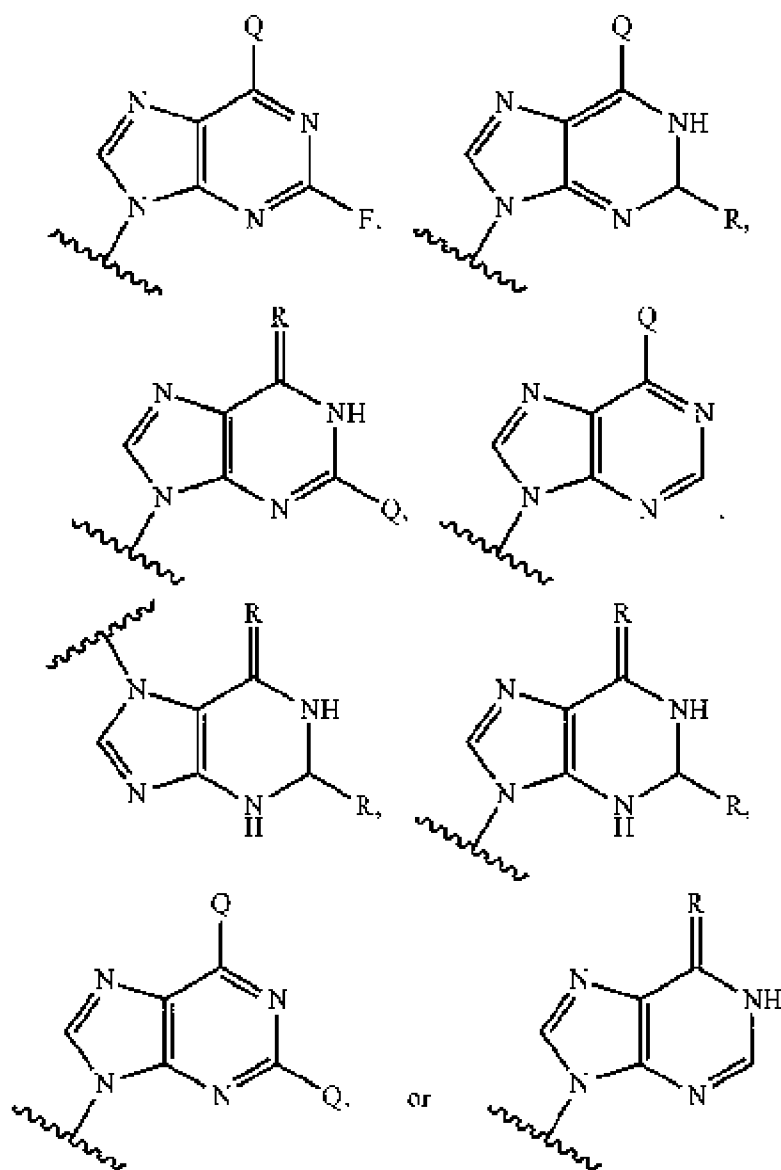
[00259] where:

[00260] A, C, A' and C' are independently selected from NH, O, and S;

[00261] X, Y, X', and Y' are independently selected from O or S;

[00262] Z and Z' are independently selected from O, S, NH, and CH₂; and

[00263] B₁ and B₂ are independently a purine selected from:



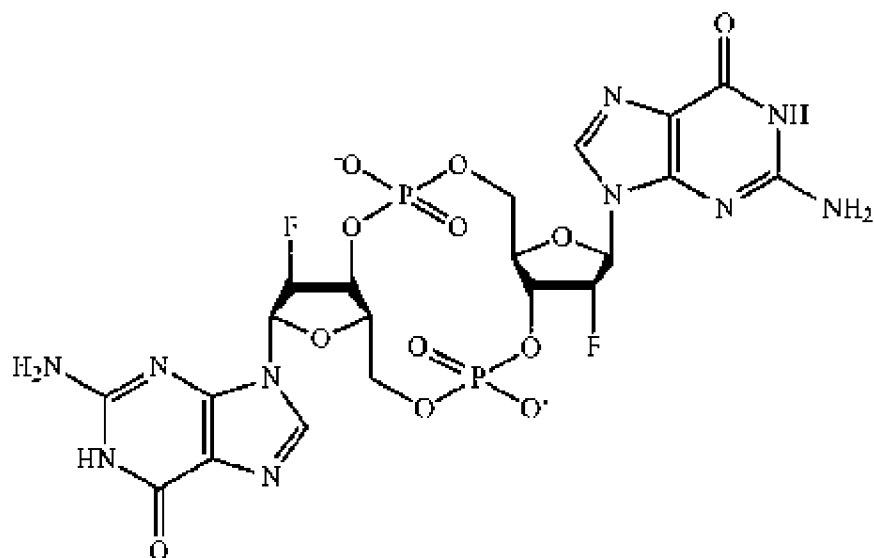
[00264] where:

[00265] Q is hydrogen or NH₂;

[00266] Nitrogen is optionally substituted with a C₁-C₆ alkyl or a C₁-C₆ acyl group; and

[00267] R is O or S.

[00268] In some cases, a CDN suitable for inclusion in an immunogenic composition of the present disclosure is a fluorinated CND. In some cases, the fluorinated CDN is 2'-F-c-diGMP having the following structure:



IMMUNOGENIC COMPOSITION COMPRISING HCV E1/E2, HCV E2, OR HCV E1 AND AN ARCHAEL GLYCOLIPID

[00269] The present disclosure provides an immunogenic composition comprising: a) an HCV E1E2 heterodimer; and b) an archaeosome. The present disclosure provides an immunogenic composition comprising: a) an HCV E2 polypeptide; and b) an archaeosome. The present disclosure provides an immunogenic composition comprising: a) an HCV E1 polypeptide; and b) an archaeosome.

[00270] In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to one or more HCV genotypes. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to one or more HCV genotypes, where the immune response is greater than the immune response induced by administration of a control composition comprising the HCV E1/E2 heterodimer (or E1 polypeptide, or E2 polypeptide) but lacking the archaeosome.

[00271] In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces CD8⁺ CTLs specific for HCV, where the number of HCV-specific CD8⁺ CTLs induced is at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% (or 2-fold), at least 2.5-fold, at least 5-fold, at least 7.5-fold, at least 10-fold, at least 20-fold, at least 50-fold, or at least 100-fold, or more than 100-fold, higher than the number of HCV-specific CD8⁺ CTLs induced

by administration of a control composition (e.g., a composition comprising the HCV E1/E2 heterodimer but lacking the archaeosome; a composition comprising an E1 polypeptide but lacking the archaeosome; a composition comprising an E2 polypeptide but lacking the archaeosome).

[00272] In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces CD4⁺ T cells specific for HCV, where the number of HCV-specific CD4⁺ T cells induced is at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% (or 2-fold), at least 2.5-fold, at least 5-fold, at least 7.5-fold, at least 10-fold, at least 20-fold, at least 50-fold, or at least 100-fold, or more than 100-fold, higher than the number of HCV-specific CD4⁺ T cells induced by administration of a control composition (e.g., a composition comprising the HCV E1/E2 heterodimer but lacking the archaeosome; a composition comprising an E1 polypeptide but lacking the archaeosome; a composition comprising an E2 polypeptide but lacking the archaeosome).

[00273] In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces production of HCV-specific CD4⁺ T cells and CD8⁺ T cells in the individual, where the number of HCV-specific CD4⁺ T cells and/or CD8⁺ T cells is increased, such that the percent of total peripheral CD4⁺ and/or CD8⁺ T cells that is HCV-specific is from 0.01% to 0.05%, from 0.05% to 0.10%, from 0.10% to 0.125%, from 0.125% to 0.25%, from 0.25% to from 0.50%, or 0.5% to 10% (e.g., from 0.5% to 1%, from 1% to 2%, from 2% to 5%, or from 5% to 10%). The number of HCV-specific CD4⁺ T cells and CD8⁺ T cells in a control individual (e.g., an individual not infected with HCV) not treated with the immunogenic composition would be undetectable.

[00274] In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, increases the number of HCV E1/E2-specific CD4⁺ T cells and CD8⁺ T cells in the individual by at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% (or 2-fold), at least 2.5-fold, at least 5-fold, at least 7.5-fold, at least 10-fold, at least 20-fold, at least 50-fold, or at least 100-fold, or more than 100-fold, compared to the number of HCV E1/E2-specific CD4⁺ T cells and CD8⁺ T cells in the individual induced by administration of a control composition comprising the HCV E1/E2 heterodimer (or HCV E2 polypeptide, or HCV E1 polypeptide) but lacking the archaeosome, or compared to the number of HCV E1/E2-specific CD4⁺ T cells and CD8⁺ T cells in the individual before administration of the immunogenic composition.

- [00275]** In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces helper T lymphocytes (e.g., CD4⁺ T cells) specific for HCV, where the number of HCV-specific helper T lymphocytes induced is at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% (or 2-fold), at least 2.5-fold, at least 5-fold, at least 7.5-fold, at least 10-fold, at least 20-fold, at least 50-fold, or at least 100-fold, or more than 100-fold, higher than the number of HCV-specific helper T cells induced by administration of a control composition comprising the HCV E1/E2 heterodimer (or HCV E2 polypeptide, or HCV E1 polypeptide) but lacking the archaeosome, or compared to the number of HCV-specific CD4⁺ T cells in the individual before administration of the immunogenic composition.
- [00276]** In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces antibody specific for HCV, where the level of HCV-specific antibody induced is at least as high as the level of HCV-specific antibody induced by administration of a control composition comprising the HCV E1/E2 heterodimer (or HCV E2 polypeptide, or HCV E1 polypeptide) but lacking the archaeosome.
- [00277]** In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces antibody specific for HCV, where the level of HCV-specific antibody induced is at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 75%, at least 100% (or 2-fold), at least 2.5-fold, at least 5-fold, at least 7.5-fold, at least 10-fold, at least 20-fold, at least 50-fold, or at least 100-fold, or more than 100-fold, higher than the level of HCV-specific antibody induced by administration of a control composition comprising the HCV E1/E2 heterodimer (or HCV E2 polypeptide, or HCV E1 polypeptide) but lacking the archaeosome, or compared the level of HCV-specific antibody in the individual before administration of the immunogenic composition.
- [00278]** An immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response (e.g., a cellular immune response) in the individual to one or more HCV genotypes. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to HCV genotype 1. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to HCV genotype 2. In some cases, an immunogenic composition of the present disclosure when administered to an individual in need thereof, induces an immune response in the individual to HCV genotype 3. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune

response in the individual to HCV genotype 1 and HCV genotype 3. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to HCV genotype 1, HCV genotype 2, and HCV genotype 3. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to HCV genotype 1, HCV genotype 2, HCV genotype 3, and HCV genotype 7. In some cases, an immunogenic composition of the present disclosure, when administered to an individual in need thereof, induces an immune response in the individual to HCV genotype 1, HCV genotype 2, HCV genotype 3, HCV genotype 4, HCV genotype 5, HCV genotype 6, and HCV genotype 7.

HCV E1E2 heterodimers, HCV E2 polypeptides, and HCV E1 polypeptides.

[00279] The present disclosure provides an immunogenic composition comprising: a) an HCV E1E2 heterodimer; and b) an archaeosome. The present disclosure provides an immunogenic composition comprising: a) an HCV E2 polypeptide; and b) an archaeosome. The present disclosure provides an immunogenic composition comprising: a) an HCV E1 polypeptide; and b) an archaeosome. Suitable HCV E1E2 heterodimers, HCV E2 polypeptides, and HCV E1 polypeptides are as described above.

Archaeal lipids and archaeosomes

[00280] An archaeal lipid suitable for use in an immunogenic composition of the present disclosure comprises a polar lipid based on a 2, 3-dialkylglycerol skeleton. These 2, 3-dialkylglycerol groups are isoprenoid and the simplest molecules are derivatives of 2,3-dibiphytanyl-O-sn-glycerol (archeol); for instance, two isoprenoid units of 20 carbons joined at positions sn-2 and sn-3 of glycerol. These alkyl chains are generally saturated; nevertheless, some forms have double bonds in different positions. These lipids have one or two groups of polar head, which may be different with units 2, 3-sn-glycerol joined by C40 alkyl components which are also isoprenoid molecules. For instance, calarcheol (so called because it is the predominant form in some thermophile archaeobacteria), has two C40 isoprenoid units bonded from positions 2 to 3' and from position 3 to 2'.

[00281] In some cases, an archaeal adjuvant suitable for use in an immunogenic composition of the present disclosure comprises multivalent cations in association with aggregates of a plurality of spherical archaeal polar lipid structures containing aqueous compartments (e.g., an "AMVAD structure"), where the archaeal polar lipid is a total polar lipids extract or archaetidyl glycerophosphate-O-methyl, obtained from an archaeal species. The multivalent cations can be divalent or trivalent cations. The multivalent cations can be divalent Ca^{2+} or Mg^{2+} , or trivalent Al^{3+} . The Ca^{2+} can be provided as CaCl_2 . The Al^{3+} can be provided as AlCl_3 or $\text{AlK}(\text{SO}_4)_2$. In

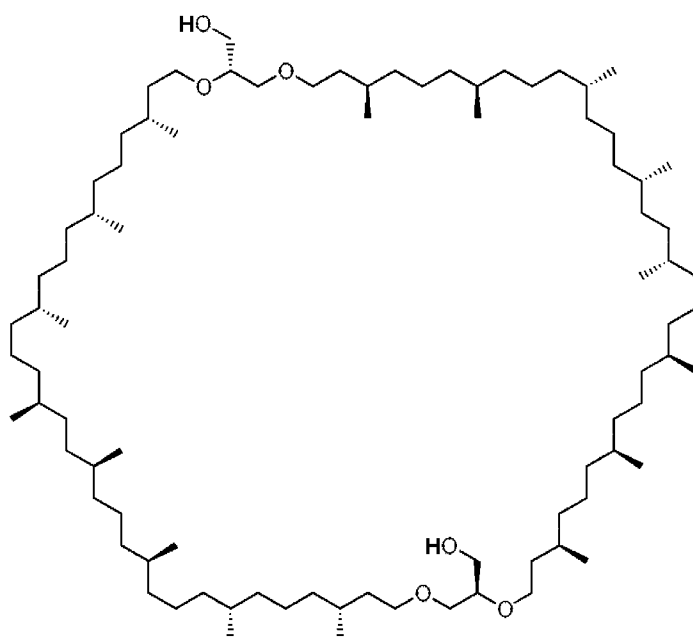
some cases, the total polar lipids extract from an archaeal species is mixed with neutral lipids from the archaeal species. See, e.g., U.S. Patent Publication No. 2013/0195932.

[00282] In some cases, lipids suitable for use in an immunogenic composition of the present disclosure comprises 1,2-di-O-hexadecyl-sn-glycero-3-phosphatidylcholine and 1,2-di-O-phytanyl-sn-glycero-3-phosphatidylethanolamine. In some cases, the 1,2-di-O-hexadecyl-sn-glycero-3-phosphatidylcholine and 1,2-di-O-phytanyl-sn-glycero-3-phosphatidylethanolamine form uniformly sized particles; for example, the particles can comprise: liposomes, nanoliposomes, niosomes, microspheres, nanospheres, nanoparticles, micelles or archaeosomes.

[00283] In some cases, an archaeosome comprises at least one polar synthetic lipid, where the at least one polar synthetic lipid comprises at least one carbohydrate or anionic group linked by covalent bonding to at least one free hydroxyl group of an archaeal core lipid. In some cases, the archaeal core lipid is archaeol (2,3-di-O-diphytanyl-sn-glycerol). In some cases, the archaeal core lipid is caldarchaeol (2,2',3,3'-tetra-O-dibiphytanyl-sn-diglycerol). In some cases, the carbohydrate group is selected from the group consisting of: β -D-Glc-(1,6)- β -D-Glc-; β -D-Glc-(1,6)- α -D-Glc-; α -D-Glc-(1,6)- β -D-Glc-; β -D-Glc-(1,4)- β -D-Glc-; α -D-Glc-(1,4)- β -D-Glc-; β -D-Gal-(1,4)- β -D-Glc-; α -D-Gal-(1,6)- β -D-Glc-; β -D-Glc-(1,6)- β -D-Glc-(1,6)- β -D-Glc-; α -D-Glc-(1,4)- α -D-Glc-(1,4)- β -D-Glc-; α -D-Man-(1,2)- α -D-Man-(1,2)- α -D-Man-; and α -D-Man-(1,2)- α -D-Man-(1,2)- α -D-Man-. In some cases, the carbohydrate group comprises two or three β -D-Glc- units in (1,6) linkage. In some cases, the carbohydrate group is a Galactose-Glucose (gal-glc) group. In some cases, the anionic group is selected from the group consisting of phosphoserine, phosphoethanolamine, phosphoinositol and phosphoglycerol. In some cases, the at least one anionic lipid is selected from the group consisting of archaetidylglycerol, archaetidylglycerolphosphate-methyl, archaetidylserine, and archaetidylinositol. In some cases, the archaeosome comprises at least one conventional lipid. In some cases, the at least one conventional lipid is selected from a group consisting of phosphatidylglycerol, phosphatidylserine, sulfoquinovosyl diacylglycerol (SQDG), and cholesterol. In some cases, the at least one conventional lipid comprises cholesterol, and wherein cholesterol is present in an amount of between 10 and 45 mol % of the total lipid composition. In some cases, the phosphatidylglycerol is present in an amount of between 20 and 80 mol % of the lipid composition. In some cases, the phosphatidylserine is present in an amount of between 10 and 30 mol % of the lipid composition. In some cases, the at least one polar synthetic lipid comprises at least one synthetic immunoactive glycolipid and at least one anionic lipid, and the archaeosome further comprises at least one stabilizing lipid. In some cases, the at least one polar synthetic lipid comprises caldarchaeol having one carbohydrate head group and one anionic head group. In some cases, the carbohydrate head group comprises gentiobiose and the anionic head

group comprises phosphoinositol. In some cases, the at least one polar synthetic lipid comprises a first caldarchaeol having two carbohydrate head groups and a second caldarchaeol having two anionic head groups, and wherein the at least one stabilizing lipid is the first and/or second caldarchaeol. In some cases, the at least one polar synthetic lipid comprises gentiotriose-archaeol and wherein the at least one stabilizing lipid comprises cholesterol and at least one of phosphatidylethanolamine, archaetidylglycerol, archaetidylserine or archaetidylglycerolphosphate-methyl.

[00284] Caldarchaeol is also known as dibiphytanyldiglycerol tetraether. Two glycerol units are linked together by two strains that consist of two phytanes linked together to form a linear chain of 32 carbon atoms. Caldarchaeol has the following structure:



[00285] Archaeal lipids can be obtained from any archaea of the phyla Euryarchaeota, Crenarchaeota, Korarchaeota, or, Nanoarchaea. Archaeal lipids can be obtained from any archaea of the genus *Thermococcus*, *Sulfolobus*, *Halobacterium*, *Methanococcus*, *Ferroplasma*, *Thermoplasma*, *Archaeoglobus*, *Haloquadratum*, or *Halorubrum*. Suitable sources of archaeal lipids include, but are not limited to, *Thermus aquaticus*, *Thermus thermophilus*; *Methanobrevibacter smithii*; *Thermoplasma acidophilum*; a *Sulfolobus* species, e.g. *Sulfolobus acidocaldarius*, *Sulfolobus solfataricus*, *Sulfolobus islandicus*, *Sulfolobus tokodaii*, etc.; a *Pyrobaculum* species, e.g. *Pyrobaculum islandicum* or *Pyrobaculum aerophilum*; a *Methanococcus* species, e.g., *Methanocaldococcus vulcanius*, *Methanocaldococcus jannaschii*, *Methanococcus acolicus*, *Methanococcus voltae*; or a *Halobacterium* species such as *Halobacterium salinarum*; *Methanopyrus kandleri*; *Methanobacterium espanolae*; *Methanosphaera stadtmanae*; *Methanosarcina mazei*; *Natronobacterium magadii*; etc.

- [00286] Total polar lipids (TPL) can be extracted from archaea and collected as the acetone-insoluble fraction. Choquet et al. (1994) *Appl. Microbiol. Biotechnol.* 42:375; Bligh and Dyer (1959) *Can. J. Biochem. Physiol.* 37:911. The polar lipids consist of regularly branched, and usually fully saturated, phytanyl chains of 20, 25, or 40 carbon length, with the 20 and 40 being most common. Archaeosomes can be prepared by hydrating TPL in a buffer (e.g., phosphate-buffered saline). The TPL-buffer solution can be sonicated (e.g., at 60 Hz for 10 min).
- [00287] TPL can be extracted from archaea by stirring the cells (which may be lyophilized) with chloroform-methanol (2 : 1, v/v) for 1 hour at room temperature. The suspension is passed through a sintered glass filter, and the residue reextracted for an additional hour. Combined filtrates are evaporated, taken up in chloroform-methanol-water (60 : 30 : 4.5, v/v/v), and passed through Sephadex G-25 for removal of nonlipid contaminations. Langworthy et al. (1977) *J. Bacteriol.* 130:1326.
- [00288] The mean diameter of archaeosomes in an archaeosomal formulation can range from about 50 nm to 600 nm, e.g., from 50 nm to 100 nm, from 100 nm to 150 nm, from 150 nm to 200 nm, from 200 nm to 250 nm, from 250 nm to 300 nm, from 300 nm to 400 nm, from 400 nm to 450 nm, from 450 nm to 500 nm, from 500 nm to 550 nm, or from 550 nm to 600 nm.

T-cell epitope polypeptides

- [00289] In some cases, one or both of the polypeptide chains of the E1/E2 heterodimer present in an immunogenic composition of the present disclosure can include a T-cell epitope polypeptide. In some cases, an E2 polypeptide present in an E1/E2 heterodimer present in an immunogenic composition of the present disclosure includes a T-cell epitope polypeptide. In some cases, an E1 polypeptide present in an E1/E2 heterodimer present in an immunogenic composition of the present disclosure includes a T-cell epitope polypeptide. In some cases, an HCV E2 polypeptide present in an immunogenic composition of the present disclosure includes a T-cell epitope polypeptide. In some cases, an HCV E1 polypeptide present in an immunogenic composition of the present disclosure includes a T-cell epitope polypeptide. In these embodiments, the T-cell epitope is covalently linked to the E1 and/or E2 polypeptide. For example, in some cases, the T-cell epitope is covalently linked to the amino terminus (N-terminus) of the HCV E1 polypeptide. In some cases, the T-cell epitope is covalently linked to the carboxyl terminus (C-terminus) of the HCV E1 polypeptide. Thus, e.g., in some cases, an immunogenic composition of the present disclosure comprises: a) a fusion polypeptide comprising, in order from N-terminus to C-terminus: i) an HCV E1 polypeptide; and ii) a T-cell epitope polypeptide; and b) an archaeosome. In some cases, an immunogenic composition of the present disclosure comprises: a) a fusion polypeptide comprising, in order from N-terminus to C-terminus: i) an HCV E2 polypeptide; and ii) a T-cell epitope polypeptide; and b) an archaeosome. In some cases, an

immunogenic composition of the present disclosure comprises: a) a fusion polypeptide comprising, in order from N-terminus to C-terminus: i) a T-cell epitope polypeptide; and ii) an HCV E1 polypeptide; and b) an archaeosome. In some cases, an immunogenic composition of the present disclosure comprises: a) a fusion polypeptide comprising, in order from N-terminus to C-terminus: i) a T-cell epitope polypeptide; and ii) an HCV E2 polypeptide; and b) an archaeosome. In some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E1E2 heterodimer comprising i) a fusion polypeptide comprising, in order from N-terminus to C-terminus: an HCV E1 polypeptide; and a T-cell epitope polypeptide; and ii) an HCV E2 polypeptide; and b) an archaeosome. In some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E1E2 heterodimer comprising i) a fusion polypeptide comprising, in order from N-terminus to C-terminus: an HCV E2 polypeptide; and a T-cell epitope polypeptide; and ii) an HCV E2 polypeptide; and b) an archaeosome. In some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E1E2 heterodimer comprising i) a fusion polypeptide comprising, in order from N-terminus to C-terminus: a T-cell epitope polypeptide; and an HCV E1 polypeptide; and ii) an HCV E2 polypeptide; and b) an archaeosome. In some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E1E2 heterodimer comprising i) a fusion polypeptide comprising, in order from N-terminus to C-terminus: a T-cell epitope polypeptide; and an HCV E1 polypeptide; and ii) an HCV E2 polypeptide; and b) an archaeosome.

[00290] In some cases, an immunogenic composition of the present disclosure comprises a T-cell epitope polypeptide, where the T-cell epitope polypeptide is not covalently linked to the HCV E1/E2 heterodimer, the HCV E1 polypeptide or the HCV E2 polypeptide. For example, in some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E1/E2 heterodimer; b) an archaeosome; and c) a T-cell epitope polypeptide. In some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E2 polypeptide; b) an archaeosome; and c) a T-cell epitope polypeptide. In some cases, an immunogenic composition of the present disclosure comprises: a) an HCV E1 polypeptide; b) an archaeosome; and c) a T-cell epitope polypeptide.

[00291] Suitable T-cell epitope polypeptides are as described above.

COMPOSITIONS COMPRISING A T-CELL EPITOPE POLYPEPTIDE COMPRISING T-CELL EPITOPES PRESENT IN AN HCV POLYPEPTIDE OTHER THAN E1 AND E2

[00292] The present disclosure provides an immunogenic composition comprising: a) a T-cell epitope polypeptide comprising T-cell epitopes present in an HCV polypeptide other than E1 and E2; and b) a CDN. The present disclosure provides an immunogenic composition comprising: a)

a T-cell epitope polypeptide comprising T-cell epitopes present in an HCV polypeptide other than E1 and E2; and b) an archaeosome.

[00293] Suitable T-cell epitope polypeptides are as described above. Suitable CDNs are as described above. Suitable archaeosomes are as described above.

NUCLEIC ACID IMMUNOGENIC COMPOSITIONS

[00294] The present disclosure provides nucleic acid compositions comprising: a) one or more nucleic acids comprising a nucleotide sequence(s) encoding polypeptides (e.g., HCV E1/E2; HCV E1; HCV E2; T-cell epitope polypeptide) as described above; and b) a CDN. The present disclosure provides nucleic acid compositions comprising: a) one or more nucleic acids comprising a nucleotide sequence(s) encoding polypeptides (e.g., HCV E1/E2; HCV E1; HCV E2; T-cell epitope polypeptide) as described above; and b) an archaeosome. The present disclosure provides an immunogenic composition comprising: a) a nucleic acid (e.g., a recombinant viral expression vector(s)) comprising nucleotide sequence(s) encoding one or more of: an HCV E1/E2 heterodimer; an HCV E1 polypeptide; an HCV E2 polypeptide; and a T-cell epitope polypeptide, where such polypeptides are described above; and b) a CDN. The present disclosure provides an immunogenic composition comprising: a) a nucleic acid (e.g., a recombinant viral expression vector(s)) comprising nucleotide sequence(s) encoding one or more of: an HCV E1/E2 heterodimer; an HCV E1 polypeptide; an HCV E2 polypeptide; and a T-cell epitope polypeptide, where such polypeptides are described above; and b) an archaeosome. The polypeptides can be encoded in the same nucleic acid, or on separate nucleic acids. For example, where the nucleic acid(s) are recombinant expression vectors, the polypeptides can be encoded in the same or separate recombinant expression vectors.

[00295] In some cases, the nucleic acid(s) is/are DNA. In some cases, the nucleic acid(s) is/are RNA. In some cases, the nucleic acid(s) is/are present in expression vector(s), generating recombinant expression vector(s) comprising the nucleic acid(s). In some cases, the recombinant expression vector(s) is/are recombinant bacterial vectors. In some cases, the recombinant expression vector(s) is/are recombinant viral vector(s). In some cases, the recombinant viral vector(s) are packaged into viral particles. In some cases, the nucleic acid(s) are present in bacteria (e.g., non-pathogenic bacteria (e.g., attenuated bacteria) suitable for delivery of nucleic acids to an individual). Where the recombinant expression vector is a bacterial vector or a viral vector, the vector is suitably attenuated so as not to cause significant pathology in an individual.

[00296] In some cases, the nucleic acid is present in an expression vector. Suitable expression vectors include, but are not limited to, a replication-defective adenovirus vector; a replication-defective vaccinia virus vector; a lentivirus vector (e.g., a self-inactivating lentivirus vector); a retroviral vector (e.g., a self-inactivating retroviral vector); an adeno-associated virus vector; and

the like. In some cases, the vector is a modified vaccinia Ankara (MVA) vector, or an MVA-based vector (see, e.g., Verheust et al. (2012) *Vaccine* 30:2623). In some cases, the vector is a replication-defective adenovirus vector. In some cases, the vector is a replication-defective adenovirus 6 (Ad6) vector. In some cases, the vector is a replication-defective simian adenovirus vector (e.g., ChAd3). Suitable viral vectors are described in, e.g., Zhou et al. (2012) *Invest. Ophthalmol. Vis. Sci.* 53:2804; Swadling et al. (2014) *Sci. Transl. Med.* 6:261ra153; and Choi and Chang (2013) *Clin. Exp. Vaccine Res.* 2:97. In many cases, the recombinant viral vectors are packaged into viral particles; and the viral particles are formulated in an immunogenic composition along with a pharmaceutically acceptable carrier. Suitable pharmaceutically acceptable carriers are described above.

[00297] In some cases, an immunogenic composition of the present disclosure comprises: a) a recombinant viral vector comprising nucleotide sequences encoding one or more of: an HCV E1/E2 heterodimer; an HCV E1 polypeptide; an HCV E2 polypeptide; and a T-cell epitope polypeptide; and b) a CDN or an archaeosome. In some cases, an immunogenic composition of the present disclosure comprises: a) a recombinant viral vector comprising nucleotide sequences encoding: an HCV E1/E2 heterodimer; and a T-cell epitope polypeptide; and b) a CDN or an archaeosome. In some cases, an immunogenic composition of the present disclosure comprises: a) a recombinant viral vector comprising nucleotide sequences encoding: an HCV E1 polypeptide; and a T-cell epitope polypeptide; and b) a CDN or an archaeosome. In some cases, an immunogenic composition of the present disclosure comprises: a) a recombinant viral vector comprising nucleotide sequences encoding: an HCV E2 polypeptide; and a T-cell epitope polypeptide; and b) a CDN or an archaeosome. In some cases, an immunogenic composition of the present disclosure comprises: a) a recombinant viral vector comprising nucleotide sequences encoding an HCV E1/E2 heterodimer; and b) a CDN or an archaeosome. In some cases, an immunogenic composition of the present disclosure comprises: a) a recombinant viral vector comprising nucleotide sequences encoding an HCV E2 polypeptide; and b) a CDN or an archaeosome. In some cases, an immunogenic composition of the present disclosure comprises: a) a recombinant viral vector comprising nucleotide sequences encoding an HCV E1 polypeptide; and b) a CDN or an archaeosome.

[00298] In some cases, the present disclosure provides: a) a first immunogenic composition comprising: i) a recombinant viral vector comprising nucleotide sequences encoding one or more of: an HCV E1/E2 heterodimer; an HCV E1 polypeptide; an HCV E2 polypeptide; and a T-cell epitope polypeptide; and ii) a CDN; and b) a second immunogenic composition comprising: i) a recombinant viral vector comprising nucleotide sequences encoding one or more of: an HCV E1/E2 heterodimer; an HCV E1 polypeptide; an HCV E2 polypeptide; and a T-cell epitope

polypeptide; and ii) a CDN. In some cases, the present disclosure provides: a) a first immunogenic composition comprising: i) a recombinant viral vector comprising nucleotide sequences encoding one or more of: an HCV E1/E2 heterodimer; an HCV E1 polypeptide; an HCV E2 polypeptide; and a T-cell epitope polypeptide; and ii) an archaeosome; and b) a second immunogenic composition comprising: i) a recombinant viral vector comprising nucleotide sequences encoding one or more of: an HCV E1/E2 heterodimer; an HCV E1 polypeptide; an HCV E2 polypeptide; and a T-cell epitope polypeptide; and ii) an archaeosome.

[00299] In some cases, the present disclosure provides: a) a first immunogenic composition comprising: i) a first recombinant viral vector comprising nucleotide sequences encoding one or more of: an HCV E1/E2 heterodimer; an HCV E1 polypeptide; an HCV E2 polypeptide; and a T-cell epitope polypeptide; and ii) a CDN or an archaeosome; and b) a second immunogenic composition comprising: i) a second recombinant viral vector comprising nucleotide sequences encoding one or more of: an HCV E1/E2 heterodimer; an HCV E1 polypeptide; an HCV E2 polypeptide; and a T-cell epitope polypeptide; and ii) a CDN or an archaeosome. In some cases, the first recombinant viral vector is a replication-defective adenovirus-based recombinant viral vector; and the second recombinant viral vector is an MVA-based recombinant viral vector. In some cases, the first recombinant viral vector is a chimpanzee adenovirus-based recombinant viral vector; and the second recombinant viral vector is an MVA-based recombinant viral vector.

[00300] In some cases, the nucleic acid(s) are present in bacteria (e.g., non-pathogenic bacteria suitable for delivery of nucleic acids to an individual). In some cases, the nucleic acid(s) are present in recombinant expression vector(s) present in bacteria (e.g., non-pathogenic bacteria suitable for delivery of nucleic acids to an individual). Thus, the present disclosure provides an immunogenic composition comprising a non-pathogenic, bacterium that harbors a nucleic acid(s) comprising nucleotide sequences encoding one or more of: an HCV E1/E2 heterodimer; an HCV E1 polypeptide; an HCV E2 polypeptide; and a T-cell epitope polypeptide, where such polypeptides are described above. The present disclosure provides an immunogenic composition comprising a non-pathogenic bacterium that harbors a recombinant expression vector(s) comprising nucleotide sequences encoding one or more of: an HCV E1/E2 heterodimer; an HCV E1 polypeptide; an HCV E2 polypeptide; and a T-cell epitope polypeptide, where such polypeptides are described above. In some cases, the bacteria are live. In some cases, the bacteria are live attenuated bacteria. In some cases, the bacteria are killed.

[00301] Bacteria suitable for delivery of nucleic acid(s) (which nucleic acid(s) may be present in expression vector(s)) include, but are not limited to, *Lactobacillus*; *Lactococcus* (e.g., *Lactococcus lactis*); *Salmonella*, e.g., attenuated, non-pathogenic *Salmonella*, e.g., *Salmonella enterica* serovar Typhi, *Salmonella enterica* serovar Typhimurium; non-pathogenic strains of

Francisella; non-pathogenic strains of *Escherichia coli*; non-pathogenic strains of *Bordetella pertussis*; non-pathogenic strains of *Listeria*; non-pathogenic strains of *Shigella*; non-pathogenic strains of *Vibrio* (e.g., *Vibrio cholera*); *Streptococcus gordonii*; non-pathogenic strains of *Yersinia enterocolitica*; non-pathogenic strains of *Shigella flexneri*; non-pathogenic strains of *Pseudomonas aeruginosa*; non-pathogenic strains of *Bacillus subtilis*; and the like.

[00302] In some cases, one or more virulence genes in the bacterium is all or partially deleted. For example, for *Salmonella enterica* serovar Typhi and *Salmonella enterica* serovar Typhimurium, an *aroA*, *aroC*, and *aroD* mutation can be made. Other mutations that can attenuate pathogenicity affect biosynthesis of the nucleotides adenine (*pur*) and guanine (*guaBA*), and outer membrane proteins C and F (*ompC*, *ompF*), as well as expression of the cAMP receptor (*cya/crp*), the conversion of UDP-galactose to UDP-glucose (*galE*), DNA recombination and repair (*recA*, *recBC*), and regulation of virulence genes (*phoP*, *phoQ*). For *Listeria monocytogenes*, attenuation can be achieved with auxotrophic mutants, or deletion of virulence factors such as the genes *actA* and internalin B (*intB*).

METHODS OF INDUCING AN IMMUNE RESPONSE TO HCV

[00303] The present disclosure provides a method of inducing an immune response (e.g., a protective immune response) to at least one HCV genotype in a mammalian subject (e.g., a human). In some cases, a method of the present disclosure for inducing an immune response in an individual to at least one HCV genotype comprises administering an immunogenic composition of the present disclosure, where the immunogenic composition comprises polypeptides (e.g., HCV E1/E2, HCV E1, or HCV E2; and optionally a T-cell epitope polypeptide). In some cases, a method of the present disclosure for inducing an immune response in an individual to at least one HCV genotype comprises administering an immunogenic composition of the present disclosure, where the immunogenic composition comprises one or more nucleic acids comprising nucleotide sequences encoding polypeptides (e.g., e.g., HCV E1/E2, HCV E1, or HCV E2; and optionally a T-cell epitope polypeptide).

Administering an immunogenic composition comprising polypeptides

[00304] In some cases, the methods comprise administering to an individual in need thereof an effective amount of an immunogenic composition of the present disclosure, where the immunogenic composition comprises: a) an HCV E1/E2 heterodimer; and b) a CDN; or where the immunogenic composition comprises: a) an HCV E2 polypeptide; and b) a CDN; or where the immunogenic composition comprises: a) an HCV E1 polypeptide; and b) a CDN. In some cases, the methods comprise administering to an individual in need thereof an effective amount of an immunogenic composition of the present disclosure, where the immunogenic composition comprises: a) an HCV E1/E2 heterodimer; and b) an archaeosome; or where the immunogenic

composition comprises: a) an HCV E2 polypeptide; and b) an archaeosome; or where the immunogenic composition comprises: a) an HCV E1 polypeptide; and b) an archaeosome.

[00305] In some cases, the methods comprise administering to an individual in need thereof an effective amount of an immunogenic composition of the present disclosure, where the immunogenic composition comprises: a) an HCV E1/E2 heterodimer; b) a T-cell epitope polypeptide comprising a T-cell epitope present in an HCV polypeptide other than E1 and E2; and c) a CDN; or where the immunogenic composition comprises: a) an HCV E2 polypeptide; b) a T-cell epitope polypeptide comprising a T-cell epitope present in an HCV polypeptide other than E1 and E2; and c) a CDN; or where the immunogenic composition comprises: a) an HCV E1 polypeptide; b) a T-cell epitope polypeptide comprising a T-cell epitope present in an HCV polypeptide other than E1 and E2; and c) a CDN.

[00306] In some cases, the methods comprise administering to an individual in need thereof an effective amount of an immunogenic composition of the present disclosure, where the immunogenic composition comprises: a) an HCV E1/E2 heterodimer; b) a T-cell epitope polypeptide comprising a T-cell epitope present in an HCV polypeptide other than E1 and E2; and c) an archaeosome; or where the immunogenic composition comprises: a) an HCV E2 polypeptide; b) a T-cell epitope polypeptide comprising a T-cell epitope present in an HCV polypeptide other than E1 and E2; and c) an archaeosome; or where the immunogenic composition comprises: a) an HCV E1 polypeptide; b) a T-cell epitope polypeptide comprising a T-cell epitope present in an HCV polypeptide other than E1 and E2; and c) an archaeosome.

[00307] In some cases, an immunogenic composition of the present disclosure comprising an HCV E1/E2 heterodimer and a CDN is administered via intramuscular administration. In some cases, an immunogenic composition of the present disclosure comprising an HCV E1/E2 heterodimer and a CDN is administered via intranasal administration. In some cases, an immunogenic composition of the present disclosure comprising an HCV E1/E2 heterodimer and a CDN is administered: a) first via intramuscular administration; b) followed by a second administration via intranasal administration; c) followed by a third administration via intranasal administration.

[00308] In some cases, an immunogenic composition of the present disclosure comprising an HCV E1/E2 heterodimer and an archaeosome is administered via intramuscular administration.

Administering an immunogenic composition comprising nucleic acid(s)

[00309] In some cases, a method of the present disclosure for inducing an immune response to HCV in an individual comprises administering to the individual an effective amount of an immunogenic composition comprising: a) nucleic acid(s) comprising nucleotide sequences

encoding: 1) an HCV E1/E2 heterodimer and a T-cell epitope polypeptide; 2) an HCV E2 polypeptide and a T-cell epitope polypeptide; 3) an HCV E1 polypeptide and a T-cell epitope polypeptide; 4) an HCV E1/E2 heterodimer; 5) an HCV E2 polypeptide; or 6) an HCV E1 polypeptide; and b) a CDN or an archaeosome. The polypeptides can be encoded in the same nucleic acid, or on separate nucleic acids. For example, where the nucleic acid(s) are recombinant expression vectors, the polypeptides can be encoded in the same or separate recombinant expression vectors.

[00310] In some cases, the nucleic acid(s) is/are DNA. In some cases, the nucleic acid(s) is/are RNA. In some cases, the nucleic acid(s) is/are present in expression vector(s) such that a recombinant expression vector(s) comprising the nucleic acid(s) are administered. In some cases, the recombinant expression vector(s) is/are recombinant viral vector(s). In some cases, the recombinant viral vector(s) are packaged into viral particles. In some cases, the nucleic acid(s) are present in bacteria (e.g., non-pathogenic bacteria (e.g., attenuated bacteria) suitable for delivery of nucleic acids to an individual).

[00311] In some cases, the nucleic acid is present in an expression vector, thereby generating a recombinant expression vector. Suitable expression vectors include, but are not limited to, a replication-defective adenovirus vector; a replication-defective vaccinia virus vector; a lentivirus vector (e.g., a self-inactivating lentivirus vector); a retroviral vector (e.g., a self-inactivating retroviral vector); an adeno-associated virus vector; and the like. In some cases, the vector is a modified vaccinia Ankara (MVA) vector, or an MVA-based vector (see, e.g., Verheust et al. (2012) *Vaccine* 30:2623). In some cases, the vector is a replication-defective adenovirus vector. In some cases, the vector is a replication-defective adenovirus 6 (Ad6) vector. In some cases, the vector is a replication-defective simian adenovirus vector (e.g., ChAd3). Suitable viral vectors are described in, e.g., Zhou et al. (2012) *Invest. Ophthalmol. Vis. Sci.* 53:2804; Swadling et al. (2014) *Sci. Transl. Med.* 6:261ra153; and Choi and Chang (2013) *Clin. Exp. Vaccine Res.* 2:97. In many cases, the recombinant viral vectors are packaged into viral particles; and the viral particles are formulated in an immunogenic composition along with a pharmaceutically acceptable carrier.

[00312] In some cases, an HCV E1/E2 heterodimer is encoded by nucleotide sequences present in a first recombinant viral vector, e.g., an adenovirus vector, a vaccinia virus vector, an MVA vector or MVA-based vector; and a T-cell epitope polypeptide is encoded by nucleotide sequences present in a second recombinant viral vector, e.g., an adenovirus vector, a vaccinia virus vector, an MVA vector or MVA-based vector.

[00313] In some cases, a prime-boost vaccine protocol is used. In some cases, a first (priming) immunogenic composition is administered, where the first immunogenic composition comprises

a recombinant viral vector comprising nucleotide sequences encoding one or more of: a) an HCV E1/E2 heterodimer; b) an HCV E2 polypeptide; c) an HCV E1 polypeptide; and d) a T-cell epitope polypeptide; and, after a time, a second (booster) immunogenic composition is administered, where the second immunogenic composition comprises a recombinant viral vector comprising nucleotide sequences encoding one or more of: a) an HCV E1/E2 heterodimer; b) an HCV E2 polypeptide; c) an HCV E1 polypeptide; and d) a T-cell epitope polypeptide. In some cases, the first recombinant viral vector and the second recombinant viral vector are the same. In some cases, the first recombinant viral vector and the second recombinant viral vector are different. For example, in some cases, the first recombinant viral vector is a vaccinia-based recombinant viral vector; and the second recombinant viral vector is an adenovirus-based recombinant viral vector. In general, the recombinant viral vectors are packaged into viral particles. A second immunogenic composition can be administered at a time period of from 1 day to 1 year following administration of the first immunogenic composition. For example, a second immunogenic composition can be administered at a time period of from 1 day to 1 week, from 1 week to 2 weeks, from 2 weeks to 1 month, from 1 month to 2 months, from 2 months to 6 months, or from 6 months to 1 year following administration of the first immunogenic composition.

[00314] For example, in some cases, a first (priming) vaccine comprising a recombinant adenovirus (e.g., Ad6 or chimpanzee Ad (e.g., ChAd3)) that comprises a nucleotide sequence encoding an HCV E1/E2 heterodimer is followed by a second (booster) vaccine comprising a recombinant MVA vector that comprises a nucleotide sequence encoding a T-cell epitope polypeptide. Other prime-boost protocols can be used. For example, multiple primes and/or multiple boosts can be administered.

[00315] In some cases, a first (priming) immunogenic composition is administered, where the first immunogenic composition comprises one or more of: a) an HCV E1/E2 heterodimer; b) an HCV E2 polypeptide; c) an HCV E1 polypeptide; and d) a T-cell epitope polypeptide, as described above; and a second (boosting) immunogenic composition is administered, where the second immunogenic composition comprises a recombinant viral vector comprising nucleotide sequence(s) encoding one or more of: a) an HCV E1/E2 heterodimer; b) an HCV E2 polypeptide; c) an HCV E1 polypeptide; and d) a T-cell epitope polypeptide, as described above.

[00316] In some cases, a first (priming) immunogenic composition is administered, where the first immunogenic composition comprises a recombinant viral vector comprising nucleotide sequence(s) encoding one or more of: a) an HCV E1/E2 heterodimer; b) an HCV E2 polypeptide; c) an HCV E1 polypeptide; and d) a T-cell epitope polypeptide, as described above; and a second (boosting) immunogenic composition is administered, where the second

immunogenic composition comprises one or more of: a) an HCV E1/E2 heterodimer; b) an HCV E2 polypeptide; c) an HCV E1 polypeptide; and d) a T-cell epitope polypeptide, as described above.

[00317] In some cases, a co-immunization regimen is carried out, in which a polypeptide(s) *per se* is administered substantially concomitantly with a nucleic acid(s) encoding the polypeptide(s). For example, in some cases, a method of the present disclosure for inducing an immune response to an HCV polypeptide can comprise administering: a) a first immunogenic composition of the present disclosure, as described above, where the immunogenic composition comprises: i) an HCV E1/E2 heterodimer; ii) a T-cell epitope polypeptide; and iii) a pharmaceutically acceptable carrier; or i) an HCV E1 polypeptide; ii) a T-cell epitope polypeptide; and iii) a pharmaceutically acceptable carrier; or i) an HCV E2 polypeptide; ii) a T-cell epitope polypeptide; and iii) a pharmaceutically acceptable carrier; and b) a second immunogenic composition of the present disclosure, as described above, where the immunogenic composition comprises: i) one or more nucleic acids comprising nucleotide sequence encoding one or more of: an HCV E1/E2 heterodimer, an HCV E1 polypeptide, an HCV E2 polypeptide, and a T-cell epitope polypeptide; and ii) a pharmaceutically acceptable carrier. In some cases, the first and the second immunogenic compositions are in a single formulation. In some cases, the first and the second immunogenic compositions are in separate formulations. In some cases, the first and the second immunogenic compositions are administered via the same route of administration. In some cases, the first and the second immunogenic compositions are administered via different routes of administration. In some cases, the first and the second immunogenic compositions are in separate formulations that are administered substantially simultaneously, e.g., within 1 minute, within 1 minute to 5 minutes, within 5 minutes to 15 minutes, or within 15 minutes to 30 minutes, of one another. In some cases, the first and the second immunogenic compositions are administered multiple times to an individual.

[00318] In some cases, a co-immunization regimen is carried out, in which a polypeptide(s) *per se* is administered substantially concomitantly with a nucleic acid(s) encoding the polypeptide(s). For example, in some cases, a method of the present disclosure for inducing an immune response to an HCV polypeptide can comprise administering: a) a first immunogenic composition of the present disclosure, as described above, where the immunogenic composition comprises: i) an HCV E1/E2 heterodimer; ii) a T-cell epitope polypeptide; and iii) a CDN; and b) a second immunogenic composition of the present disclosure, as described above, where the immunogenic composition comprises: i) one or more nucleic acids comprising nucleotide sequences encoding an HCV E1/E2 heterodimer and a T-cell epitope polypeptide; and ii) a CDN. In some cases, the first and the second immunogenic compositions are in a single formulation. In some cases, the

first and the second immunogenic compositions are in separate formulations. In some cases, the first and the second immunogenic compositions are administered via the same route of administration. In some cases, the first and the second immunogenic compositions are administered via different routes of administration. In some cases, the first and the second immunogenic compositions are in separate formulations that are administered substantially simultaneously, e.g., within 1 minute, within 1 minute to 5 minutes, within 5 minutes to 15 minutes, or within 15 minutes to 30 minutes, of one another. In some cases, the first and the second immunogenic compositions are administered multiple times to an individual. In some cases, the one or more nucleic acids are recombinant viral vectors.

[00319] In some cases, a method of the present disclosure for inducing an immune response to HCV in an individual comprises administering to the individual an effective amount of an immunogenic composition comprising: a) nucleic acid(s) comprising nucleotide sequences encoding 1) an HCV E1/E2 heterodimer and a T-cell epitope polypeptide; 2) an HCV E2 polypeptide and a T-cell epitope polypeptide; 3) an HCV E1 polypeptide and a T-cell epitope polypeptide; 4) an HCV E1/E2 polypeptide; 5) an HCV E2 polypeptide; or 6) an HCV E1 polypeptide; and b) a CDN or an archaeosome. In some cases, the nucleic acid is an RNA comprising nucleotide sequences encoding a polypeptide of the present disclosure (e.g., an HCV E1/E2 heterodimer; an HCV E1 polypeptide; an HCV E2 polypeptide; a T-cell epitope polypeptide, as described herein. See, e.g., Weiner (2013) *Molec. Therapy* 21:506; and Ulmer et al. (2012) *Vaccine* 30:4414. In some cases, an RNA (e.g., a single mRNA molecule; or 2 mRNA molecules; or 3 mRNA molecules) comprising nucleotide sequences encoding a polypeptide of the present disclosure is formulated with a liposome. In some cases, an RNA (e.g., a single mRNA molecule; or 2 mRNA molecules) comprising nucleotide sequences encoding a polypeptide of the present disclosure is complexed with protamine. In some cases, an RNA (e.g., a single mRNA molecule; or 2 mRNA molecules) comprising nucleotide sequences encoding a polypeptide of the present disclosure is complexed with 1,2-dioleoyl-3-trimethylammonium-propane/1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOTAP/DOPE).

[00320] In some cases, the nucleic acid(s) are present in bacteria (e.g., non-pathogenic bacteria suitable for delivery of nucleic acids to an individual). In some cases, the nucleic acid(s) are present in recombinant expression vector(s) present in bacteria (e.g., non-pathogenic bacteria suitable for delivery of nucleic acids to an individual). In some cases, the bacteria are live. In some cases, the bacteria are live attenuated bacteria. In some cases, the bacteria are killed. Bacteria suitable for delivery of nucleic acid(s) (which may be present in expression vectors) include, but are not limited to, *Lactobacillus*; *Lactococcus* (e.g., *Lactococcus lactis*); *Salmonella*, e.g., attenuated, non-pathogenic *Salmonella*, e.g., *Salmonella enterica* serovar Typhi, *Salmonella*

enterica serovar Typhimurium; non-pathogenic strains of *Escherichia coli*; non-pathogenic strains of *Bordetella pertussis*; non-pathogenic strains of *Listeria*; non-pathogenic strains of *Shigella*; non-pathogenic strains of *Vibrio* (e.g., *Vibrio cholera*); *Streptococcus gordonii*; non-pathogenic strains of *Yersinia enterocolitica*; non-pathogenic strains of *Shigella flexneri*; non-pathogenic strains of *Pseudomonas aeruginosa*; non-pathogenic strains of *Bacillus subtilis*; and the like. In some cases, one or more virulence genes in the bacterium is all or partially deleted. For example, for *Salmonella enterica* serovar Typhi and *Salmonella enterica* serovar Typhimurium, an *aroA*, *aroC*, and *aroD* mutation can be made. Other mutations that can attenuate pathogenicity affect biosynthesis of the nucleotides adenine (*pur*) and guanine (*guaBA*), and outer membrane proteins C and F (*ompC*, *ompF*), as well as expression of the cAMP receptor (*cya/crp*), the conversion of UDP-galactose to UDP-glucose (*galE*), DNA recombination and repair (*recA*, *recBC*), and regulation of virulence genes (*phoP*, *phoQ*). For *Listeria monocytogenes*, attenuation can be achieved with auxotrophic mutants, or deletion of virulence factors such as the genes *actA* and internalin B (*intB*).

General considerations

[00321] An immunogenic composition of the present disclosure is generally administered to a human subject who has an HCV infection or who is at risk of acquiring an HCV infection (e.g., is at greater risk than the general population of acquiring an HCV infection) so as to prevent or at least partially arrest the development of disease and its complications. An amount adequate to accomplish this is defined as a “therapeutically effective dose” or a “therapeutically effective amount.” “Prophylactic” use of a subject immunogenic composition generally refers to administration to an individual who has not been infected with HCV. “Therapeutic” use of a subject immunogenic composition can refer to “prophylactic” use (administration to an individual who has not been infected with HCV) and/or to administration to an individual who has an HCV infection. A “therapeutically effective amount” of an immunogenic composition of the present disclosure, can be an amount that, when administered in one or more doses to an individual who is not infected with HCV, is effective to induce an immune response in the individual to HCV. A “therapeutically effective amount” of an immunogenic composition of the present disclosure, can be an amount that, when administered in one or more doses to an individual who is infected with HCV, is effective to enhance an immune response in the individual to HCV.

[00322] Amounts effective for therapeutic use will depend on, e.g., the manner of administration, the weight and general state of health of the patient, and the judgment of the prescribing physician. Single or multiple doses of a subject immunogenic composition can be administered

depending on the dosage and frequency required and tolerated by the patient, and route of administration.

- [00323]** In some cases, an effective amount of an immunogenic composition of the present disclosure is an amount that, when administered to an individual in one or more doses, is effective to induce an antibody response (e.g., a neutralizing antibody response) to HCV in the individual. For example, antibody to HCV (e.g., extracellular HCV), and/or to an HCV-infected cell, can be induced.
- [00324]** An effective amount of an immunogenic composition of the present disclosure can be an amount that, when administered to an individual in one or more doses, is effective to induce a neutralizing antibody response to HCV of a variety of genotypes (e.g., genotype 1; genotype 3; etc.). A neutralizing antibody response reduces binding of HCV to one or more host receptors for HCV and inhibits entry of HCV into a cell.
- [00325]** In some cases, an effective amount (e.g., a therapeutically effective amount) of an immunogenic composition of the present disclosure is an amount that, when administered to an individual in one or more doses, is effective to induce a cytotoxic T lymphocyte (CTL) response to HCV. For example, a CTL response to an HCV-infected cell can be induced.
- [00326]** In some cases, an effective amount (e.g., a therapeutically effective amount) of an immunogenic composition of the present disclosure is an amount that, when administered to an individual in one or more doses, is effective to induce a helper T lymphocyte (e.g., CD4⁺ T cell) to HCV in an individual.
- [00327]** In some cases, an effective amount (e.g., a therapeutically effective amount) of an immunogenic composition of the present disclosure is an amount that, when administered to an individual in one or more doses, is effective to induce an antibody response (e.g., a neutralizing antibody response) and/or a CTL response and/or a helper T cell response to HCV genotype 1. In some cases, an effective amount (e.g., a therapeutically effective amount) of an immunogenic composition of the present disclosure is an amount that, when administered to an individual in one or more doses, is effective to induce an antibody response (e.g., a neutralizing antibody response) and/or a CTL response and/or a helper T cell response to HCV genotype 3. In some cases, an effective amount (e.g., a therapeutically effective amount) of an immunogenic composition of the present disclosure is an amount that, when administered to an individual in one or more doses, is effective to induce an antibody response (e.g., a neutralizing antibody response) and/or a CTL response and/or a helper T cell response to HCV genotype 1 and HCV genotype 3. In some cases, an effective amount (e.g., a therapeutically effective amount) of an immunogenic composition of the present disclosure is an amount that, when administered to an

individual in one or more doses, is effective to induce an antibody response (e.g., a neutralizing antibody response) and/or a CTL response and/or a helper T cell response to HCV of any genotype.

[00328] An immunogenic composition of the present disclosure is generally administered in an amount effective to elicit an immune response, e.g., a humoral immune response (e.g., an antibody response) and/or a CTL response, in the mammalian subject. Effective amounts for immunization will vary, and can generally range from about 1 µg to 100 µg per 70 kg patient, e.g., from about 5 µg/70 kg to about 50 µg/70 kg. Substantially higher dosages (e.g. 10 mg to 100 mg or more) may be suitable in oral, nasal, or topical administration routes. The initial administration can be followed by booster immunization of the same immunogenic composition or a different immunogenic composition. In some instances, a subject method of inducing an immune response involves an initial administration of an immunogenic composition of the present disclosure, followed by at least one booster, and in some instances involves two or more (e.g., three, four, or five) boosters. The interval between an initial administration and a booster, or between a give booster and a subsequent booster, can be from about 1 week to about 12 weeks, e.g., from about 1 week to about 2 weeks, from about 2 weeks to about 4 weeks, from about 4 weeks to about 6 weeks, from about 6 weeks to about 8 weeks, from about 8 weeks to about 10 weeks, or from about 10 weeks to about 12 weeks. The interval between an initial administration and a booster, or between a give booster and a subsequent booster, can be from 4 months to 6 months, or from 6 months to 1 year.

[00329] In general, immunization can be accomplished by administration of an immunogenic composition of the present disclosure by any suitable route, including administration of the composition orally, nasally, nasopharyngeally, parenterally, enterically, gastrically, topically, transdermally, subcutaneously, intramuscularly, in tablet, solid, powdered, liquid, aerosol form, locally or systemically, with or without added excipients. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art and are described in more detail in such publications as Remington's Pharmaceutical Science, 15th ed., Mack Publishing Company, Easton, Pa. (1980). In some instances, immunization is accomplished by intramuscular injection of an immunogenic composition of the present disclosure.

INDIVIDUALS SUITABLE FOR ADMINISTRATION

[00330] Individuals who are suitable for administration with an immunogenic composition of the present disclosure include immunologically naïve individuals (e.g., individuals who have not been infected with HCV and/or who have not been administered with an HCV vaccine).

Individuals suitable for administration include humans. Individuals who are suitable for administration with an immunogenic composition of the present disclosure are also referred to as “an individual in need thereof.”

[00331] Individuals who are suitable for administration with an immunogenic composition of the present disclosure include individuals who are at greater risk than the general population of becoming infected with HCV, where such individuals include, e.g., intravenous drug users; individuals who are the recipients, or the prospective recipients, of blood or blood products from another (donor) individual(s); individuals who are the recipients, or the prospective recipients, of non-autologous cells, tissues, or organs from another (donor) individual; health care workers; emergency medical and non-medical personnel (e.g., first responders; fire fighters; emergency medical team personnel; etc.) and the like.

[00332] Individuals who are suitable for administration with an immunogenic composition of the present disclosure include individuals who recently became exposed to HCV or who recently became infected with HCV. For example, a subject immunogenic composition can be administered to an individual within from about 24 hours to about 48 hours, from about 48 hours to about 1 week, or from about 1 week to about 4 weeks, following possible or suspected exposure to HCV or following infection with HCV.

[00333] Individuals who are suitable for administration with an immunogenic composition of the present disclosure include individuals who have been diagnosed as having an HCV infection, and include chronically infected individuals. In some cases, an individual who has been diagnosed as having an HCV infection is treated with an anti-viral agent and an immunogenic composition of the present disclosure. Suitable anti-viral agents for treating HCV infection include, e.g., ribavirin (1- β -D-ribofuranosyl-1H-1,2,4-triazole-3-carboxamide); interferon-alpha (IFN- α) (where “IFN- α ” includes IFN- α 2a; IFN- α 2b; IFN- α that is conjugated with poly(ethylene glycol) (“pegylated IFN- α), where the pegylated IFN- α can be pegylated IFN- α 2a or pegylated IFN- α 2b); an HCV NS3 protease inhibitor (e.g., boceprevir; telaprevir); and an HCV NS5 protease inhibitor. In some cases, an individual who has been diagnosed as having an HCV infection is treated with, e.g.: 1) IFN- α + ribavirin; and an immunogenic composition of the present disclosure; or 2) IFN- α + ribavirin + an HCV protease inhibitor (e.g., boceprevir or telaprevir); and an immunogenic composition of the present disclosure. Suitable anti-viral agents for treating HCV infection include Sovaldi (Sofosbuvir; a nucleotide analog that functions as an NS5B polymerase inhibitor), alone or in combination with pegylated IFN- α and ribavirin.

Examples of Non-Limiting Aspects of the Disclosure

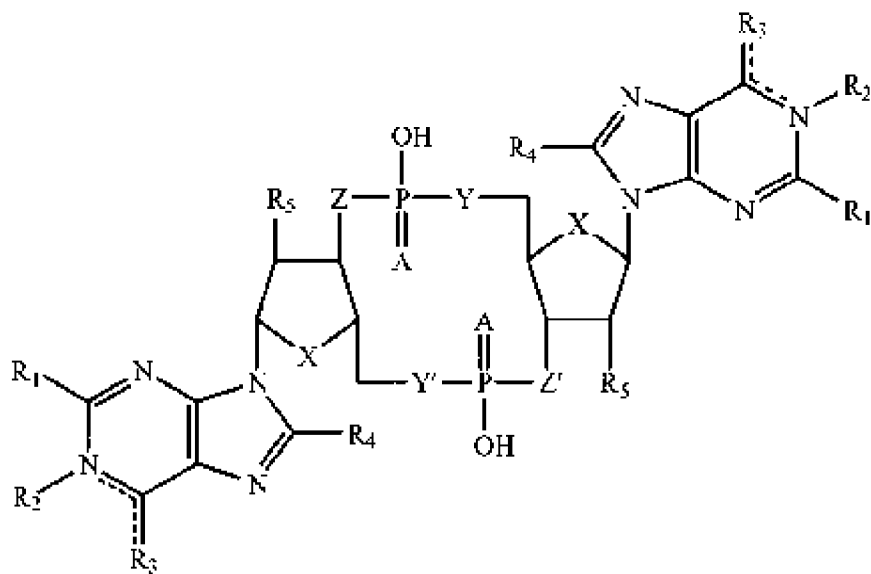
[00334] Aspects, including embodiments, of the present subject matter described above may be beneficial alone or in combination, with one or more other aspects or embodiments. Without limiting the foregoing description, certain non-limiting aspects of the disclosure numbered 1-136 are provided below. As will be apparent to those of skill in the art upon reading this disclosure, each of the individually numbered aspects may be used or combined with any of the preceding or following individually numbered aspects. This is intended to provide support for all such combinations of aspects and is not limited to combinations of aspects explicitly provided below:

[00335] Aspect 1. An immunogenic composition comprising: a) an HCV E1/E2 heterodimer; and b) a cyclic dinucleotide (CDN); or a) an HCV E2 polypeptide; and b) a CDN; or a) an HCV E1 polypeptide; and b) a CDN.

[00336] Aspect 2. The immunogenic composition of aspect 1A, aspect 1B, or aspect 1C, wherein the CDN is fluorinated.

[00337] Aspect 3. The immunogenic composition of aspect 2, wherein the CDN is 2'-F-c-di-GMP.

[00338] Aspect 4. The immunogenic composition of aspect 1A, aspect 1B, or aspect 1C, wherein the CDN is of Formula (I):



[00339] wherein:

[00340] A is S or O;

[00341] X is S, N, O, CH₂;

[00342] Y, Y' is NH, CH₂, O;

[00343] Z, Z' is NH, CH₂, O;

- [00344] R1 represents hydrogen or NH₂ which may be substituted;
- [00345] R2 is hydrogen or absent;
- [00346] R3 represents NH₂, O, OH, H, or a halogen;
- [00347] R4 represents hydrogen, halogen, or a straight or branched C₁-C₆ alkyl group which may optionally be substituted;
- [00348] R5 represents hydrogen, OH or a straight or branched C₁-C₆ alkyl chain or C₁-C₆ straight or branched alkoxy chain which may optionally be substituted;
- [00349]  is a single or double bond;
- [00350] or conjugates thereof, and salts or solvates thereof.
- [00351] Aspect 5. The immunogenic composition of aspect 4, wherein the CDN is c-diGMP, c-diAMP, c-diIMP, or c-dXMP.
- [00352] Aspect 6. The immunogenic composition of aspect 4, wherein the CDN is c-GpAp, c-Gplp, c-GpXp, c-ApIp, c-ApXp, or c-lpXp.
- [00353] Aspect 7. The immunogenic composition of aspect 1, wherein the CDN is cyclic-GMP-AMP (cGAMP).
- [00354] Aspect 8. The immunogenic composition of aspect 7, wherein the cGAMP is 2'3'-cGAMP, 2'2'-cGAMP, 3'2'-cGAMP or 3'3'-GAMP.
- [00355] Aspect 9. The immunogenic composition of any one of aspect aspects 1-8, wherein the composition comprises an HCV E1/E2 heterodimer.
- [00356] Aspect 10. The immunogenic composition of aspect 9, wherein:
- [00357] a) the HCV E2 polypeptide is derived from an HCV of major genotype 1, 2, 3, 4, 5, 6, or 7; and
- [00358] b) the HCV E1 polypeptide is derived from an HCV of major genotype 1, 2, 3, 4, 5, 6, or 7.
- [00359] Aspect 11. The immunogenic composition of any one of aspects 1-10, wherein the HCV E2 polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to an E2 polypeptide depicted in one of FIG. 1A-1C, FIG. 2A-2C, FIG. 3A-3C, and FIG. 4A-4B.
- [00360] Aspect 12. The immunogenic composition of any one of aspects 1-10, wherein the HCV E1 polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to an E1 polypeptide depicted in FIG. 1A-1C, FIG. 2A-2C, FIG. 3A-3C, and FIG. 4A-4B.
- [00361] Aspect 13. The immunogenic composition of any one of aspects 1-12, wherein the E2 polypeptide and/or the E1 polypeptide lacks a C-terminal transmembrane domain.

- [00362] Aspect 14. The immunogenic composition of any one of aspects 1-13, wherein the HCV E2 polypeptide and the HCV E1 polypeptide are derived from an HCV of the same genotype.
- [00363] Aspect 15. The immunogenic composition of any one of aspects 1-13, wherein the HCV E2 polypeptide and the HCV E1 polypeptide are derived from an HCV of different genotypes.
- [00364] Aspect 16. The immunogenic composition of any one of aspects 1-15, wherein the HCV E1/E2 heterodimeric polypeptide comprises:
- [00365] a) an HCV E1 polypeptide; and
- [00366] b) a modified E2 polypeptide comprising, in order from N-terminus to C-terminus:
- [00367] i) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are C-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; and
- [00368] ii) an HCV E2 polypeptide; or
- [00369] a) an HCV E2 polypeptide; and
- [00370] b) a modified E1 polypeptide comprising, in order from N-terminus to C-terminus:
- [00371] i) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are C-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; and
- [00372] ii) an HCV E1 polypeptide; or
- [00373] a) an HCV E1 polypeptide; and
- [00374] b) a modified E2 polypeptide comprising, in order from N-terminus to C-terminus:
- [00375] i) an HCV E2 polypeptide; and
- [00376] ii) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are N-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; or
- [00377] a) an HCV E2 polypeptide; and
- [00378] b) a modified E1 polypeptide comprising, in order from N-terminus to C-terminus:
- [00379] i) an HCV E1 polypeptide; and
- [00380] ii) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are N-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker.
- [00381] Aspect 17. The immunogenic composition of aspect 16, wherein:
- [00382] a) the from 1 to 6 heterologous amino acids at the N-terminus of the modified E2 polypeptide or the modified E1 polypeptide are Gly-Pro, Ser, Gly, or Gly-Ser; or
- [00383] b) the from 1 to 6 heterologous amino acids at the C-terminus of the modified E2 polypeptide or the modified E1 polypeptide are LEVLFQGP (SEQ ID NO:117), ENLYYFQ (SEQ ID NO:150), LVPR (SEQ ID NO:124), I(E/D)GR (SEQ ID NO:125), or DDDDK.
- [00384] Aspect 18. The immunogenic composition of any one of aspects 1-17, wherein the HCV E1 polypeptide, the HCV E2 polypeptide, or one or both chains of the HCV E1/E2 heterodimer

comprises a covalently linked T-cell epitope polypeptide comprising a T-cell epitope present in an HCV protein other than E1 and E2.

- [00385]** Aspect 19. The immunogenic composition of any one of aspects 1-18, comprising a T-cell epitope polypeptide comprising a T-cell epitope present in an HCV protein other than E1 and E2, wherein the T-cell epitope polypeptide is not covalently linked to the HCV E1E2 heterodimer, the HCV E1 polypeptide, or the HCV E2 polypeptide.
- [00386]** Aspect 20. The immunogenic composition of aspect 18 or aspect 19, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in one or more of:
- [00387]** a) an HCV non-structural polypeptide-3 (NS3) polypeptide;
 - [00388]** b) an HCV non-structural polypeptide-2 (NS2) polypeptide;
 - [00389]** c) an HCV non-structural polypeptide-4A (NS4A) polypeptide;
 - [00390]** d) an HCV non-structural polypeptide-4B (NS4B) polypeptide;
 - [00391]** e) an HCV non-structural polypeptide-5A (NS5A) polypeptide;
 - [00392]** f) an HCV non-structural polypeptide-5B (NS5B) polypeptide;
 - [00393]** g) an HCV core polypeptide; and
 - [00394]** h) an HCV p7 polypeptide.
- [00395]** Aspect 21. The immunogenic composition of any one of aspects 18-20, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 3000 amino acids.
- [00396]** Aspect 22. The immunogenic composition of any one of aspects 18-20, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 50 amino acids, from about 100 amino acids to about 230 amino acids, from about 230 amino acids to about 550 amino acids, from about 550 amino acids to about 780 amino acids, or from about 780 amino acids to about 2000 amino acids.
- [00397]** Aspect 23. The immunogenic composition of any one of aspects 18-22, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in an HCV NS3 polypeptide.
- [00398]** Aspect 24. The immunogenic composition of any one of aspects 18-23, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to the amino acid sequence of one of TP29, TP50, TP52, TP70, TP100, TP171, TP228, TP553, TP778, and TP1985.
- [00399]** Aspect 25. The immunogenic composition of aspect any one of aspects 18-24, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to a polypeptide depicted in any one of FIG. 9A, 9B, 10A-10D, and 11A-11N.

- [00400] Aspect 26. The immunogenic composition of any one of 18-25, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in:
- [00401] a) cholera toxin or toxoid; and/or
- [00402] b) tetanus toxin or toxoid; and/or
- [00403] c) diphtheria toxin or toxoid; and/or
- [00404] d) CRM197.
- [00405] Aspect 27. The immunogenic composition of any one of aspects 1-25, wherein the composition comprises a polypeptide comprising one or more T cell epitopes present in:
- [00406] a) cholera toxin or toxoid; and/or
- [00407] b) tetanus toxin or toxoid; and/or
- [00408] c) diphtheria toxin or toxoid; and/or
- [00409] d) CRM197.
- [00410] Aspect 28. A method of inducing an immune response to HCV in an individual, the method comprising administering to the individual an effective amount of the immunogenic composition of any one of aspects 1-27.
- [00411] Aspect 29. The method of aspect 28, wherein said administering is via intramuscular administration, intranasal administration, subcutaneous administration, or a combination thereof.
- [00412] Aspect 30. The method of aspect 28, wherein said administering comprises a prime and a boost.
- [00413] Aspect 31. An immunogenic composition comprising:
- [00414] a) one or more nucleic acids comprising nucleotide sequences encoding the hepatitis C virus (HCV) E1 polypeptide, the HCV E2 polypeptide, or the HCV E1/E2 heterodimer as recited in any one of aspects 1-28; and
- [00415] b) a cyclic dinucleotide as recited in any one of aspects 1-28.
- [00416] Aspect 32. The immunogenic composition of aspect 31, wherein the one or more nucleic acids are recombinant expression vectors.
- [00417] Aspect 33. The immunogenic composition of aspect 32, wherein the one or more recombinant expression vectors are recombinant viral vectors.
- [00418] Aspect 34. The immunogenic composition of aspect 32, wherein the one or more recombinant viral vectors are packaged into viral particles.
- [00419] Aspect 35. The immunogenic composition of any one of aspects 31-34, wherein the one or more nucleic acids are present within non-pathogenic bacteria.

- [00420] Aspect 36. A method of inducing an immune response to HCV in an individual, the method comprising administering to the individual an effective amount of any one of aspects 31-35.
- [00421] Aspect 37. The method of aspect 36, wherein said administering is via intramuscular administration, intranasal administration, subcutaneous administration, or a combination thereof.
- [00422] Aspect 38. The method of aspect 36, wherein said administering comprises a prime and a boost.
- [00423] Aspect 39. The method of any one of aspects 28-30 or aspects 36-38, wherein the immune response comprises one or more of a CD4⁺ response, a CD8⁺ response, and a neutralizing antibody response.
- [00424] Aspect 40. The method of any one of aspects 28-30 or aspects 36-38, wherein the immune response induced is to more than one HCV genotype.
- [00425] Aspect 41. An immunogenic composition comprising: a) an HCV E1/E2 heterodimer; and b) an archaeosome comprising at least one polar synthetic lipid, wherein the at least one polar synthetic lipid comprises at least one carbohydrate or anionic group linked by covalent bonding to at least one free hydroxyl group of an archaeal core lipid; or a) an HCV E2 polypeptide; and b) an archaeosome comprising at least one polar synthetic lipid, wherein the at least one polar synthetic lipid comprises at least one carbohydrate or anionic group linked by covalent bonding to at least one free hydroxyl group of an archaeal core lipid; or a) an HCV E1 polypeptide; and b) an archaeosome comprising at least one polar synthetic lipid, wherein the at least one polar synthetic lipid comprises at least one carbohydrate or anionic group linked by covalent bonding to at least one free hydroxyl group of an archaeal core lipid.
- [00426] Aspect 42. The immunogenic composition of aspect 41, wherein the archaeal core lipid is archaeol (2,3-di-O-diphytanyl-sn-glycerol).
- [00427] Aspect 43. The immunogenic composition of aspect 41, wherein the archaeal core lipid is caldarchaeol (2,2',3,3'-tetra-O-dibiphytanyl-sn-diglycerol).
- [00428] Aspect 44. The immunogenic composition of aspect 41, wherein the carbohydrate group is selected from the group consisting of: β -D-Glc-(1,6)- β -D-Glc-; β -D-Glc-(1,6)-.alpha.-D-Glc-; .alpha.-D-Glc-(1,6)- β -D-Glc-; β -D-Glc-(1,4)- β -D-Glc-; α -D-Glc-(1,4)- β -D-Glc-; β -D-Gal-(1,4)- β -D-Glc-; α -D-Gal-(1,6)- β -D-Glc-; β -D-Glc-(1,6)- β -D-Glc-(1,6)- β -D-Glc-; α -D-Glc-(1,4)- α -D-Glc-(1,4)- β -D-Glc-; α -D-Man-(1,2)- α -D-Man-(1,2)- α -D-Man-; and α -D-Man-(1,2)- α -D-Man-(1,2)- α -D-Man-.
- [00429] Aspect 45. The immunogenic composition of aspect 41, wherein the carbohydrate group comprises two or three β -D-Glc- units in (1,6) linkage.

- [00430] Aspect 46. The immunogenic composition of aspect 41, wherein the carbohydrate group is a gal-glc-group.
- [00431] Aspect 47. The immunogenic composition of aspect 41, wherein the anionic group is selected from the group consisting of phosphoserine, phosphoethanolamine, phosphoinositol and phosphoglycerol.
- [00432] Aspect 48. The immunogenic composition of aspect 41, wherein the at least one polar synthetic lipid comprises at least one anionic lipid.
- [00433] Aspect 49. The immunogenic composition of aspect 48, wherein the at least one anionic lipid is selected from the group consisting of archaetidylglycerol, archaetidylglycerolphosphate-methyl, archaetidylserine, and archaetidylinositol.
- [00434] Aspect 50. The immunogenic composition of aspect 48, wherein the archaeosome comprises at least one conventional lipid.
- [00435] Aspect 51. The immunogenic composition of aspect 50, wherein the at least one conventional lipid is selected from a group consisting of phosphatidylglycerol, phosphatidylserine, SQDG, and cholesterol.
- [00436] Aspect 52. The immunogenic composition of aspect 51, wherein the at least one conventional lipid comprises cholesterol, and wherein cholesterol is present in an amount of between 10 and 45 mol % of the total lipid composition.
- [00437] Aspect 53. The immunogenic composition of aspect 51, wherein the phosphatidylglycerol is present in an amount of between 20 and 80 mol % of the lipid composition.
- [00438] Aspect 54. The immunogenic composition of aspect 51, wherein the phosphatidylserine is present in an amount of between 10 and 30 mol % of the lipid composition.
- [00439] Aspect 55. The immunogenic composition of aspect 51, wherein the at least one polar synthetic lipid comprises at least one synthetic immunoactive glycolipid and at least one anionic lipid, and the archaeosome further comprises at least one stabilizing lipid.
- [00440] Aspect 56. The immunogenic composition of aspect 55, wherein the at least one polar synthetic lipid comprises caldarchaeol having one carbohydrate head group and one anionic head group.
- [00441] Aspect 57. The immunogenic composition of aspect 56, wherein the carbohydrate head group comprises gentiobiose and the anionic head group comprises phosphoinositol.
- [00442] Aspect 58. The immunogenic composition of aspect 55, wherein the at least one polar synthetic lipid comprises a first caldarchaeol having two carbohydrate head groups and a second

caldarchaeol having two anionic head groups, and wherein the at least one stabilizing lipid is the first and/or second caldarchaeol.

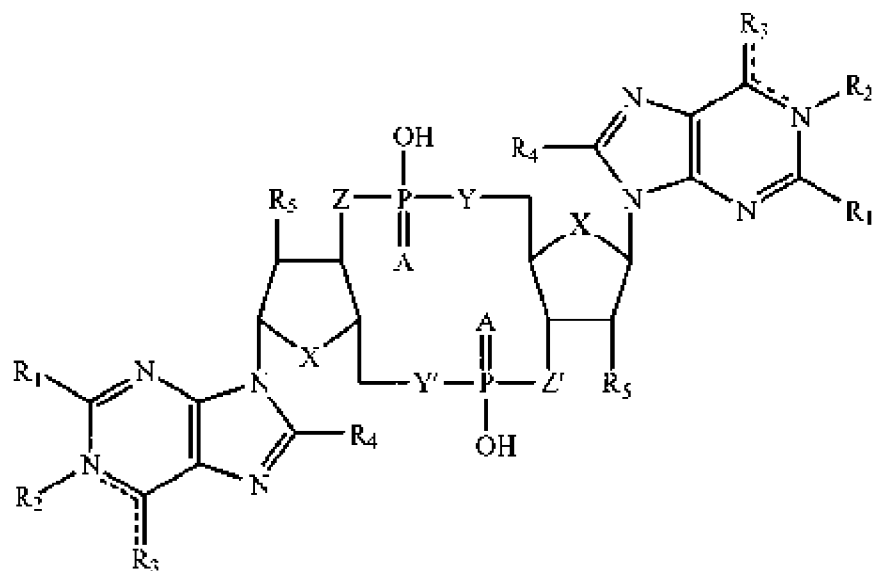
- [00443]** Aspect 59. The immunogenic composition of aspect 55, wherein the at least one polar synthetic lipid comprises gentiotriose-archaeol and wherein the at least one stabilizing lipid comprises cholesterol and at least one of phosphatidylethanolamine, archaetidylglycerol, archaetidylserine or archaetidylglycerolphosphate-methyl.
- [00444]** Aspect 60. The immunogenic composition of any one of aspects 41-59, wherein the composition comprises an HCV E1/E2 heterodimer.
- [00445]** Aspect 61. The immunogenic composition of aspect 60, wherein:
- [00446]** a) the HCV E2 polypeptide is derived from an HCV of major genotype 1, 2, 3, 4, 5, 6, or 7; and
- [00447]** b) the HCV E1 polypeptide is derived from an HCV of major genotype 1, 2, 3, 4, 5, 6, or 7.
- [00448]** Aspect 62. The immunogenic composition of any one of aspects 41-61, wherein the HCV E2 polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to an E2 polypeptide depicted in one of FIG. 1A-1C, FIG. 2A-2C, FIG. 3A-3C, and FIG. 4A-4B.
- [00449]** Aspect 63. The immunogenic composition of any one of aspects 41-61, wherein the HCV E1 polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to an E1 polypeptide depicted in FIG. 1A-1C, FIG. 2A-2C, FIG. 3A-3C, and FIG. 4A-4B.
- [00450]** Aspect 64. The immunogenic composition of any one of aspects 41-63, wherein the E2 polypeptide and/or the E1 polypeptide lacks a C-terminal transmembrane domain.
- [00451]** Aspect 65. The immunogenic composition of any one of aspects 41-64, wherein the HCV E2 polypeptide and the HCV E1 polypeptide are derived from an HCV of the same genotype.
- [00452]** Aspect 66. The immunogenic composition of any one of aspects 41-64, wherein the HCV E2 polypeptide and the HCV E1 polypeptide are derived from an HCV of different genotypes.
- [00453]** Aspect 67. The immunogenic composition of any one of aspects 41-66, wherein the HCV E1/E2 heterodimeric polypeptide comprises:
- [00454]** a) an HCV E1 polypeptide; and
- [00455]** b) a modified E2 polypeptide comprising, in order from N-terminus to C-terminus:

- [00456] i) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are C-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; and
- [00457] ii) an HCV E2 polypeptide; or
- [00458] a) an HCV E2 polypeptide; and
- [00459] b) a modified E1 polypeptide comprising, in order from N-terminus to C-terminus:
- [00460] i) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are C-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; and
- [00461] ii) an HCV E1 polypeptide; or
- [00462] a) an HCV E1 polypeptide; and
- [00463] b) a modified E2 polypeptide comprising, in order from N-terminus to C-terminus:
- [00464] i) an HCV E2 polypeptide; and
- [00465] ii) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are N-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; or
- [00466] a) an HCV E2 polypeptide; and
- [00467] b) a modified E1 polypeptide comprising, in order from N-terminus to C-terminus:
- [00468] i) an HCV E1 polypeptide; and
- [00469] ii) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are N-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker.
- [00470] Aspect 68. The immunogenic composition of aspect 67, wherein:
- [00471] a) the from 1 to 6 heterologous amino acids at the N-terminus of the modified E2 polypeptide or the modified E1 polypeptide are Gly-Pro, Ser, Gly, or Gly-Ser; or
- [00472] b) the from 1 to 6 heterologous amino acids at the C-terminus of the modified E2 polypeptide or the modified E1 polypeptide are LEVLFQGP (SEQ ID NO:117), ENLYYFQ (SEQ ID NO:150), LVPR (SEQ ID NO:124), I(E/D)GR (SEQ ID NO:125), or DDDDK.
- [00473] Aspect 69. The immunogenic composition of any one of aspects 41-68, wherein the HCV E1 polypeptide, the HCV E2 polypeptide, or one or both chains of the HCV E1/E2 heterodimer comprises a covalently linked T-cell epitope polypeptide comprising a T-cell epitope present in an HCV protein other than E1 and E2.
- [00474] Aspect 70. The immunogenic composition of any one of aspects 41-68, comprising a T-cell epitope polypeptide comprising a T-cell epitope present in an HCV protein other than E1 and E2, wherein the T-cell epitope polypeptide is not covalently linked to the HCV E1/E2 heterodimer, the HCV E1 polypeptide, or the HCV E2 polypeptide.
- [00475] Aspect 71. The immunogenic composition of aspect 69 or aspect 70, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in one or more of:

- [00476] a) an HCV non-structural polypeptide-3 (NS3) polypeptide;
- [00477] b) an HCV non-structural polypeptide-2 (NS2) polypeptide;
- [00478] c) an HCV non-structural polypeptide-4A (NS4A) polypeptide;
- [00479] d) an HCV non-structural polypeptide-4B (NS4B) polypeptide;
- [00480] e) an HCV non-structural polypeptide-5A (NS5A) polypeptide;
- [00481] f) an HCV non-structural polypeptide-5B (NS5B) polypeptide;
- [00482] g) an HCV core polypeptide; and
- [00483] h) an HCV p7 polypeptide.
- [00484] Aspect 72. The immunogenic composition of any one of aspects 69-71, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 3000 amino acids.
- [00485] Aspect 73. The immunogenic composition of any one of aspects 69-71, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 50 amino acids, from about 100 amino acids to about 230 amino acids, from about 230 amino acids to about 550 amino acids, from about 550 amino acids to about 780 amino acids, or from about 780 amino acids to about 2000 amino acids.
- [00486] Aspect 74. The immunogenic composition of any one of aspects 69-73, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in an HCV NS3 polypeptide.
- [00487] Aspect 75. The immunogenic composition of aspect any one of aspects 69-74, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to the amino acid sequence of one of TP29, TP50, TP52, TP70, TP100, TP171, TP228, TP553, TP778, and TP1985.
- [00488] Aspect 76. The immunogenic composition of aspect any one of aspects 69-74, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to a polypeptide depicted in any one of FIG. 9A, 9B, 10A-10D, and 11A-11N.
- [00489] Aspect 77. The immunogenic composition of any one of 69-76, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in:
- [00490] a) cholera toxin or toxoid; and/or
- [00491] b) tetanus toxin or toxoid; and/or
- [00492] c) diphtheria toxin or toxoid; and/or
- [00493] d) CRM197.
- [00494] Aspect 78. The immunogenic composition of any one of aspects 41-76, wherein the composition comprises a polypeptide comprising one or more T cell epitopes present in:
- [00495] a) cholera toxin or toxoid; and/or

- [00496] b) tetanus toxin or toxoid; and/or
- [00497] c) diphtheria toxin or toxoid; and/or
- [00498] d) CRM197.
- [00499] Aspect 79. A method of inducing an immune response to HCV in an individual, the method comprising administering to the individual an effective amount of the immunogenic composition of any one of aspects 41-78.
- [00500] Aspect 80. The method of aspect 79, wherein said administering is via intramuscular administration, intranasal administration, subcutaneous administration, or a combination thereof.
- [00501] Aspect 81. The method of aspect 79, wherein said administering comprises a prime and a boost.
- [00502] Aspect 82. An immunogenic composition comprising:
- [00503] a) one or more nucleic acids comprising nucleotide sequences encoding the hepatitis C virus (HCV) E1 polypeptide, the HCV E2 polypeptide, or the HCV E1/E2 heterodimer as recited in any one of aspects 41-78; and
- [00504] b) an archaeosome as recited in any one of aspects 41-78.
- [00505] Aspect 83. The immunogenic composition of aspect 82, wherein the one or more nucleic acids are recombinant expression vectors.
- [00506] Aspect 84. The immunogenic composition of aspect 83, wherein the one or more recombinant expression vectors are recombinant viral vectors.
- [00507] Aspect 85. The immunogenic composition of aspect 84, wherein the one or more recombinant viral vectors are packaged into viral particles.
- [00508] Aspect 86. The immunogenic composition of any one of aspects 82-84, wherein the one or more nucleic acids are present within non-pathogenic bacteria.
- [00509] Aspect 87. A method of inducing an immune response to HCV in an individual, the method comprising administering to the individual an effective amount of any one of aspects 82-86.
- [00510] Aspect 88. The method of aspect 87, wherein said administering is via intramuscular administration, intranasal administration, subcutaneous administration, or a combination thereof.
- [00511] Aspect 89. The method of aspect 87, wherein said administering comprises a prime and a boost.
- [00512] Aspect 90. The method of any one of aspects 79-81 or aspects 87-89, wherein the immune response comprises one or more of a CD4⁺ response, a CD8⁺ response, and a neutralizing antibody response.

- [00513] Aspect 91. The method of any one of aspects 79-81 or aspects 87-89, wherein the immune response induced is to more than one HCV genotype.
- [00514] Aspect 92. An immunogenic composition comprising:
- [00515] a) a T-cell epitope polypeptide comprising a T-cell epitope present in a hepatitis C virus (HCV) protein other than E1 and E2; and
- [00516] b) a cyclic dinucleotide (CDN).
- [00517] Aspect 93. The immunogenic composition of aspect 92, wherein the CDN is fluorinated.
- [00518] Aspect 94. The immunogenic composition of aspect 93, wherein the CDN is 2'-F-c-di-GMP.
- [00519] Aspect 95. The immunogenic composition of aspect 92, wherein the CDN is of Formula



(I):

- [00520] wherein:
- [00521] A is S or O;
- [00522] X is S, N, O, CH₂;
- [00523] Y, Y' is NH, CH₂, O;
- [00524] Z, Z' is NH, CH₂, O;
- [00525] R1 represents hydrogen or NH₂ which may be substituted;
- [00526] R2 is hydrogen or absent;
- [00527] R3 represents NH₂, O, OH, H, or a halogen;
- [00528] R4 represents hydrogen, halogen, or a straight or branched C₁-C₆ alkyl group which may optionally be substituted;

- [00529] R5 represents hydrogen, OH or a straight or branched C₁-C₆ alkyl chain or C₁-C₆ straight or branched alkoxy chain which may optionally be substituted;
- [00530]  is a single or double bond;
- [00531] or conjugates thereof, and salts or solvates thereof.
- [00532] Aspect 96. The immunogenic composition of aspect 95, wherein the CDN is c-diGMP, c-diAMP, c-dilMP, or c-dXMP.
- [00533] Aspect 97. The immunogenic composition of aspect 95, wherein the CDN is c-GpAp, c-Gplp, c-GpXp, c-Aplp, c-ApXp, or c-lpXp.
- [00534] Aspect 98. The immunogenic composition of aspect 92, wherein the CDN is cyclic-GMP-AMP (cGAMP).
- [00535] Aspect 99. The immunogenic composition of aspect 98, wherein the cGAMP is 2'3'-cGAMP, 2'2'-cGAMP, 3'2'-cGAMP or 3'3'-GAMP.
- [00536] Aspect 100. The immunogenic composition of any one of aspects 92-99, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in one or more of:
- [00537] a) an HCV non-structural polypeptide-3 (NS3) polypeptide;
 - [00538] b) an HCV non-structural polypeptide-2 (NS2) polypeptide;
 - [00539] c) an HCV non-structural polypeptide-4A (NS4A) polypeptide;
 - [00540] d) an HCV non-structural polypeptide-4B (NS4B) polypeptide;
 - [00541] e) an HCV non-structural polypeptide-5A (NS5A) polypeptide;
 - [00542] f) an HCV non-structural polypeptide-5B (NS5B) polypeptide;
 - [00543] g) an HCV core polypeptide; and
 - [00544] h) an HCV p7 polypeptide.
- [00545] Aspect 101. The immunogenic composition of any one of aspects 92-100, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 3000 amino acids.
- [00546] Aspect 102. The immunogenic composition of any one of aspects 92-100, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 50 amino acids, from about 100 amino acids to about 230 amino acids, from about 230 amino acids to about 550 amino acids, from about 550 amino acids to about 780 amino acids, or from about 780 amino acids to about 2000 amino acids.
- [00547] Aspect 103. The immunogenic composition of any one of aspects 92-102, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in an HCV NS3 polypeptide.
- [00548] Aspect 104. The immunogenic composition of aspect any one of aspects 92-103, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20%

amino acid sequence identity to the amino acid sequence of one of TP29, TP50, TP52, TP70, TP100, TP171, TP228, TP553, TP778, and TP1985.

- [00549] Aspect 105. The immunogenic composition of aspect any one of aspects 1-20, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to a polypeptide depicted in any one of FIG. 9A, 9B, 10A-10D, and 11A-11N.
- [00550] Aspect 106. The immunogenic composition of any one of 92-105, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in:
- [00551] a) cholera toxin or toxoid; and/or
- [00552] b) tetanus toxin or toxoid; and/or
- [00553] c) diphtheria toxin or toxoid; and/or
- [00554] d) CRM197.
- [00555] Aspect 107. The immunogenic composition of any one of aspects 92-105, wherein the composition comprises a polypeptide comprising one or more T cell epitopes present in:
- [00556] a) cholera toxin or toxoid; and/or
- [00557] b) tetanus toxin or toxoid; and/or
- [00558] c) diphtheria toxin or toxoid; and/or
- [00559] d) CRM197.
- [00560] Aspect 108. A method of inducing an immune response to an antigen in an individual, the method comprising administering to the individual an effective amount of:
- [00561] a) the composition of any one of aspects 92-107; and
- [00562] b) the antigen.
- [00563] Aspect 109. An immunogenic composition comprising:
- [00564] a) a T-cell epitope polypeptide comprising a T-cell epitope present in a hepatitis C virus (HCV) protein other than E1 and E2; and
- [00565] b) an archaeosome comprising at least one polar synthetic lipid, wherein the at least one polar synthetic lipid comprises at least one carbohydrate or anionic group linked by covalent bonding to at least one free hydroxyl group of an archaeal core lipid.
- [00566] Aspect 110. The immunogenic composition of aspect 109, wherein the archaeal core lipid is archaeol (2,3-di-O-diphytanyl-sn-glycerol).
- [00567] Aspect 111. The immunogenic composition of aspect 109, wherein the archaeal core lipid is caldarchaeol (2,2',3,3'-tetra-O-dibiphytanyl-sn-diglycerol).
- [00568] Aspect 112. The immunogenic composition of aspect 109, wherein the carbohydrate group is selected from the group consisting of: β -D-Glc-(1,6)- β -D-Glc-; β -D-Glc-(1,6)-.alpha.-D-Glc-; .alpha.-D-Glc-(1,6)- β -D-Glc-; β -D-Glc-(1,4)- β -D-Glc-; α -D-Glc-(1,4)- β -D-Glc-; β -D-

Gal-(1,4)- β -D-Glc-; α -D-Gal-(1,6)- β -D-Glc-; β -D-Glc-(1,6)- β -D-Glc-(1,6)- β -D-Glc-; α -D-Glc-(1,4)- α -D-Glc-(1,4)- β -D-Glc-; α -D-Man-(1,2)- α -D-Man-(1,2)- α -D-Man-; and α -D-Man-(1,2)- α -D-Man-(1,2)- α -D-Man-.

- [00569] Aspect 113. The immunogenic composition of aspect 109, wherein the carbohydrate group comprises two or three β -D-Glc- units in (1,6) linkage.
- [00570] Aspect 114. The immunogenic composition of aspect 109, wherein the carbohydrate group is a gal-glc-group.
- [00571] Aspect 115. The immunogenic composition of aspect 109, wherein the anionic group is selected from the group consisting of phosphoserine, phosphoethanolamine, phosphoinositol and phosphoglycerol.
- [00572] Aspect 116. The immunogenic composition of aspect 109, wherein the at least one polar synthetic lipid comprises at least one anionic lipid.
- [00573] Aspect 117. The immunogenic composition of aspect 116, wherein the at least one anionic lipid is selected from the group consisting of archaetidylglycerol, archaetidylglycerolphosphate-methyl, archaetidylserine, and archaetidylinositol.
- [00574] Aspect 118. The immunogenic composition of aspect 116, wherein the archaeosome comprises at least one conventional lipid.
- [00575] Aspect 119. The immunogenic composition of aspect 118, wherein the at least one conventional lipid is selected from a group consisting of phosphatidylglycerol, phosphatidylserine, SQDG, and cholesterol.
- [00576] Aspect 120. The immunogenic composition of aspect 119, wherein the at least one conventional lipid comprises cholesterol, and wherein cholesterol is present in an amount of between 10 and 45 mol % of the total lipid composition.
- [00577] Aspect 121. The immunogenic composition of aspect 119, wherein phosphatidylglycerol is present in an amount of between 20 and 80 mol % of the lipid composition.
- [00578] Aspect 122. The immunogenic composition of aspect 119, wherein phosphatidylserine is present in an amount of between 10 and 30 mol % of the lipid composition.
- [00579] Aspect 123. The immunogenic composition of aspect 109, wherein the at least one polar synthetic lipid comprises at least one synthetic immunoactive glycolipid and at least one anionic lipid, and the archaeosome further comprises at least one stabilizing lipid.
- [00580] Aspect 124. The immunogenic composition of aspect 123, wherein the at least one polar synthetic lipid comprises caldarchaeol having one carbohydrate head group and one anionic head group.

- [00581]** Aspect 125. The immunogenic composition of aspect 124, wherein the carbohydrate head group comprises gentiobiose and the anionic head group comprises phosphoinositol.
- [00582]** Aspect 126. The immunogenic composition of aspect 123, wherein the at least one polar synthetic lipid comprises a first caldarchaeol having two carbohydrate head groups and a second caldarchaeol having two anionic head groups, and wherein the at least one stabilizing lipid is the first and/or second caldarchaeol.
- [00583]** Aspect 127. The immunogenic composition of aspect 123, wherein the at least one polar synthetic lipid comprises gentiotriose-archaeol and wherein the at least one stabilizing lipid comprises cholesterol and at least one of phosphatidylethanolamine, archaetidylglycerol, archaetidylserine or archaetidylglycerolphosphate-methyl.
- [00584]** Aspect 128. The immunogenic composition of any one of aspects 109-127, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in one or more of:
- [00585]** a) an HCV non-structural polypeptide-3 (NS3) polypeptide;
 - [00586]** b) an HCV non-structural polypeptide-2 (NS2) polypeptide;
 - [00587]** c) an HCV non-structural polypeptide-4A (NS4A) polypeptide;
 - [00588]** d) an HCV non-structural polypeptide-4B (NS4B) polypeptide;
 - [00589]** e) an HCV non-structural polypeptide-5A (NS5A) polypeptide;
 - [00590]** f) an HCV non-structural polypeptide-5B (NS5B) polypeptide;
 - [00591]** g) an HCV core polypeptide; and
 - [00592]** h) an HCV p7 polypeptide.
- [00593]** Aspect 129. The immunogenic composition of any one of aspects 109-128, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 3000 amino acids.
- [00594]** Aspect 130. The immunogenic composition of any one of aspects 109-128, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 50 amino acids, from about 100 amino acids to about 230 amino acids, from about 230 amino acids to about 550 amino acids, from about 550 amino acids to about 780 amino acids, or from about 780 amino acids to about 2000 amino acids.
- [00595]** Aspect 131. The immunogenic composition of any one of aspects 109-130, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in an HCV NS3 polypeptide.
- [00596]** Aspect 132. The immunogenic composition of aspect any one of aspects 109-131, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to the amino acid sequence of one of TP29, TP50, TP52, TP70, TP100, TP171, TP228, TP553, TP778, and TP1985.

- [00597] Aspect 133. The immunogenic composition of aspect any one of aspects 109-132, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to a polypeptide depicted in any one of FIG. 9A, 9B, 10A-10D, and 11A-11N.
- [00598] Aspect 134. The immunogenic composition of any one of 109-133, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in:
- [00599] a) cholera toxin or toxoid; and/or
- [00600] b) tetanus toxin or toxoid; and/or
- [00601] c) diphtheria toxin or toxoid; and/or
- [00602] d) CRM197.
- [00603] Aspect 135. The immunogenic composition of any one of aspects 109-133, wherein the composition comprises a polypeptide comprising one or more T cell epitopes present in:
- [00604] a) cholera toxin or toxoid; and/or
- [00605] b) tetanus toxin or toxoid; and/or
- [00606] c) diphtheria toxin or toxoid; and/or
- [00607] d) CRM197.
- [00608] Aspect 136. A method of inducing an immune response to an antigen in an individual, the method comprising administering to the individual an effective amount of:
- [00609] a) the composition of any one of aspects 109-135; and
- [00610] b) the antigen.

EXAMPLES

- [00611] The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the present invention, and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all or the only experiments performed. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Celsius, and pressure is at or near atmospheric. Standard abbreviations may be used, e.g., bp, base pair(s); kb, kilobase(s); pl, picoliter(s); s or sec, second(s); min, minute(s); h or hr, hour(s); aa, amino acid(s); kb, kilobase(s); bp, base pair(s); nt, nucleotide(s); i.m., intramuscular(ly); i.p., intraperitoneal(ly); s.c., subcutaneous(ly); and the like.

Example 1: Induction of an immune response with HCV E1/E2 and a CDN or an archaeosome.

[00612] Various adjuvants including MF59, aluminum hydroxide/monophosphoryl lipid A (Alum/MPLA), cyclic di-adenosine monophosphate (C-di-AMP) and archaeosomes, were formulated with rE1E2 to immunize mice. 6-8 weeks mice were immunized three times on day 0, day 14, and day 35 and sera was collected two weeks after last immunization (FIG. 13). The ability of the antibodies to neutralize HCV was evaluated using HCV pseudo-particle (HCVpp) carrying a luciferase reported gene, where the particles were incubated with serum before culturing and the level of luciferase expression was used to measure the neutralization activity of the given serum. Spleens were also collected, and isolated splenocytes were restimulated *ex vivo* with short peptides to evaluate cellular immunity using multicolor flow cytometry to detect intracellular production of cytokines. Different groups of mice received rE1E2 formulated with MF59, Alum/MPLA, C-di-AMP, or archaeosomes along with appropriate controls

[00613] FIG. 13 depicts the immunization protocol.

RESULTS

[00614] *The sera collected from immunized mice is able to neutralize and prevent the entry of HCV pseudo-particles in vitro:* As compared to the controls, the sera collected from immunized mice with adjuvanted rE1E2, showed significant increase in preventing the entry of HCVpp in an *in vitro* neutralization assay (FIG. 14). When the antigen was formulated with MF59 or Alum-MPLA, this effect was highly comparable to neutralization activity of anti-CD81 against HCVpp. However, this effect was lower than that of anti-CD81 in the case of C-di-AMP and archaeosomes formulations. The route seemed to be playing a significant role for C-di-AMP, since the sera from mice with three intranasal administration (IN-IN-IN) of rE1E2 + C-di-AMP did not neutralize HCVpp, as opposed to an intramuscular immunization followed by two intranasal boost (IM-IN-IN) regimen.

[00615] FIG. 14. Neutralization activity of rE1E2 in combination with adjuvant in mice. The sera from mice immunized with rE1E2 were able to neutralize the entry of HCV pseudoparticle *in vitro*. Percentage of neutralization was calculated based on the neutralizing activity for post-vaccination bleed divided by neutralization activity of pre-vaccination bleed.

[00616] Horizontal lines are the medians in each group.

[00617] ** = p value < 0.01; * = p value < 0.05.

[00618] *Robust T cell immune response in C-di-AMP and archaeosomes groups:* *In vitro* stimulation of mice splenocytes with a pool of 55 peptides that span the whole length of HCV E1E2 induced a strong memory T cell response in the groups, where the antigen was formulated

with C-di-AMP and archaeosomes (p value < 0.005). A moderate response was also detected in Alum/MPLA group (p value < 0.05). The data show that while C-di-AMP and archaeosomes elicit strong neutralizing antibodies comparable to MF59 and Alum/MPLA, both induced a more robust cellular immune response which was confirmed by the detection of vaccine-specific poly-functional CD4⁺ T cells (FIG. 15).

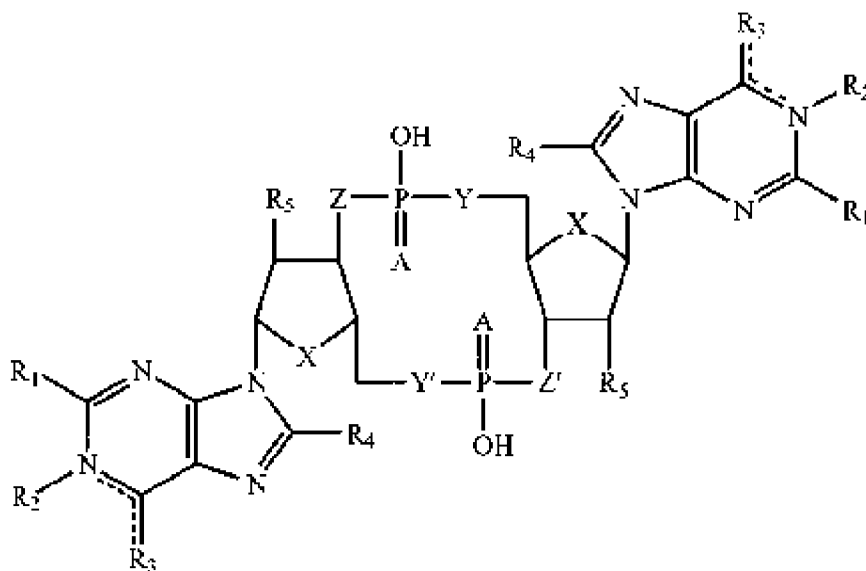
[00619] **FIG. 15. Differential detection of T cell immune response in mice**. The splenocytes from vaccinated mice with rE1E2 in combination with different adjuvants were stimulated in vitro and intracellular production of cytokine was detected by multi-color flow cytometry. IM = Intramuscular; IN = Intranasal; Neg = Negative control splenocytes; E1E2 = Splenocytes that are stimulated with a pool of 55 peptides spanning E1E2.

[00620] While the present invention has been described with reference to the specific embodiments thereof, it should be understood by those skilled in the art that various changes may be made and equivalents may be substituted without departing from the true spirit and scope of the invention. In addition, many modifications may be made to adapt a particular situation, material, composition of matter, process, process step or steps, to the objective, spirit and scope of the present invention. All such modifications are intended to be within the scope of the claims appended hereto.

CLAIMS

What is claimed is:

1. An immunogenic composition comprising:
 - a) a hepatitis C virus (HCV) E1 polypeptide, an HCV E2 polypeptide, or an HCV E1/E2 heterodimer; and
 - b) a cyclic dinucleotide (CDN).
2. The immunogenic composition of claim 1, wherein the CDN is fluorinated.
3. The immunogenic composition of claim 2, wherein the CDN is 2'-F-c-di-GMP.
4. The immunogenic composition of claim 1, wherein the CDN is of Formula (I):



wherein:

A is S or O;

X is S, N, O, CH₂;

Y, Y' is NH, CH₂, O;

Z, Z' is NH, CH₂, O;

R1 represents hydrogen or NH₂ which may be substituted;

R2 is hydrogen or absent;

R3 represents NH₂, O, OH, H, or a halogen;

R4 represents hydrogen, halogen, or a straight or branched C₁-C₆ alkyl group which may optionally be substituted;

R5 represents hydrogen, OH or a straight or branched C₁-C₆ alkyl chain or C₁-C₆ straight or branched alkoxy chain which may optionally be substituted;

 is a single or double bond;

or conjugates thereof, and salts or solvates thereof.

5. The immunogenic composition of claim 4, wherein the CDN is c-diGMP, c-diAMP, c-dilMP, or c-dXMP.

6. The immunogenic composition of claim 4, wherein the CDN is c-GpAp, c-Gplp, c-GpXp, c-Aplp, c-ApXp, or c-lpXp.

7. The immunogenic composition of claim 1, wherein the CDN is cyclic-GMP-AMP (cGAMP).

8. The immunogenic composition of claim 7, wherein the cGAMP is 2'3'-cGAMP, 2'2'-cGAMP, 3'2'-cGAMP or 3'3'-GAMP.

9. The immunogenic composition of any one of claims 1-8, wherein the composition comprises an HCV E1/E2 heterodimer.

10. The immunogenic composition of claim 9, wherein:

- a) the HCV E2 polypeptide is derived from an HCV of major genotype 1, 2, 3, 4, 5, 6, or 7; and
- b) the HCV E1 polypeptide is derived from an HCV of major genotype 1, 2, 3, 4, 5, 6, or 7.

11. The immunogenic composition of any one of claims 1-10, wherein the HCV E2 polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to an E2 polypeptide depicted in one of FIG. 1A-1C, FIG. 2A-2C, FIG. 3A-3C, and FIG. 4A-4B.

12. The immunogenic composition of any one of claims 1-10, wherein the HCV E1 polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to an E1 polypeptide depicted in FIG. 1A-1C, FIG. 2A-2C, FIG. 3A-3C, and FIG. 4A-4B.

13. The immunogenic composition of any one of claims 1-12, wherein the E2 polypeptide and/or the E1 polypeptide lacks a C-terminal transmembrane domain.

14. The immunogenic composition of any one of claims 1-13, wherein the HCV E2 polypeptide and the HCV E1 polypeptide are derived from an HCV of the same genotype.

15. The immunogenic composition of any one of claims 1-13, wherein the HCV E2 polypeptide and the HCV E1 polypeptide are derived from an HCV of different genotypes.

16. The immunogenic composition of any one of claims 1-15, wherein the HCV E1/E2 heterodimeric polypeptide comprises:

- a) an HCV E1 polypeptide; and
- b) a modified E2 polypeptide comprising, in order from N-terminus to C-terminus:
 - i) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are C-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; and
 - ii) an HCV E2 polypeptide; or
- a) an HCV E2 polypeptide; and
- b) a modified E1 polypeptide comprising, in order from N-terminus to C-terminus:
 - i) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are C-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; and
 - ii) an HCV E1 polypeptide; or
- a) an HCV E1 polypeptide; and
- b) a modified E2 polypeptide comprising, in order from N-terminus to C-terminus:
 - i) an HCV E2 polypeptide; and
 - ii) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are N-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; or
- a) an HCV E2 polypeptide; and
- b) a modified E1 polypeptide comprising, in order from N-terminus to C-terminus:
 - i) an HCV E1 polypeptide; and
 - ii) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are N-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker.

17. The immunogenic composition of claim 16, wherein:

- a) the from 1 to 6 heterologous amino acids at the N-terminus of the modified E2 polypeptide or the modified E1 polypeptide are Gly-Pro, Ser, Gly, or Gly-Ser; or

b) the from 1 to 6 heterologous amino acids at the C-terminus of the modified E2 polypeptide or the modified E1 polypeptide are LEVLFQGP, ENLYYFQ, LVPR, I(E/D)GR, or DDDDK.

18. The immunogenic composition of any one of claims 1-17, wherein the HCV E1 polypeptide, the HCV E2 polypeptide, or one or both chains of the HCV E1/E2 heterodimer comprises a covalently linked T-cell epitope polypeptide comprising a T-cell epitope present in an HCV protein other than E1 and E2.

19. The immunogenic composition of any one of claims 1-18, comprising a T-cell epitope polypeptide comprising a T-cell epitope present in an HCV protein other than E1 and E2, wherein the T-cell epitope polypeptide is not covalently linked to the HCV E1E2 heterodimer, the HCV E1 polypeptide, or the HCV E2 polypeptide.

20. The immunogenic composition of claim 18 or claim 19, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in one or more of:

- a) an HCV non-structural polypeptide-3 (NS3) polypeptide;
- b) an HCV non-structural polypeptide-2 (NS2) polypeptide;
- c) an HCV non-structural polypeptide-4A (NS4A) polypeptide;
- d) an HCV non-structural polypeptide-4B (NS4B) polypeptide;
- e) an HCV non-structural polypeptide-5A (NS5A) polypeptide;
- f) an HCV non-structural polypeptide-5B (NS5B) polypeptide;
- g) an HCV core polypeptide; and
- h) an HCV p7 polypeptide.

21. The immunogenic composition of any one of claims 18-20, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 3000 amino acids.

22. The immunogenic composition of any one of claims 18-20, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 50 amino acids, from about 100 amino acids to about 230 amino acids, from about 230 amino acids to about 550 amino acids, from about 550 amino acids to about 780 amino acids, or from about 780 amino acids to about 2000 amino acids.

23. The immunogenic composition of any one of claims 18-22, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in an HCV NS3 polypeptide.

24. The immunogenic composition of any one of claims 18-23, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to the amino acid sequence of one of TP29, TP50, TP52, TP70, TP100, TP171, TP228, TP553, TP778, and TP1985.

25. The immunogenic composition of claim any one of claims 18-24, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to a polypeptide depicted in any one of FIG. 9A, 9B, 10A-10D, and 11A-11N.

26. The immunogenic composition of any one of 18-25, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in:

- a) cholera toxin or toxoid; and/or
- b) tetanus toxin or toxoid; and/or
- c) diphtheria toxin or toxoid; and/or
- d) CRM197.

27. The immunogenic composition of any one of claims 1-25, wherein the composition comprises a polypeptide comprising one or more T cell epitopes present in:

- a) cholera toxin or toxoid; and/or
- b) tetanus toxin or toxoid; and/or
- c) diphtheria toxin or toxoid; and/or
- d) CRM197.

28. A method of inducing an immune response to HCV in an individual, the method comprising administering to the individual an effective amount of the immunogenic composition of any one of claims 1-27.

29. The method of claim 28, wherein said administering is via intramuscular administration, intranasal administration, subcutaneous administration, or a combination thereof.

30. The method of claim 28, wherein said administering comprises a prime and a boost.

31. An immunogenic composition comprising:

a) one or more nucleic acids comprising nucleotide sequences encoding the hepatitis C virus (HCV) E1 polypeptide, the HCV E2 polypeptide, or the HCV E1/E2 heterodimer as recited in any one of claims 1-28; and

b) a cyclic dinucleotide as recited in any one of claims 1-28.

32. The immunogenic composition of claim 31, wherein the one or more nucleic acids are recombinant expression vectors.

33. The immunogenic composition of claim 32, wherein the one or more recombinant expression vectors are recombinant viral vectors.

34. The immunogenic composition of claim 32, wherein the one or more recombinant viral vectors are packaged into viral particles.

35. The immunogenic composition of any one of claims 31-34, wherein the one or more nucleic acids are present within non-pathogenic bacteria.

36. A method of inducing an immune response to HCV in an individual, the method comprising administering to the individual an effective amount of any one of claims 31-35.

37. The method of claim 36, wherein said administering is via intramuscular administration, intranasal administration, subcutaneous administration, or a combination thereof.

38. The method of claim 36, wherein said administering comprises a prime and a boost.

39. The method of any one of claims 28-30 or claims 36-38, wherein the immune response comprises one or more of a CD4⁺ response, a CD8⁺ response, and a neutralizing antibody response.

40. The method of any one of claims 28-30 or claims 36-38, wherein the immune response induced is to more than one HCV genotype.

41. An immunogenic composition comprising:

a) a hepatitis C virus (HCV) E1 polypeptide, an HCV E2 polypeptide, or an HCV E1/E2 heterodimer; and

b) an archaeosome comprising at least one polar synthetic lipid, wherein the at least one polar synthetic lipid comprises at least one carbohydrate or anionic group linked by covalent bonding to at least one free hydroxyl group of an archaeal core lipid.

42. The immunogenic composition of claim 41, wherein the archaeal core lipid is archaeol (2,3-di-O-diphytanyl-sn-glycerol).

43. The immunogenic composition of claim 41, wherein the archaeal core lipid is caldarchaeol (2,2',3,3'-tetra-O-dibiphytanyl-sn-diglycerol).

44. The immunogenic composition of claim 41, wherein the carbohydrate group is selected from the group consisting of: β -D-Glc-(1,6)- β -D-Glc-; β -D-Glc-(1,6)-.alpha.-D-Glc-; .alpha.-D-Glc-(1,6)- β -D-Glc-; β -D-Glc-(1,4)- β -D-Glc-; α -D-Glc-(1,4)- β -D-Glc-; β -D-Gal-(1,4)- β -D-Glc-; α -D-Gal-(1,6)- β -D-Glc-; β -D-Glc-(1,6)- β -D-Glc-(1,6)- β -D-Glc-; α -D-Glc-(1,4)- α -D-Glc-(1,4)- β -D-Glc-; α -D-Man-(1,2)- α -D-Man-(1,2)- α -D-Man-; and α -D-Man-(1,2)- α -D-Man-(1,2)- α -D-Man-(1,2)- α -D-Man-.

45. The immunogenic composition of claim 41, wherein the carbohydrate group comprises two or three β -D-Glc- units in (1,6) linkage.

46. The immunogenic composition of claim 41, wherein the carbohydrate group is a gal-glc-group.

47. The immunogenic composition of claim 41, wherein the anionic group is selected from the group consisting of phosphoserine, phosphoethanolamine, phosphoinositol and phosphoglycerol.

48. The immunogenic composition of claim 41, wherein the at least one polar synthetic lipid comprises at least one anionic lipid.

49. The immunogenic composition of claim 48, wherein the at least one anionic lipid is selected from the group consisting of archaetidylglycerol, archaetidylglycerolphosphate-methyl, archaetidylserine, and archaetidylinositol.

50. The immunogenic composition of claim 48, wherein the archaeosome comprises at least one conventional lipid.

51. The immunogenic composition of claim 50, wherein the at least one conventional lipid is selected from a group consisting of phosphatidylglycerol, phosphatidylserine, SQDG, and cholesterol.

52. The immunogenic composition of claim 51, wherein the at least one conventional lipid comprises cholesterol, and wherein cholesterol is present in an amount of between 10 and 45 mol % of the total lipid composition.

53. The immunogenic composition of claim 51, wherein the phosphatidylglycerol is present in an amount of between 20 and 80 mol % of the lipid composition.

54. The immunogenic composition of claim 51, wherein the phosphatidylserine is present in an amount of between 10 and 30 mol % of the lipid composition.

55. The immunogenic composition of claim 51, wherein the at least one polar synthetic lipid comprises at least one synthetic immunoactive glycolipid and at least one anionic lipid, and the archaeosome further comprises at least one stabilizing lipid.

56. The immunogenic composition of claim 55, wherein the at least one polar synthetic lipid comprises caldarchaeol having one carbohydrate head group and one anionic head group.

57. The immunogenic composition of claim 56, wherein the carbohydrate head group comprises gentiobiose and the anionic head group comprises phosphoinositol.

58. The immunogenic composition of claim 55, wherein the at least one polar synthetic lipid comprises a first caldarchaeol having two carbohydrate head groups and a second caldarchaeol having two anionic head groups, and wherein the at least one stabilizing lipid is the first and/or second caldarchaeol.

59. The immunogenic composition of claim 55, wherein the at least one polar synthetic lipid comprises gentiotriose-archaeol and wherein the at least one stabilizing lipid comprises cholesterol and at least one of phosphatidylethanolamine, archaetidylglycerol, archaetidylserine or archaetidylglycerolphosphate-methyl.

60. The immunogenic composition of any one of claims 41-59, wherein the composition comprises an HCV E1/E2 heterodimer.

61. The immunogenic composition of claim 60, wherein:

- a) the HCV E2 polypeptide is derived from an HCV of major genotype 1, 2, 3, 4, 5, 6, or 7; and
- b) the HCV E1 polypeptide is derived from an HCV of major genotype 1, 2, 3, 4, 5, 6, or 7.

62. The immunogenic composition of any one of claims 41-61, wherein the HCV E2 polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to an E2 polypeptide depicted in one of FIG. 1A-1C, FIG. 2A-2C, FIG. 3A-3C, and FIG. 4A-4B.

63. The immunogenic composition of any one of claims 41-61, wherein the HCV E1 polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to an E1 polypeptide depicted in FIG. 1A-1C, FIG. 2A-2C, FIG. 3A-3C, and FIG. 4A-4B.

64. The immunogenic composition of any one of claims 41-63, wherein the E2 polypeptide and/or the E1 polypeptide lacks a C-terminal transmembrane domain.

65. The immunogenic composition of any one of claims 41-64, wherein the HCV E2 polypeptide and the HCV E1 polypeptide are derived from an HCV of the same genotype.

66. The immunogenic composition of any one of claims 41-64, wherein the HCV E2 polypeptide and the HCV E1 polypeptide are derived from an HCV of different genotypes.

67. The immunogenic composition of any one of claims 41-66, wherein the HCV E1/E2 heterodimeric polypeptide comprises:

- a) an HCV E1 polypeptide; and
- b) a modified E2 polypeptide comprising, in order from N-terminus to C-terminus:
 - i) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are C-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; and
 - ii) an HCV E2 polypeptide; or
- a) an HCV E2 polypeptide; and
- b) a modified E1 polypeptide comprising, in order from N-terminus to C-terminus:
 - i) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are C-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; and
 - ii) an HCV E1 polypeptide; or
- a) an HCV E1 polypeptide; and

- b) a modified E2 polypeptide comprising, in order from N-terminus to C-terminus:
 - i) an HCV E2 polypeptide; and
 - ii) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are N-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker; or
- a) an HCV E2 polypeptide; and
- b) a modified E1 polypeptide comprising, in order from N-terminus to C-terminus:
 - i) an HCV E1 polypeptide; and
 - ii) from 1 to 6 heterologous amino acids, wherein the from 1 to 6 heterologous amino acids are N-terminal to a site of proteolytic cleavage in a proteolytically cleavable linker.

68. The immunogenic composition of claim 67, wherein:

- a) the from 1 to 6 heterologous amino acids at the N-terminus of the modified E2 polypeptide or the modified E1 polypeptide are Gly-Pro, Ser, Gly, or Gly-Ser; or
- b) the from 1 to 6 heterologous amino acids at the C-terminus of the modified E2 polypeptide or the modified E1 polypeptide are LEVLFQGP, ENLYYFQ, LVPR, I(E/D)GR, or DDDDK.

69. The immunogenic composition of any one of claims 41-68, wherein the HCV E1 polypeptide, the HCV E2 polypeptide, or one or both chains of the HCV E1/E2 heterodimer comprises a covalently linked T-cell epitope polypeptide comprising a T-cell epitope present in an HCV protein other than E1 and E2.

70. The immunogenic composition of any one of claims 41-68, comprising a T-cell epitope polypeptide comprising a T-cell epitope present in an HCV protein other than E1 and E2, wherein the T-cell epitope polypeptide is not covalently linked to the HCV E1E2 heterodimer, the HCV E1 polypeptide, or the HCV E2 polypeptide.

71. The immunogenic composition of claim 69 or claim 70, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in one or more of:

- a) an HCV non-structural polypeptide-3 (NS3) polypeptide;
- b) an HCV non-structural polypeptide-2 (NS2) polypeptide;
- c) an HCV non-structural polypeptide-4A (NS4A) polypeptide;
- d) an HCV non-structural polypeptide-4B (NS4B) polypeptide;
- e) an HCV non-structural polypeptide-5A (NS5A) polypeptide;
- f) an HCV non-structural polypeptide-5B (NS5B) polypeptide;

- g) an HCV core polypeptide; and
- h) an HCV p7 polypeptide.

72. The immunogenic composition of any one of claims 69-71, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 3000 amino acids.

73. The immunogenic composition of any one of claims 69-71, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 50 amino acids, from about 100 amino acids to about 230 amino acids, from about 230 amino acids to about 550 amino acids, from about 550 amino acids to about 780 amino acids, or from about 780 amino acids to about 2000 amino acids.

74. The immunogenic composition of any one of claims 69-73, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in an HCV NS3 polypeptide.

75. The immunogenic composition of claim any one of claims 69-74, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to the amino acid sequence of one of TP29, TP50, TP52, TP70, TP100, TP171, TP228, TP553, TP778, and TP1985.

76. The immunogenic composition of claim any one of claims 69-74, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to a polypeptide depicted in any one of FIG. 9A, 9B, 10A-10D, and 11A-11N.

77. The immunogenic composition of any one of 69-76, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in:

- a) cholera toxin or toxoid; and/or
- b) tetanus toxin or toxoid; and/or
- c) diphtheria toxin or toxoid; and/or
- d) CRM197.

78. The immunogenic composition of any one of claims 41-76, wherein the composition comprises a polypeptide comprising one or more T cell epitopes present in:

- a) cholera toxin or toxoid; and/or
- b) tetanus toxin or toxoid; and/or
- c) diphtheria toxin or toxoid; and/or

d) CRM197.

79. A method of inducing an immune response to HCV in an individual, the method comprising administering to the individual an effective amount of the immunogenic composition of any one of claims 41-78.

80. The method of claim 79, wherein said administering is via intramuscular administration, intranasal administration, subcutaneous administration, or a combination thereof.

81. The method of claim 79, wherein said administering comprises a prime and a boost.

82. An immunogenic composition comprising:

a) one or more nucleic acids comprising nucleotide sequences encoding the hepatitis C virus (HCV) E1 polypeptide, the HCV E2 polypeptide, or the HCV E1/E2 heterodimer as recited in any one of claims 41-78; and

b) an archaeosome as recited in any one of claims 41-78.

83. The immunogenic composition of claim 82, wherein the one or more nucleic acids are recombinant expression vectors.

84. The immunogenic composition of claim 83, wherein the one or more recombinant expression vectors are recombinant viral vectors.

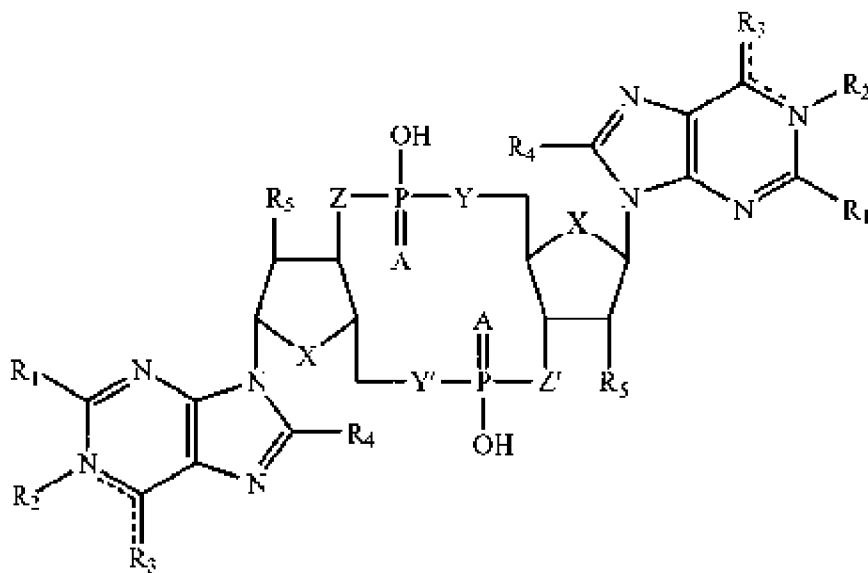
85. The immunogenic composition of claim 84, wherein the one or more recombinant viral vectors are packaged into viral particles.

86. The immunogenic composition of any one of claims 82-84, wherein the one or more nucleic acids are present within non-pathogenic bacteria.

87. A method of inducing an immune response to HCV in an individual, the method comprising administering to the individual an effective amount of any one of claims 82-86.

88. The method of claim 87, wherein said administering is via intramuscular administration, intranasal administration, subcutaneous administration, or a combination thereof.

89. The method of claim 87, wherein said administering comprises a prime and a boost.
90. The method of any one of claims 79-81 or claims 87-89, wherein the immune response comprises one or more of a CD4⁺ response, a CD8⁺ response, and a neutralizing antibody response.
91. The method of any one of claims 79-81 or claims 87-89, wherein the immune response induced is to more than one HCV genotype.
92. An immunogenic composition comprising:
 a) a T-cell epitope polypeptide comprising a T-cell epitope present in a hepatitis C virus (HCV) protein other than E1 and E2; and
 b) a cyclic dinucleotide (CDN).
93. The immunogenic composition of claim 92, wherein the CDN is fluorinated.
94. The immunogenic composition of claim 93, wherein the CDN is 2'-F-c-di-GMP.
95. The immunogenic composition of claim 92, wherein the CDN is of Formula (I):



wherein:

A is S or O;

X is S, N, O, CH₂;

Y, Y' is NH, CH₂, O;

Z, Z' is NH, CH₂, O;

R1 represents hydrogen or NH₂ which may be substituted;

R2 is hydrogen or absent;

R3 represents NH₂, O, OH, H, or a halogen;

R4 represents hydrogen, halogen, or a straight or branched C₁-C₆ alkyl group which may optionally be substituted;

R5 represents hydrogen, OH or a straight or branched C₁-C₆ alkyl chain or C₁-C₆ straight or branched alkoxy chain which may optionally be substituted;

 is a single or double bond;

or conjugates thereof, and salts or solvates thereof.

96. The immunogenic composition of claim 95, wherein the CDN is c-diGMP, c-diAMP, c-dilMP, or c-dXMP.

97. The immunogenic composition of claim 95, wherein the CDN is c-GpAp, c-Gplp, c-GpXp, c-ApIp, c-ApXp, or c-lpXp.

98. The immunogenic composition of claim 92, wherein the CDN is cyclic-GMP-AMP (cGAMP).

99. The immunogenic composition of claim 98, wherein the cGAMP is 2'3'-cGAMP, 2'2'-cGAMP, 3'2'-cGAMP or 3'3'-GAMP.

100. The immunogenic composition of any one of claims 92-99, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in one or more of:

- a) an HCV non-structural polypeptide-3 (NS3) polypeptide;
- b) an HCV non-structural polypeptide-2 (NS2) polypeptide;
- c) an HCV non-structural polypeptide-4A (NS4A) polypeptide;
- d) an HCV non-structural polypeptide-4B (NS4B) polypeptide;
- e) an HCV non-structural polypeptide-5A (NS5A) polypeptide;
- f) an HCV non-structural polypeptide-5B (NS5B) polypeptide;
- g) an HCV core polypeptide; and
- h) an HCV p7 polypeptide.

101. The immunogenic composition of any one of claims 92-100, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 3000 amino acids.

102. The immunogenic composition of any one of claims 92-100, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 50 amino acids, from about 100 amino acids to about 230 amino acids, from about 230 amino acids to about 550 amino acids, from about 550 amino acids to about 780 amino acids, or from about 780 amino acids to about 2000 amino acids.

103. The immunogenic composition of any one of claims 92-102, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in an HCV NS3 polypeptide.

104. The immunogenic composition of claim any one of claims 92-103, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to the amino acid sequence of one of TP29, TP50, TP52, TP70, TP100, TP171, TP228, TP553, TP778, and TP1985.

105. The immunogenic composition of claim any one of claims 92-103, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to a polypeptide depicted in any one of FIG. 9A, 9B, 10A-10D, and 11A-11N.

106. The immunogenic composition of any one of 92-105, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in:

- a) cholera toxin or toxoid; and/or
- b) tetanus toxin or toxoid; and/or
- c) diphtheria toxin or toxoid; and/or
- d) CRM197.

107. The immunogenic composition of any one of claims 92-105, wherein the composition comprises a polypeptide comprising one or more T cell epitopes present in:

- a) cholera toxin or toxoid; and/or
- b) tetanus toxin or toxoid; and/or
- c) diphtheria toxin or toxoid; and/or
- d) CRM197.

108. A method of inducing an immune response to an antigen in an individual, the method comprising administering to the individual an effective amount of:

- a) the composition of any one of claims 92-107; and
- b) the antigen.

109. An immunogenic composition comprising:

- a) a T-cell epitope polypeptide comprising a T-cell epitope present in a hepatitis C virus (HCV) protein other than E1 and E2; and
- b) an archaeosome comprising at least one polar synthetic lipid, wherein the at least one polar synthetic lipid comprises at least one carbohydrate or anionic group linked by covalent bonding to at least one free hydroxyl group of an archaeal core lipid.

110. The immunogenic composition of claim 109, wherein the archaeal core lipid is archaeol (2,3-di-O-diphytanyl-sn-glycerol).

111. The immunogenic composition of claim 109, wherein the archaeal core lipid is caldarchaeol (2,2',3,3'-tetra-O-dibiphytanyl-sn-diglycerol).

112. The immunogenic composition of claim 109, wherein the carbohydrate group is selected from the group consisting of: β -D-Glc-(1,6)- β -D-Glc-; β -D-Glc-(1,6)-.alpha.-D-Glc-; .alpha.-D-Glc-(1,6)- β -D-Glc-; β -D-Glc-(1,4)- β -D-Glc-; α -D-Glc-(1,4)- β -D-Glc-; β -D-Gal-(1,4)- β -D-Glc-; α -D-Gal-(1,6)- β -D-Glc-; β -D-Glc-(1,6)- β -D-Glc-(1,6)- β -D-Glc-; α -D-Glc-(1,4)- α -D-Glc-(1,4)- β -D-Glc-; α -D-Man-(1,2)- α -D-Man-(1,2)- α -D-Man-; and α -D-Man-(1,2)- α -D-Man-(1,2)- α -D-Man-(1,2)- α -D-Man-.

113. The immunogenic composition of claim 109, wherein the carbohydrate group comprises two or three β -D-Glc- units in (1,6) linkage.

114. The immunogenic composition of claim 109, wherein the carbohydrate group is a gal-glc-group.

115. The immunogenic composition of claim 109, wherein the anionic group is selected from the group consisting of phosphoserine, phosphoethanolamine, phosphoinositol and phosphoglycerol.

116. The immunogenic composition of claim 109, wherein the at least one polar synthetic lipid comprises at least one anionic lipid.

117. The immunogenic composition of claim 116, wherein the at least one anionic lipid is selected from the group consisting of archaetidylglycerol, archaetidylglycerolphosphate-methyl, archaetidylserine, and archaetidylinositol.

118. The immunogenic composition of claim 116, wherein the archaeosome comprises at least one conventional lipid.

119. The immunogenic composition of claim 118, wherein the at least one conventional lipid is selected from a group consisting of phosphatidylglycerol, phosphatidylserine, SQDG, and cholesterol.

120. The immunogenic composition of claim 119, wherein the at least one conventional lipid comprises cholesterol, and wherein cholesterol is present in an amount of between 10 and 45 mol % of the total lipid composition.

121. The immunogenic composition of claim 119, wherein phosphatidylglycerol is present in an amount of between 20 and 80 mol % of the lipid composition.

122. The immunogenic composition of claim 119, wherein phosphatidylserine is present in an amount of between 10 and 30 mol % of the lipid composition.

123. The immunogenic composition of claim 109, wherein the at least one polar synthetic lipid comprises at least one synthetic immunoactive glycolipid and at least one anionic lipid, and the archaeosome further comprises at least one stabilizing lipid.

124. The immunogenic composition of claim 123, wherein the at least one polar synthetic lipid comprises caldarchaeol having one carbohydrate head group and one anionic head group.

125. The immunogenic composition of claim 124, wherein the carbohydrate head group comprises gentiobiose and the anionic head group comprises phosphoinositol.

126. The immunogenic composition of claim 123, wherein the at least one polar synthetic lipid comprises a first caldarchaeol having two carbohydrate head groups and a second caldarchaeol having two anionic head groups, and wherein the at least one stabilizing lipid is the first and/or second caldarchaeol.

127. The immunogenic composition of claim 123, wherein the at least one polar synthetic lipid comprises gentiatriose-archaeol and wherein the at least one stabilizing lipid comprises cholesterol and at least one of phosphatidylethanolamine, archaetidylglycerol, archaetidylserine or archaetidylglycerolphosphate-methyl.

128. The immunogenic composition of any one of claims 109-127, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in one or more of:

- a) an HCV non-structural polypeptide-3 (NS3) polypeptide;
- b) an HCV non-structural polypeptide-2 (NS2) polypeptide;
- c) an HCV non-structural polypeptide-4A (NS4A) polypeptide;
- d) an HCV non-structural polypeptide-4B (NS4B) polypeptide;
- e) an HCV non-structural polypeptide-5A (NS5A) polypeptide;
- f) an HCV non-structural polypeptide-5B (NS5B) polypeptide;
- g) an HCV core polypeptide; and
- h) an HCV p7 polypeptide.

129. The immunogenic composition of any one of claims 109-128, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 3000 amino acids.

130. The immunogenic composition of any one of claims 109-128, wherein the T-cell epitope polypeptide has a length of from about 10 amino acids to about 50 amino acids, from about 100 amino acids to about 230 amino acids, from about 230 amino acids to about 550 amino acids, from about 550 amino acids to about 780 amino acids, or from about 780 amino acids to about 2000 amino acids.

131. The immunogenic composition of any one of claims 109-130, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in an HCV NS3 polypeptide.

132. The immunogenic composition of claim any one of claims 109-131, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to the amino acid sequence of one of TP29, TP50, TP52, TP70, TP100, TP171, TP228, TP553, TP778, and TP1985.

133. The immunogenic composition of claim any one of claims 109-132, wherein the T-cell epitope polypeptide comprises an amino acid sequence having at least 20% amino acid sequence identity to a polypeptide depicted in any one of FIG. 9A, 9B, 10A-10D, and 11A-11N.

134. The immunogenic composition of any one of 109-133, wherein the T-cell epitope polypeptide comprises one or more T cell epitopes present in:

- a) cholera toxin or toxoid; and/or
- b) tetanus toxin or toxoid; and/or
- c) diphtheria toxin or toxoid; and/or
- d) CRM197.

135. The immunogenic composition of any one of claims 109-133, wherein the composition comprises a polypeptide comprising one or more T cell epitopes present in:

- a) cholera toxin or toxoid; and/or
- b) tetanus toxin or toxoid; and/or
- c) diphtheria toxin or toxoid; and/or
- d) CRM197.

136. A method of inducing an immune response to an antigen in an individual, the method comprising administering to the individual an effective amount of:

- a) the composition of any one of claims 109-135; and
- b) the antigen.

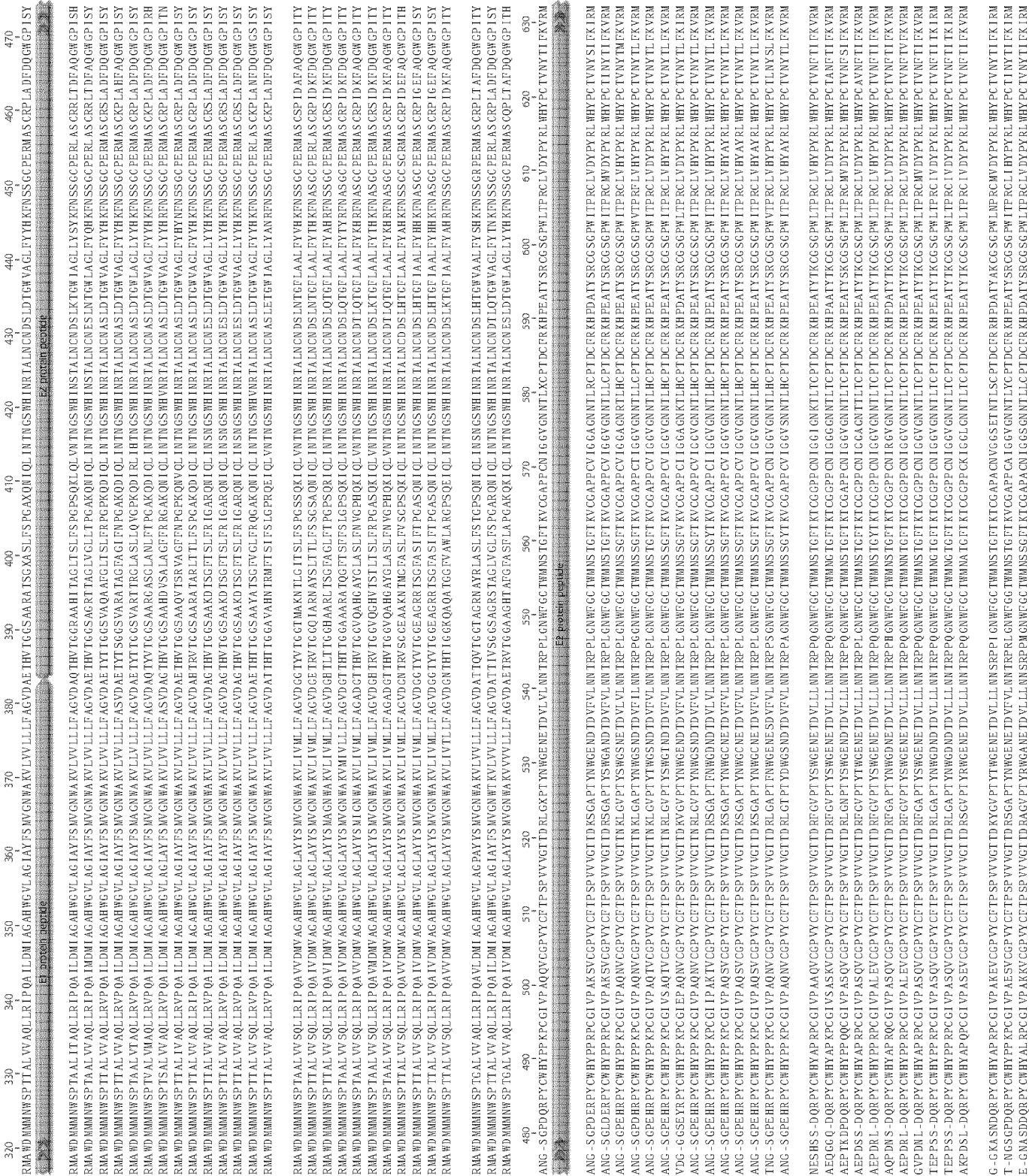


FIG. 1B

Consensus	1	10	20	30	40	50	60	70	80	
	M	S	T	N	P	K	P	Q	R	K
	T	K	R	N	T	N	R	R	P	Q
	D	V	K	F	P	G	G	Q	I	V
	G	V	G	V	L	L	P	R	R	G
	P	R	L	G	P	R	L	G	V	R
	A	T	R	K	T	S	E	R	S	Q
	P	R	R	R	Q	P	I	P	K	D
	R	R	S	T	G	K	S	W	G	K
	P	L	Y	G						
AB047639 (JFH1)	M	S	T	N	P	K	P	Q	R	K
AB047645	T	K	R	N	T	N	R	R	P	Q
AF238482	D	V	K	F	P	G	G	Q	I	V
AF169005	G	V	G	V	L	L	P	R	R	G
AY746460	P	R	L	G	P	R	L	G	V	R
HPCPOLP	A	T	R	K	T	S	E	R	S	Q
NC_009823	P	R	R	Q	P	I	P	K	D	R
	R	R	S	T	G	K	S	W	G	K
	P	L	Y	G						
Core										
HPCJ8G HC-J8	M	S	T	N	P	K	P	Q	R	K
AY232730	T	K	R	N	T	N	R	R	P	Q
AY232747	D	V	K	F	P	G	G	Q	I	V
AB030907	G	V	G	V	L	L	P	R	R	G
DQ430817	P	R	L	G	P	R	L	G	V	R
	A	T	R	K	T	S	E	R	S	Q
	P	R	R	Q	P	I	P	K	D	R
	R	R	S	T	G	K	S	W	G	K
	P	L	Y	G						
Consensus	90	100	110	120	130	140	150	160	170	
	N	E	G	L	G	W	A	G	W	L
	L	S	P	R	G	S	R	P	S	W
	G	T	D	P	R	H	R	S	R	N
	V	G	K	I	D	T	L	T	C	G
	F	A	D	L	M	G	I	P	V	V
	G	A	P	L	G	V	A	R	A	L
	A	H	G	V	R	V	L	E	D	G
	V	N	A	T	G	N	L	P	G	C
	S	F								
AB047639 (JFH1)	N	E	G	L	G	W	A	G	W	L
AB047645	L	S	P	R	G	S	R	P	S	W
AF238482	G	T	D	P	R	H	R	S	R	N
AF169005	V	G	K	I	D	T	L	T	C	G
AY746460	F	A	D	L	M	G	I	P	V	V
HPCPOLP	G	A	P	L	G	V	A	R	A	L
NC_009823	A	H	G	V	R	V	L	E	D	G
	V	N	A	T	G	N	L	P	G	C
	S	F								
Core										
HPCJ8G HC-J8	N	E	G	L	G	W	A	G	W	L
AY232730	L	S	P	R	G	S	R	P	S	W
AY232747	G	T	D	P	R	H	R	S	R	N
AB030907	V	G	K	I	D	T	L	T	C	G
DQ430817	F	A	D	L	M	G	I	P	V	V
	G	A	P	L	G	V	A	R	A	L
	A	H	G	V	R	V	L	E	D	G
	V	N	A	T	G	N	L	P	G	C
	S	F								
Consensus	180	190	200	210	220	230	240	250	260	
	S	I	F	L	L	A	L	L	S	C
	I	T	P	V	S	A	E	V	K	N
	I	S	T	S	Y	M	V	T	N	D
	C	S	N	D	S	I	T	W	Q	L
	A	A	V	L	H	V	P	G	C	V
	P	C	E	R	-	V	G	N	T	S
	R	C	W	I	P	V	S	P	N	V
	A	V	R	Q	P	G	A	L	T	Q
	G	L	R	T						
AB047639 (JFH1)	S	I	F	L	L	A	L	L	S	C
AB047645	I	T	P	V	S	A	E	V	K	N
AF238482	I	S	T	S	Y	M	V	T	N	D
AF169005	C	S	N	D	S	I	T	W	Q	L
AY746460	A	A	V	L	H	V	P	G	C	V
HPCPOLP	P	C	E	R	-	V	G	N	T	S
NC_009823	R	C	W	I	P	V	S	P	N	V
	A	V	R	Q	P	G	A	L	T	Q
	G	L	R	T						
Core										
HPCJ8G HC-J8	S	I	F	L	L	A	L	L	S	C
AY232730	I	T	P	V	S	A	E	V	K	N
AY232747	I	S	T	S	Y	M	V	T	N	D
AB030907	C	S	N	D	S	I	T	W	Q	L
DQ430817	A	A	V	L	H	V	P	G	C	V
	P	C	E	R	-	V	G	N	T	S
	R	C	W	I	P	V	S	P	N	V
	A	V	R	Q	P	G	A	L	T	Q
	G	L	R	T						
Consensus	260	270	280	290	300	310	320	330	340	
	S	I	F	L	L	A	L	L	S	C
	I	T	P	V	S	A	E	V	K	N
	I	S	T	S	Y	M	V	T	N	D
	C	S	N	D	S	I	T	W	Q	L
	A	A	V	L	H	V	P	G	C	V
	P	C	E	R	-	V	G	N	T	S
	R	C	W	I	P	V	S	P	N	V
	A	V	R	Q	P	G	A	L	T	Q
	G	L	R	T						
AB047639 (JFH1)	S	I	F	L	L	A	L	L	S	C
AB047645	I	T	P	V	S	A	E	V	K	N
AF238482	I	S	T	S	Y	M	V	T	N	D
AF169005	C	S	N	D	S	I	T	W	Q	L
AY746460	A	A	V	L	H	V	P	G	C	V
HPCPOLP	P	C	E	R	-	V	G	N	T	S
NC_009823	R	C	W	I	P	V	S	P	N	V
	A	V	R	Q	P	G	A	L	T	Q
	G	L	R	T						
Core										
HPCJ8G HC-J8	S	I	F	L	L	A	L	L	S	C
AY232730	I	T	P	V	S	A	E	V	K	N
AY232747	I	S	T	S	Y	M	V	T	N	D
AB030907	C	S	N	D	S	I	T	W	Q	L
DQ430817	A	A	V	L	H	V	P	G	C	V
	P	C	E	R	-	V	G	N	T	S
	R	C	W	I	P	V	S	P	N	V
	A	V	R	Q	P	G	A	L	T	Q
	G	L	R	T						

FIG. 2A

2A	Consensus	HIDMVVMSATLCSALYVGDLCGGVMLAAQXFIVSPQRHWFVQECNCISIYPGTITGHRMAWDMMMNNWSPATMILAYAMRVPEVIID
	AB047639 (JFH1)	HIDMVVMSATFCSALYVGDLCGGVMLAAQVFIIVSPQYHWFVQECNCISIYPGTITGHRMAWDMMMNNWSPATMILAYVMRVPEVIID
	AB047645	HIDMVVMSATLCSALYVGDLCGGVMLAAQMFIIISPQHHWFVQECNCISIYPGTITGHRMAWDMMMNNWSPTTMILAYVMRVPEVIID
	AF238482	HIDMVVMSATLCSALYVGDLCGGVMLAAQOLFIVSPRRHHWFVQECNCISIYPGATGHRMAWDMMMNNWSPTTMVLAYAMRVPEVIID
	AF169005	HIDMVVMSATLCSALYVGDLCGGVMLAAQMFIVSPQHHWFVQECNCISIYPGATITGHRMAWDMMMNNWSPATMILAYAMRVPEVIID
	AY746460	HIDIIVMSATLCSALYVGDLCGGVMLAAQMFIVSPQHHWFVQECNCISIYPGATITGHRMAWDMMMNNWSPATMILAYAMRVPEVIID
	HPCPOLP	HIDMVVMSATLCSALYVGDLCGGVMLAAQMFIVSPQHHWFVQDCNCISIYPGTITGHRMAWDMMMNNWSPATMILAYAMRVPEVIID
	NC_009823	HIDMVVMSATLCSALYVGDLCGGVMLAAQMFIVSPQHHWFVQDCNCISIYPGTITGHRMAWDMMMNNWSPATMILAYAMRVPEVIID
	Consensus	HVDMIVMAATACSAALYVGDVCGAVMILSQAFMVSPQRHNFTQECNCISIYQGHITGHRMAWDMMLWSPTLTMILAYAAARVPELVLEI
	HPCJ8G HC-J8	HVDIVVAAATVCSALYVGDVCGAVMIASQALIVSPARHNFTQECNCISIYQGRITGHHMAWDMMLNWSPTITMILAYAARIPELVLEI
2B	AY232730	HVDIVVMAATVCSALYVGDICGAVMIVSQAFIISPERHNFTQECNCISMYQGHITGHRMAWDMMLNWSPTLTMILAYAAARVPELVLEI
	AY232747	HVDIVVMAATVCSALYVGDVCGAVMIVSQALIVSPERHNFTQECNCISIYQGHITGHRMAWDMMLNWSPTLTMILAYAAARVPELVLEI
	AB030907	HVDIVVMAATVCSALYVGDVCGAVMIVSQAFIMS?ERHNFTQECNCISIYQGHITGHRMAWDMMLGWSPTLTMILAYAAARVPE?VLEI
	DQ430817	I?GAHWGVMFGLAYFSMQGAWAKVIVILLXAGVDARTHTVGGSGXGRTTSGXAGLFFSSGPKQNIQLINTNGSWHINRTALNCNDSLQ
	Consensus	VSGAHWGVMFGLAYFSMQGAWAKVIVILLXAGVDAGTTTVGGAVARSTNVIIAGVFSHGPOQNIQLINTNGSWHINRTALNCNDSLN
	AB047639 (JFH1)	IGGAHWGVMFGLAYFSMQGAWAKVVVILLXAGVDAHTRT-GSSVGYATSGIVGLFTSGPKQNIQLINTNGSWHINRTALNCNDSLN
	AB047645	ISGAHWGVMFGLAYFSMQGAWAKVAVILLITAGVEARTHTTGSAVAGRTTSGFAGIFTSGPKQNIQLINTNGSWHINRTALNCNDSLN
	AF238482	ISGAHWGVMFGLAYFSMQGAWAKVVVILLITAGVDAHTRSIAGSAHATSGLAGLFTSGAKQNIQLINTNGSWHINRTALNCNDSLN
	AF169005	ISGAHWGVMFGLAYFSMQGAWAKVVVILLXAGVDAYTHTVGGAAASTANSIAGLSRGPQRNLQINSGSWHINRTALNCNDSLQ
	AY746460	ISGAHWGVMFGLAYFSMQGAWAKVVVILLXAGVDAQYTHTVGGSTAHNARTLTGMEFSLGARQKIQLINTNGSWHINRTALNCNDSLH
2B	HPCPOLP	ISGAHWGVMFGLAYFSMQGAWAKVVVILLXAGVDARTHTVGGSAQAQTTGRLTSLFDMGPRQKIQLVNTNGSWHINRTALNCNDSLH
	NC_009823	IFGGHWGVVFGFLAYFSMQGAWAKVIAILLXAGVDAATYSSGQEAQRTVAGFAGLFTTGAKQNIQLINTNGSWHINRTALNCNDSLQ
	HPCJ8G HC-J8	IFGGHWGVVFGFLAYFSMQGAWAKVIVILLXAGVDARHHTTGLQAQKTLARVTSLFSIGAKQNIQLINTNGSWHINRTALNCNDSLQ
	AY232730	IFGGHWGVVFGFLAYFSMQGAWAKVIAILLXAGVDANTYSSGVTGHTTSTFANIFSVGPSQKINLINTNGSWHINRTALNCNDSLQ
	AY232747	VFGGHWGVVFGFLAYFSMQGAWAKVIAILLXAGVDAATYSTGATVGRVTGSAFLFKLGAQQNVQLINTNGSWHINRTALNCNDSLH
	AB030907	VFGGHWGVVFGFLAYFSMQGAWAKVIAILLXAGVDAGTSSGATIGQGTGRLV?LFSAGPSQKISLINTNGSWHINRT?LNCNDSLQ
	DQ430817	TGFIASLFYTXNFNSSGCPERLSACRGIEAFRIGWGTLOVEDVNTNPEDMRPVCWHYPPKXCXGIVPARSVCGPVYCFPTSPVVVGT
	Consensus	TGFLAALFYTNRFNSSGCPERLSACRNIEAFRIGWGTLOVEDVNTNPEDMRPYCWHYPPKQCGIVPARSVCGPVYCFPTSPVVVGT
	AB047639 (JFH1)	TGFIASLFYTNRFNSSGCPERLSACRNIEAFRIGWGTLOVEDVNTNPEDMRPYCWHYPPKQCGIVPARSVCGPVYCFPTSPVVVGT
	AB047645	TGFIASLFYTNRFNSSGCPERLSACRNIEAFRIGWGTLOVEDVNTNPEDMRPYCWHYPPKQCGIVPARSVCGPVYCFPTSPVVVGT
2A	AF238482	TGFIASLFYTNRFNSSGCPERLSACRNIEAFRIGWGTLOVEDVNTNPEDMRPYCWHYPPKQCGIVPARSVCGPVYCFPTSPVVVGT
	AF169005	TGFIASLFYTNRFNSSGCPERLSACRNIEAFRIGWGTLOVEDVNTNPEDMRPYCWHYPPKQCGIVPARSVCGPVYCFPTSPVVVGT
	AY746460	TGFIASLFYTNRFNSSGCPERLSACRNIEAFRIGWGTLOVEDVNTNPEDMRPYCWHYPPKQCGIVPARSVCGPVYCFPTSPVVVGT
	HPCPOLP	TGFIASLFYTNRFNSSGCPERLSACRNIEAFRIGWGTLOVEDVNTNPEDMRPYCWHYPPKQCGIVPARSVCGPVYCFPTSPVVVGT
	NC_009823	TGFIASLFYTNRFNSSGCPERLSACRNIEAFRIGWGTLOVEDVNTNPEDMRPYCWHYPPKQCGIVPARSVCGPVYCFPTSPVVVGT
	Consensus	TGFLASLFYTHKFNSSGCPERLSACRGLDDFRIGWGTLEYEYETVNTNDGDMRPPCYCWHYPPRPPCGIVPARTVCGPVYCFPTSPVVVGT
	HPCJ8G HC-J8	TGFLASLFYTHKFNSSGCPERLSACRGLDDFRIGWGTLEYEYETVNTNDGDMRPPCYCWHYPPRPPCGIVPARTVCGPVYCFPTSPVVVGT
	AY232730	TGFLASLFYTHKFNSSGCPERLSACRGLDDFRIGWGTLEYEYETVNTNDGDMRPPCYCWHYPPRPPCGIVPARTVCGPVYCFPTSPVVVGT
	AY232747	TGFLASLFYTHKFNSSGCPERLSACRGLDDFRIGWGTLEYEYETVNTNDGDMRPPCYCWHYPPRPPCGIVPARTVCGPVYCFPTSPVVVGT
	AB030907	TGFLASLFYTHKFNSSGCPERLSACRGLDDFRIGWGTLEYEYETVNTNDGDMRPPCYCWHYPPRPPCGIVPARTVCGPVYCFPTSPVVVGT
	DQ430817	TGFLASLFYTHKFNSSGCPERLSACRGLDDFRIGWGTLEYEYETVNTNDGDMRPPCYCWHYPPRPPCGIVPARTVCGPVYCFPTSPVVVGT

Consensus

AB047639 (JFH1)

AB047645

AF238482

AF169005

AY746460

HPCPOLP

NC_009823

2A

DR

LG

VP

TY

TW

GE

NE

TD

VF

LL

NS

TR

PP

RG

SW

FG

CT

WM

NS

TG

FT

KT

CG

AP

CR

IR

AD

FN

AS

TD

LL

CP

TD

CF

RK

HP

DA

TY

JK

CG

GP

WL

E2

DR

RG

VP

TY

TW

GE

NE

TD

VF

LL

NS

TR

PP

QG

SW

FG

CT

WM

NS

TG

FT

KT

CG

AP

CR

TR

AD

FN

AS

TD

LL

CP

TD

CF

RK

HP

DA

TY

IK

CG

GP

WL

DR

LG

VP

TY

TW

GE

NE

TD

VF

LL

NS

TR

PP

VG

SW

FG

CT

WM

NS

TG

FT

KT

CG

AP

CR

IR

AD

FN

AS

TD

LL

CP

TD

CF

RK

HP

DA

TY

IK

CG

GP

WL

NK

LG

VP

TY

TW

GE

NE

TD

VF

LL

NS

TR

PP

RG

SW

FG

CT

WM

NS

TG

FT

KT

CG

AP

CR

IR

AD

FN

AS

TD

LL

CP

TD

CF

RK

HP

DA

TY

IK

CG

GP

WL

DR

LG

VP

TY

TW

GE

NE

TD

VF

LL

NS

TR

PP

RG

SW

FG

CT

WM

NS

TG

FT

KT

CG

AP

CR

IR

AD

FN

AS

MD

LL

CP

TD

CF

RK

HP

DA

TY

IK

CG

GP

WL

DK

LG

VP

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TW

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LL

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CG

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	10	20	30	40	50	60	70	80	
Consensus	MSTLPKPQRKTKRNTIRRPQDVVKFPGGGQIVGGVYVLPFRRGPRLGVRATRKTKTSERSQPRGRRRQPIPKARRSEGRSWAQP GYPWPPLYGN								
	Core								
AVI3a177	MSTLPKPQRKTKRNTIRRPQDVVKFPGGGQIVGGVYVLPFRRGPRLGVRATRKTKTSERSQPRGRRRQPIPKARRSDGRSWAQP GYPWPPLYGN								
ADF97232(S52)	MSTLPKPQRKTKRNTIRRPQDVVKFPGGGQIVGGVYVLPFRRGPRLGVRATRKTKTSERSQPRGRRRQPIPKARRSEGRSWAQP GYPWPPLYGN								
YP_001469631	MSTLPKPQRKTKRNTIRRPQDVVKFPGGGQIVGGVYVLPFRRGPRLGVRATRKTKTSERSQPRGRRRQPIPKARRSEGRSWAQP GYPWPPLYGN								
CAA54244	MSTLPKPQRKTKRNTIRRPQDVVKFPGGGQIVGGVYVLPFRRGPRLGVRATRKTKTSERSQPRGRRRQPIPKARRSEGRSWAQP GYPWPPLYGN								
AAC03058	MSTLPKPQRKTKRNTIRRPQDVVKFPGGGQIVGGVYVLPFRRGPRLGVRATRKTKTSERSQPRRRRQPIPKARRSEGRSWAQP GYPWPPLYGN								
AAV29642	MSTLPKPQRKTKRNTIRRPQDVVKFPGGGQIVGGVYVLPFRRGPRLGVRATRKTKTSERSQPRRRRQPIPKARRSEGRSWAQP GYPWPPLYGN								
ABD85062	MSTLPKPQRKTKRNTIRRPQDVVKFPGGGQIVGGVYVLPFRRGPRLGVRATRKTKTSERSQPRRRRQPIPKARRSEGRSWAQP GYPWPPLYGN								
ABD85063	MSTLPKPQRKTKRNTIRRPQDVVKFPGGGQIVGGVYVLPFRRGPRLGVRATRKTKTSERSQPRRRRQPIPKARRSEGRSWAQP GYPWPPLYGN								
ABD97104	MSTLPKPQRKTKRNTIRRPQDVVKFPGGGQIVGGVYVLPFRRGPRLGVRATRKTKTSERSQPRRRRQPIPKARRSEGRSWAQP GYPWPPLYGN								
BAA06044	MSTLPKPQRKTKRNTIRRPQDVVKFPGGGQIVGGVYVLPFRRGPRLGVRATRKTKTSERSQPRRRRQPIPKARRSEGRSWAQP GYPWPPLYGN								
	Core								
BAA08372	MSTLPKPQRKTKRNTIRRPQDVVKFPGGGQIVGGVYVLPFRRGPRLGVRATRKTKTSERSQPRGRRRQPIPKARRSEGRSWAQP GYPWPPLYGN								
	Core								
BAA09890	MSTLPKPQRITKRNINRRRPQDVVKFPGGGQIVGGVYVLPFRRGPKLGVRATRKTKTSERSQPRSRRRQPIPKARRTEGRSWAQP GYPWPPLYGN								
Consensus	EGCGWAGWLLSPRGSRPSWGPNDP RRRSRNLGKVIDTLTCGFA DLMGYIPLVGA PVGGVARALAHGVRALEDGINFATGNLPGCSFSI								
	Core								
AVI3a177	EGCGWAGWLLSPRGSRPSWGPNDP RRRSRNLGKVIDTLTCGFA DLMGYIPLVGA PVGGVARALAHGVRALEDGINFATGNLPGCSFSI								
ADF97232(S52)	EGCGWAGWLLSPRGSRPSWGPNDP RRRSRNLGKVIDTLTCGFA DLMGYIPLVGA PVGGVARALAHGVRALEDGINFATGNLPGCSFSI								
YP_001469631	EGCGWAGWLLSPRGSRPSWGPNDP RRRSRNLGKVIDTLTCGFA DLMGYIPLVGA PVGGVARALAHGVRALEDGINFATGNLPGCSFSI								
CAA54244	EGCGWAGWLLSPRGSRPSWGPNDP RRRSRNLGKVIDTLTCGFA DLMGYIPLVGA PVGGVARALAHGVRALEDGINFATGNLPGCSFSI								
AAC03058	EGCGWAGWLLSPRGSRPSWGPNDP RRRSRNLGKVIDTLTCGFA DLMGYIPLVGA PVGGVARALAHGVRALEDGINFATGNLPGCSFSI								
AAV29642	EGCGWAGWLLSPRGSRPSWGPNDP RRRSRNLGKVIDTLTCGFA DLMGYIPLVGA PVGGVARALAHGVRALEDGINFATGNLPGCSFSI								
ABD85062	EGCGWAGWLLSPRGSRPSWGPNDP RRRSRNLGKVIDTLTCGFA DLMGYIPLVGA PVGGVARALAHGVRALEDGINFATGNLPGCSFSI								
ABD85063	EGCGWAGWLLSPRGSRPSWGPNDP RRRSRNLGKVIDTLTCGFA DLMGYIPLVGA PVGGVARALAHGVRALEDGINFATGNLPGCSFSI								
ABD97104	EGCGWAGWLLSPRGSRPSWGPNDP RRRSRNLGKVIDTLTCGFA DLMGYIPLVGA PVGGVARALAHGVRALEDGINFATGNLPGCSFSI								
BAA06044	EGCGWAGWLLSPRGSRPNWAPNDP RRRSRNLGKVIDTLTCGFA DLMGYIPLVGA PLGGARALAHGVRALEDGINFATGNLPGCSFSI								
	Core								
BAA08372	EGCGWAGWLLPPRGSRPSWGPNDP RRRSRNLGKVIDTLTCGFA DLMGYIPLVGA PVGGVARALAHGVRALEDGVNYYATGNLPGCSFSI								
	Core								
BAA09890	EGCGWAGWLLSPRGSRPSWGPNDP RRRSRNLGKVIDTLTCGFA DLMGYIPLVGA PVGGVARALAHGVRALEDGINFATGNLPGCSFSI								
Consensus	FLALFSCLIHPAASLEWRNTSGLYVLTNDCSNSSIVYEADDVILHTPGCVPCVQ-DGNTSTCWTPTPTVA VRYVGA TTASIRSHVD								
	Core								
AVI3a177	FLALFSCLIHPAASLEWRNTSGLYVLTNDCPNSSIVYEADDVILHTPGCIPCVQ-DGNTSTCWTSPVPTVA VRYVGA TTASIRSHVD								
ADF97232(S52)	FLALFSCLIHPAASLEWRNTSGLYVLTNDCSNSSIVYEADDVILHTPGCVPCVQ-DDNTSTCWTPTPTVA VRYVGA TTASIRSHVD								
YP_001469631	FLALFSCLIHPAASLEWRNTSGLYVLTNDCSNSSIVYEADDVILHTPGCVPCVQ-DGNTSTCWTPTPTVA VRYVGA TTASIRSHVD								
CAA54244	FLALFSCLIHPAASLEWRNTSGLYVLTNDCSNSSIVYEADDVILHTPGCVPCVQ-DGNTSTCWTPTPTVA VRYVGA TTASIRSHVD								
AAC03058	FLALFSCLIHPAASLEWRNTSGLYVLTNDCSNSSIVYEADDVILHTPGCVPCVQ-DGNTSTCWTPTPTVA VRYVGA TTASIRSHVD								
AAV29642	FLALFSCLIHPAASLEWRNTSGLYVLTNDCPNSSIVYEADDVILHTPGCIPCVQ-DGNTSTCWTPTPTVA VRYVGA TTASIRSHVD								
ABD85062	FLALFSCLIHPAASLEWRNTSGLYVLTNDCSNSSIVYEADDVILHTPGCVPCVQ-DGNTSTCWTPTPTVA VRYVGA TTASIRSHVD								
ABD85063	FLALFSCLIHPAASLEWRNTSGLYVLTNDCSNSSIVYEADDVILHTPGCVPCVQ-DGNTSTCWTPTPTVA VRYVGA TTASIRSHVD								
ABD97104	FLALFSCLIHPAASLEWRNTSGLYVLTNDCPNSSIVYEADDVILHTPGCIPCVQ-DGNTSTCWTPTPTVA VRYVGA TTASIRSHVD								
BAA06044	FLALFSCLIHPAASLEWRNTSGLYVLTNDCSNSSIVYEADDVILHTPGCIPCVQ-DGNTSTCWTPTPTVA VRYVGA TTASIRSHVD								
	Core								
BAA08372	FLALFSCLTCPA SSLEYRNA SGLYLLTNDCSNRSIVYEADDVILHLPGCVPVETDNNNTS CWTPTPTVA VKHPGVTTASIRNHVN								
	Core								
BAA09890	FLALFSCLLTPTAGLEYRNA SGLYTVTNDCSNGSIVYEAGDVILHLPGCIPCVR-LNNA SKCWTPTPTVA VSRPGAA TASLRTHVD								

FIG. 3A

3A	Consensus	270	280	290	300	310	320	330	340	350																											
	AVI3a177	LLVGAATLCSALYVVD	MC	GAVFLVGQA	FTFRPRRHQT	VQTCNC	SLYPGHL	SGHRMA	WDMMMN	WSPA	VGMVVA	HVLR	LPQT	FLDI	IAGA																						
	ADF97232(S52)	LLVGAATLCSALYVVD	MC	GAVFLVGQA	FTFRPRRHQT	VQTCNC	SLYPGHL	SGHRMA	WDMMMN	WSPA	VGMVVA	HVLR	LPQT	FLDI	IAGA																						
	YP_001469631	LLVGAATLCSALYVVD	MC	GAVFLVGQA	FTFRPRRHQT	VQTCNC	SLYPGHL	SGHRMA	WDMMMN	WSPA	VGMVVA	HVLR	LPQT	FLDI	IAGA																						
	CAAS4244	LLVGAATLCSALYVVD	MC	GAVFLVGQA	FTFRPRRHQT	VQTCNC	SLYPGHL	SGHRMA	WDMMMN	WSPA	VGMVVA	HVLR	LPQT	FLDI	IAGA																						
	AAC03058	LLVGAATLCSALYVVD	MC	GAVFLVGQA	FTFRPRRHQT	VQTCNC	SLYPGHL	SGHRMA	WDMMMN	WSPA	VGMVVA	HVLR	LPQT	FLDI	IAGA																						
	AAY29642	LLVGAATLCSALYVVD	MC	GAVFLVGQA	FTFRPRRHQT	VQTCNC	SLYPGHL	SGHRMA	WDMMMN	WSPA	VGMVVA	HVLR	LPQT	FLDI	IAGA																						
	ABD85062	LLVGAATLCSALYVVD	MC	GAVFLVGQA	FTFRPRRHQT	VQTCNC	SLYPGHL	SGHRMA	WDMMMN	WSPA	VGMVVA	HVLR	LPQT	FLDI	IAGA																						
	ABD85063	LLVGAATLCSALYVVD	MC	GAVFLVGQA	FTFRPRRHQT	VQTCNC	SLYPGHL	SGHRMA	WDMMMN	WSPA	VGMVVA	HVLR	LPQT	FLDI	IAGA																						
	ABD97104	LLVGAATLCSALYVVD	MC	GAVFLVGQA	FTFRPRRHQT	VQTCNC	SLYPGHL	SGHRMA	WDMMMN	WSPA	VGMVVA	HVLR	LPQT	FLDI	IAGA																						
BAA06044	LLVGAATLCSALYVVD	MC	GAVFLVGQA	FTFRPRRHQT	VQTCNC	SLYPGHL	SGHRMA	WDMMMN	WSPA	VGMVVA	HVLR	LPQT	FLDI	IAGA																							
3B	Consensus	360	370	380	390	400	410	420	430	440																											
	BAA08372	MLVAPPTLCSALYVED	AF	GAVSLVGQA	FTFRPRRHQT	VQTCNC	SIYPGHV	SGHRMA	WDMMMN	WSPA	IGLVI	SHLM	RLPQT	FFFD	LVVGA																						
	BAA09890	MMVGAATLCSALYVGD	LC	GALFLVGQGF	SWRRHRQH	TWVQDCNC	SIYPGH	LTGHRMA	WDMMMN	WSPA	MTLIV	SQVLR	LPQT	MTFM	DLVIGA																						
	Consensus	HWGILAGLA	YYSM	QGNWAKVA	IIMVMF	SGVDA	TTYTTG	GSAA	RGARGL	TS	LS	FSVGA	KQKL	QLVNT	NGSWHIN	STALNC	XSINT	GF	FA																		
	AVI3a177	HWGILAGLA	YYSM	QGNWAKVA	IIMVMF	SGVDA	ETHTTG	CTAARNA	F	TLTGL	FTQGAR	OKLE	ILINT	NGSWHIN	RTALNC	NESINT	GF	FA																			
	ADF97232(S52)	HWGILAGLA	YYSM	QGNWAKVA	IIMVMF	SGVDA	EYVTG	GSVAH	SARGL	TS	LS	FSMGA	KQKL	QLVNT	NGSWHIN	STALNC	NESINT	GF	FA																		
	YP_001469631	HWGILAGLA	YYSM	QGNWAKVA	IIMVMF	SGVDA	EYVTG	CTAARNA	F	TLTGL	FTQGAR	OKLE	ILINT	NGSWHIN	RTALNC	NESINT	GF	FA																			
	CAAS4244	HWGILAGLA	YYSM	QGNWAKVA	IIMVMF	SGVDA	EYVTG	CTAARNA	F	TLTGL	FTQGAR	OKLE	ILINT	NGSWHIN	RTALNC	NESINT	GF	FA																			
	AAC03058	HWGILAGLA	YYSM	QGNWAKVA	IIMVMF	SGVDA	VYTTG	GSAA	AHA	TRGL	TS	LS	FSVGA	KQKL	QLVNT	NGSWHIN	STALNC	NESINT	GF	FA																	
	AAY29642	HWGILAGLA	YYSM	QGNWAKVI	IIMVMF	SGVDA	THVTG	CTAGL	TAFRL	TGL	FTVGP	QOKL	QLVNT	NGSWHIN	RTALNC	NDSINT	GF	FA																			
ABD85062	HWGILAGLA	YYSM	QGNWAKVA	IIMVMF	SGVDA	TTYTS	CGSVA	QQA	RG	LAD	LS	FSVGA	KQKL	QLVNT	NGSWHIN	STALNC	NDSINT	GF	FA																		
ABD85063	HWGILAGLA	YYSM	QGNWAKVA	IIMVMF	SGVDA	TTYTS	CGSVA	QQA	RG	LAD	LS	FSVGA	KQKL	QLVNT	NGSWHIN	STALNC	NDSINT	GF	FA																		
ABD97104	HWGILAGLA	YYSM	QGNWAKVA	IIMVMF	SGVDA	TTYTTG	CGNA	ARGAS	G	IV	SL	TPGA	KQKL	QLVNT	NGSWHIN	RTALNC	NDSINT	GF	FA																		
BAA06044	HWGILAGLA	YYSM	QGNWAKVA	IIMVMF	SGVDA	STHVTA	GQAARNA	Y	G	IT	LS	FSVGA	KQKL	QLVNT	NGSWHIN	RTALNC	NESINT	GF	FA																		
3B	Consensus	450	460	470	480	490	500	510	520																												
	BAA08372	HWGVMAGLA	YFSM	QGNWAKV	IVLIMF	SGVDA	TTHTTG	GSAAQ	A	TAG	FTS	FFTRGP	SQNL	QLVNS	NGSWHIN	STALNC	NDSINT	GF	FA																		
	BAA09890	HWGVMAGVA	YYSM	QGNWAKV	FLVLC	FS	GVDA	STTTIT	CGVA	AS	G	AFT	IT	SL	FS	TGA	KQPL	HLVNT	NGSWHIN	RTALNC	NDSINT	GF	FA														
	Consensus	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFXQ	GWG	PLTD	ANI	TG	PSDD	KPY	CWH	YAP	RPCD	VVP	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DA	KGVPT											
	AVI3a177	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	LT	DANI	TG	PSDD	KPY	CWH	YAP	RPCD	VVP	PALN	VCG	VP	YCF	TPSP	VV	VGTT	DR	QGVPT											
	ADF97232(S52)	GLFY	YHKFN	STGCP	QRL	SSCKP	ITIS	FRQ	WG	PLTD	DANI	TG	PSDD	R	Y	PCV	SV	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DI	KGKPT											
	YP_001469631	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	PLTD	DANI	TG	PSDD	R	Y	PCV	SV	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DA	R	GVPT											
	CAAS4244	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	LT	DANI	TG	PSDD	KPY	CWH	YAP	RPCD	VVP	PALN	VCG	VP	YCF	TPSP	VV	VGTT	DR	KGVPT											
	AAC03058	GLFY	YHRFN	STGCP	QRL	SSCKP	ITFFKQ	QWGS	PLTD	DANI	SG	PSDD	KPY	CWH	YAP	RPCV	PKV	VV	PAS	GC	VP	YCF	TPSP	VV	VGTT	DA	KGVPT										
	AAY29642	GLFR	FRHFN	STGCP	PE	MLSSCKP	ITS	FKQ	WG	PLTD	DANI	IT	PSDD	R	Y	PCV	SV	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DA	KGVPT											
ABD85062	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFKQ	QWGS	PLTD	DANI	IT	PSDD	KPY	CWH	YAP	RR	CGV	VV	PAS	VC	GPV	YCF	TPSP	VV	VGTT	DA	KGVPT											
ABD85063	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFKQ	QWGS	PLTD	DANI	IT	PSDD	KPY	CWH	YAP	RR	CGV	VV	PAS	VC	GPV	YCF	TPSP	VV	VGTT	DA	KGVPT											
ABD97104	GLI	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	LT	DANI	TG	PSDD	KPY	CWH	Y	PR	PCD	TI	RAS	SV	CG	VP	YCF	TPSP	VV	VGTT	DA	KGAPT										
BAA06044	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFKQ	QWGS	PLTD	DANI	TG	PSDD	KPY	CWH	YAP	RPCG	IV	PALN	VCG	VP	YCF	TPSP	VV	VGTT	DA	KGAPT												
3B	Consensus	530	540	550	560	570	580	590	600	610																											
	BAA08372	GLFY	YHKFN	SSGCP	PER	MS	SSCKP	ITYFN	QWGS	PLTD	DANI	ING	P	SE	DR	P	CW	HY	PP	R	PC	NI	TK	PLN	VCG	VP	YCF	TPSP	VV	VGTT	DI	KGLPT					
	BAA09890	GLLY	YHKFN	SSGCP	VER	MS	AC	SP	LD	R	FA	QWGS	PL	GP	ANI	SG	PS	SE	K	P	CW	HY	AP	R	PCD	TV	PA	Q	S	VCG	VP	YCF	TPSP	VV	VGAT	DI	KRGAPT
	Consensus	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	PLTD	DANI	TG	PSDD	KPY	CWH	YAP	RPCD	VVP	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DA	KGVPT											
	AVI3a177	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	PLTD	DANI	TG	PSDD	KPY	CWH	YAP	RPCD	VVP	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DA	R	GVPT										
	ADF97232(S52)	GLFY	YHKFN	STGCP	QRL	SSCKP	ITIS	FRQ	WG	PLTD	DANI	TG	PSDD	R	Y	PCV	SV	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DI	KGKPT											
	YP_001469631	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	PLTD	DANI	TG	PSDD	R	Y	PCV	SV	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DA	R	GVPT											
	CAAS4244	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	LT	DANI	TG	PSDD	KPY	CWH	YAP	RPCD	VVP	PALN	VCG	VP	YCF	TPSP	VV	VGTT	DR	KGVPT											
	AAC03058	GLFY	YHRFN	STGCP	QRL	SSCKP	ITFFKQ	QWGS	PLTD	DANI	SG	PSDD	KPY	CWH	YAP	RPCV	PKV	VV	PAS	GC	VP	YCF	TPSP	VV	VGTT	DA	KGVPT										
	AAY29642	GLFR	FRHFN	STGCP	PE	MLSSCKP	ITS	FKQ	WG	PLTD	DANI	IT	PSDD	R	Y	PCV	SV	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DA	KGVPT											
ABD85062	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFKQ	QWGS	PLTD	DANI	IT	PSDD	KPY	CWH	YAP	RR	CGV	VV	PAS	VC	GPV	YCF	TPSP	VV	VGTT	DA	KGVPT											
ABD85063	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFKQ	QWGS	PLTD	DANI	IT	PSDD	KPY	CWH	YAP	RR	CGV	VV	PAS	VC	GPV	YCF	TPSP	VV	VGTT	DA	KGVPT											
ABD97104	GLI	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	LT	DANI	TG	PSDD	KPY	CWH	Y	PR	PCD	TI	RAS	SV	CG	VP	YCF	TPSP	VV	VGTT	DA	KGAPT										
BAA06044	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFKQ	QWGS	PLTD	DANI	TG	PSDD	KPY	CWH	YAP	RPCG	IV	PALN	VCG	VP	YCF	TPSP	VV	VGTT	DA	KGAPT												
3K	Consensus	620	630	640	650	660	670	680	690	700																											
	BAA08372	GLFY	YHKFN	SSGCP	PER	MS	SSCKP	ITYFN	QWGS	PLTD	DANI	ING	P	SE	DR	P	CW	HY	PP	R	PC	NI	TK	PLN	VCG	VP	YCF	TPSP	VV	VGTT	DI	KGLPT					
	BAA09890	GLLY	YHKFN	SSGCP	VER	MS	AC	SP	LD	R	FA	QWGS	PL	GP	ANI	SG	PS	SE	K	P	CW	HY	AP	R	PCD	TV	PA	Q	S	VCG	VP	YCF	TPSP	VV	VGAT	DI	KRGAPT
	Consensus	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	PLTD	DANI	TG	PSDD	KPY	CWH	YAP	RPCD	VVP	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DA	KGVPT											
	AVI3a177	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	PLTD	DANI	TG	PSDD	KPY	CWH	YAP	RPCD	VVP	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DA	R	GVPT										
	ADF97232(S52)	GLFY	YHKFN	STGCP	QRL	SSCKP	ITIS	FRQ	WG	PLTD	DANI	TG	PSDD	R	Y	PCV	SV	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DI	KGKPT											
	YP_001469631	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	PLTD	DANI	TG	PSDD	R	Y	PCV	SV	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DA	R	GVPT											
	CAAS4244	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	LT	DANI	TG	PSDD	KPY	CWH	YAP	RPCD	VVP	PALN	VCG	VP	YCF	TPSP	VV	VGTT	DR	KGVPT											
	AAC03058	GLFY	YHRFN	STGCP	QRL	SSCKP	ITFFKQ	QWGS	PLTD	DANI	SG	PSDD	KPY	CWH	YAP	RPCV	PKV	VV	PAS	GC	VP	YCF	TPSP	VV	VGTT	DA	KGVPT										
	AAY29642	GLFR	FRHFN	STGCP	PE	MLSSCKP	ITS	FKQ	WG	PLTD	DANI	IT	PSDD	R	Y	PCV	SV	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DA	KGVPT											
ABD85062	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFKQ	QWGS	PLTD	DANI	IT	PSDD	KPY	CWH	YAP	RR	CGV	VV	PAS	VC	GPV	YCF	TPSP	VV	VGTT	DA	KGVPT											
ABD85063	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFKQ	QWGS	PLTD	DANI	IT	PSDD	KPY	CWH	YAP	RR	CGV	VV	PAS	VC	GPV	YCF	TPSP	VV	VGTT	DA	KGVPT											
ABD97104	GLI	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	LT	DANI	TG	PSDD	KPY	CWH	Y	PR	PCD	TI	RAS	SV	CG	VP	YCF	TPSP	VV	VGTT	DA	KGAPT										
BAA06044	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFKQ	QWGS	PLTD	DANI	TG	PSDD	KPY	CWH	YAP	RPCG	IV	PALN	VCG	VP	YCF	TPSP	VV	VGTT	DA	KGAPT												
3K	Consensus	720	730	740	750	760	770	780	790	800																											
	BAA08372	GLFY	YHKFN	SSGCP	PER	MS	SSCKP	ITYFN	QWGS	PLTD	DANI	ING	P	SE	DR	P	CW	HY	PP	R	PC	NI	TK	PLN	VCG	VP	YCF	TPSP	VV	VGTT	DI	KGLPT					
	BAA09890	GLLY	YHKFN	SSGCP	VER	MS	AC	SP	LD	R	FA	QWGS	PL	GP	ANI	SG	PS	SE	K	P	CW	HY	AP	R	PCD	TV	PA	Q	S	VCG	VP	YCF	TPSP	VV	VGAT	DI	KRGAPT
	Consensus	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	PLTD	DANI	TG	PSDD	KPY	CWH	YAP	RPCD	VVP	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DA	KGVPT											
	AVI3a177	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS	PLTD	DANI	TG	PSDD	KPY	CWH	YAP	RPCD	VVP	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DA	R	GVPT										
	ADF97232(S52)	GLFY	YHKFN	STGCP	QRL	SSCKP	ITIS	FRQ	WG	PLTD	DANI	TG	PSDD	R	Y	PCV	SV	PASS	VC	GPV	YCF	TPSP	VV	VGTT	DI	KGKPT											
	YP_001469631	GLFY	YHKFN	STGCP	QRL	SSCKP	ITFFRQ	QWGS																													

3A	Consensus	530 540 550 560 570 580 590 600 610 YTWGENETDVFLLESRLRPPSGRWFGGCTWMNSTGFVKTCGAPPCNIYGGGGNPH-NESDLFCPTDCFRKHPDA TYSRCGAGPWLTPRCM
	AVI3a177	E2 YTWGENETDVFLLESRLRPPSGRWFGGCTWMNSTGFVKTCGAPPCDIYGGGGNRC-NESDLFCPTDCFRKHPDA TYSRCGAGPWLTPRCL
	ADF97232(S52)	YTWGENETDVFLLESRLRPPSGRWFGGCAWMNSTGFLKTCGAPPCNIYGGEGDPE-NETDLFCPTDCFRKHPDA TYSRCGAGPWLTPRCM
	YP_001469631	YTWGENEKDVFLLESRLRPPSGRWFGGCAWMNSTGFLKTCGAPPCNIYGGEGNPH-NESDLFCPTDCFRKHPDA TYSRCGAGPWLTPRCM
3A	Consensus	620 630 640 650 660 670 680 690 700 VDYPYRLWHYPCTVNFVTLFKVRMFVGGFEHRTAAACNWTGRCRCDIEDRRSEQHPLHSHSTTELA ILPCSTPMPALSTGLIHLHQNI
	AVI3a177	E2 VDYPYRLWHYPCTVNFVTLFKVRMFVGGFEHRTAAACNWTGRCRCDIEDRRSEQHPLHSHSTTELA ILPCSTPMPALSTGLIHLHQNI
	ADF97232(S52)	VDYPYRLWHYPCTVNFVTLFKVRMFVGGFEHRTAAACNWTGRCRCDIEDRRSEQHPLHSHSTTELA ILPCSTPMPALSTGLIHLHQNI
	YP_001469631	VDYPYRLWHYPCTVNFVTLFKVRMFVGGFEHRTAAACNWTGRCRCDIEDRRSEQHPLHSHSTTELA ILPCSTPMPALSTGLIHLHQNI
3A	Consensus	710 720 730 740 750 754 VDVQYLYGVGSGMVGWALKWFEFVILVFLLLADARVCVALWMLMISQAEA
	AVI3a177	E2 VDVQYLYGVGSGVVGWALKWFEFVILVFLLLADARVCVALWMLMISQAEA
	ADF97232(S52)	VDVQYLYGVGSDMVGWALKWFEFVILVFLLLADARVCVALWMLMVSQAEA
	YP_001469631	VDVQYLYGVGSGMVGWALKWFEFVILVFLLLADARVCVALWMLMISQTEA
3A	Consensus	760 770 780 790 800 810 VDVQYLYGVGSGMVGWALKWFEFVILVFLLLADARVCVALWMLMISQAEA
	AVI3a177	E2 VDVQYLYGVGSGMVGWALKWFEFVILVFLLLADARVCVALWMLMISQAEA
	ADF97232(S52)	VDVQYLYGVGSGMVGWALKWFEFVILVFLLLADARVCVALWMLMISQAEA
	YP_001469631	VDVQYLYGVGSGMVGWALKWFEFVILVFLLLADARVCVALWMLMISQAEA
3B	Consensus	820 830 840 850 860 870 880 890 900 VDVQYLYGVGSAVVGWALKWFEFVILVFLLLADARVCVALWMLMISQAEA
	AVI3a177	E2 VDVQYLYGVGSAVVGWALKWFEFVILVFLLLADARVCVALWMLMISQAEA
	ADF97232(S52)	VDVQYLYGVGSAVVGWALKWFEFVILVFLLLADARVCVALWMLMISQAEA
	YP_001469631	VDVQYLYGVGSAVVGWALKWFEFVILVFLLLADARVCVALWMLMISQAEA
3K	Consensus	910 920 930 940 950 960 970 980 990 VDVQYLYGIGSGLVGWAIKWEFVILVFLLLADARVCVALWMLMISQAEA
	AVI3a177	E2 VDVQYLYGIGSGLVGWAIKWEFVILVFLLLADARVCVALWMLMISQAEA
	ADF97232(S52)	VDVQYLYGIGSGLVGWAIKWEFVILVFLLLADARVCVALWMLMISQAEA
	YP_001469631	VDVQYLYGIGSGLVGWAIKWEFVILVFLLLADARVCVALWMLMISQAEA

FIG. 3C

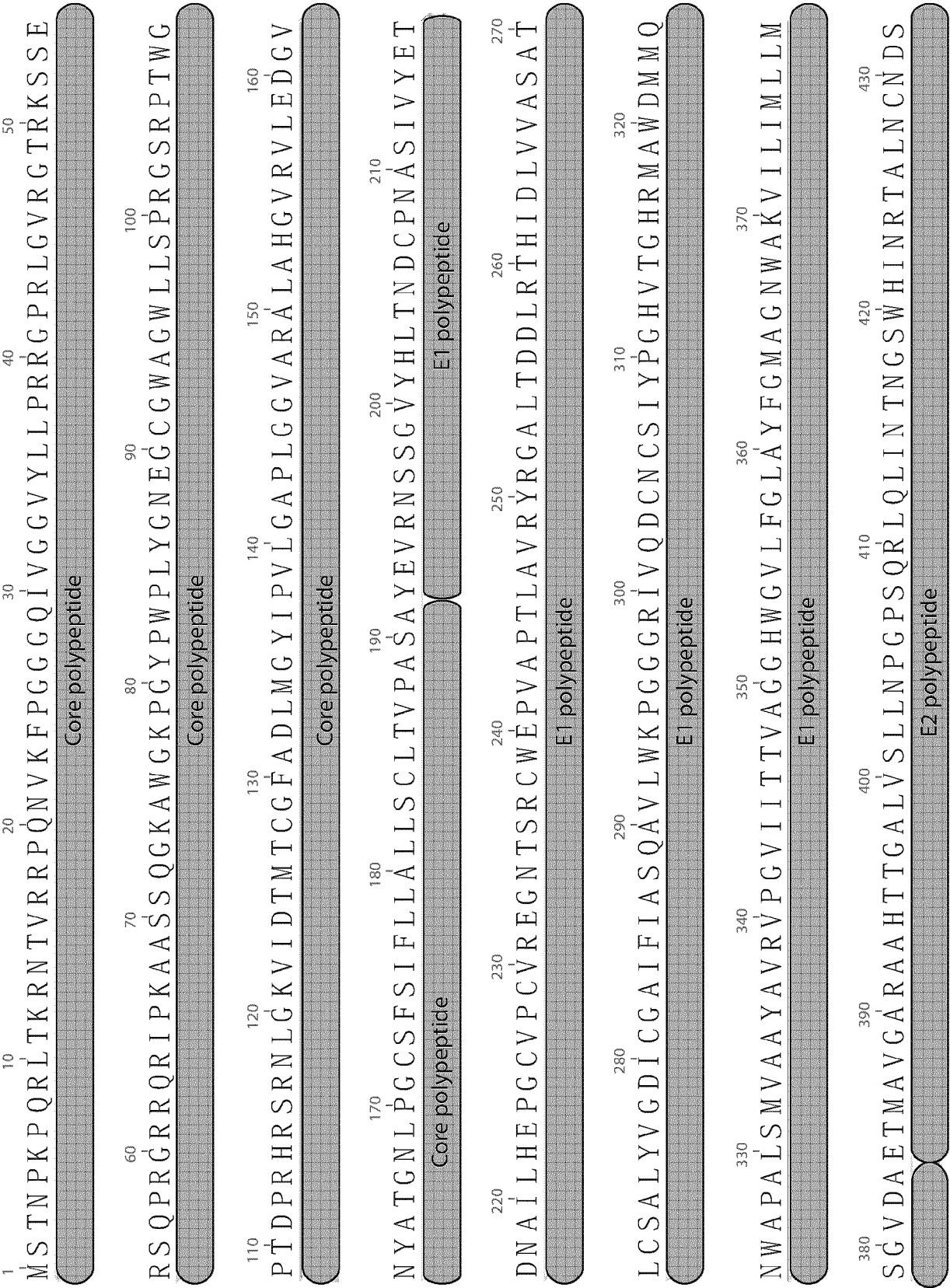


FIG. 4A

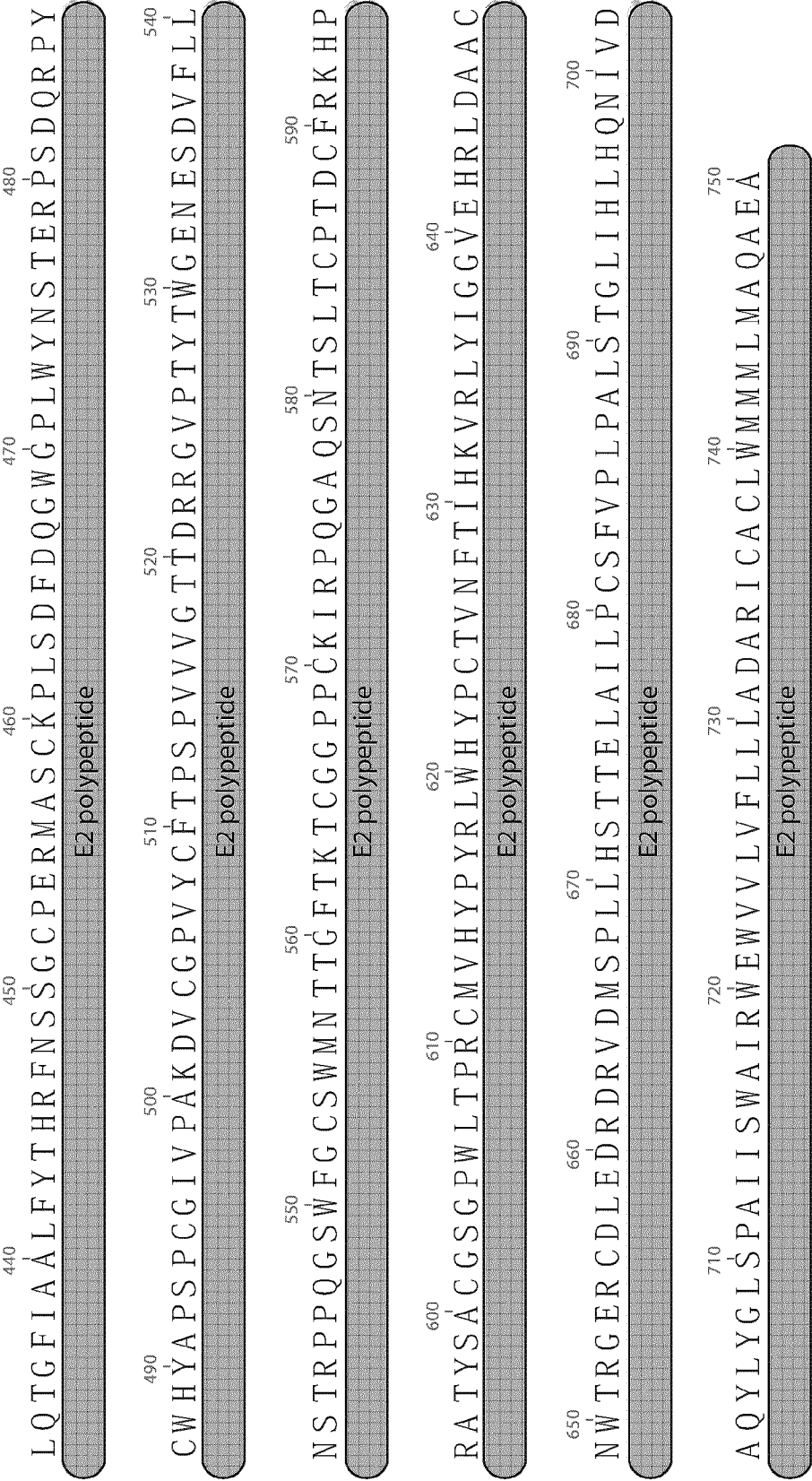


FIG. 4B

FIG. 5A

GenBank 3S7G_A

Homo sapiens **IgG1** Fc

227 aa

1 dkthtccppcp apellggpsv flfppkpkdt lmisrtpevt cvvvdvshed pevknwyvd
 61 gvevhnatk preeqnsty rvsvltvlh qdwlngkeyk ckvsnkappa piektiskak
 121 gqprepqvyt lppsrdeitk nqvsitclvk gfypsdiave wesngqpenn ykttppvlds
 181 dgsfflyskl tvdksrwqgg nvfscsvmhe alnhytqks lslspgk

GenBank AAN76044

Homo sapiens **IgG2** Fc (amino acids 99-325)

227 aa

1 stkgpsvfpl apcsrstses taalglvkd yfpepvtvsw nsgaltsgvh tfpavlqssg
 61 lyslssvvtv pssnfgtqty tcnvdhkpsn tkvdktverk ccvecppcpa ppvagpsvfl
 121 fppkpkdtlm isrtpevtcv vvdvshedpe vqfnwyvdgv evhnaktkpr eeqfnstfrv
 181 vsvltvvhqdw lngkeykck vsnkglpapi ektisktkgq prepqvvtlp psreemtknq
 241 vsltclvkgf ypsdiavewe sngqpennyy ttpmldsdg sfflyskltv dksrwqqgnv
 301 fscsvmheal hnhytqksls lspgk

GenBank AAW65947

Homo sapiens **IgG3** Fc (amino acids 19-246)

238 aa

1 hkpsntkvdk rvelktplgd tthtccppcpa pellggpsvf lfppkpkdtl misrtpevtc
 61 vvvdvshedp evkfnwyvdg vevhnaktkp reeqnstyrv vsvltvlhqw dwlngkeykc
 121 kvsnkappa iektiskakg qprepqvytl ppsrdeltkn qvsltclvkg fypsdiavew
 181 esngqpenny kttppvldsds gsfflysklt vdksrwqqgn vfcscsvmhea lnhytqksl
 241 slspgk

FIG. 5B

GenBank AAA52770
Homo sapiens IgD Fc (amino acids 162-383)
222 aa

```
1 ptkapdvfpi isgcrhpkdn spvvlacilit gyhptsvtvt wymgtqspq rtfpeiqrdd
61 syymtssqls tplqqwrqge ykcvvqhtas kskkeifrwp espkaqassv ptaqpqaegs
121 lakattapat trntgrggee kkekekeeq eeretktpec pshtqplgvy lltpavqdlw
181 lrdkatftcf vvgdldkdah ltwevagkvp tggveeglle rhsgsqsqh srltlprslw
241 nagtsvtctl nhpslppqrl malrepaaqa pvklslnlla ssdppeaasw llcevsgfsp
301 pnillmwled qrevntsgfa parpppqrpr ttfwawsvlr vpappspqa tytvcvshed
361 srllnasrs levsyvtldhg pmk
```

GenBank 0308221A
Homo sapiens IgM Fc
276 aa

```
1 vtstltikzs dwlgesmftc rvdhrgltfq qnassmcpvd qdtairvfai ppsfasiflt
61 kstkltclvt dltybsvti swtreengav kthtnishes pnatfsavge asicedbdws
121 gerftctvth tdlpsplkqt isrpkgvalh rpbvylppa rzzlnlresa titclvtgfs
181 padvfviewmq rgeplspqky vtsapmpepq apgryfahsi ltvseeewnt ggtytcvvah
241 ealpnrvter tvdkstgkpt lynvslvmsd tagtcy
```

FIG. 5C

GenBank P01876

Homo sapiens **IgA** Fc (amino acids 120-353)

234 aa

```

1 asptspkvfp lslcstqpdg nvviaclvqg ffpqeplsvt wsesgggvta rnfpssqdas
61 gdlyttssql tlpataqlag ksvtchvkhy tnpdqdvtp cpvpstptp spstptpsp
121 scchprlslh rpaledlllg seanltctlt glrdasgvtf twtpssgksa vggpperdlc
181 gcysvssvlp gcaepwnhkg tftctaaype sktpltatls ksgntfrpev hllpppseel
241 alnelvtltc largfspkdv lvrwlqgsqe lprekyltwa srqepsqgtt tfavtsilrv
301 aedwkkgt fscmvgheal plaftqktid rlagkpthvn vsvmaevdg tcy

```

GenBank 1F6A_B

Homo sapiens **IgE** Fc (amino acids 6-222)

212 aa

```

1 adpcdsnprg vsaylsrpsp fdllfirspt itclvvdlap skgtvnltws rasgkpvnhs
61 trkeekqrng tltvtstlpv gtrdwieget yqcrvthphl pralmrsttk tsgpraapev
121 yafatpewpg srdkrtlacl ignfmpedis vqwlhnevql pdarhsttqp rktkgsqffv
181 fsrlevtrae weqkdeficr avheaaspsq tvqravsvnp gk

```

GenBank P01861

Homo sapiens **IgG4** Fc (amino acids 100-327)

228 aa

```

1 astkgpsvfp lapcsrste staaalgclvk dyfpepvtvs wnsгалtsgv htfpavllqss
61 glyslssvvt vpssslgtkt ytcnvdhkps ntkvdkrves kygppcpscp afeilggpsv
121 flfppkpkdt lmisrtpevt cvvvdvsqed pevqfnwyvd gvevhnaktk preeqfnsty
181 rvsvltvlh qdwlngkeyk ckvsnkglps siektiskak gqprepvyt lppsqeemtk
241 nqvsltclvk gfypsdiave wesngqpenn ykttppvlds dgsfflyslr tvdksrwqeg
301 nvfscsvmhe alnhhytqks lsllslgk

```

FIG. 6

Table 1. Conserved Regions based on the conserved CD4 epitopes

No.	Residues*	Length	Sequence	Genotype Conservancy	# of included Epitopes
CD4-R1	1251-1265	15	VLVLNPSVAATLGFG	HCV1a, 1b, 2a, 2b, 3, 4, 5, 6, 7	2
CD4-R2	1295-1309	15	TYGKFLADGGCSGGA	HCV1a, 1b, 3, 4, 5, 6, 7	2
CD4-R3	1387-1401	15	GGRHLIFCHSKKKCD	HCV1a, 1b, 2a, 2b, 3, 4, 5, 6, 7	4
CD4-R4	1415-1425	11	VAYYRGLDVSV	HCV1a, 1b, 2b, 3, 4, 7	4
CD4-R5	1436-1453	18	ATDALMTGFTGDFDSV ID	HCV1a, 1b, 3, 4, 7	2
CD4-R6	1563-1577	15	TGLTHIDAHFLSQTk	HCV1a, 1b, 2a, 2b, 3, 7	1
CD4-R7	1773-1785	13	QYLAGLSTLPGNP	HCV1a, 1b, 2a, 2b, 3, 4, 5, 6, 7	4
CD4-R8	1881-1888	8	NLLPAILS	HCV1a, 1b, 2b, 3, 4, 7	1
CD4-R9	1904-1930	27	RHVGPGEgAVQWMN RLIAFASRGNHVS	HCV1a, 1b, 3, 4	3
CD4-R10	2201-2215	15	SSASQLSAPSLKATC	HCV1a, 1b, 2b, 3, 4, 5, 6	1
CD4-R11	2788-2792	5	SNVSV	HCV1a, 1b, 2a, 2b, 3, 4, 5, 6, 7	1

* Numbers are based on HCV1a genotype sequence. R = region

FIG. 7

Table 2. Number of located HCV CD8 T cell epitopes and anchor positions for common each HLA-I Alleles in USA

MHC-I Allele	Total Epitopes (#)	Located Epitopes (#)	Allele-specific Anchor Positions			
			2	9	Others	Others
A*02:01	48	29	M#, L, Q, V, I	V, L, I, A, M	F (1, 3, 7)	
A*24:02	33	20	Y, W, F	F, I, W, L, M	F, W (7)	
A*03:01	10	6	M, L, I, V, T, S, Q, A	K, Y, R	F & Y (3), K & R (1)	
A*01:01	4	3	T, S, A, V, M, I, L	Y, F	D (3)	
B*35:01	1	1	P, G, A	Y, M, F, H	M (1), A (8), W (1), F (1), Y (1), P (8)	
			5	9	Others	Others
B*08:01	2	1	R, K, H, F	L, M, I, F, V, A, W	K (3), R (3), L (2), F (6), M (1, 2, 3), P (2), S (8)	
			1	2	9	Others
B*40:02	2	2	Y, K, R, A, H, W, G, F, Q, L, S, C, I, T, M, V	E, D	I, L, A, V, F, M, T, W, S, C	F (3), P (8), A (8)
C*03:03	2	2	NA##	NA	NA	NA
A*33:03	1	0	-	-	-	-
A*02:06	1	0	-	-	-	-
A*26:01	1	0	-	-	-	-
A*31:01	1	0	-	-	-	-
Total	106	64				

Bold Anchor positions describe the optimal amino acid for that location. ## Not Available

FIG. 8

Table 3. Conserved Regions based on the conserved CD8 Epitopes

No.	Residues*	Length	Sequence	Conserved HCV1a, 1b, & 3	Conserved 9** Genotypes	# of epitopes
CD8-R1	1292-1300	9	TYSTYGKFL	Yes	Yes	2
CD8-R2	1391-1399	9	LIFCHSKKK	Yes	Yes	2
CD8-R3	1436-1451	16	ATDALMTGFTGDFDSV	Yes	No	2
CD8-R4	1666-1675	10	VLAALAAAYCL	Yes	No	1
CD8-R5	1851-1859	9	ILAGYGAGV	Yes	No	1
CD8-R6	1373-1380	8	IPFYGKAI	Yes	No	1
CD8-R7	1596-1604	9	RAQA PPPSW	Yes	No	1
CD8-R8	1910-1945	36	EGAVQWMNRLIAFASRGN HVSPTHYVPESDAAARVT	Yes	No	3
CD8-R9	2290-2298	9	RPDYNPPLL	Yes	No	1
CD8-R10	2557-2565	9	TIMAKNEVF	Yes	Yes	1

* Numbers are based on HCV1a genotype sequence.

** Nine genotypes include HCV1a, 1b, 2a, 2b, 3, 4, 5, 6, and 7

FIG. 9A. CD4 and CD8 epitopes for Core, P7, and NS2 regions

Name	Type of epitope	Start*	End*
Core-1	CD4	1	20
Core-2	CD4	11	30
Core-3	CD4	21	40
Core-4	CD4	39	63
Core-5	CD4	47	70
Core-6	CD4	61	80
Core-7	CD4	71	90
Core-8	CD4	81	100
Core-9	CD4	91	110
Core-10	CD4	101	115
Core-11	CD4	111	130
Core-12	CD4	125	139
Core-13	CD4	131	150
Core-14	CD4	151	170
Core-15	CD4	161	180
Core-16	CD8	35	44
Core-17	CD8	43	51
Core-18	CD8	51	59
Core-19	CD8	129	137
Core-20	CD8	131	140
Core-21	CD8	150	158
Core-22	CD8	154	162
Core-23	CD8	168	176
Core-24	CD8	177	187
Core-25	CD8	178	187
P7-1	CD8	803	811
NS2-1	CD4	955	974
NS2-2	CD4	975	994
NS2-3	CD4	985	1,004
NS2-4	CD4	1,015	1,034
NS2-5	CD4	1,035	1,054
NS2-6	CD8	924	933
NS2-7	CD8	961	970
NS2-8	CD8	989	997

* Start and End numbers are based on sequence designated "Consensus" in Fig. 12A-12L.

FIG. 9B. CD4 and CD8 epitopes that are conserved among genotypes 1a, 1b, 2a, 2b, and 3

Name	Type of epitope	Start*	End*
NS3-1	CD4	1,265	1,279
NS3-2	CD4	1,309	1,323
NS3-3	CD4	1,401	1,415
NS3-4	CD4	1,402	1,412
NS3-5	CD4	1,429	1,439
NS3-6	CD4	1,450	1,464
NS3-7	CD4	1,453	1,467
NS3-8	CD4	1,577	1,591
NS3-9	CD8	1,306	1,314
NS3-10	CD8	1,387	1,394
NS3-11	CD8	1,405	1,413
NS3-12	CD8	1,450	1,458
NS3-13	CD8	1,457	1,465
NS3-14	CD8	1,610	1,618
NS4a-1	CD8	1,683	1,692
NS4b-1	CD4	1,790	1,801
NS4b-2	CD4	1,792	1,802
NS4b-3	CD4	1,898	1,905
NS4b-4	CD4	1,921	1,935
NS4b-5	CD4	1,922	1,941
NS4b-6	CD4	1,928	1,947
NS4b-7	CD8	1,868	1,876
NS4b-8	CD8	1,927	1,942
NS4b-9	CD8	1,932	1,940
NS4b-10	CD8	1,948	1,962
NS5a-1	CD4	2,218	2,232
NS5a-2	CD8	2,309	2,317
NS5b-1	CD4	2,847	2,851
NS5b-2	CD8	2,602	2,610

* Start and End numbers are based on sequence designated "Consensus" in Fig. 12A-12L.

FIG. 10A

Name	Sequence*	Start**	End**	Contained Epitopes
TP29	AIPLEVIKGGRLIFCHSKKKCDELAAKL	1,393	1,421	NS3-3, NS3-4, NS3-11
TP50	LGALTGTYYVYNHLTPLRDWAHNGLRDLA VAVEPVVFSQMETKLITWGADT	955	1,004	NS2-1, NS2-2, NS2-3, NS2-7, NS2-8
TP52	AIPLEVIKGGRLIFCHSKKKCDELAAKLV ALGINAVAYYRGLDVSVIPTSG	1,393	1,444	NS3-3, NS3-4, NS3-5, NS3-11
TP70	KGGRHLIFCHSKKKCDELAAKLVALGINA VAYYRGLDVSVIPTSGDVVVVATDALMTG FTGDFDSVIDCN	1,400	1,469	NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-11, NS3-12, NS3-13
TP100	VALSTTGEIPFYGKAIPLEVIKGGRLIFCHS KKKCDELAAKLVALGINAVAYYRGLDVS VIPTSGDVVVVATDALMTGFTGDFDSVIDC NTCVTQTVDF	1,379	1,478	NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-10, NS3-11, NS3-12, NS3-13
TP171	MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVG GVYLLPRRGPRLGVRATRKTSESRQPRGRRQPI PKARRPEGRTWAQPGYPWPLYGNEGCGWAG WLLSPRGSRPSWGPTDPRRRSRNLGKVIDTLT CGFADLMGYIPLVGAPLGGAARALAHGVRVLED GVNYATGNLPG	1	171	Core-1, Core-2, Core-3, Core-4, Core-5, Core-6, Core-7, Core-8, Core-9, Core-10, Core-11, Core-12, Core-13, Core-14, Core-16, Core-17, Core-18, Core-19, Core-20, Core-21, Core-22
TP228	LHAPTGSgKSTKVPAAAYAAQGYKVLVLNP SVAATLGFGAYMSKAHGIDPNIRTGVRTIT TGSPITYSTYGKFLADGGCSGGAYDIIICDE CHSTDATSILGIGTVLDQAETAGARLVVLA TATPPGSVTVPHPNIEEVALSTTGEIPFYGK AIPLEVIKGGRLIFCHSKKKCDELAAKLV ALGINAVAYYRGLDVSVIPTSGDVVVVAT DALMTGFTGDFDSVIDCN	1,242	1,469	NS3-1, NS3-2, NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-9, NS3-10, NS3-11, NS3-12, NS3-13
TP553	QASLLKVPYFVRVQGLLRICALARKMAGG HYVQMAIIKLGAALTGTYYVYNALTPLRDWA HNGLRDLAVAVEPVVFSQMETKLITWGAD TAACGDIINGLPVSARRGREILLGPADGMV SKGWRLAPITAYAQQTRGLLGCIITSLTG RDKNQVEGEVQIVSTAAQTFLATCINGVC WTVYHGAGTRTIA SPKGPVIQMYTNVDQD LVGWPA PQGARSLTPCTCGSSDLVLRH ADVIPVRRRGDSRGSLLSPRPISYLKGSAGG PLLCPAGHAVGIFRAAVCTRGVAKAVDFIP VENLETTMRSPVFTDNSSPPAVPQSFQVAH LHAPTGSgKSTKVPAAAYAAQGYKVLVLNP SVAATLGFGAYMSKAHGIDPNIRTGVRTIT TGSPITYSTYGKFLADGGCSGGAYDIIICDE CHSTDATSILGIGTVLDQAETAGARLVVLA TATPPGSVTVPHPNIEEVALSTTGEIPFYGK	917	1,469	NS2-1, NS2-2, NS2-3, NS2-4, NS2-5, NS2-6, NS2-7, NS2-8, NS3-1, NS3-2, NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-9, NS3-10, NS3-11, NS3-12, NS3-13

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FIG. 10B

	AIPLEVIKGGRLIFCHSKKKCDELAACKLV ALGINAVAYYRGLDVSVIPTSGDVVVVAT DALMTGFTGDFDSVIDCN			
TP778	LHAPTGS GKSTKVPAA YAAQGYKVLVLNP SVAATLGFGAYMSKAHGIDPNIRTGVRTIT TGSPITYSTY GKFLADGGCSGGAYDIIICDE CHSTDATSILGIGTVLDQAETAGARLVVLA TATPPGSVTVPHPNIEEVALSTTGEIPFYGK AIPLEVIKGGRLIFCHSKKKCDELAACKLV ALGINAVAYYRGLDVSVIPTSGDVVVVAT DALMTGFTGDFDSVIDCNTCVTQTVDFSL DPTFTIETTTLPQDAVSRTQRRGRTGRGKP GIYRFVAPGERPSGMFDSSVLCECYDAGCA WYELTPAETTVRLRAYMNTPLPVCQDHL EFWEGVFTGLTHIDAHFLSQTQSGENLPY LVAYQATVCARAQAPPSWDQMWKCLIR LKPTLHGPTPLLYRLGAVQNEVTLTHPITK YIMTCMSADLEVVTSTWVLVGGVLAALA AYCLSTGCVVIVGRIVLSGKPAIIPDREVL REFDEMEEC SQHLPYIEQGMMLAEQFKQK ALGLLQTASRQAEVIAPAVQTNWQKLEAF WAKHMWNFISGIQYLAGLSTLPGNPAIASL MAFTA AVTSPLTTSQTLLFNILGGWVAAQ LAAPGAATAFVGAGLAGAAIGSVGLGKVL VDILAGYGAGVAGALVAFKIMSGEVPSTE DLVNLLPAILSPGALVVGVVCAAILRRHVG PGEGAVQWMNRLIAFASRGNHVSPTHYVP ESDAAARVTAILSSLTVTQLLRRLHQWISS ECTTPCSGSWLRDIWDWICEVLSDFKTWL KAKLMPQLPG	1,242	2,022	NS3-1, NS3-2, NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-8, NS3-9, NS3-10, NS3-11, NS3-12, NS3-13, NS3-14, NS4a-1, NS4b-1, NS4b-2, NS4b-3, NS4b-4, NS4b-5, NS4b-6, NS4b-7, NS4b-8, NS4b-9, NS4b-10

FIG. 10C

TP1985	APITAYAQQTRGLLGCIITSLTGRDKNQVE GEVQIVSTAAQTFLATCINGVCWTVYHGA GTRTIASPKGPVIQMYTNVDQDLVGWPAP QGARS LTPCTCGSSDLYLVTRHADVIPVRR RGDSRGSLLSPRPISYLKGSAGGPLLCPAG HAVGIFRAAVCTRGVAKAVDFIPVENLETT MRSPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATL GFGAYMSKAHGIDPNIRTGVRTITTGSPITY STYGKFLADGGCSGGAYDIIICDECHSTDA TSILGIGTVLDQAETAGARLVVLATATPPG SVTVPHPNIEEVALSTTGEIPFYGKAIPLEVI KGGRHLIFCHSKKKCDELA AKLVALGINA VAYYRGLDVSVIPTSGDVVVVATDALMTG FTGDFDSVIDCNTCVTQTVD FSLDPTFTIET TTL PQDAVSRTQRRGRTGRGKPGIYRFVAP GERPSGMFDSSVLCECYDAGCAWYELTPA ETTVRLRAYMNTPLPVCQDHLEFWEGVF TGLTHIDAHFLSQTKQSGENLPYLVAYQAT VCARAQAPPPSWDQMWKCLIRL KPTLHGP TPLLYRLGAVQNEVT LTHPITKYIMTCMSA DLEVVTSTWVLVGGVLAALAAAYCLSTGC VVIVGRIVLSGKPAIIPDREVL YREFDEMEE CSQHLPYIEQGMMLAEQFKQKALG LLQTA SRQAEVIAPAVQTNWQKLEAFWAKHMWN FISGIQYLAGLSTLPGNPAIASLMAFTAAVT SPLTTSQTLLFNILGGWVAAQLAAPGAATA FVGAGLAGAAIGSVGLGKVLVDILAGYGA GVAGALVAFKIMSGEVPSTEDLVNLLPAIL SPGALVVG VVCAAILRRHVGPGE GAVQW MNRLIAFASRGNHVSPTHYVPESDAAARV TAILSSLTVTQLLRRLHQWISSECTTPCSGS WLRDIWDWICEVLSDFKTWLKAKLMPQLP GIPFVSCQRGYRGVWRGDGIMHTRCHCGA EITGHVKNGTMRIVGPRTCRNMWSGTFPIN AYTTGPCTPLPAPNYTFALWRVSAEEYVEI RQVGDFHYVTGMTTDNLKCPCQVPSPEFF TELDGVR LHRFAPPCKPLLREEVSFRVGLH EYPVGSQLPCEPEPDVAVLTSM L TDPSHIT AEAAGRRLARGSPPSVASSASQLSAPSLK ATCTANHDSPDAELIEANLLWRQEMGGNI TRVESENKVVILDSFDPLVAEEDEREISVPA EILRKSRRFAPALPIWARPDYNPPLLETWK KPDYEPPVVHGCPLPPPQSPVP PPRKKRT VVLTESTVSTALAE L ATKSFGSSSTSGITGD NTTTSSEPA PS GCPPDSDAESYSSMPPLEGE	1041	3073	NS3-1, NS3-2, NS3-3, NS3-4, NS3-5, NS3-6, NS3-7, NS3-8, NS3-9, NS3-10, NS3-11, NS3-12, NS3-13, NS3-14, NS4a-1, NS4b-1, NS4b-2, NS4b-3, NS4b-4, NS4b-5, NS4b-6, NS4b-7, NS4b-8, NS4b-9, NS4b-10, NS5a-1, NS5a-2, NS5b-1, NS5b-2
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FIG. 10D

PGDPDLSDGSWSTVSSEADTEDVVCCSMS YSWTGALVTPCAAEEQKL PINALSNSLLRH HNLVYSTTSRSACQRQKKVTFDRLQVLDS HYQDVLKEVKAAASKVKANLLSVEEACSL TPPHSAKSKFGYGAKDVRCHARKAVNHIN SVWKDLEDSTPIDTTIMAKNEVFCVQPE KGGRKPARLIVFIDLGV RVCEKMALYDVV SKLPLAVMGSSYGQYSPGQ RVEFLVQAW KSKKTPMGFSYDTRCFDSTV TESDIRTEEI YQCCDLDPQARVAIKSLTERLYVGGPLTNS RGENCGYRRCRASGVLT TSCGNTLTCTYIK ARAACRAAGLQDCTMLVCGNNLVVICESA GVQEDAASLRAFTEAMTRYSA PPGDPPQP EYDLELITSCSSNVSV AHDGAGKRVYYLTR DPTTPLARAAWETARHTPVNSWLGNIIMF APTLWARMILMTHFFSVLIARDQLEQALD CEIYGACYSIEPLDLPPIIQLHGLSAFSLHS YSPGEINRVAACLRKLGVPPLRAWRHRAR SVRARLLSRGGRAAICGKYLFNWAVRTKL KLTPIAAAGQLDL SGWFTAGYSGGDIYHS VSHARPRWFWFCLLLLAAGVGIYLLPNR			
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* TP sequences are based on HCV1a consensus sequence and gaps were removed

** Start and End numbers are based on sequence designated "Consensus" in Fig. 16A-16L.

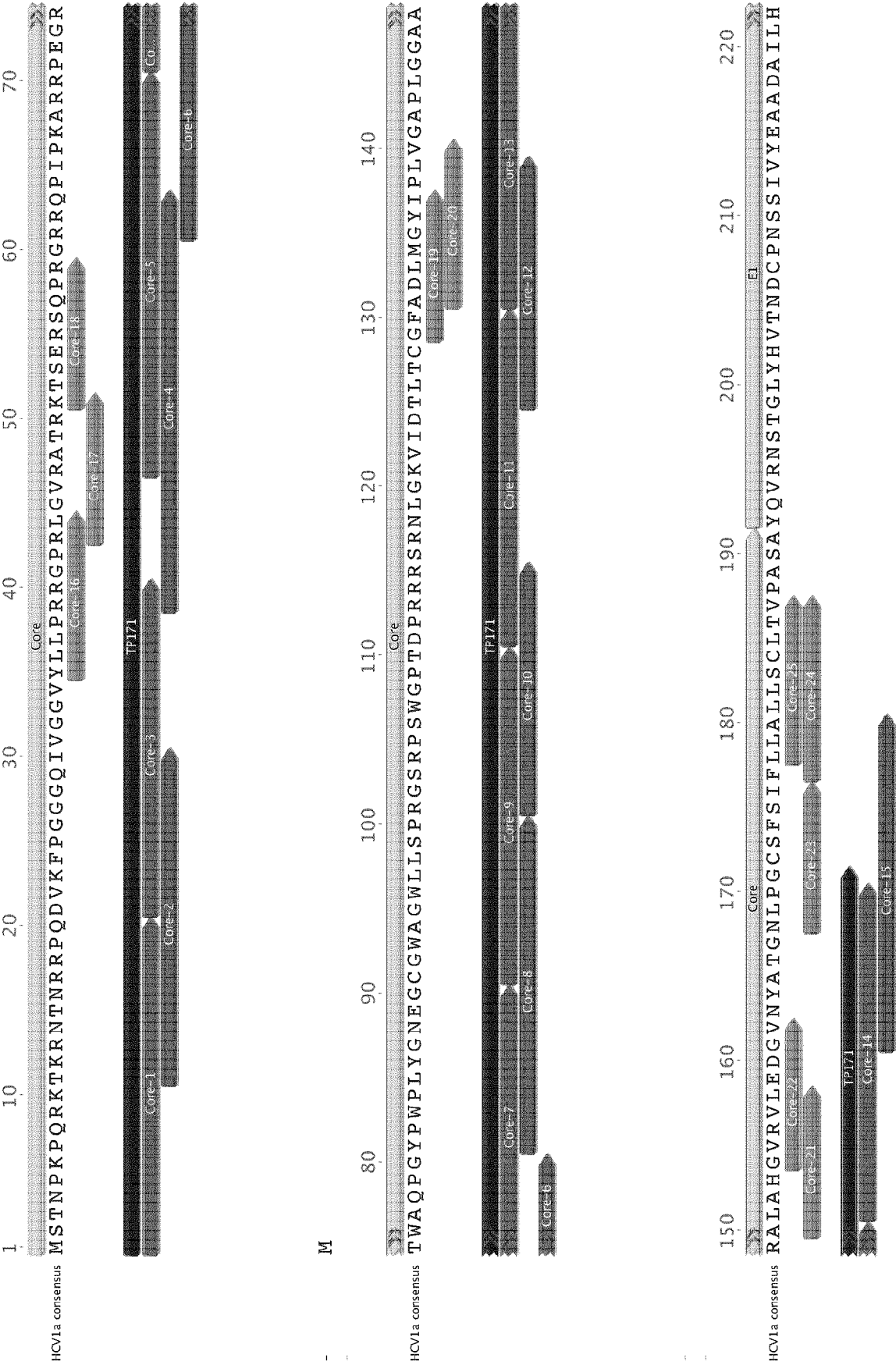


FIG. 11A

HCv1a consensus
TPGCVPCVR-EGNASRCWVAVTPTVATRDGKLPQTQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSP
230 240 250 260 270 280 290

HCv1a consensus
RRHWTQDCNC SIYPGHI TGHRMAWDMMNWSPTTALVVAQLLRIPQAILDMIAGAHWGLAGIAYFSMVGNWA
300 310 320 330 340 350 360 370

HCv1a consensus
KVLVLLLFAGVDAETHVTGGSAARTTSGLASLFTPGAKQNIQLINTNGSWHINRTALNCNDSLNTGWLAGLFY
380 390 400 410 420 430 440

FIG. 11B

HCv1a consensus
YHKFNSSGCCPERLASCRPLTDFDQGWGPISYANG-SGP-DQRPYCWHPKPCGIVPAKSVCGPVCFTP--SP
450 460 470 480 490 500 510

HCv1a consensus
VVVGTTDRSGAPTYNWGENDTDVFLNNTTRPPPLGNWFGCTWMNST-GFTKVCGAPPCVI-GGVGN-----NTLH
520 530 540 550 560 570 580 590

HCv1a consensus
CPTDCFRKHPAATYSRCGSGPWITPRCLVDYPYRLWHYPCTINITYTIFKVRMYVGGVEHRLAACNWTGERCDL
600 610 620 630 640 650 660

FIG. 11C

HCv1a consensus
EDDRSELSPILLSTTQWQVLPCTTLPALSTGLIHLHQNIVDVQYLYGVGSSIASWAIKWEYVLLFLLAD

HCv1a consensus
ARVCCLWMMLLISQAEAALENLVVLNAAAGTHGLVSFLVFFCFAWYLK--GRWVPGAAAYALYGMWPLLLLL

HCv1a consensus
LALPQRAYALDTEVAASCGGVVLVGLMALTLSPYYKRYISWCLWWLQYFLTRVEAQLHVWVPLNVRGGRDAVI

FIG. 11D

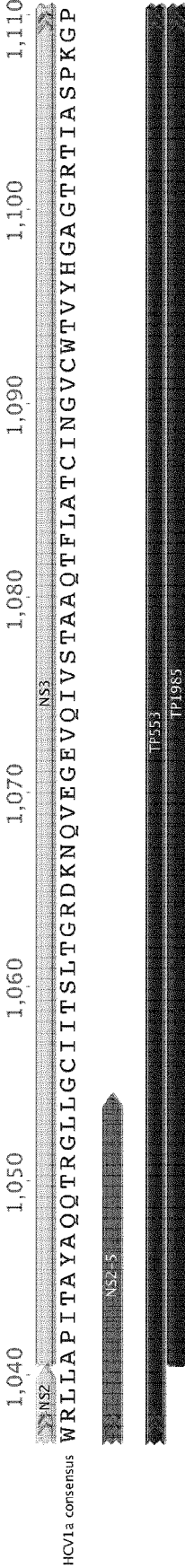
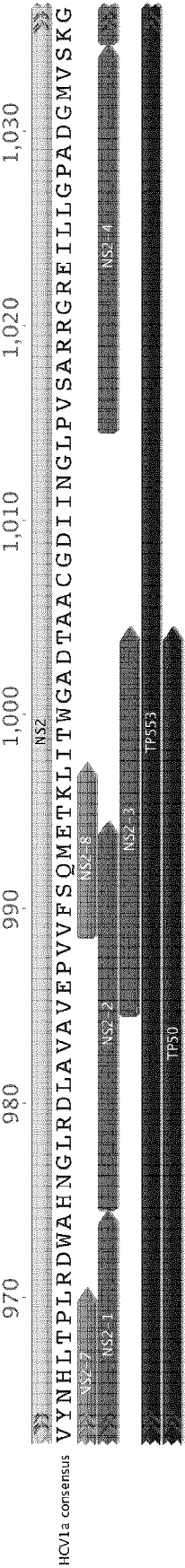
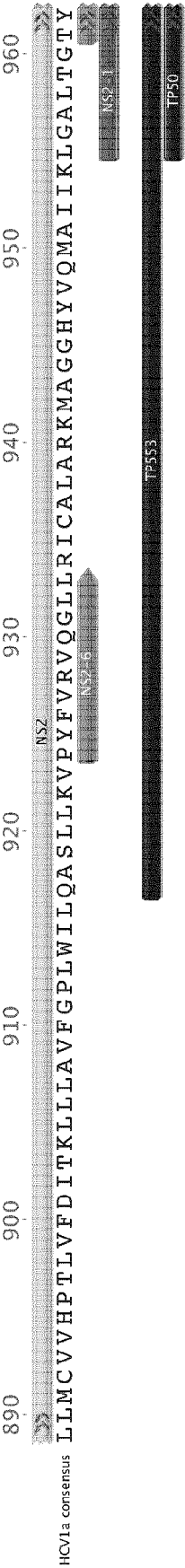


FIG. 11E

1,120 1,130 1,140 1,150 1,160 1,170 1,180
HC/1a consensus
VIQMYTNVDQDLVGWPA PQGARS LTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISY LKGS SGGPLL

TP553
TP1985
A

1,190 1,200 1,210 1,220 1,230 1,240 1,250
HC/1a consensus
CPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMRSPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAY

TP553
TP1985
TP228
TP778

1,260 1,270 1,280 1,290 1,300 1,310 1,320 1,330
HC/1a consensus
AAQGYKVLVLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGA YDIICDEC

TP553
TP1985
TP228
TP778

NS3-2

NS3-1

FIG. 11F

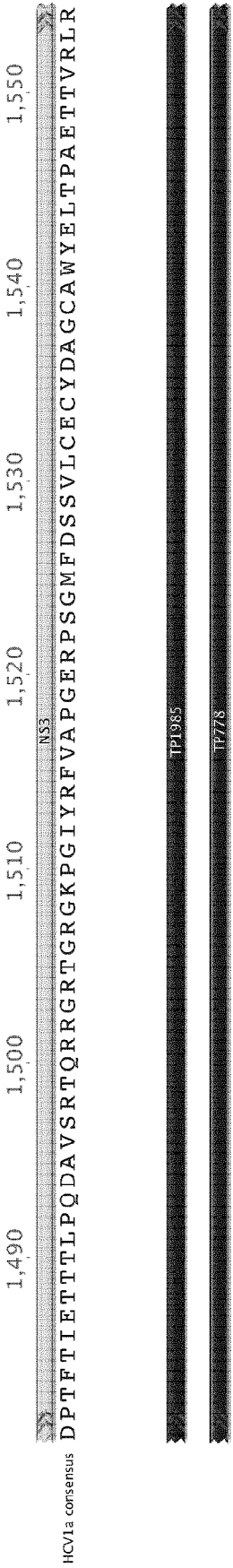
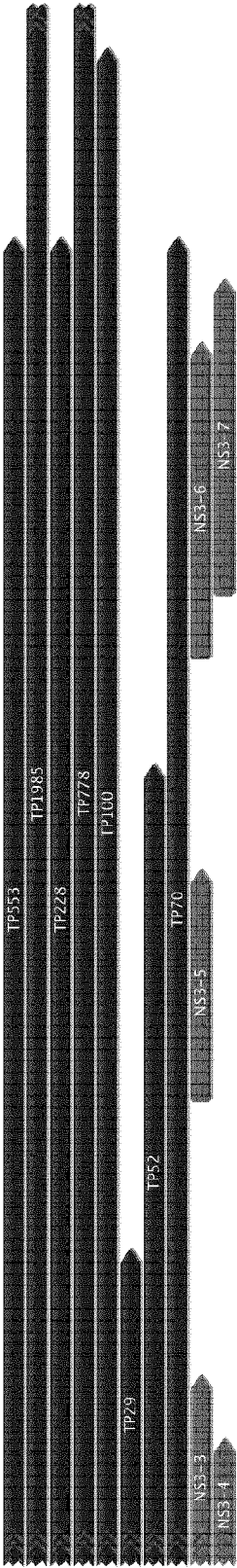
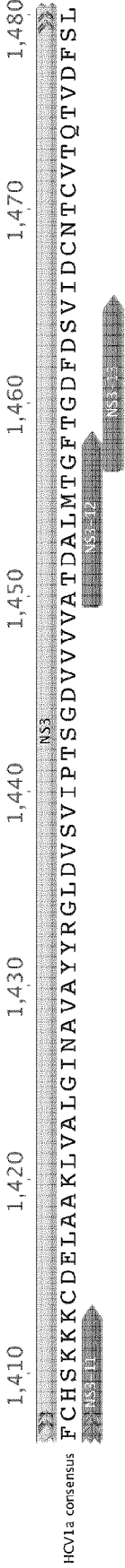
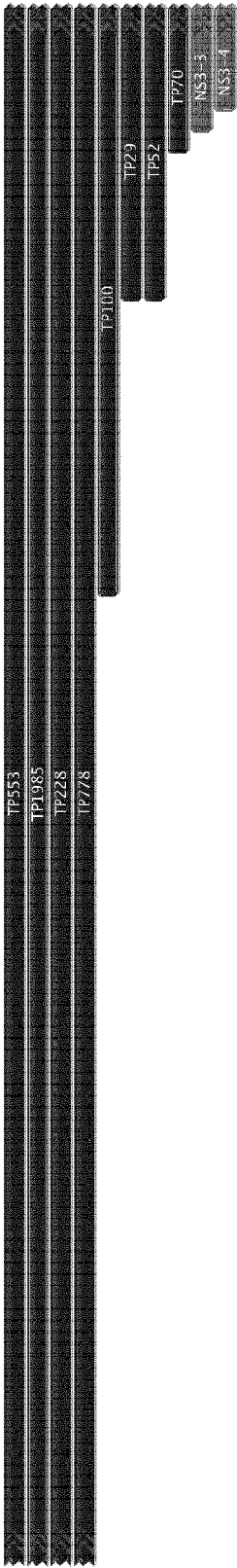
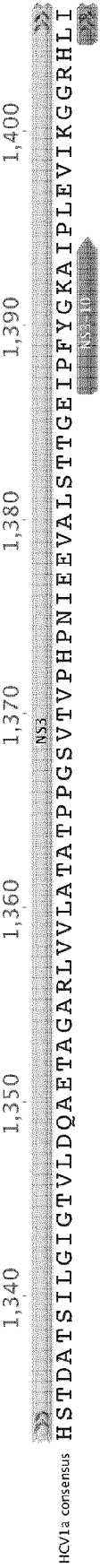


FIG. 11G

1,560 1,570 1,580 1,590 1,600 1,610 1,620
HCV1a consensus
AYMNTPGLPVCQDHLFEFWEGVFTGLTHIDAHFLSQTKQSGENLPYLVA YQATVCARAQAAPPSPWDQMWKCLIRL

TP1985
TP778

NS3-8

1,630 1,640 1,650 1,660 1,670 1,680 1,690 1,700
HCV1a consensus
KPTLHGPTPLL YRLGAVQNEVTLTHPITKYIMTCMSADLEVVT--STWVLVGGVLAALAA YCLSTGCVVI VGR

TP1985
TP778

1,710 1,720 1,730 1,740 1,750 1,760 1,770
HCV1a consensus
IVLSGKPAIIPDREVLVREFDEMEEC SQHLPYIEQGMMLAEQFKQKALGLLQTA SRQAEVIAPAVQTNWQKLEA

TP1985
TP778

FIG. 11H

1,780 1,790 1,800 1,810 1,820 1,830 1,840 1,850
HCV1a consensus
FWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAFTAAVTSPLTTSQTLLFNILGGWVAAQLAAPGAATAFVGAG

NS4b
TP1985
TP778

NS4b-1
NS4b-2

1,860 1,870 1,880 1,890 1,900 1,910 1,920
HCV1a consensus
LAGAAIGSVGLGKVLVDILAGYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVCAAILRRHVHG

NS4b
NS4b-7

TP1985
TP778

NS4b-3
NS...

1,930 1,940 1,950 1,960 1,970 1,980 1,990
HCV1a consensus
PGEGAVQWMNRLIAFASRGNHVSPTHYVPESDAAARVTAIILSSLTVTQLLRRLHQWISSECTTPCSCSWLRDIW

NS4b
NS4b-8
NS4b-9
NS4b-10
NS5a

TP1985
TP778

NS4b-4
NS4b-5
NS4b-6

FIG. 11I

HCV1a consensus
2,000 2,010 2,020 2,030 2,040 2,050 2,060 2,070
NS5a
DWICEVLSDFKTLKAKLMPQLPGIPFVSCQRGYRGVWRGDGIMHTRCHCGAEITGHVKNGTMRIVGPRTCRNM

TP1985
TP278

HCV1a consensus
2,080 2,090 2,100 2,110 2,120 2,130 2,140
NS5a
WSTFPINAYTTGPGCTPLPAPNYTFALWRVSAEEYVEIRQVGDFHYVTGMTTDNLKPCQVPSPEFFTELDGVR

TP1985

HCV1a consensus
2,150 2,160 2,170 2,180 2,190 2,200 2,210 2,220
NS5a
LHRFAPPCKPLLREEVSFRVGLHEYPVGSQLPCEPEPDVAVLTSMLTDP SHITAEAAARRRLARGSPPSVASSSA

TP1985

N

FIG. 11J

2,230 2,240 2,250 2,260 2,270 2,280 2,290
HCV1a consensus NS5a
SQLSAPSLKATCTANHDSFDAELIEANLLWRQEMGGNITRVESENKVVILDSFDPLVAE-EDEREISVPAEILR

TP1985

NS5a-1

2,300 2,310 2,320 2,330 2,340 2,350 2,360
HCV1a consensus NS5a
KSR-RFAPALPIWARPDYNPPILLETWKKKPDYEPVVHGCPLPPPPQSPVPVPPRKK-RTVVLTSTVSTALAE

NS5a-2

TP1985

2,370 2,380 2,390 2,400 2,410 2,420 2,430 2,440
HCV1a consensus NS5a
TKSFGSSSTSGI-----TGDNTTTSSEPAPS-GCPPDSDAESYSSMPPLEGEGPGDPPDLSD-----

TP1985

FIG. 11K

2,450 2,460 2,470 2,480 2,490 2,500 2,510
HCV1a consensus NS5a
-----GSWSTVSSEADTEDVCCSMSYSWTGALVTPCAAEEQKLPINALSNSLLRHHNLVYSTTSRSACQRQKK

TP1985

2,520 2,530 2,540 2,550 2,560 2,570 2,580 2,590
HCV1a consensus NS5b
VTFDRLOVLD SHYQDVLKEVKAAASKVKANLLSVEEACSLTPPHSAKSKFGYGA KDVRCHARKAVNHINSVWKD

TP1985

2,600 2,610 2,620 2,630 2,640 2,650 2,660
HCV1a consensus NS5b
LLED SVTPIDTTIMAKNEVFCVQPEKGGRRKPARLIVFPDL-GVRVCEKMALYDVVSKLPLAVMGSSYGFQYSPG

TP1985

FIG. 11L

HCV1a consensus
2,670 2,680 2,690 2,700 2,710 2,720 2,730
QRVEFLVQAWKSKKTPMG--FSYDTRCFDSTVT-ESDIRTEEAIIYQCCDLDPQARVAIKSLTERLYVGGPLTNS

NS5b
TP1985

HCV1a consensus
2,740 2,750 2,760 2,770 2,780 2,790 2,800 2,810
RGENCGYRRCRASGVLTTSCGNTLTCTCYIKARAAACRAAGLQDCTMLVCGDDL VVICESAGVQEDAAASLRAFTEAM

NS5b
TP1985 GNN

HCV1a consensus
2,820 2,830 2,840 2,850 2,860 2,870 2,880
TR-----YSAPPGDPP-----QPEYDLELITSCSSNVSAHDGAGKRVYLLTRDPTTPLARAAWETARHTP---

NS5b
TP1985

NS5b-1

FIG. 11M

HCV1a consensus
2,890 2,900 2,910 2,920 2,930 2,940 2,950 2,960
VNSWLGNIIMFAPT LWARMILMTHFFSVLIARDQLEQALDCEIYGACYSIEPLDLPPIIQRLHGLSAFSLHSYS

NS5b
TP1985

2,970 2,980 2,990 3,000 3,010 3,020 3,030
PGEINRVAACLRLKLGVPPLRAWRRHARSVRARLLSRGGRAAICGKYLFNWAVRTKLLTPIAAAGQLDLSGWFT

NS5b
TP1985

3,040 3,050 3,060 3,070 3,074
AGYSGGDIYHSVSHARPRWFCLLLAAGVGIYLLPNRX

NS5b
TP1985

FIG. 11N

	1	10	20	30	40	50	60	70	80
Consensus	MSTNPKPQKTKRNTNRRPQDVKFFPGCGQIVGGVYLLPRRCPRLGVRAATKTSERSQPRRRQP IPKARRSEGRSWAQP GYPWPLY								
	Core								
1. HCV1a consensus	MSTNPKPQKTKRNTNRRPQDVKFFPGCGQIVGGVYLLPRRCPRLGVRAATKTSERSQPRRRQP IPKARRSEGRSWAQP GYPWPLY								
2. HCV1b consensus	MSTNPKPQKTKRNTNRRPQDVKFFPGCGQIVGGVYLLPRRCPRLGVRAATKTSERSQPRRRQP IPKARRSEGRSWAQP GYPWPLY								
3. HCV2a Consensus	MSTNPKPQKTKRNTNRRPQDVKFFPGCGQIVGGVYLLPRRCPRLGVRAATKTSERSQPRRRQP IPKARRSEGRSWAQP GYPWPLY								
4. HCV2b Consensus	MSTNPKPQKTKRNTNRRPQDVKFFPGCGQIVGGVYLLPRRCPRLGVRAATKTSERSQPRRRQP IPKARRSEGRSWAQP GYPWPLY								
5. HCV 3 Consensus	MSTNPKPQKTKRNTNRRPQDVKFFPGCGQIVGGVYLLPRRCPRLGVRAATKTSERSQPRRRQP IPKARRSEGRSWAQP GYPWPLY								
6. HCV 4 Consensus	MSTNPKPQKTKRNTNRRPQDVKFFPGCGQIVGGVYLLPRRCPRLGVRAATKTSERSQPRRRQP IPKARRSEGRSWAQP GYPWPLY								
7. HCV5 consensus	MSTNPKPQKTKRNTNRRPQDVKFFPGCGQIVGGVYLLPRRCPRLGVRAATKTSERSQPRRRQP IPKARRSEGRSWAQP GYPWPLY								
8. HCV6 consensus	MSTNPKPQKTKRNTNRRPQDVKFFPGCGQIVGGVYLLPRRCPRLGVRAATKTSERSQPRRRQP IPKARRSEGRSWAQP GYPWPLY								
9. HCV7: ABN05226	MSTNPKPQKTKRNTNRRPQDVKFFPGCGQIVGGVYLLPRRCPRLGVRAATKTSERSQPRRRQP IPKARRSEGRSWAQP GYPWPLY								
14. AV1a-129	MSTNPKPQKTKRNTNRRPQDVKFFPGCGQIVGGVYLLPRRCPRLGVRAATKTSERSQPRRRQP IPKARRSEGRSWAQP GYPWPLY								
15. AV3a-177	MSTNPKPQKTKRNTNRRPQDVKFFPGCGQIVGGVYLLPRRCPRLGVRAATKTSERSQPRRRQP IPKARRSEGRSWAQP GYPWPLY								
	90	100	110	120	130	140	150	160	170
Consensus	GNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLGKV IDTLTCGFADLMGY IPLVCGAPLGGVARALAHGVRVLEDGINYATGNLPCC								
	Core								
1. HCV1a consensus	GNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLGKV IDTLTCGFADLMGY IPLVCGAPLGGVARALAHGVRVLEDGINYATGNLPCC								
2. HCV1b consensus	GNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLGKV IDTLTCGFADLMGY IPLVCGAPLGGVARALAHGVRVLEDGINYATGNLPCC								
3. HCV2a Consensus	GNEGLWAGWLLSPRGRSPSWGPTDPRRRSRNLGKV IDTLTCGFADLMGY IPVVGAPLGGVARALAHGVRVLEDGINYATGNLPCC								
4. HCV2b Consensus	GNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLGKV IDTLTCGFADLMGY IPVVGAPLGGVARALAHGVRVLEDGINYATGNLPCC								
5. HCV 3 Consensus	GNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLGKV IDTLTCGFADLMGY IPLVCGAPLGGVARALAHGVRVLEDGINYATGNLPCC								
6. HCV 4 Consensus	GNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLGKV IDTLTCGFADLMGY IPLVCGAPLGGVARALAHGVRVLEDGINYATGNLPCC								
7. HCV5 consensus	ANEGLWAGWLLSPRGRSPSWGPTDPRRRSRNLGKV IDTLTCGFADLMGY IPLVGGPVGVARALAHGVRVLEDGINYATGNLPCC								
8. HCV6 consensus	GNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLGKV IDTLTCGFADLMGY IPVVGAPLGGVARALAHGVRVLEDGINYATGNLPCC								
9. HCV7: ABN05226	GNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLGKV IDTLTCGFADLMGY IPLVCGAPLGGVARALAHGVRVLEDGINYATGNLPCC								
14. AV1a-129	GNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLGKV IDTLTCGFADLMGY IPLVCGAPLGGVARALAHGVRVLEDGINYATGNLPCC								
15. AV3a-177	GNECGWAGWLLSPRGRSPSWGPTDPRRRSRNLGKV IDTLTCGFADLMGY IPLVCGAPLGGVARALAHGVRVLEDGINYATGNLPCC								
	180	190	200	210	220	230	240	250	
Consensus	SFSIFLLALLSCLTVPASAYEVRNKSGLYHVTNDCPNSS IVEEADDA ILHTPGCVPCVR-EGNTSRCWVXVPTTVA VRYXGAPTTS								
	Core								
1. HCV1a consensus	SFSIFLLALLSCLTVPASAYEVRNKSGLYHVTNDCPNSS IVEEADDA ILHTPGCVPCVR-EGNTSRCWVXVPTTVA VRYXGAPTTS								
2. HCV1b consensus	SFSIFLLALLSCLTVPASAYEVRNKSGLYHVTNDCPNSS IVEEADDA ILHTPGCVPCVR-EGNTSRCWVXVPTTVA VRYXGAPTTS								
3. HCV2a Consensus	SFSIFLLALLSCLTVPASAYEVRNKSGLYHVTNDCPNSS IVEEADDA ILHTPGCVPCVR-EGNTSRCWVXVPTTVA VRYXGAPTTS								
4. HCV2b Consensus	SFSIFLLALLSCLTVPASAYEVRNKSGLYHVTNDCPNSS IVEEADDA ILHTPGCVPCVR-EGNTSRCWVXVPTTVA VRYXGAPTTS								
5. HCV 3 Consensus	SFSIFLLALLSCLTVPASAYEVRNKSGLYHVTNDCPNSS IVEEADDA ILHTPGCVPCVR-EGNTSRCWVXVPTTVA VRYXGAPTTS								
6. HCV 4 Consensus	SFSIFLLALLSCLTVPASAYEVRNKSGLYHVTNDCPNSS IVEEADDA ILHTPGCVPCVR-EGNTSRCWVXVPTTVA VRYXGAPTTS								
7. HCV5 consensus	SFSIFXLLALLSCLTVPASAYEVRNKSGLYHVTNDCPNSS IVEEADDA ILHTPGCVPCVR-EGNTSRCWVXVPTTVA VRYXGAPTTS								
8. HCV6 consensus	SFSIFLLALLSCLTVPASAYEVRNKSGLYHVTNDCPNSS IVEEADDA ILHTPGCVPCVR-EGNTSRCWVXVPTTVA VRYXGAPTTS								
9. HCV7: ABN05226	SFSIFLLALLSCLTVPASAYEVRNKSGLYHVTNDCPNSS IVEEADDA ILHTPGCVPCVR-EGNTSRCWVXVPTTVA VRYXGAPTTS								
14. AV1a-129	SFSIFLLALLSCLTVPASAYEVRNKSGLYHVTNDCPNSS IVEEADDA ILHTPGCVPCVR-EGNTSRCWVXVPTTVA VRYXGAPTTS								
15. AV3a-177	SFSIFLLALLSCLTVPASAYEVRNKSGLYHVTNDCPNSS IVEEADDA ILHTPGCVPCVR-EGNTSRCWVXVPTTVA VRYXGAPTTS								

260	270	280	290	300	310	320	330	340
Consensus	LRRHVDLLVGAATLCSALYVVDLCGAVFLVGQXFTFSRRHWTVDQNCNCSYIPGCHITGHRMAWDMMNWSPPTXLVXAQLLRIPQX							
	E1							
1. HCV1a consensus	LRRHIDLLVGSATLCSALYVVDLCGSVFLVGQLFTFSRRHWTQDCNCSYIPGCHITGHRMAWDMMNWSPPTALVVAQLLRIPQA							
2. HCV1b consensus	LRRHVDLLVGAFAAFCSAMYVDLCSVFLVSQFLFTFSRRHETVQDCNCSYIPGHVSGHRMAWDMMNWSPPTALVVSQQLRIPQA							
3. HCV2a Consensus	LRTIDMVMSATLCSALYVVDLCGVMIAAQMFIYSPQHWFVQECNCSYIPGTHITGHRMAWDMMNWSPPTATMILAYAMRVPEV							
4. HCV2b Consensus	LRTHVDIMVMAATVCSALYVVDLCGVMIVSQALIVSPERHNTQECNCSYIPGCHITGHRMAWDMMLNWSPTLTMILAYAAARVPEL							
5. HCV 3 Consensus	LRRHVDLLVGAATMCSALYVVDLCGVMIVSQALIVSPERHNTQECNCSYIPGCHITGHRMAWDMMNWSPPTALVVAQLLRIPQT							
6. HCV 4 Consensus	LRRHVDLLVGAATVCSALYIGDLGGFLVVGQMFISPRRHWTQDCNCSYIPGCHITGHRMAWDMMNWSPPTALVVAQLLRIPQT							
7. HCV5 Consensus	LRRHVDLLVGAATVCSALYIGDLGGFLVVGQMFISPRRHWTQDCNCSYIPGCHITGHRMAWDMMNWSPPTALVVAQLLRIPQT							
8. HCV6 consensus	LRRHVDLLVGAATVCSALYIGDLGGFLVVGQMFISPRRHWTQDCNCSYIPGCHITGHRMAWDMMNWSPPTALVVAQLLRIPQT							
9. HCV7: ABN05226	LRRHVDLLVGAATVCSALYIGDLGGFLVVGQMFISPRRHWTQDCNCSYIPGCHITGHRMAWDMMNWSPPTALVVAQLLRIPQT							
14. AV1a-129	LRRHVDLLVGAATVCSALYIGDLGGFLVVGQMFISPRRHWTQDCNCSYIPGCHITGHRMAWDMMNWSPPTALVVAQLLRIPQT							
15. AV13a-177	LRRHVDLLVGAATVCSALYIGDLGGFLVVGQMFISPRRHWTQDCNCSYIPGCHITGHRMAWDMMNWSPPTALVVAQLLRIPQT							
Consensus	XLDIIAGAHWGVLAGLAYFMSQGNWAKVJXVLLIFAGVDAETHTTGCGXAARTTSLTSLFSPCPXQNLQILINTNGSWHINRTALNC							
	E1							
	E2							
1. HCV1a consensus	ILDMIAGAHWGVLAGLAYFMSQGNWAKVJXVLLIFAGVDAETHTTGCGXAARTTSLTSLFSPCPXQNLQILINTNGSWHINRTALNC							
2. HCV1b consensus	VVDMAGAHWGVLAGLAYFMSQGNWAKVJXVLLIFAGVDAETHTTGCGXAARTTSLTSLFSPCPXQNLQILINTNGSWHINRTALNC							
3. HCV2a Consensus	IIDIISGAHWGVLAGLAYFMSQGNWAKVJXVLLIFAGVDAETHTTGCGXAARTTSLTSLFSPCPXQNLQILINTNGSWHINRTALNC							
4. HCV2b Consensus	VLEVFGGHGVLAGLAYFMSQGNWAKVJXVLLIFAGVDAETHTTGCGXAARTTSLTSLFSPCPXQNLQILINTNGSWHINRTALNC							
5. HCV 3 Consensus	LFDIIAGAHWGVLAGLAYFMSQGNWAKVJXVLLIFAGVDAETHTTGCGXAARTTSLTSLFSPCPXQNLQILINTNGSWHINRTALNC							
6. HCV 4 Consensus	LVDLLAGGHGVLAGLAYFMSQGNWAKVJXVLLIFAGVDAETHTTGCGXAARTTSLTSLFSPCPXQNLQILINTNGSWHINRTALNC							
7. HCV5 Consensus	VIDIIAGAHWGVLAGLAYFMSQGNWAKVJXVLLIFAGVDAETHTTGCGXAARTTSLTSLFSPCPXQNLQILINTNGSWHINRTALNC							
8. HCV6 consensus	LIDIFLGGHGVLAGLAYFMSQGNWAKVJXVLLIFAGVDAETHTTGCGXAARTTSLTSLFSPCPXQNLQILINTNGSWHINRTALNC							
9. HCV7: ABN05226	IITTVAGGHGVLAGLAYFMSQGNWAKVJXVLLIFAGVDAETHTTGCGXAARTTSLTSLFSPCPXQNLQILINTNGSWHINRTALNC							
14. AV1a-129	ILDMIAGAHWGVLAGLAYFMSQGNWAKVJXVLLIFAGVDAETHTTGCGXAARTTSLTSLFSPCPXQNLQILINTNGSWHINRTALNC							
15. AV13a-177	VFDIIAGAHWGVLAGLAYFMSQGNWAKVJXVLLIFAGVDAETHTTGCGXAARTTSLTSLFSPCPXQNLQILINTNGSWHINRTALNC							
Consensus	NDSLXTGFIAGLFIYTHKFNSSGCPERLASCRPLTDFDQGWGPLYANXISGPDSDRPYCWHPYPRPCGIVPARSVCGPVYCFPT--							
	E1							
	E2							
1. HCV1a consensus	NDSLNTGWLAGLFIYTHKFNSSGCPERLASCRPLTDFDQGWGPLYANXISGPDSDRPYCWHPYPRPCGIVPARSVCGPVYCFPT--							
2. HCV1b consensus	NDSLQGTGFLAALFIYTHKFNSSGCPERLASCRPLTDFDQGWGPLYANXISGPDSDRPYCWHPYPRPCGIVPARSVCGPVYCFPT--							
3. HCV2a Consensus	NDSLNTGFLASLFIYTHKFNSSGCPERLASCRPLTDFDQGWGPLYANXISGPDSDRPYCWHPYPRPCGIVPARSVCGPVYCFPT--							
4. HCV2b Consensus	NDSLQGTGFIAGLFIYTHKFNSSGCPERLASCRPLTDFDQGWGPLYANXISGPDSDRPYCWHPYPRPCGIVPARSVCGPVYCFPT--							
5. HCV 3 Consensus	NDSLINTGFIAGLFIYTHKFNSSGCPERLASCRPLTDFDQGWGPLYANXISGPDSDRPYCWHPYPRPCGIVPARSVCGPVYCFPT--							
6. HCV 4 Consensus	NDSLNTGFLASLFIYTHKFNSSGCPERLASCRPLTDFDQGWGPLYANXISGPDSDRPYCWHPYPRPCGIVPARSVCGPVYCFPT--							
7. HCV5 Consensus	NDSLQGTGFIAGLFIYTHKFNSSGCPERLASCRPLTDFDQGWGPLYANXISGPDSDRPYCWHPYPRPCGIVPARSVCGPVYCFPT--							
8. HCV6 consensus	NDSLQGTGFIAGLFIYTHKFNSSGCPERLASCRPLTDFDQGWGPLYANXISGPDSDRPYCWHPYPRPCGIVPARSVCGPVYCFPT--							
9. HCV7: ABN05226	NDSLQGTGFIAGLFIYTHKFNSSGCPERLASCRPLTDFDQGWGPLYANXISGPDSDRPYCWHPYPRPCGIVPARSVCGPVYCFPT--							
14. AV1a-129	NDSLQGTGFIAGLFIYTHKFNSSGCPERLASCRPLTDFDQGWGPLYANXISGPDSDRPYCWHPYPRPCGIVPARSVCGPVYCFPT--							
15. AV13a-177	NDSLQGTGFIAGLFIYTHKFNSSGCPERLASCRPLTDFDQGWGPLYANXISGPDSDRPYCWHPYPRPCGIVPARSVCGPVYCFPT--							

	520	530	540	550	560	570	580	590	600
Consensus	SPVVVGTTDRXGVPYTTWGENETDVFLNSTRPPQGNWFGCTWMNST-GFTKTCGAPPCNI-GCGCN-----NDLLCPTDCFRKHP								
	E2								
1. HCV1a consensus	SPVVVGTTDRSGAPTYNWGENDTVFVLNNTTRPPLGNWFGCTWMNST-GFTKVCAPPVCI-GGVGN-----NTLHCPTDCFRKHP								
2. HCV1b consensus	SPVVVGTTDRFGVPTYSWGENETDVLLNNTTRPPQGNWFGCTWMNST-GFTKTCGGPPCNI-GGVGN-----NTLTCTDCFRKHP								
3. HCV2a Consensus	SPVVVGTTDRGLGVPTYSWGENETDVFLNSTRPPQGSWFGCTWMNST-GFTKTCGAPPCR I-RADFNAS-----TDLLCPTDCFRKHP								
4. HCV2b Consensus	SPVVVGTTDRQGVPYTSWGENETDVFLNSTRPPQGAWFGCTWMNGT-GFTKTCGAPPCR I-RRDYNST-----LDLLCPTDCFRKHP								
5. HCV 3 Consensus	SPVVVGTTDAKGVPYTSWGENETDVFLLESRLPPSGWFGCTWMNSTGRFVKTCGAPPCNIYGGGNPXNNESDLFCPTDCFRKHP								
6. HCV 4 Consensus	SPVVVGTTDRGLGVPTYSWGENESDVFLNSTRPPQGAWFGCVWMNST-GFTKACGAPPCNL-GPTGN-----TDWPCPTDCFRKHP								
7. HCV5 Consensus	SPVVVGTTDRXGXPYXWGXNETDIFLLNNTTRPPXGNWFGCTWMNST-GFVKTCGAPPCNL-GPTGN-----NSLKCPTDCFRKHP								
8. HCV6 consensus	SPVVVGTTDRRGLPYTWGENETDVFLLESRLPPTGGWFGCTWMNST-GFVKTCGAPPCNI-XPNSSN-----NSLLCPTDCFRKHP								
9. HCV7: ABN05226	SPVVVGTTDRRGVPYTSWGENESDVFLNSTRPPQGSWFGCSWMNTT-GFTKTCGGPPCKIRPQGAQSN-----TSLTCP TDCFRKHP								
14. AV1a-129	SPVVVGTTDKSGAPTYNWGENDWDVFLNNTTRPPLGNWFGCTWMNST-GFTKVCAPPVCI-GGAGN-----NLTLCPTDCFRKHP								
15. AV13a-177	SPVVVGTTDRQGVPYTTWGENETDVFLLSRLRPPSGWFGCTWMNST-GFVKTCGAPPCDIYGGGNRCN-ESDLFCPTDCFRKHP								
	610	620	630	640	650	660	670	680	
Consensus	EATYXCGSGPWLTPRCLVDYPYRLWHYPCTVNFTIFKVRMYVGVGVEHRLAACNWTTRGERCDLEDRDRSELSPLLHSTTEWA ILP								
	E2								
1. HCV1a consensus	EATYSRCGSGPWITPRCLVDYPYRLWHYPCTINFTIFKVRMYVGVGVEHRLAACNWTTRGERCDLEDRDRSELSPLLSTTQWQVLP								
2. HCV1b consensus	EATYKCGSGPWLTPRCLVDYPYRLWHYPCTVNFTIFKVRMYVGVGVEHRLAACNWTTRGERCDLEDRDRSELSPLLSTTTEWQ ILP								
3. HCV2a Consensus	EATYKCGSGPWLTPRCLVDYPYRLWHYPCTVNFTIFKIRMYVGVGVEHRLTAACNFTTRGDRCNLEDRDRSQSPLLHSTTEWA ILP								
4. HCV2b Consensus	DATYKCGAGPWLTPRCLVDYPYRLWHYPCTVNFTIFKVRMYVGVGVEHRLSAAACNFTTRGDRCLDRDRGQSQSPLLHSTTEWA VLP								
5. HCV 3 Consensus	EATYSRCGAGPWLTPRCMDVPYRLWHYPCTVNFTIFKVRMEFVGGEHRTAAACNWTTRGERCDIEDRDRSEQHPLHSTTELA ILP								
6. HCV 4 Consensus	ETTYAKCGSGPWITPRCLIHYPYRLWHYPCTVNFTVFRTFFIGGIEHRMEAACNWTTRGEVCGLEHRRDRAELSPLLSTTTWQXLP								
7. HCV5 Consensus	DATYKCGSGPWLTPRCLVHYPYRLWHYPCTVNFTIFKVRMF IGGLHRLAACNWTTRGERCDLEDRDRRAELSPLLHTTTQWA ILP								
8. HCV6 consensus	EATYARCGSGPWLTPRCLVDYPYRLWHYPCTVNFTIFKVRMFVGVGVEHRTAAACNWTTRGERCELDLDRDIEMSPLLFSTTELA ILP								
9. HCV7: ABN05226	RATYACGSGPWLTPRCMVHYPYRLWHYPCTVNFTIFKVRVLYIGGVEHRLDAACNWTTRGERCDLEDRDRVDMSPLLHSTTELA ILP								
14. AV1a-129	DATYSRCGSGPWITPRCLVDYPYRLWHYPCTVNFTIFKIRMYLGGVEHRLAACNWTTRGERCDLEDRDRSELSPLLSTTQWQVLP								
15. AV13a-177	EATYSRCGAGPWLTPRCLVDYPYRLWHYPCTVNFTIFKVRMEFVGGEHRTAAACNWTTRGERCNIEDRDRSEQHPLHSTTELA ILP								
	690	700	710	720	730	740	750	760	770
Consensus	CSFTTLPALSTGLIHLHQNIVDVQYLYGVGSAAVSWAXKWEYVVLFLLLADARVCACLWMMLLISQAEAALENLVVNAASAAGT								
	E2								
1. HCV1a consensus	CSFTTLPALSTGLIHLHQNIVDVQYLYGVGS IASWA IKWEYVVLFLLLADARVCCLWMMLLISQAEAALENLVVNAASLAGT								
2. HCV1b consensus	CSFTTLPALSTGLIHLHQNIVDVQYLYIGSAVVSFAIKWEYVVLFLLLADARVCACLWMMLL IQAEEAALENLVVNAASVAGA								
3. HCV2a Consensus	CSYSDLPALSTGLIHLHQNIVDVQYMYGLSPALTKYVVRWEWVVLFLLLADARVCACLWMML ILLGQAEAALEKLVVLAASAASC								
4. HCV2b Consensus	CSFSDLPALSTGLIHLHQNIVDVQYLYGLSPA ITRY IVKWEWVVLFLLLADARVCACLWMML ILLGQAEAALEKL I ILHSAASA								
5. HCV 3 Consensus	CSFTTLPALSTGLIHLHQNIVDVQYLYGVSGMVAWKWEFVILVFLLLADARVCVALWMLMISQAEAALENLVTLNAVAAAGT								
6. HCV 4 Consensus	CSFTTLPALSTGLIHLHQNIVDVQYLYGVGSAAVSWALKWEYVVLFLLLADARVCACLWMFMVSVQEAALSNL ININAAASAAGT								
7. HCV5 Consensus	CSFTTLPALSTGLIHLHQNIVDQYLYGLSS IVSWAVKWEY IVLXFLLLADAR ICTCLV ILLXQCQAEAALENV IVLNAASAAGX								
8. HCV6 consensus	CSFTTLPALSTGLIHLHQNIVDVQYLYGVSSSVSWAKWEYVVLAFVLADARICACLWMMLL IGAEEAALENV IVINAAASAAGT								
9. HCV7: ABN05226	CSFVPLPALSTGLIHLHQNIVDAQYLYGLSPA IISWA IRWEWVVLVFLLLADARICACLWMMLMAQAEAALENL IHLNAASLAGT								
14. AV1a-129	CSFTTLPALSTGLIHLHQNIVDVQYLYGVGSVAASWA IKWDYVVLFLLLADAR ICSCLWMMLLISQAEAALENV IVLNAASLAGT								
15. AV13a-177	CSFTTLPALSTGLIHLHQNIVDVQYLYGVGSVGVGVALRWEFVVLVFLLLADARVCVALWMLMISQAEAALENV IVTLNAVAAAGT								
	P7								

	780	790	800	810	820	830	840	850	860
Consensus	HGIKWFLLVFFCAAWYK--GRLVPXATYALXGLWPLILLLLALPQRAYALDREVAASLXAVLVXLTIFTLSPHYKHLLSRXLWWL								
	P7								
	NS2								
1. HCV1a consensus	HGLVSFLVFFCFAWYK--GRWVPGAAYALVGMWPLLLLLALPQRAYALDTEVAASCGGVVLVGLMALTLSPYKRYISWCLWWL								
2. HCV1b consensus	HGLVSFLVFFCAAWYK--GRLVPGAAYAFYGVWPLLLLLALPQRAYAMDRMAASCGGAVFVGLALLTLSPHYKVFLARLIWWL								
3. HCV2a Consensus	NGFLYFVIFFFVAAWYK--GRAVPLAAYSLSLGLWPFCLLLALPQQAAYADASVHGQIGAAALLILITLFTLTPGYKTLSSRCLWWL								
4. HCV2b Consensus	NGPLWFFIFFTAAWYK--GRVVPVATYSVLGLWSFLLLVALLPQQAAYALDAAEQEGELGVILVLIISIFTLTPAYKILLRSRVWWL								
5. HCV 3 Consensus	HGIWYLVAFCAAWHVRRAAGKLVPLVTSYSLTGLWSLALLVLLPQRAYAYSGEDSATLGAGILVLFGGFTLSPWYKHWIGRLMWWN								
6. HCV 4 Consensus	HGFWYAIFFICIAWHVK--GRLPAAATYACGMWPLLLLLALPQRAYAYDREVAASLGGAVVVALTILTLSPHYKSWLARGLWWI								
7. HCV5 Consensus	HGFVWGLLVXCXAWHXK--GRLVPGATYCLGXWPLLLLLALPQRAYALDSSDGGTVGCLVLXILITLFTLTPGYKXVVLVXWWL								
8. HCV6 consensus	QGWWGLFLFCCAWYK--GRLVPACTYALLOLWPLLLLLALPQRAYAYDNEQAASLGGALVLIITIFTLTPAYKQLLVSLFWWN								
9. HCV7: ABN05226	HGIWMLLVFCAWHLR--GRVPLVTVYICGMWPFLLMLSLPQRAYALDREVAASLGGTGLMAIILLVTLGPHYKRLALILWWV								
14. AV1a-129	HGLAPFLVFFCLAWYK--GKWPAGVAVYVGMWPLLLLLALPQRAYALDTEVAASCGGAVLGLMVLTLSPHYKHYISWCLWWL								
15. AV13a-177	HGIWYLVAFCAAWHLR--GKLVPLVTSYSLTGLWSLAVLVLPLPQRAYAYSGEDSATLGAGILVLFGGFTLSPWYKHWIGRLMWWN								
	870	880	890	900	910	920	930	940	
Consensus	QYFITRAEAXLQVWVPPPLNVRGGRDXXILLTCLLHPXILVFDITKLLAVLGLPLYLLOASLLRVPYFVRAHALLRXCMLVRXLGGK								
	NS2								
1. HCV1a consensus	QYFLTRVEAQLHVWVPPPLNVRGGRDAVILLMCVVHPTLVFDITKLLAVFGPLWILQASLLKVPYFVRVQGLLRICALARKMAGGH								
2. HCV1b consensus	QYFITRAEAXLQVWVPPPLNVRGGRDAIILLTCAVHPELIFDITKLLAILGLPMLVQAGITRVPYFVRAQGLIRACMLVRKVAGGH								
3. HCV2a Consensus	CYLLTGEAMVQEWAPPQARGRDGIWAATIFCPGVVFDITKLLAVLGLPALLRDALTRVPYFVRAHALLRMCMTVRHLAGGR								
4. HCV2b Consensus	SYMLVLAEAQIQWVPPPLEARGRDGIWAVILHPRLVFEVTKWLLAILGPAYLLKASLLRVPYFVRAHALLRVCTLRHLAGAR								
5. HCV 3 Consensus	QYTCRCEAALQVWVPPPLARGRDGVIILTSLLYPSLIFDITKLLIAVLGPLYLIQAAITTPYFVRAHVLVRLCMLVRSVMGGK								
6. HCV 4 Consensus	QYFIARAEALLHYVPSFVDRGPRDSLIIILAVLACPHLVFDITKYLAILGLPYILOASLLRVPYFVRAHALVKICSLRGVYVGK								
7. HCV5 Consensus	QYFLARVEAXIHVVVPPPLQVRGGRDAIIMLTCLFHPALGFEVTKILGLILGLPYLLOXSLKVPYFVRARALLRACLLAKHLVXGK								
8. HCV6 consensus	QYFIARAEAMLHVWVPPPLRVGGRDAVILLTCLLHPQLGFEVTKILLALGLPYLLOXSLKVPYFVRALIRACLLVRLRLLAGGK								
9. HCV7: ABN05226	TYFLTRCEAALQVWVPPPLNVRGGRDGVILCVLLCYPLGVFDITKLLVMMCPYLLQCLVTRVPYFVRAQALIRVCSLFTKLAGGR								
14. AV1a-129	QYFLTRAEALQVWVPPPLNVRGGRDAVILLMCVVHPTLVFDITKLLAV?GPLVILQTSLLKVPYFVRVQGLLRICALARKIAGGH								
15. AV13a-177	QYTCRCEAALQVWVPPPLARGSRDGAILLTSLLYPSLIFDITKLLIAVLGPLYLIQAAITTPYFVRAHVLVRLCMLVRSVMGGK								
	950	960	970	980	990	1,000	1,010	1,020	1,030
Consensus	YVQMAILLKGRWTGTYIYDHLXPLSDWAAAGLRDLAVAVEPVIFSPMEKKVITWGADTAACGDILCGLPVSARLGREILLGPADDY								
	NS2								
1. HCV1a consensus	YVQMAIILKLGALTGTYVYNHLLTPLRDWAHNGLRDLAVAVEPVVFSQMETKLTWGADTAACGDIINGLPVSARRGREILLGPADGM								
2. HCV1b consensus	YVQMAFMKLAALTGTYYVDHLTPLRDWAHAGLRDLAVAVEPVVFSDMETKIITWGADTAACGDIILGLPVSARRGREILLGPADSL								
3. HCV2a Consensus	YVQMAILLALGRWTGTYIYDHLTPMSDWAAAGLRDLAVAVEPVIFSPMEKKVIVWGAETAACGDILHGLPVSARLGREILLGPADGY								
4. HCV2b Consensus	YIQMLLITIGRWGTYYVDHLSPSLSTWAAQGLRDLAVAVEPVVFSQMETKIVWGAETVACGDILHGLPVSARLGREILLGPADSY								
5. HCV 3 Consensus	YFQMIILSIGRWFTYLYDHLAPMQHWAAGLRDLAVATEPVIFSPMEIKVITWGADTAACGDILCGLPVSARLGREILLGPADDY								
6. HCV 4 Consensus	YQMAVLKVGAALTGTYYDHLTPLSDWAAAGLRDLAVALEPVVFTSPMEIKVITWGADTAACGDIIXGLPVSARLGREILLGPADSE								
7. HCV5 Consensus	YVQAALLHLGLTGTYYVDHLAPMKDWAAGLRDLAVATEPVIFSPMETKVITWGADTAACGDILAGLPVSARRGREIFLGPADDI								
8. HCV6 consensus	YVQACLLRLGAWTGTYYDHLAPLSDWASDGLRDLAVATEPVIFSPMEKKVITWGADTAACGDILAGLPVSARRGNLVLGPADDI								
9. HCV7: ABN05226	YVQAALLTIGRWGTYYIYNHLLAPLETWAAAGLRDLAVATEPVIFSPMEKKIIVWGAETACGDILCGLPVSARLGREILLGPADDY								
14. AV1a-129	YVQMAIILKLGALTGTYIYDHLTPLRDWAHNGLRDLAVATEPVVFSRMEIKVITWGADTAACGDIINGLPVSARRCQEILLGPADGM								
15. AV13a-177	YFQMIILSIGRWFTYLYDHLAPMQHWAAGLRDLAVATEPVIFSPMEIKVITWGADTAACGDILCGLPVSARLGREILLGPADDY								

	1,040	1,050	1,060	1,070	1,080	1,090	1,100	1,110	
Consensus	XSKGWRLIAP	ITAYAAQOTRGLLGT	IVTSLTGRDKNEVEGEVQ	IVLSTATQTFLGTC	INGVMTVYHGA	CSKTLACPKG	PVXQMYTNV		
	NS2								
	NS3								
1. HCV1a consensus	VSKGWRLIAP	ITAYAAQOTRGLLGC	IITSLTGRDKNQVEGEVQ	IVSTAAQTFLATC	INGVCWTVYHGA	CSKTLACPKG	PVVIQMYTNV		
2. HCV1b consensus	EGQGWRLIAP	ITAYSQOTRGLLGC	IITSLTGRDKNQVEGEVQ	IVSTAAQTFLATC	INGVCWTVYHGA	CSKTLACPKG	PVITQMYTNV		
3. HCV2a Consensus	TSKGWRLIAP	ITAYAAQOTRGLLGA	IVVMTGRDKTEQAGE	IQVLSTVTSQFLGTS	ISGVLWTVYHGA	GNKTLAGSRG	PVTQMYSSA		
4. HCV2b Consensus	TSKGWKLLAP	ITAYTQOTRGLLGA	IVVSLTGRDKNEAGQVQ	VLSSVTQFLGTS	ISGVLWTVYHGA	GNKTLAGPKG	PVTQMYTSA		
5. HCV 3 Consensus	REMGWRLIAP	ITAYAAQOTRGLLGT	IVTSLTGRDKNVTEGEVQ	IVLSTATQTFLGTC	INGVMTVYHGA	GNKTLAGAKHP	ALQMYTNV		
6. HCV 4 Consensus	TSKGWRLIAP	ITAYAAQOTRGLFST	IITSLTGRDKNENCGEVEVQ	IVLSTATQSFLLG	GTAVNGVMTVYHGA	GNKTLAGPKG	PVNVQMYTNV		
7. HCV5 Consensus	XXAGWRLIAP	ITAYAAQOTRGLVGA	IVVSLTGRDKNEAGEVQ	IVLSTATQFLGTC	INGVMTVYHGA	GNKTLAGPKG	PVNVQMYTNV		
8. HCV6 consensus	KRGWRLIAP	ITAYAAQOTRGLLGT	IVTSLTGRDKNEVEGEVQ	IVLSTATQSFLLG	INGVMTVYHGA	GNKTLAGPKG	PVNVQMYTNV		
9. HCV7: ABN05226	RSMGWQLLAP	ISAYAAQOTRGLIST	LVVSLTGRDKNETAGEVQ	IVLSTSTQFLGTC	INGVMTVYHGA	GNKTLAGPKG	PVNVQMYTNV		
14. AV1a-129	VSKGWRLIAP	ITAYAAQOTRGLLGC	IITSLTGRDKNQVEGEVQ	IVSTAAQTFLATC	INGVCWTVYHGA	GNKTLAGPKG	PVVIQMYTNV		
15. AV13a-177	REMGWRLIAP	ITAYAAQOTRGLLGT	IVTSLTGRDKNVTEGEVQ	IVLSTATQTFLGTC	INGVMTVYHGA	GNKTLAGPKG	PVVIQMYTNV		
	1,120	1,130	1,140	1,150	1,160	1,170	1,180	1,190	1,200
Consensus	DQDLVGPAPP	CAKSLTPCTCGSSD	LYLVTRHADV	IPXRRRCDSRGS	LLSPRP	ISXLKSSG	CGPVLCP	SGHAGV	IFRAAVCTR
	NS3								
1. HCV1a consensus	DQDLVGPAPP	QAGARSLTPCTCGSSD	LYLVTRHADV	IPVRRRCDSRGS	LLSPRP	ISYLKSSG	CGPVLCP	AGHAGV	IFRAAVCTR
2. HCV1b consensus	DQDLVGPAPP	QAGARSLTPCTCGSSD	LYLVTRHADV	IPVRRRCDSRGS	LLSPRP	ISYLKSSG	CGPVLCP	AGHAGV	IFRAAVCTR
3. HCV2a Consensus	EGDLVGPAPP	PGTKSLPCTCGAVD	LYLVTRHADV	IPARRRCDSRGS	LLSPRP	ISLTKSSG	CGPVLCP	RGHAGV	IFRAAVCTR
4. HCV2b Consensus	EGDLVGPAPP	PGTKSLPCTCGAVD	LYLVTRHADV	IPARRRCDSRGS	LLSPRP	ISLTKSSG	CGPVLCP	RGHAGV	IFRAAVCTR
5. HCV 3 Consensus	DQDLVGPAPP	PGAKSLPCTCGASD	LYLVTRHADV	IPARRRCDSRGS	LLSPRP	ISLTKSSG	CGPVLCP	RGHAGV	IFRAAVCTR
6. HCV 4 Consensus	DQDLVGPAPP	PGVKSAPCTCGASD	LYLVTRHADV	IPARRRCDSRGS	LLSPRP	ISLTKSSG	CGPVLCP	RGHAGV	IFRAAVCTR
7. HCV5 Consensus	DKDLVGPAPP	XPXGXRSLTPCTCGASD	LYLVTRHADV	IPARRRCDSRGS	LLSPRP	ISLTKSSG	CGPVLCP	RGHAGV	IFRAAVCTR
8. HCV6 consensus	DQDLVGPAPP	PGARSLTPCTCGSSD	LYLVTRHADV	IPARRRCDSRGS	LLSPRP	ISLTKSSG	CGPVLCP	RGHAGV	IFRAAVCTR
9. HCV7: ABN05226	SDDL VGPAPP	PGSKSLPCTCGASD	LYLVTRHADV	IPARRRCDSRGS	LLSPRP	ISLTKSSG	CGPVLCP	RGHAGV	IFRAAVCTR
14. AV1a-129	DKDLVGPAPP	PGSRSLPCTCGSSD	LYLVTRHADV	IPARRRCDSRGS	LLSPRP	ISLTKSSG	CGPVLCP	RGHAGV	IFRAAVCTR
15. AV13a-177	DQDLVGPAPP	PGAKSLPCTCGSSD	LYLVTRHADV	IPARRRCDSRGS	LLSPRP	ISLTKSSG	CGPVLCP	RGHAGV	IFRAAVCTR
	1,210	1,220	1,230	1,240	1,250	1,260	1,270	1,280	1,290
Consensus	KAVDFIPVES	LETMRSPXFTDN	STPPAVPQXYQVGYLHAPT	CGSKSTKVP	AAAYAAQYKVL	INP	SVAATL	CGAYMSKA	HGIDP
	NS3								
1. HCV1a consensus	KAVDFIPVEN	LETMRSPVFTDN	SSPPAVPQSFQVAHLHAPT	CGSKSTKVP	AAAYAAQYKVL	INP	SVAATL	CGAYMSKA	HGIDP
2. HCV1b consensus	KAVDFIPVES	METMRSPVFTDN	SSPPAVPQTFQVAHLHAPT	CGSKSTKVP	AAAYAAQYKVL	INP	SVAATL	CGAYMSKA	HGIDP
3. HCV2a Consensus	KSIDFIPVET	LDIVTRSPFTSD	NSTPPAVPQTYQVGYLHAPT	CGSKSTKVP	AAAYAAQYKVL	INP	SVAATL	CGAYMSKA	HGIDP
4. HCV2b Consensus	KSIDFIPVES	LDIATRTPSFSD	NSTPPAVPQSYQVGYLHAPT	CGSKSTKVP	AAAYAAQYKVL	INP	SVAATL	CGAYMSKA	HGIDP
5. HCV 3 Consensus	KALQFIPVET	LSQARS	PSFSDNSTPPAVPQSYQVGYLHAPT	CGSKSTKVP	AAAYAAQYKVL	INP	SVAATL	CGAYMSKA	HGIDP
6. HCV 4 Consensus	KAVDFIPVES	LETMRSPVFTDN	STPPAVPQTYQVAHLHAPT	CGSKSTKVP	AAAYAAQYKVL	INP	SVAATL	CGAYMSKA	HGIDP
7. HCV5 Consensus	KALQFIPVEN	LETMRSPVFTDN	STPPAVPHEFQVGYLHAPT	CGSKSTKVP	AAAYAAQYKVL	INP	SVAATL	CGAYMSKA	HGIDP
8. HCV6 consensus	KSLDFIPVEN	METMRSPFTSD	NSTPPAVPQTYQVGYLHAPT	CGSKSTKVP	AAAYAAQYKVL	INP	SVAATL	CGAYMSKA	HGIDP
9. HCV7: ABN05226	KAVQFVP	IEKMQVARS	PSFSDNSTPPAVPSTYQVGYLHAPT	CGSKSTKVP	AAAYAAQYKVL	INP	SVAATL	CGAYMSKA	HGIDP
14. AV1a-129	KAVDFIPVES	LETMRSPVFTDN	SSPPAVPQSFQVAHLHAPT	CGSKSTKVP	AAAYAAQYKVL	INP	SVAATL	CGAYMSKA	HGIDP
15. AV13a-177	KALQFIPVET	LSAQRS	PSFSDNSTPPIVPQSYQVGYLHAPT	CGSKSTKVP	AAAYAAQYKVL	INP	SVAATL	CGAYMSKA	HGIDP

	1,300	1,310	1,320	1,330	1,340	1,350	1,360	1,370	
Consensus	NIRTVRTVTTGAPITYSTYCKFLADGCCSGGAYDIIICDECHSTDATIILGICTVLDQAEAGVRLVVLATATPPGCVTVPHPNINS3								
1. HCV1a consensus	NIRTVRTITTGSPITYSTYCKFLADGCCSGGAYDIIICDECHSTDATSIILGICTVLDQAEAGVRLVVLATATPPGCVTVPHPNINS3								
2. HCV1b consensus	NIRTVRTITTGAPITYSTYCKFLADGCCSGGAYDIIICDECHSTSTTILGICTVLDQAEAGVRLVVLATATPPGCVTVPHPNINS3								
3. HCV2a Consensus	NIRTVRTVTTGEAITYSTYCKFLADGCCAGGAYDIIICDECHAVDATIILGICTVLDQAEAGVRLVVLATATPPGCVTVPHPNINS3								
4. HCV2b Consensus	NIRTVRTVTTGDPITYSTYCKFLADGCCSAGAYDIIICDECHSVDATIILGICTVLDQAEAGVRLVVLATATPPGCVTVPHPNINS3								
5. HCV 3 Consensus	NIRTVRTVTTGAKLTITYSTYCKFLADGCCSGGAYDIIICDECHAQDATSIILGICTVLDQAEAGVRLVVLATATPPGCVTVPHPNINS3								
6. HCV 4 Consensus	NIRTVRTITTGAPITYSTYCKFLADGCCSGGAYDIIICDECHSQDATSIILGICTVLDQAEAGVRLVVLATATPPGCVTVPHPNINS3								
7. HCV5 Consensus	NIRTVRTVTTGAAITYSTYCKFLADGCCSGGAYDIIICDECHSQDATSIILGICTVLDQAEAGVRLVVLATATPPGCVTVPHPNINS3								
8. HCV6 consensus	NIRTVRTITTGGAITYSTYCKFLADGCCSGGAYDIIICDECHSTPTTILGICTVLDQAEAGVRLVVLATATPPGCVTVPHPNINS3								
9. HCV7: ABN05226	SVRTGARTVTTGAPITYSTYCKFLADGCCSGGAYDIIICDECHAIIDATTVVGICTVLDQAEAGVRLVVLATATPPGCVTVPHPNINS3								
14. AV1a-129	NIRTVRTITTGSPITYSTYCKFLADGCCSGGAYDIIICDECHSTDATSIILGICTVLDQAEAGVRLVVLATATPPGCVTVPHPNINS3								
15. AV13a-177	NIRTVRTVTTGAKLTITYSTYCKFLADGCCSGGAYDIIICDECHAQDATSIILGICTVLDQAEAGVRLVVLATATPPGCVTVPHPNINS3								
Consensus	1,380	1,390	1,400	1,410	1,420	1,430	1,440	1,450	1,460
	EEVALGTXGEIPFYCKAIPLEXIKGGRHLIFCHSKKKKDELAACKLXGLGNNAVAYRGLDVS IPTSGDVVVVATDALMTGFTGDFNS3								
1. HCV1a consensus	EEVALSTTGEIPFYGKAIPLEVIKGGRHLIFCHSKKKKDELAACKLVALGINAVAYRGLDVS IPTSGDVVVVATDALMTGFTGDF								
2. HCV1b consensus	EEVALSNTGEIPFYGKAIPLETIKGGRHLIFCHSKKKKDELAACKLGLGNNAVAYRGLDVS IPTSGDVVVVATDALMTGFTGDF								
3. HCV2a Consensus	EEVALGQEGEIPFYGRAIPLSYIKGGRHLIFCHSKKKKDELAACKLRCMGLNAVAYRGLDVS IPTSGDVVVVATDALMTGFTGDF								
4. HCV2b Consensus	EEVALGHEGEIPFYGKAIPLEAFIKGGRHLIFCHSKKKKDELAACKLRGMGNNAVAYRGLDVS IPTQGDVVVVATDALMTGYTGDF								
5. HCV 3 Consensus	EEVALGSEGEIPFYGKAIPIAQLKGGRHLIFCHSKKKKDEIASKLRGMGLNAVAYRGLDVS IPTTGDVVVVCATDALMTGFTGDF								
6. HCV 4 Consensus	EEVALPTTGEIPFYGKAIPLELIKGGGRHLIFCHSKKKKDELAACKLTSGLNAVAYRGLDVS IPTSGDVVVVCATDALMTGFTGDF								
7. HCV5 Consensus	EEVALPSEGEIPFYGRAIPLXLIKGGGRHLIFCHSKKKKDELAACKLTSGLNAVAYRGLDVAIPATGDDVVVVCSTDALMTGFTGDF								
8. HCV6 consensus	TETALPTTGEIPFYGKAIPLEYIKGGRHLIFCHSKKKKDELAACKLTSGLNAVAFYRGVDVS IPTSGDVVVVCATDALMTGYTGDF								
9. HCV7: ABN05226	EEVALGNDGEIPFYGKAIPLOHIKGGGRHLIFCHSKKKKDELAACKLTSGLTAVAYRGLDVS IPTSGDVVVVATDALMTGFTGDF								
14. AV1a-129	EEVALSTTGEIPFYGKAIPLEVIKGGRHLIFCHSKKKKDELAACKLVALGINAVAYRGLDVS IPTSGDVVVVATDALMTGYTGDF								
15. AV13a-177	EEVALGSEGEIPFYGKAIPLAQLKGGRHLIFCHSKKKKDEMAASKLRGMGLNAVAYRGLDVS IPTAGDVVVVCATDALMTGFTGDF								
Consensus	1,470	1,480	1,490	1,500	1,510	1,520	1,530	1,540	
	DSVIDCNVAVTQTVDFSLDPTFTIETTVPQDAVSRSQRRGRTGGRGLGIYRVSPGERPSGMFDSVVLCECYDAGCAWYELTPAES3								
1. HCV1a consensus	DSVIDCNTCVTQTVDFSLDPTFTIETTLPQDAVSRQTQRRGRTGRGKPGIYRFVAPGERPSGMFDSVVLCECYDAGCAWYELTPAES3								
2. HCV1b consensus	DSVIDCNTCVTQTVDFSLDPTFTIETTVPQDAVSRSQRRGRTGRRRGIRYFVTPGERPSGMFDSVVLCECYDAGCAWYELTPAES3								
3. HCV2a Consensus	DSVIDCNVAVTQVDFSLDPTFTITQTVQDAVSRSQRRGRTGRRGLGIYRVSTGERASGMFDSVVLCECYDAGCAWYELTPAES3								
4. HCV2b Consensus	DSVIDCNVAVTQIVDFSLDPTFTITQTVQDAVSRSQRRGRTGRRGLGIYRVSSGERPSGMFDSVVLCECYDAGCAWYELTPAES3								
5. HCV 3 Consensus	DSVIDCNVAVEQYVDFSLDPTFTSIETRTAPQDAVSRSQRRGRTGRRGLGIYRVTPGERPSGMFDSVVLCECYDAGCAWYELTPAES3								
6. HCV 4 Consensus	DSVIDCNTSVIQTVDFSLDPTFTSIETTVQDAVSRSQRRGRTGRRGLGIYRVTPGERPSGMFDSVVLCECYDAGCAWYELTPAES3								
7. HCV5 Consensus	DSVIDCNTAVTQTVDFSLDPTFTIETTVPQDAVSRSQRRGRTGRRHGIRYVSSGERPSGMFDSVVLCECYDAGCAWYELTPAES3								
8. HCV6 consensus	DSVIDCNVAVTQVDFSLDPTFTSIETTVQDAVSRSQRRGRTGRRGPGIYRVSSQGERPSGMFDTVVLCEAYDTGCAWYELTPAES3								
9. HCV7: ABN05226	DSVIDCNVAVTQTVDFSLDPTFTIETTLPQDAVSRSQRRGRTGRRGLGIYRVSSGERPSGMFDTSVLCECYDAGCAWYELTPAES3								
14. AV1a-129	DSVIDCNTCVTQTVDFSLDPTFTIETTLPQDAVSRQTQRRGRTGRRGPGIYRFVAPGERPSGMFDSVVLCECYDAGCAWYELTPAES3								
15. AV13a-177	DSVIDCNVTEQYVDFSLDPTFTSIETRTAPQDAVSRSQRRGRTGRRGLGIYRVVAPGERPSGMFDSVVLCECYDAGCAWYELTPAES3								

	1,550	1,560	1,570	1,580	1,590	1,600	1,610	1,620	1,630
Consensus	TTVRLRAYLNTPLPVCQDHLFEWEGVFTGLTH IDAHFLSQTKQSGENFPYLVAIQATVCARAXAPPPSWDXMWKCLIRLKPTLHG								
	NS3								
1. HCV1a consensus	TTVRLRAYMNTPLPVCQDHLFEWEGVFTGLTH IDAHFLSQTKQSGENFPYLVAIQATVCARAXAPPPSWDXMWKCLIRLKPTLHG								
2. HCV1b consensus	TSVRLRAYLNTPLPVCQDHLFEWESVFTGLTH IDAHFLSQTKQAGDNFPYLVAIQATVCARAXAPPPSWDXMWKCLIRLKPTLHG								
3. HCV2a Consensus	TTVRLRAYFNTPLPVCQDHLFEWAVFTGLTH IDAHFLSQTKQSGENFAYLVAIQATVCARAKAPPPSWDXMWKCLIRLKPTLHG								
4. HCV2b Consensus	TTVRLRAYFNTPLPVCQDHLFEWAVFTGLTH IDAHFLSQTKQGGDNFAYLVAIQATVCARAKAPPPSWDXMWKCLIRLKPTLHG								
5. HCV 3 Consensus	TTVRLRAYLSTPLPVCQDHLDFWESVFTGLTH IDAHFLSQTKQGGNFPYLVAIQATVCARAXAPPPSWDXMWKCLIRLKPTLHG								
6. HCV 4 Consensus	TTVRLRAYFNTPLPVCQDHLFEWESVFTGLTH IDAHFLSQTKQGGNFPYLVAIQATVCARAXAPPPSWDXMWKCLIRLKPTLHG								
7. HCV5 Consensus	TTVRLRAYLNTPLPVCQDHLFEWEGVFTGLTN IDAHMSLQTKQGGNFPYLVAIQATVCARAXAPPPSWDXMWKCLIRLKPTLHG								
8. HCV6 consensus	TTVRLRAYLNTPLPVCQDHLFEWEGVFTGLTH IDAHFLSQTKQGGNFPYLVAIQATVCARAXAPPPSWDXMWKCLIRLKPTLHG								
9. HCV7: ABN05226	TTVRLRAYLNTPLPVCQDHLFEWEGVFTGLTH IDAHFLSQTKQGGNFPYLVAIQATVCARAXAPPPSWDXMWKCLIRLKPTLHG								
14. AV1a-129	TTVRLRAYLNTPLPVCQDHLFEWEGVFTGLTH IDAHFLSQTKQGGNFPYLVAIQATVCARAXAPPPSWDXMWKCLIRLKPTLHG								
15. AV13a-177	TTVRLRAYLNTPLPVCQDHLFEWEGVFTGLTH IDAHFLSQTKQGGNFPYLVAIQATVCARAXAPPPSWDXMWKCLIRLKPTLHG								
	1,640	1,650	1,660	1,670	1,680	1,690	1,700	1,710	1,720
Consensus	PTPLLYRLGAVQNEVTLTHP ITKY IMTCMSADLEVVT--STWVLVGGVLAALAAAYCLSTGCVV IVGRIVLSGKPAX IPDREVLYQ								
	NS3								
	NS4a								
1. HCV1a consensus	PTPLLYRLGAVQNEVTLTHP ITKY IMTCMSADLEVVT--STWVLVGGVLAALAAAYCLSTGCVV IVGRIVLSGKPAX IPDREVLYR								
2. HCV1b consensus	PTPLLYRLGAVQNEVTLTHP ITKY IMTCMSADLEVVT--STWVLVGGVLAALAAAYCLSTGCVV IVGRIVLSGKPAX IPDREVLYR								
3. HCV2a Consensus	PTPLLYRLGAVQNEVTLTHP ITKY IMTCMSADLEVVT--STWVLVGGVLAALAAAYCLSTGCVV IVGRIVLSGKPAX IPDREVLYR								
4. HCV2b Consensus	PTPLLYRLGAVQNEVTLTHP ITKY IMTCMSADLEVVT--STWVLVGGVLAALAAAYCLSTGCVV IVGRIVLSGKPAX IPDREVLYR								
5. HCV 3 Consensus	PTPLLYRLGAVQNEVTLTHP ITKY IMTCMSADLEVVT--STWVLVGGVLAALAAAYCLSTGCVV IVGRIVLSGKPAX IPDREVLYR								
6. HCV 4 Consensus	PTPLLYRLGAVQNEVTLTHP ITKY IMTCMSADLEVVT--STWVLVGGVLAALAAAYCLSTGCVV IVGRIVLSGKPAX IPDREVLYR								
7. HCV5 Consensus	PTPLLYRLGAVQNEVTLTHP ITKY IMTCMSADLEVVT--STWVLVGGVLAALAAAYCLSTGCVV IVGRIVLSGKPAX IPDREVLYR								
8. HCV6 consensus	PTPLLYRLGAVQNEVTLTHP ITKY IMTCMSADLEVVT--STWVLVGGVLAALAAAYCLSTGCVV IVGRIVLSGKPAX IPDREVLYR								
9. HCV7: ABN05226	PTPLLYRLGAVQNEVTLTHP ITKY IMTCMSADLEVVT--STWVLVGGVLAALAAAYCLSTGCVV IVGRIVLSGKPAX IPDREVLYR								
14. AV1a-129	PTPLLYRLGAVQNEVTLTHP ITKY IMTCMSADLEVVT--STWVLVGGVLAALAAAYCLSTGCVV IVGRIVLSGKPAX IPDREVLYR								
15. AV13a-177	PTPLLYRLGAVQNEVTLTHP ITKY IMTCMSADLEVVT--STWVLVGGVLAALAAAYCLSTGCVV IVGRIVLSGKPAX IPDREVLYR								
	1,730	1,740	1,750	1,760	1,770	1,780	1,790	1,800	
Consensus	QFDEMEECASHLPY IEQCGQ IAEQFKQKALGLLQATKQAEV IAPAVQXNWQKLEQFWAKHMWNF ISGIQYLAGLSTLPCNPAS								
	NS4b								
	NS4a								
1. HCV1a consensus	EFDMEECASHLPY IEQGMMLAEQFKQKALGLLQATKQAEV IAPAVQXNWQKLEAFWAKHMWNF ISGIQYLAGLSTLPCNPAS								
2. HCV1b consensus	EFDMEECASHLPY IEQGMMLAEQFKQKALGLLQATKQAEV IAPAVQXNWQKLEAFWAKHMWNF ISGIQYLAGLSTLPCNPAS								
3. HCV2a Consensus	AFDEMEECASHLPY IEQGMMLAEQFKQKALGLLQATKQAEV IAPAVQXNWQKLEAFWAKHMWNF ISGIQYLAGLSTLPCNPAS								
4. HCV2b Consensus	AFDEMEECASHLPY IEQGMMLAEQFKQKALGLLQATKQAEV IAPAVQXNWQKLEAFWAKHMWNF ISGIQYLAGLSTLPCNPAS								
5. HCV 3 Consensus	QYDEMEECASHLPY IEQGMMLAEQFKQKALGLLQATKQAEV IAPAVQXNWQKLEAFWAKHMWNF ISGIQYLAGLSTLPCNPAS								
6. HCV 4 Consensus	QYDEMEECASHLPY IEQGMMLAEQFKQKALGLLQATKQAEV IAPAVQXNWQKLEAFWAKHMWNF ISGIQYLAGLSTLPCNPAS								
7. HCV5 Consensus	QYDEMEECASHLPY IEQGMMLAEQFKQKALGLLQATKQAEV IAPAVQXNWQKLEAFWAKHMWNF ISGIQYLAGLSTLPCNPAS								
8. HCV6 consensus	QYDEMEECASHLPY IEQGMMLAEQFKQKALGLLQATKQAEV IAPAVQXNWQKLEAFWAKHMWNF ISGIQYLAGLSTLPCNPAS								
9. HCV7: ABN05226	HFDMEECASHLPY IEQGMMLAEQFKQKALGLLQATKQAEV IAPAVQXNWQKLEAFWAKHMWNF ISGIQYLAGLSTLPCNPAS								
14. AV1a-129	EFDMEECASHLPY IEQGMMLAEQFKQKALGLLQATKQAEV IAPAVQXNWQKLEAFWAKHMWNF ISGIQYLAGLSTLPCNPAS								
15. AV13a-177	QYDEMEECASHLPY IEQGMMLAEQFKQKALGLLQATKQAEV IAPAVQXNWQKLEAFWAKHMWNF ISGIQYLAGLSTLPCNPAS								

	1,810	1,820	1,830	1,840	1,850	1,860	1,870	1,880	1,890
Consensus	LMAFTAAVTSPLTTSQTLLFNILGGWVASQLAPPTAATAFVVSGLAGAAVGSIGLGVKLVLDILAGYGAGVAGALVAFKIMSGEXPS								
	NS4b								
1. HCV1a consensus	LMAFTAAVTSPLTTSQTLLFNILGGWVAAQLAAPGAATAFVAGLAGAAAIGSVGLGVKLVLDILAGYGAGVAGALVAFKIMSGEVPS								
2. HCV1b consensus	LMAFTASITSPITTTQHTLLFNILGGWVAAQLAPPSAASAFVAGIAGAAVGSIGLGVKLVLDILAGYGAGVAGALVAFKIMSGEMPS								
3. HCV2a Consensus	MMAFSAALTSPITSTTTILLNILGGWLASQIAPPAGATGFVVSGLVGAAGVGSIGLGVKLVLDILAGYGAGISGALVAFKIMSGEKPS								
4. HCV2b Consensus	MMAFSAALTSPITSTTTILLNIMGGWLASQIAPPAGATGFVVSGLVGAAGVGSIGLGVKLVLDILAGYGAGISGALVAFKIMSGEKPS								
5. HCV 3 Consensus	LMAFTASVTSPLTTNQTMFFNILGGWVATHLAGPQSSAFVVSGLAGAAAIGGIGLGRVLLDILAGYGAGVSGALVAFKIMSGELPT								
6. HCV 4 Consensus	LMSFTAAVTSPLTTQHTLLFNILGGWVASQIATPTASTAFVVSGLAGAAVGSIGLGRVLDILAGYGAGVAGALVAFKIMSGERPT								
7. HCV5 Consensus	LMSFTAAVTSPLTTQHTLLFNILGGWVASQIAPPTAATAFVVSGLAGAAVGSIGLGRVLDILAGYGAGVAGALVAFKIMSGERPT								
8. HCV6 consensus	LMSFSASLTSPITSTTTLLNILGGWVASQLAPPTASTAFVVSGLAGAAVGSIGLGRVLDILAGYGAGVSGALVAFKIMSGETPA								
9. HCV7: ABN05226	LMAFTASVTSPLATSTLLVNILGGWFAASQLAPPSAATFVVSGLAGAAVGSIGLGVKLVLDILAGYGAGIAGALVAFKIMSGEVPS								
14. AV1a-129	LMAFTAAVTSPLTTSQTLLFNILGGWVAAQLAAPGAATAFVAGLAGAAAIGSVGLGVKLVLDILAGYGAGVAGALVAFKIMSGE?PS								
15. AV13a-177	LMAFTASVTSPLTTNQTMFFNILGGWVATHLAGPQSSAFVVSGLAGAAAIGGIGLGRVLLDILAGYGAGVSGALVAFKIMSGEIPT								

	1,900	1,910	1,920	1,930	1,940	1,950	1,960	1,970
Consensus	TEDLVNLLPAILSPGALVVGVCVCAAILRRHVGPCEGAVQWMNRLIAFASRCNHVSPHYVPESDAAARVTQILSSLTVTSLRLRLH							
	NS4b							

1. HCV1a consensus	TEDLVNLLPAILSPGALVVGVCVCAAILRRHVGPCEGAVQWMNRLIAFASRCNHVSPHYVPESDAAARVTQILSSLTVTQTLRLRLH							
2. HCV1b consensus	TEDLVNLLPAILSPGALVVGVCVCAAILRRHVGPCEGAVQWMNRLIAFASRCNHVSPHYVPESDAAARVTQILSSLTITQLLRLRLH							
3. HCV2a Consensus	MEDVVNLLPGILSPGALVVGVCVCAAILRRHVGPCEGAVQWMNRLIAFASRCNHVSPHYVPESDASQRTQLLGSITITSLRLRLH							
4. HCV2b Consensus	VEDVVNLLPAILSPGALVVGVCVCAAILRRHVGPCEGAVQWMNRLIAFASRCNHVSPHYVPESDASQRTQLLGSITITSLRLRLH							
5. HCV 3 Consensus	AEDMVNLLPAILSPGALVVGVCVCAAILRRHVGPCEGAVQWMNRLIAFASRCNHVSPHYVPESDAAARVTQILSSLTVTSLRLRLH							
6. HCV 4 Consensus	TEDLVNLLPAILSPGALVVGVCVCAAILRRHVGPCEGAVQWMNRLIAFASRCNHVSPHYVPESDAAARVTQILSSLTVTSLRLRLH							
7. HCV5 Consensus	AEDLVNLLPSILCPGALVVGVCVCAAIVLRRHIGPCEGAVQWMNRLIAFASRCNHVSPHYVPESDAAARVTQILSSLTVTSLRLRLH							
8. HCV6 consensus	XEDMVNLLPALILSPGALVVGVCVCAAILRRHVGPCEGAVQWMNRLIAFASRCNHVSPHYVPESDASQRTQLLGSITITSLRLRLH							
9. HCV7: ABN05226	TEDLVNLLPAILSPGALVVGVCVCAAIIKRHTGTSEGVQWMNRLIAFASRCNHVSPHYIQDDASAKRVMGILSSLTITSLIKRVL							
14. AV1a-129	TEDLVNLLPAILSPGALVVGVCVCAAILRRHVGPCEGAVQWMNRLIAFASRCNHVSPHYVPESDAAARVTQILSSLTVTQTLRLRLH							
15. AV13a-177	AEDMVNLLPAILSPGALVVGVCVCAAILRRHVGPCEGAVQWMNRLIAFASRCNHVSPHYVPESDAAARVTQILSSLTVTSLRLRLH							

	1,980	1,990	2,000	2,010	2,020	2,030	2,040	2,050	2,060
Consensus	QWINEDCSTPCSGSWLRDIWDWVCTVLSDFKTWLKALLPQLPGIPFLSCQRYKGVWRGDCVMHTRCPCGAEITGHVKNMGSMRIV								
	NS4b								
	NS5a								

1. HCV1a consensus	QWISSECTTPCSGSWLRDIWDWICEVLSDFKTWLKALLPQLPGIPFVSCQRYKGVWRGDCIMHTRCHCGAEITGHVKNMGSMRIV								
2. HCV1b consensus	QWINEDCSTPCSGSWLRDIWDWICTVLTDFKTWLQSKLLPRLPGVPFLSCQRYKGVWRGDCIMQTTCPGAGITGHVKNMGSMRIV								
3. HCV2a Consensus	NWITEDCPICAGSWLRDIWDWVCTILTDFKNWLTSLFKPMPLPFISCKQRYKGVWAGTGMTTRCPCGANISGNVRLGSMRIT								
4. HCV2b Consensus	AWITEDCPVPCSGSWLRDIWDWVCSILTDFKNWLTSLFKPMPLPFISCKQRYKGVWAGTGMTTRCPCGANISGNVRLGSMRIT								
5. HCV 3 Consensus	QWINEDCSTPCSGSWLRDIWDWVCTVLSDFKTWLKALLPQLPGIPFLSCQRYKGVWRGDCVMHTRCPCGAEITGHVKNMGSMRIV								
6. HCV 4 Consensus	QWINEDCSTPCAESWLRDIWDWVCTVLSDFKTWLKALLPQLPGIPFLSCQRYKGVWRGDCVMHTRCPCGAEITGHVKNMGSMRIV								
7. HCV5 Consensus	TWIGEDYSTPCDGTWLRDIWDWVCTALTDFKAWLQKLLPQLPGIPFLSCQRYKGVWRGDCVMHTRCPCGAEITGHVKNMGSMRIV								
8. HCV6 consensus	EWINXDWSTPCATSWLRDIWDWVCTVLSDFKTWLKALLPQLPGIPFLSCQRYKGVWRGDCVMHTRCPCGAEITGHVKNMGSMRIV								
9. HCV7: ABN05226	AWAQTDYSAPCAGSWLRDIWDWVCMVLSDFASWLRKAVLPSLPGIPFLSCQRYKGVWRGDCIMHTRCHCGAEITGHVKNMGSMRIV								
14. AV1a-129	QWISSECTTPCSGSWLRDIWDWICEVLSDFKTWLKALLPQLPGIPFVSCQRYKGVWRGDCIMHTRCHCGAEITGHVKNMGSMRIV								
15. AV13a-177	HWINEDYSPCSGSWLRDIWDWVCMVLSDFRTWLSAKIMPALPGLPFLSCQRYKGVWRGDCVMHTRCPCGAEITGHVKNMGSMRIV								

Consensus

2,070 2,080 2,090 2,100 2,110 2,120 2,130 2,140 2,150

GPKTCSTNTHGTFP INAYTTGPPXPPAPNYKRALWRVXAEYVEVRRVGDHFHYVTGXTTDLKCPQVPAPEFFTEVDGVLHRX

NS5a

1. HCV1a consensus
 2. HCV1b consensus
 3. HCV2a Consensus
 4. HCV2b Consensus
 5. HCV 3 Consensus
 6. HCV 4 Consensus
 7. HCV5 Consensus
 8. HCV6 consensus
 9. HCV7: ABN05226
 14. AV1a-129
 15. AV13a-177

3,160 3,170 3,180 3,190 3,200 3,210 3,220 3,230

APPCKPLLRDEVTFSVGLNSYVVGSQLPCEPEPDVAVLTSMLTDPISHITAETAARRLARGSPPLASSASQLSAPSLKATCTTHH

NS5a

Consensus

1. HCV1a consensus
 2. HCV1b consensus
 3. HCV2a Consensus
 4. HCV2b Consensus
 5. HCV 3 Consensus
 6. HCV 4 Consensus
 7. HCV5 Consensus
 8. HCV6 consensus
 9. HCV7: ABN05226
 14. AV1a-129
 15. AV13a-177

2,240 2,250 2,260 2,270 2,280 2,290 2,300 2,310 2,320

DHPDAEL IEANLLWRQEMGGNITRVESENKVV ILDSFDPLVAE-EDDRE ISVPAECLRKXR-KFPFALP IWARPDYNPPLLETWKR

NS5a

Consensus

1. HCV1a consensus
 2. HCV1b consensus
 3. HCV2a Consensus
 4. HCV2b Consensus
 5. HCV 3 Consensus
 6. HCV 4 Consensus
 7. HCV5 Consensus
 8. HCV6 consensus
 9. HCV7: ABN05226
 14. AV1a-129
 15. AV13a-177

DSPDAEL IEANLLWRQEMGGNITRVESENKVV ILDSFDPLVAE-EDERE ISVPAE ILRKSR-RFAPALP IWARPDYNPPLLETWKK

DSPDADL IEANLLWRQEMGGNITRVESENKVV ILDSFDPLRAE-EDEREVSVPAAE ILRKSR-KFPFAMP IWARPDYNPPLLESWKD

KTYDVMVDANLF- ---MGDDVTR IESESKVVILDSLDPM-AEERSDLEPS IPSEYMLPRN-RFPFALP IWARPDYNPPLVESWKR

MAYDCDMVDANLF- ---MGDDVTR IEESDSKV ILDSLDPM-TEVEDDDREPSVPSEYL IRRR-KFPFALP IWARPDYNPPLVETWKR

PHPDAELVDANLLWRQEMGGNITRVESETKVV ILDSFEPLRAE-TDDAELSVAAECFKPP-KYPPALP IWARPDYNPPLLDWRKA

DSPGTDLLEANLLW- ---GSTATRVEDEKVI ILDSFEPCVAEEDDDREVSAAE ILRPTK-KFPFALP IWARPDYNPPLLETWKK

HPDADL IEANLLWRQEMGGNITRVEAENKVV ILDSFEPLKXE-EDDRE ISVSAECFRGGP-AFPFALP IWARPDYNPPLLETWKR

DHPDAEL IEANLLWRQEMGGNITRVESENKVV ILDSFDPLVAE-YDDRE ISVSAECHRPPKFPFALP IWARPDYNPPLLETWKA

QHPDAEL IEANLLMWEHKVGA- IRRMETDKVI ILDSFDSA-SSVEDDMEPSTAAECLTRK-VFPFAMP IWARPDYNPPLVVENWKD

DSPDAEL IEANLLWRQEMGGNITRVESENKVV ILDSFDPLVAE-EDERE ISVPAE ILRKSR-RFTQALP IWARPDYNPPLVEAWKK

PHPDAELVDANLLWRQEMGGNITRVESETKVV ILDSFEPLRAE-ADDAELSVAAECFKPP-KYPPALP IWARPDYNPPLLDWRKT

Consensus	2,330	2,340	2,350	2,360	2,370	2,380	2,390	2,400
PDYEPPTVHGCGALPPPPXAPPVPPRRK-RTVXLTESTVSTALAEAEKSFSGSXXSXSGXDTTSSXXSXPP-DCDAXSDAE								
	NS5a							
1. HCV1a consensus	PDYEPVVHGGCLPPPPQSPVPPRRK-RTVVLTESTVSTALAEATKFGSSSTSGI----	TCGNTTTSSEPAPS-GCPDSDAE						
2. HCV1b consensus	PDYVPVVHGGCLPPPTKAPP IPPRRK-RTVVLTESTVSSALAEATKFGSSESA-----	VDSGTATAPDQPSDDGADSDVE						
3. HCV2a Consensus	PDYQPTVAGCALPPPKTPTPPRRR-RTVGLSESTIGDALQQLAIKTFGQPPSGDSLSTGADAAADSGRTTP-DELAISGTG							
4. HCV2b Consensus	PGYEPPTVHGCGALPPTPQAPVPPRRR-RAKVLTDQNVGVLREMAKVLSPQDHNDSGHSTGADTGDSVQPPS-DETAASEAG							
5. HCV 3 Consensus	PDYPPPTVHGCGALPPRGAAPPVPPRRK-RTIQLDGSNVSAALAEAKSFPSKQPEENSSSGVDTQSSSTSKVPPSPGGESDSE							
6. HCV 4 Consensus	QDYKPTVHGCGALPPSKQPPVPPRRK-RTVQLTESVSTALAEALAEAKTFGQSELGDSGADLTGPTETDTSGP ILVDDA-SDDG							
7. HCV5 Consensus	PDYDPQVSGCCLPPAGLPPVPPRRKRPVLSSTVSVQVLADLADARF-KXDTPS IEGQDSAVGTSSQXDSGPEEKRDDXSDAA							
8. HCV6 consensus	PDYEPVVSVCALPPGPP IPPRRK-KVHLDESTVSHALAEAKSFPESSSDTS-SDSGLSITSSGSPETTTDDACSEAG							
9. HCV7: ABN05226	PEYAPPQVSGCALPPAQTTPVPPRRKRAVIQLTESAVSTALAEALAEAKSFPESSSDTS-SDSA ISLSDSPAANDPPSD CDQGEI-							
14. AV1a-129	PDYEPVVHGGCLPPPKSPVPPRRK-RTVVLTESTVSTALAEATKFGSSTSGI----	TCGNTTTSSEPAPP-GCSPDSDAE						
15. AV13a-177	PDYVPPTVHGCGALPPRGAAPPVPPRRK-RTVQLDGSNVSAALAEAKSFPSLEPQGENSSSGIDIQSSTASEVPPSPGEGSDSE							
	2,410	2,420	2,430	2,440	2,450	2,460	2,470	2,480
SYSSMPPLEGEPDPLSD-----								
Consensus	NS5a							
	NS5b							
1. HCV1a consensus	SYSSMPPLEGEPDPLSD-----	GSWSTVSSEADTEDVVC CSMSYSWTGALVTPCAAAEQKLPINALSNS						
2. HCV1b consensus	SYSSMPPLEGEPDPLSD-----	GSWSTVSEAS-EDVVCMSYSWTGALITPCAAEEESKLPINALSNS						
3. HCV2a Consensus	SYSSMPPLEGEPDPLPEQVELQPPQGGEVAPGSDSGSWSTCSEED--	DVVCMSYSWTGALITPCSPPEEEKLPINALSNS						
4. HCV2b Consensus	SYSSMPPLEGEPDPLFEFEPAGSAPPSEGECEV IDSLSKSWSTVSDQE--	DSVICCSMSYSWTGALITPCGPEEEKLPINALSNS						
5. HCV 3 Consensus	SYSSMPPLEGEPDPLSCDQVELQPPQGGVAPGSGSWSTVSDSEE--	QSVCCMSYSWTGALITPCSAEEEEKLPISPLSNS						
6. HCV 4 Consensus	SYSSMPPLEGEPDPLTSDQVELQPPQGGVAPGSGSWSTVSGSE--	DTVCCMSYSWTGALVTPCAAAEEESKLPISPLSNS						
7. HCV5 Consensus	SYSSMPPLEGEPDPLSS-----	GSWSTVSDE--DSVVCMSYSWTGALITPCSAEEEEKLPINPLSNT						
8. HCV6 consensus	SYSSMPPLEGEPDPLSS-----	GSWSTVSEE--DSVVCMSYSWTGALITPCAAEEEEKLPINPLSNS						
9. HCV7: ABN05226	SFSSMPPLEGEPDPLSD-----	GSWSTVSTR--SDVICCSMSYSWTGALVTPSGPEEEERLPINALSNT						
14. AV1a-129	SYSSMPPLEGEPDPLSD-----	GSWSTVSSEADTEDVVCMSYSWTGALITPCAAEEEQKLPINALSNS						
15. AV13a-177	SCTSMPPLEGEPDPLSC-----	DSWSTVSDSEE--QSVCCMSYSWTGALITPCSAEEEEKLPISPLSNS						
	2,500	2,510	2,520	2,530	2,540	2,550	2,560	2,570
LLRHHNLVYSTTSRSASQRQKKVTFDRQLQVLDDHYXDVLKEVKAKASKVKARLLSVEEACALTPPHSARSKFCYGAKDVRSLSRKA								
Consensus	NS5b							
1. HCV1a consensus	LLRHHNLVYSTTSRSACQRQKKVTFDRQLQVLDDSHYQDVLKEVKAAASKVKANLLSVEEACSLTPPHSAKSKFCYGAKDVRSLSRKA							
2. HCV1b consensus	LLRHHNMVYATTSRSASQRQKKVTFDRQLQVLDDHYDVLKEMKAKASTVKAKLLSVEEACKLTTPPHSARSKFCYGAKDVRSLSRKA							
3. HCV2a Consensus	LLRYHNKVYCTTSKASLRQKKVTFDRMQVLDAHYDSVLKD IKLAASKVSARLLTLEEACQLTPPHSARSKYFGGAKDVRSLSGRA							
4. HCV2b Consensus	LMRFHNKVYSTTSRSASLRQKKVTFDRVQVLDAHYDSVLQDVKRAASKVSARLLSVEEACALTPPHSAKSKFCYGAKDVRSLSRRA							
5. HCV 3 Consensus	LLRHHNLVYSTTSRSASQRQKKVTFDRQLQVLDDHYKLTALKEIKERASRVKARMLTIEEACALTPPHSARSKFCYGAKDVRSLSRKA							
6. HCV 4 Consensus	LLRHHNMVYATTSRSATVRQKKVTFDRQLQVLDDHYNETLKEIKERASRVKARMLTIEEACDLTPPHSAKSKFCYGAKDVRSLSRKA							
7. HCV5 Consensus	LLRHHNLVYSTTSRSAGLRQKKVTFDRQLQVLDDHYREVVDKRLASKVKARLLPLEEACGLTPPHSARSKYFGGAKDVRSLSRKA							
8. HCV6 consensus	LLRHHNLVYSTTSRSASLRQKKVTFDRVQVLDDHYQDVLKEIKLRASQVQARLLSVEEACDLTPPHSARSKFCYGAKDVRSLSHASKA							
9. HCV7: ABN05226	MLRHHNLVYSTTSRSASQRQKKVTFDRQLQVLDDHYKRALADVKADASTVKAQLLSVEEAAALTPPHSARSKFCYGAKDVRSLSAPKA							
14. AV1a-129	LLRHHNLVYSTTSRSACQRQKKVTFDRQLQVLDDHYQDVLKEVKAAASKVKANLLSVEEACSLTPPHSAKSKFCYGAKDVRSLSRKA							
15. AV13a-177	LLRHHNLVYSTTSRSASQRQKKVTFDRQLQVLDDHYKAVLKEVKERASRVKARMLTIEEACALVPPPHSARSKFCYGAKDVRSLSGRA							

Consensus
VNHIKXSVWXLLEDSTTP IPTT IMAKNEVFCVDPKXGGRKPARL IVYPDL -GVRVCEKRALYDVXQKLPKAVMGSSYGFQYSPAQR
NS5b
2,590 2,600 2,610 2,620 2,630 2,640 2,650 2,660
1. HCV1a consensus VNHIKXSVWXLLEDSTTP IDTT IMAKNEVFCVQPEKGGKPPARL IVFPDL -GVRVCEKRALYDVVSKPLAVMGSSYGFQYSPGQR
2. HCV1b consensus VNHIKXSVWXLLEDSTTP IDTT IMAKNEVFCVQPEKGGKPPARL IVFPDL -GVRVCEKRALYDVVSKPLAVMGSSYGFQYSPGQR
3. HCV2a Consensus VNHIKXSVWXLLEDSTTP IPTT IMAKNEVFCVDPKXGGRKPARL IVYPDL -GVRVCEKRALYDVXQKLPKAVMGSSYGFQYSPAQR
4. HCV2b Consensus VNHIKXSVWXLLEDSTTP IDTT IMAKNEVFCVDPKXGGRKPARL IVYPDL -GVRVCEKRALYDVXQKLPKAVMGSSYGFQYSPAQR
5. HCV 3 Consensus VNHIKXSVWXLLEDSTTP IPTT IMAKNEVFCVDPKXGGRKPARL IVYPDL -GVRVCEKRALYDVXQKLPKAVMGSSYGFQYSPAQR
6. HCV 4 Consensus VNHIKXSVWXLLEDSTTP IPTT IMAKNEVFCVDPKXGGRKPARL IVYPDL -GVRVCEKRALYDVXQKLPKAVMGSSYGFQYSPAQR
7. HCV5 Consensus VNHIKXSVWXLLEDSTTP IPTT IMAKNEVFCVDPKXGGRKPARL IVYPDL -GVRVCEKRALYDVXQKLPKAVMGSSYGFQYSPAQR
8. HCV6 consensus VNHIKXSVWXLLEDSTTP IPTT IMAKNEVFCVDPKXGGRKPARL IVYPDL -GVRVCEKRALYDVXQKLPKAVMGSSYGFQYSPAQR
9. HCV7: ABN05226 VNHIKXSVWXLLEDSTTP IDTT IMAKNEVFCVQPEKGGKPPARL IVYPDL -GVRVCEKRALYDVXQKLPKAVMGSSYGFQYSPAQR
14. AV1a-129 VNHIKXSVWXLLEDSTTP IDTT IMAKNEVFCVQPEKGGKPPARL IVYPDL -GVRVCEKRALYDVXQKLPKAVMGSSYGFQYSPAQR
15. AV13a-177 VNHIKXSVWXLLEDSTTP IPTT IMAKNEVFCVDPKXGGRKPARL IVYPDL -GVRVCEKRALYDVXQKLPKAVMGSSYGFQYSPAQR
Consensus
VEFLKAWKSKKTPMG--FSYDTRCFDSTVT-EXD IRTEEXIYQCCDLDPQARVAIKSLTERLYVGGPMXNSKQXCGYRRCRASG
NS5b
2,670 2,680 2,690 2,700 2,710 2,720 2,730 2,740 2,750

Consensus
VEFLVQAWKSKKTPMG--FSYDTRCFDSTVT-ESD IRTEEAIVQCCDLDPQARVAIKSLTERLYVGGPLTNSRGENCYRRRCRASG
1. HCV1a consensus VEFLVQAWKSKKTPMG--FSYDTRCFDSTVT-ESD IRTEEAIVQCCDLDPQARVAIKSLTERLYVGGPLTNSRGENCYRRRCRASG
2. HCV1b consensus VEFLVQAWKSKKTPMG--FSYDTRCFDSTVT-ESD IRTEEAIVQCCDLDPQARVAIKSLTERLYVGGPLTNSRGENCYRRRCRASG
3. HCV2a Consensus VEFLVQAWKSKKTPMG--FSYDTRCFDSTVT-ERD IRTEESIVQACSLPEEARTAIHSLTERLYVGGPMFNSKQTCGYYRRCRASG
4. HCV2b Consensus VEFLVQAWKSKKTPMG--FSYDTRCFDSTVT-ERD IRTEESIVQACSLPEEARTAIHSLTERLYVGGPMFNSKQTCGYYRRCRASG
5. HCV 3 Consensus VERLLKMWTSKKTPLGVLFSYDTRCFDSTVTGEQD IRVEEIVQCCNLEPEARKV ISSLTERLYCGGPMFNSKQTCGYYRRCRASG
6. HCV 4 Consensus VEFLVQAWKSKKTPMG--FSYDTRCFDSTVT-ERD IRTEEAIVQCCDLDPQARVAIKSLTERLYVGGPMFNSKQTCGYYRRCRASG
7. HCV5 Consensus VEFLVQAWKSKKTPMG--FSYDTRCFDSTVT-ERD IRTEEAIVQCCDLDPQARVAIKSLTERLYVGGPMFNSKQTCGYYRRCRASG
8. HCV6 consensus VEFLVQAWKSKKTPMG--FSYDTRCFDSTVT-ERD IRTEEAIVQCCDLDPQARVAIKSLTERLYVGGPMFNSKQTCGYYRRCRASG
9. HCV7: ABN05226 VEFLVQAWKSKKTPMG--FSYDTRCFDSTVT-ERD IRTEEAIVQCCDLDPQARVAIKSLTERLYVGGPMFNSKQTCGYYRRCRASG
14. AV1a-129 VEFLVQAWKSKKTPMG--FSYDTRCFDSTVT-ERD IRTEEAIVQCCDLDPQARVAIKSLTERLYVGGPMFNSKQTCGYYRRCRASG
15. AV13a-177 VERLLEMWTSKKTPLGVLFSYDTRCFDSTVT-ERD IRTEEAIVQCCDLDPQARVAIKSLTERLYVGGPMFNSKQTCGYYRRCRASG
Consensus
VLTSMGNTLTCYIKAXAACRAAGLRDCTMLVCGDDLTVV ICESAGVZEDAAXLRAFTEAMTR-----YSAPPGDPP-----QPEYD
NS5b
2,760 2,770 2,780 2,790 2,800 2,810 2,820 2,830

Consensus
VLTSMGNTLTCYIKAXAACRAAGLRDCTMLVCGDDLTVV ICESAGVZEDAAXLRAFTEAMTR-----YSAPPGDPP-----QPEYD
1. HCV1a consensus VLTSMGNTLTCYIKAXAACRAAGLRDCTMLVCGDDLTVV ICESAGVZEDAAXLRAFTEAMTR-----YSAPPGDPP-----QPEYD
2. HCV1b consensus VLTSMGNTLTCYIKAXAACRAAGLRDCTMLVCGDDLTVV ICESAGVZEDAAXLRAFTEAMTR-----YSAPPGDPP-----QPEYD
3. HCV2a Consensus VLTSMGNTLTCYIKAXAACRAAGLRDCTMLVCGDDLTVV ICESAGVZEDAAXLRAFTEAMTR-----YSAPPGDPP-----QPEYD
4. HCV2b Consensus VLTSMGNTLTCYIKAXAACRAAGLRDCTMLVCGDDLTVV ICESAGVZEDAAXLRAFTEAMTR-----YSAPPGDPP-----QPEYD
5. HCV 3 Consensus VLTSMGNTLTCYIKAXAACRAAGLRDCTMLVCGDDLTVV ICESAGVZEDAAXLRAFTEAMTR-----YSAPPGDPP-----QPEYD
6. HCV 4 Consensus VLTSMGNTLTCYIKAXAACRAAGLRDCTMLVCGDDLTVV ICESAGVZEDAAXLRAFTEAMTR-----YSAPPGDPP-----QPEYD
7. HCV5 Consensus VLTSMGNTLTCYIKAXAACRAAGLRDCTMLVCGDDLTVV ICESAGVZEDAAXLRAFTEAMTR-----YSAPPGDPP-----QPEYD
8. HCV6 consensus VLTSMGNTLTCYIKAXAACRAAGLRDCTMLVCGDDLTVV ICESAGVZEDAAXLRAFTEAMTR-----YSAPPGDPP-----QPEYD
9. HCV7: ABN05226 VLTSMGNTLTCYIKAXAACRAAGLRDCTMLVCGDDLTVV ICESAGVZEDAAXLRAFTEAMTR-----YSAPPGDPP-----QPEYD
14. AV1a-129 VLTSMGNTLTCYIKAXAACRAAGLRDCTMLVCGDDLTVV ICESAGVZEDAAXLRAFTEAMTR-----YSAPPGDPP-----QPEYD
15. AV13a-177 VLTSMGNTLTCYIKAXAACRAAGLRDCTMLVCGDDLTVV ICESAGVZEDAAXLRAFTEAMTR-----YSAPPGDPP-----QPEYD

	2,840	2,850	2,860	2,870	2,880	2,890	2,900	2,910	2,920
Consensus	LELITSCSSNVSAHDXSGKRVYYLTRDPTTPLARAASETARHTP---VNSWLGNIIMYAPT IWVRMVLMTHTFFS ILQXQEQLXAXA								
	NS5b								
1. HCV1a consensus	LELITSCSSNVSAHDGAGKRVYYLTRDPTTPLARAASETARHTP---VNSWLGNIIMFAPTLWARMILMTHTFFSVLIARDQLEQA								
2. HCV1b consensus	LELITSCSSNVSAHDASGKRVYYLTRDPTTPLARAASETARHTP---VNSWLGNIIMYAPT LWARMILMTHTFFS ILLAQEQLEKA								
3. HCV2a Consensus	LELITSCSSNVSAVGPGQRRYYLTRDPTTPIARAASETVRHSP---VNSWLGNI IQYAPT IWVRMVLMTHTFFS ILLMAQDTLDQN								
4. HCV2b Consensus	LELITSCSSNVSAVDSDRGRRYYLTRDPTTPIARAASETVRHSP---VNSWLGNI IQYAPT IWVRMVIMTHFFS ILLAQDTLNQN								
5. HCV 3 Consensus	LELITSCSSNVSAVDNKGKRYYYLTRDATTPLARAASETARHTPGVNSWLGNIIMYAPT IWVRMVMTHFFS ILQSQEILDRP								
6. HCV 4 Consensus	LELITSCSSNVSAHDAATGKRVYYLTRDPEPTPLARAASETARHTP---VNSWLGNIIMYAPT IWVRMVLMTHTFFS ILQSQEALKA								
7. HCV5 Consensus	LELITSCSSNVSAHDASGNRVYYLTRDQVPLARAASETAKHSP---VNSWLGNIIMYAPT LWARMILMTHTFFS ILQSQEQLEKA								
8. HCV6 consensus	LELITSCSSNVSAHDGTGQRYYYLTRDPTTPLARAASETARHTP---VNSWLGNIIMYAPT IWVRMVLMTHTFFQ ILQSQEQLEKA								
9. HCV7: ABN05226	LEHIDSCSSNVSAVDNSGKRVYYLTRDPTNPLSRAASETARHSP---VNSWVGNIIIMFAPT IWVRMVLMTHTFFS ILLNEERLNDP								
14. AV1a-129	LELITSCSSNVSAHDGAGKRVYYLTRDPTTPLARAASETARHTP---VNSWLGNIIMFAPT LWARMVLMTHTFFS IARDQLEQA								
15. AV13a-177	LELITSCSSNVSAVDNKGKRYYYLTRDATTPLARAASETARHTP---VNSWLGNIIMYAPT IWVRMVMTHFFS ILQSQEILDRP								
	2,930	2,940	2,950	2,960	2,970	2,980	2,990	3,000	3,010
Consensus	LDFEMYGATYSVTPLDLPAAIIQRLHGLSAFSLHSYSPCELNRVAACLRKLGVPPPLRAWRHRARAVRAKLIAQGGRAAICGKYLFWN								
	NS5b								
1. HCV1a consensus	LDCEIYGACYSIEPLDLPPIIQLHGLSAFSLHSYSPGEINRVAACLRKLGVPPPLRAWRHRARSVRARLLSRGGRAAICGKYLFWN								
2. HCV1b consensus	LDCQIYGACYSIEPLDLPPIIQLHGLSAFSLHSYSPGEINRVASCLRKLGVPPPLRVWRHRARSVRARLLSQGGRAATCGKYLFWN								
3. HCV2a Consensus	LNFEMYGVSYSVPLDLPAAIIERLHGLDAFSLHTYTPHELTRVASALRKLGVPPPLRAWKSRARAVRASLISRGGRAAICGKYLFWN								
4. HCV2b Consensus	LNFEMYGAVYSVNPLDLPAAIIERLHGLDAFSLHTYSPHELSTRVAATLRKLGVPPPLRAWKSRARAVRASLISRGGRAAICGKYLFWN								
5. HCV 3 Consensus	LDFEMYGATYSVTPLDLPAAIIERLHGLSAFTLHSYSPVELNRVAGTLRKLGVPPPLRAWRHRARAVRAKLIAQGGKAKICGLYLFWN								
6. HCV 4 Consensus	LDFDMYGVYSITPLDLPAAIIQLHGLSAFTLHGYSPHELNRVAGSLRKLGVPPPLRAWRHRARAVRAKLIAQGGKAKICGLYLFWN								
7. HCV5 Consensus	LAFEMYGSVYSVTPLDLPAAIIQLHGLSAFSLHSYSPSEINRVASCLRKLGVPPPLRAWRHRARAVRAKLIAQGGKAAICGIYLFNW								
8. HCV6 consensus	LDFDIYGVYSITPLDLPAAIIQLHGLMAAFSLHGYSPCELNRVAACLRKLGVPPPLRAWRHRARAVRAKLIAQGGKAAICGKYLFWN								
9. HCV7: ABN05226	VSFEMYGATYTCPTDLPPIIQLHGLRAFAELHTYSPAELTRVAATLRKLGVPPPLRTWRQARAVRAKLIGQGGRAAICGKYLFWN								
14. AV1a-129	LDCEIYGACYSIEPLDLPPIIQLHGLSAFSLHSYSPGEINRVAACLRKLGVPPPLRTWRHRARSVRARLLSRGGRAAICGKYLFWN								
15. AV13a-177	LDFEMYGATYSVTPLDLPAAIIERLHGLSAFTLHSYSPVELNRVAGTLRKLGVPPPLRAWRHRARAVRAKLIAQGGKAKICGLYLFWN								
	3,020	3,030	3,040	3,050	3,060	3,070	3,080	3,090	3,100
Consensus	AVRTKLLTLPAAQXLDLSSWFTVAGCGDIYHSVSRARPRWLLLCILLXVGVGIFLLPARX								
	NS5b								
1. HCV1a consensus	AVRTKLLTLPAAQQLDLSGWFTAGYSGGDIYHSVSHARPRWFVFCILLAAAGVG IYLLPNRX								
2. HCV1b consensus	AVRTKLLTLPAAQQLDLSGWFTAGYSGGDIYHSLSRARPRWFVFCILLXVGVG IYLLPNRX								
3. HCV2a Consensus	AVTKLLTLPPEARLLDLSWFTVAGCGDIYHSVSRARPRWLLLCILLXVGVG IYLLPNRX								
4. HCV2b Consensus	AVTKLLTLPPEARLLDLSWFTVAGCGDIFHSVSHARPRWLLLCILLXVGVG IYLLPNRX								
5. HCV 3 Consensus	AVRTKLLTLPAAQQLDLSWFTVAGCGDIYHSVSRARPRWLLLCILLXVGVG IYLLPNRX								
6. HCV 4 Consensus	AVTKLLTLPAAANLDLSWFTVAGCGDIYHSVSRARPRWLLLCILLXVGVG IYLLPNRX								
7. HCV5 Consensus	AVTKRLLTPLADRLDLSWFTVAGCGDIYHSMRARPRWLLLCILLXVGVG IYLLPNRX								
8. HCV6 consensus	AVTKLLTPLRGASKLDLSGWFTAGYSGGDIYHSVSRARPRWLLLCILLXVGVG IYLLPNRX								
9. HCV7: ABN05226	AVRTKLLTPLAGAGRLDLSWFTVAGCGDIYHSVSHARPRWFVFCILLAAAGVG IYLLPNRX								
14. AV1a-129	AVRTKLLTLPAAQQLDLSGWFTAGYSGGDIYHSVSHARPRWFVFCILLAAAGVG IYLLPNRX								
15. AV13a-177	AVRTKLLTLPAAQQLDLSWFTVAGCGDIYHSVSRARTRHLLLCILLXVGVG IYLLPNRX								

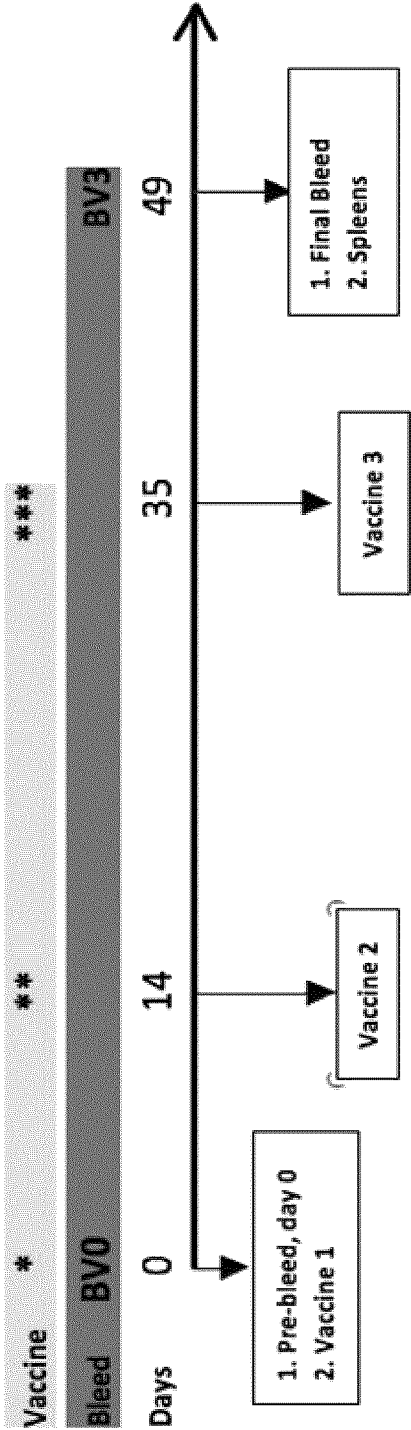


FIG. 13

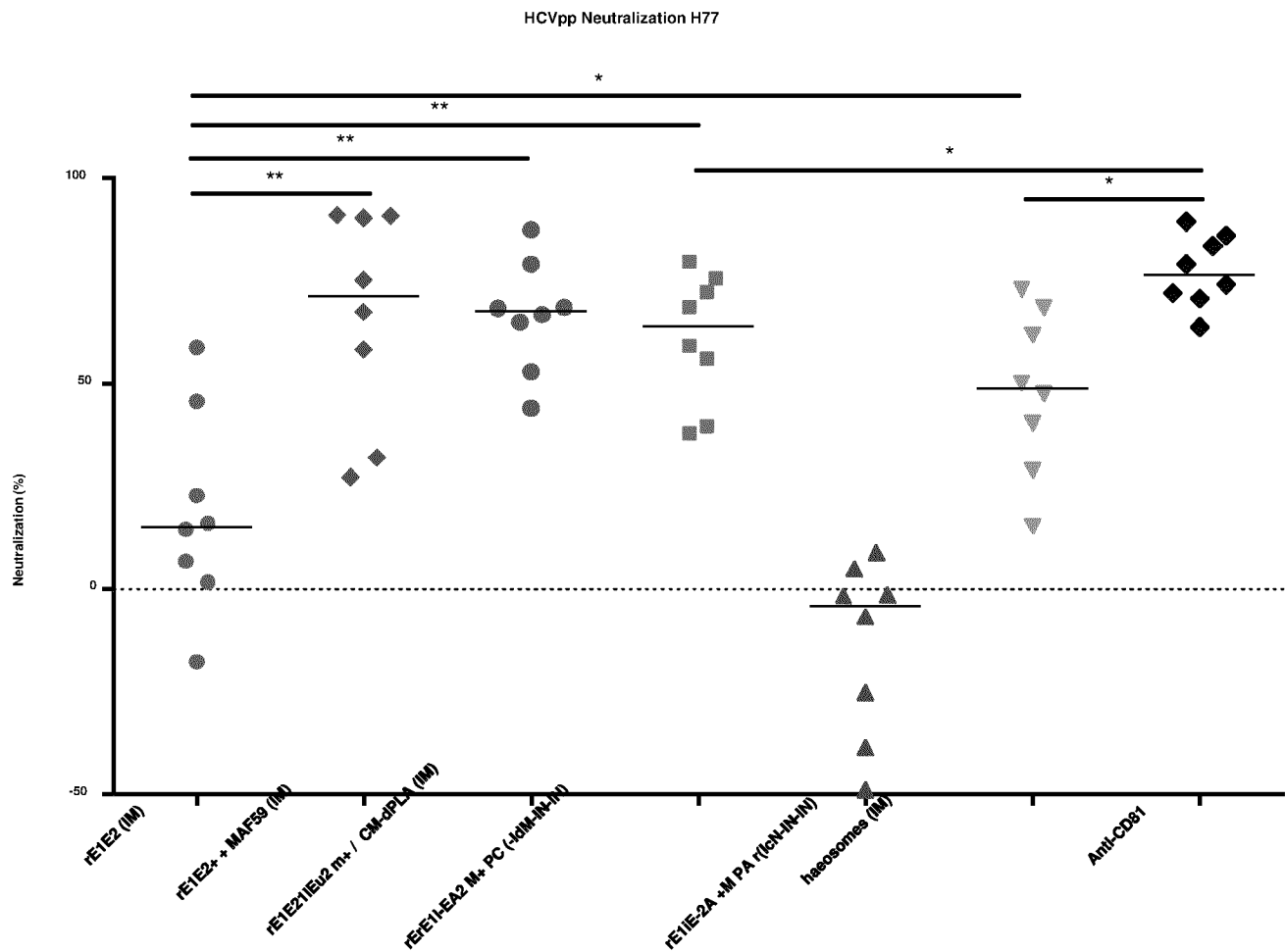


FIG. 14

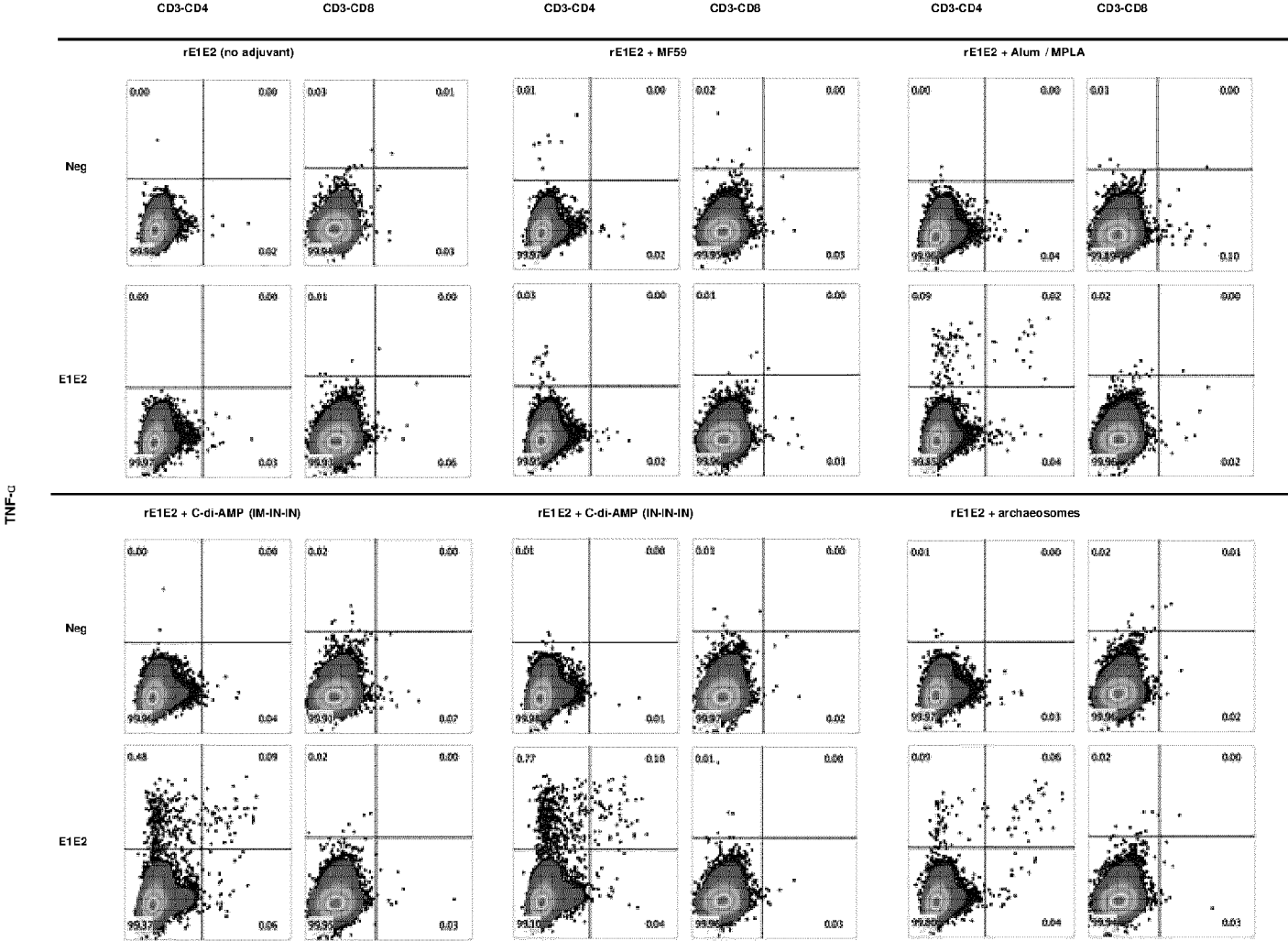


FIG. 15

INTERNATIONAL SEARCH REPORT

International application No.

PCT/CA2017/051192

A. CLASSIFICATION OF SUBJECT MATTER

IPC: **A61K 39/39** (2006.01), **A61K 39/00** (2006.01), **A61K 39/29** (2006.01), **A61P 31/14** (2006.01), **A61P 37/04** (2006.01), **C01F 11/02** (2006.01), **C07D 323/00** (2006.01) (more IPCs on page 8/9)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
All IPC classifications searched

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic database(s) consulted during the international search (name of database(s) and, where practicable, search terms used)

Database: Scopus, Orbit, STN, CIPO patent database, CIPO Library Discovery Tool

Keywords: HCV, Hepatitis, cyclic, dinucleotide, adjuvant, amp, gmp, Houghton, Landis, vaccine, archaeosomes, E1, E2, T-cell epitope, archaeal lipid, polar synthetic lipid, immunogenic composition

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO03002065 A2 (HOUGHTON, M. et al.) 9 January 2003 (09-01-2003) See whole document	1-136
Y	WO2015132619 A1 (HOUGHTON, M. et al.) 11 September 2015 (11-09-2015) See whole document	1-136
Y	WO2007121491 A1 (VON GABAIN, A. et al.) 1 November 2007 (01-11-2007) See whole document	1-136
Y	WO2014189805 A1 (DUBENSKY, T. et al.) 27 November 2014 (27-11-2014) See whole document and especially paragraphs [0016], [0020], [0083], [00157], and Table 1	1-40 and 92-108
Y	WO2005087238 A2 (KARAOLIS, D.) 22 September 2005 (22-09-2005) See whole document and especially paragraphs [0044], [0052], [0069], and [0086]	1-40 and 92-108

☒ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

* "A" "E" "L" "O" "P"	Special categories of cited documents: document defining the general state of the art which is not considered to be of particular relevance earlier application or patent but published on or after the international filing date document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) document referring to an oral disclosure, use, exhibition or other means document published prior to the international filing date but later than the priority date claimed	"T" "X" "Y" "&"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art document member of the same patent family
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Date of the actual completion of the international search
07 December 2017 (07-12-2017)

Date of mailing of the international search report
10 January 2018 (10-01-2018)

Name and mailing address of the ISA/CA
Canadian Intellectual Property Office
Place du Portage I, C114 - 1st Floor, Box PCT
50 Victoria Street
Gatineau, Quebec K1A 0C9
Facsimile No.: 819-953-2476

Authorized officer

Robin Green (819) 639-7813

INTERNATIONAL SEARCH REPORT

International application No.

PCT/CA2017/051192

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO2007112567 A1 (SPROTT, D. et al.) 11 October 2007 (11-10-2007) See whole document and especially page 3, line 30 to page 5, line 29; page 10, lines 9-26; page 11, lines 6-10; page 13, lines 18-25; page 17, line 30 to page 18, line 10; and page 21, line 3 to page 37, line 29	41-91 and 109-136
Y	HAQ, K. et al., "Archael lipid vaccine adjuvants for induction of cell-mediated immunity". Expert Rev. Vaccines. 8 June 2016 (08-06-2016), Vol. 15(12), pp. 1557-1566 See whole document and especially	41-91 and 109-136
A	MA, X. et al., "DNA-based vaccination against hepatitis C virus (HCV) : effect of expressing different forms of HCV E2 protein and use of CpG-optimized vectors in mice". Vaccine. 2002, Vol. 20, pp. 3263-3271	1-40 and 92-108
A	FREY, S. et al., "Safety and immunogenicity of HCV E1E2 vaccine adjuvanted with MF59 administered to healthy adults". Vaccine. 7 July 2010 (07-06-2010), Vol. 28, pp. 6367-6373	1-136
A	WO0126683 A2 (SPROTT, D. et al.) 19 April 2004 (19-04-2004)	41-91 and 109-136
A	US6121020 A (SELBY, M. et al.) 19 September 2000 (19-09-2000)	1-136
A	DUBENSKY, T. et al., "Rationale, progress and development of vaccines utilizing STING-activating cyclic dinucleotide adjuvants". Theor. Adv. Vaccines, 2013, Vol. 1(4), pp. 131-143 See whole document, especially page 137 and conclusion	1-40 and 92-108
A	AGHASADEGHI, M. R. et al., "Induction of strong and specific humoral and T-helper 1 cellular responses by HBsAg entrapped in the Methanobrevibacter smithii archaeosomes". Avicenna J. med. Biotech. 2014, Vol. 6(4), pp. 238-245 See whole document	41-91 and 109-136
T	LANDI, A. et al., "Superior immunogenicity of HCV envelope glycoproteins when adjuvanted with cyclic-di-AMP, a STING activator or archaeosomes", Vaccine, Epub 28 October 2017 (28-10-2017), 35(50), Pages 6949-6956	1-136

INTERNATIONAL SEARCH REPORT

International application No.

PCT/CA2017/051192**Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of the first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

The claims are directed to a plurality of inventive concepts as follows:

Group A: Claims 1-17 (in whole) and claims 18-40 (in part) are directed to an immunogenic composition comprising (a) Hepatitis C virus (HCV) E1 polypeptide; (b) HCV E2 polypeptide; or (c) HCV E1/E2 heterodimer, and a cyclic dinucleotide;

See continuation of Box No. III (extra sheet)

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claim Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claim Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

Continuation of Box No. III (Unity)

Group B: Claims 41-68 (in whole) and claims 69-91 (in part) are directed to an immunogenic composition comprising (a) Hepatitis C virus (HCV) E1 polypeptide; (b) HCV E2 polypeptide; or (c) HCV E1/E2 heterodimer, and an archaeosome comprising at least one polar synthetic lipid, wherein the at least one polar synthetic lipid comprises at least one carbohydrate or anionic group linked by covalent bonding to at least one free hydroxyl group of an archaeal core lipid;

Group C: Claims 92-108 (in whole) and claims 18-40 (in part) are directed to an immunogenic composition comprising a T cell epitope polypeptide comprising a T cell epitope present in a HCV protein other than E1 and E2, and a cyclic dinucleotide; and

Group D: Claims 109-136 (in whole) and claims 69-91 (in part) are directed to an immunogenic composition comprising a T cell epitope polypeptide comprising a T-cell epitope present on a HCV protein other than E1 and E2, and an archaeosome comprising at least one polar synthetic lipid, wherein the at least one polar synthetic lipid comprises at least one carbohydrate or anionic group linked by covalent bonding to at least one free hydroxyl group of an archaeal core lipid.

In view of *a priori* consideration, the claims do not appear to be linked by a single special technical feature and are directed to four distinct and separable alleged inventions. Moreover, in view of *a posteriori* consideration vaccines comprising HCV E1 and E2 polypeptides are known in the art (US6121020), as too are vaccines containing HCV T-cell epitope polypeptides other than E1 and E2 (WO2007/121491). Furthermore, the use of cyclic dinucleotides as an adjuvant in a vaccine (WO2005087238), and the use of archaeal lipids as vaccine adjuvants (Haq, K et al. "Archaeal lipid vaccine adjuvants for induction of cell mediated immunity", Expert reviews of vaccines. 8 June 2016 (08-06-2016), 15(12), Pages 1557-1566) are also known in the art. As such, the subject matter of the claims are not so linked because there does not appear to be an inventive special technical feature common to the groups of claims defined above.

Continuation of IPC's codes:

C07K 14/18 (2006.01), **C07K 14/28** (2006.01), **C07K 14/33** (2006.01), **C07K 14/34** (2006.01)

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.
PCT/CA2017/051192

Patent Document Cited in Search Report	Publication Date	Patent Family Member(s)	Publication Date
WO03002065A2	09 January 2003 (09-01-2003)	WO03002065A2 WO03002065A3 AU2002322358B2 CA2451739A1 CN1636015A CN1931365A CZ20033515A3 EP1572124A2 EP1572124A4 HU0400346A2 JP2005502611A JP4370161B2 JP2005298523A NZ530632A PL367526A1 RU2004102520A RU2316347C2 SK15762003A3 US2003138458A1 US2005255124A1 US2009258033A1	09 January 2003 (09-01-2003) 19 April 2007 (19-04-2007) 18 June 2009 (18-06-2009) 09 January 2003 (09-01-2003) 06 July 2005 (06-07-2005) 21 March 2007 (21-03-2007) 12 January 2005 (12-01-2005) 14 September 2005 (14-09-2005) 28 November 2007 (28-11-2007) 28 August 2007 (28-08-2007) 27 January 2005 (27-01-2005) 25 November 2009 (25-11-2009) 27 October 2005 (27-10-2005) 27 April 2007 (27-04-2007) 21 February 2005 (21-02-2005) 10 June 2005 (10-06-2005) 10 February 2008 (10-02-2008) 03 January 2005 (03-01-2005) 24 July 2003 (24-07-2003) 17 November 2005 (17-11-2005) 15 October 2009 (15-10-2009)
WO2015132619A1	11 September 2015 (11-09-2015)	WO2015132619A1 AU2014385320A1 CA2909586A1 CL2015003333A1 CN105263517A EP2996718A1 EP2996718A4 HK1216395A1 JP2016520077A US2016067332A1	11 September 2015 (11-09-2015) 12 November 2015 (12-11-2015) 11 September 2015 (11-09-2015) 30 September 2016 (30-09-2016) 20 January 2016 (20-01-2016) 23 March 2016 (23-03-2016) 21 June 2017 (21-06-2017) 11 November 2016 (11-11-2016) 11 July 2016 (11-07-2016) 10 March 2016 (10-03-2016)
WO2007121491A1	01 November 2007 (01-11-2007)	WO2007121491A1 WO2007121491A8 AU2006342608A1 CA2645832A1 CN101426514A EP2010201A1 JP2009534428A US2009186047A1	01 November 2007 (01-11-2007) 10 January 2008 (10-01-2008) 01 November 2007 (01-11-2007) 01 November 2007 (01-11-2007) 06 May 2009 (06-05-2009) 07 January 2009 (07-01-2009) 24 September 2009 (24-09-2009) 23 July 2009 (23-07-2009)

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.
PCT/CA2017/051192

Patent Document Cited in Search Report	Publication Date	Patent Family Member(s)	Publication Date
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