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(54) **RECOMBINANT ANTIBODIES AGAINST H1N1 INFLUENZA**

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(75) Inventors: **Jens Wrammert**, Decatur, GA (US);
Rafi Ahmed, Atlanta, GA (US); **Patrick Wilson**, Chicago, IL (US)

(73) Assignees: **Emory University**, Atlanta, GA (US);
The University of Chicago, Chicago, IL (US)

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See application file for complete search history.

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Primary Examiner — Agnieszka Boesen

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(57) **ABSTRACT**

Antibodies that bind with high affinity to swine H1N1 virus are described. In vivo experiments showed that one such antibody is able to fully protect mice challenged with a lethal dose of swine H1N1 virus. The antibody is also able to cure mice in a therapeutic setting when treated as late as up to 60 hours (2.5 days) after infection with swine H1N1 virus. Also described are recombinant forms of this antibody.

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Figure 1

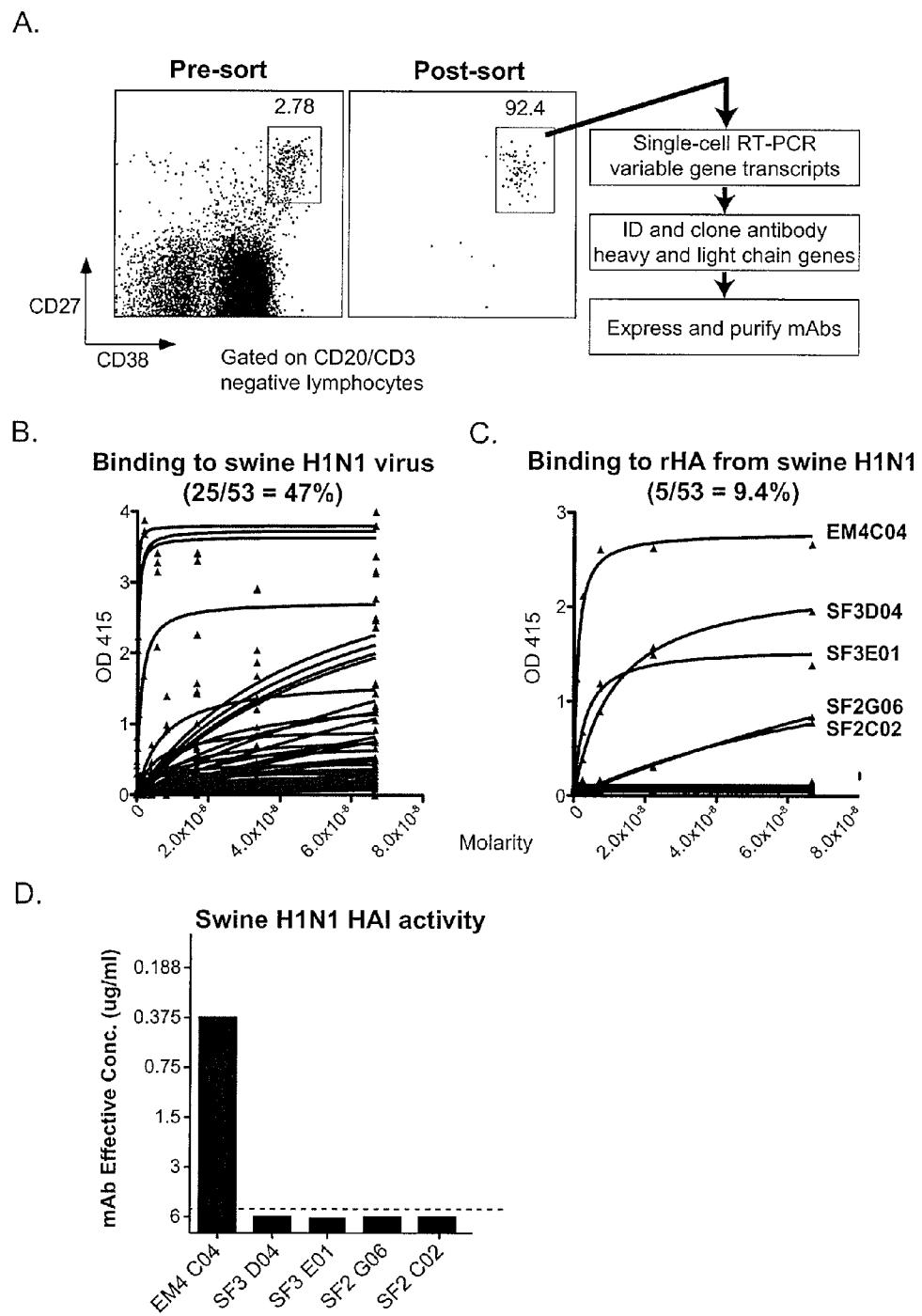


Figure 2

Crossreactivity of swine H1N1-induced mAbs to various influenza antigens
(Analysis of ELISA area under the curves)

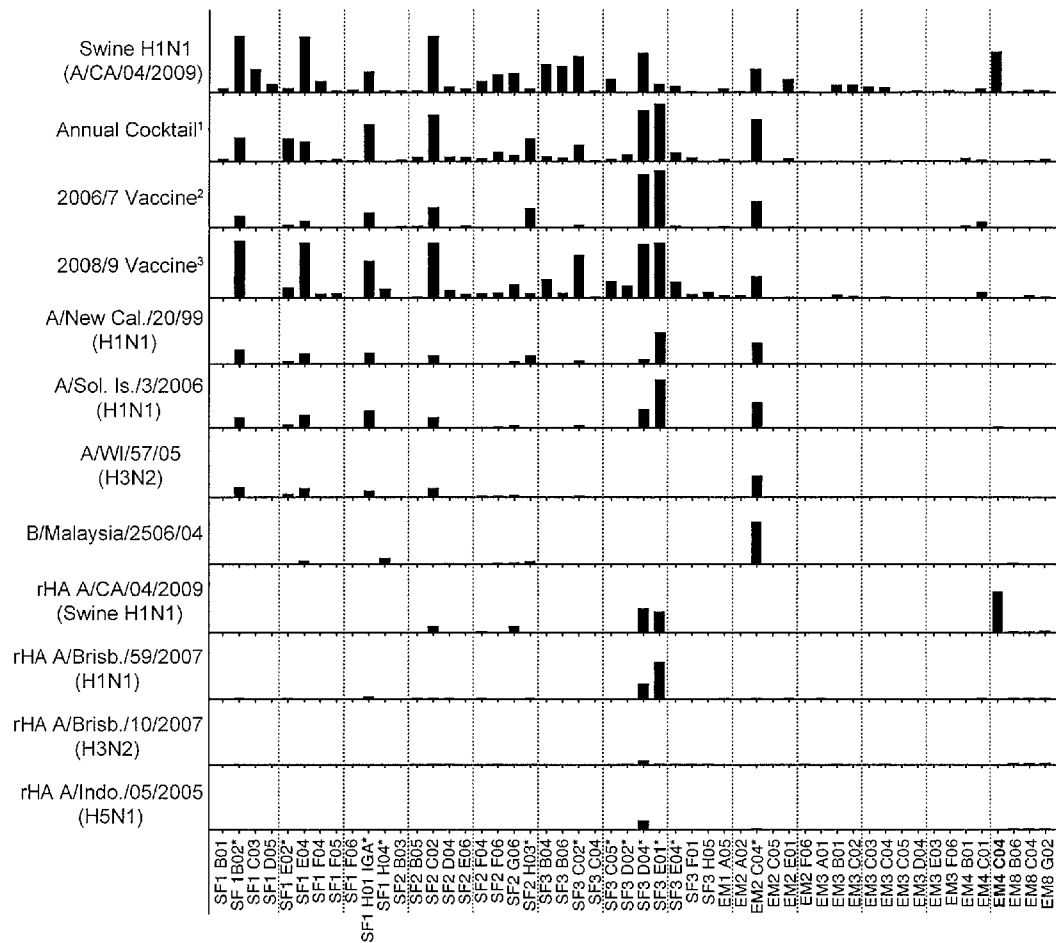
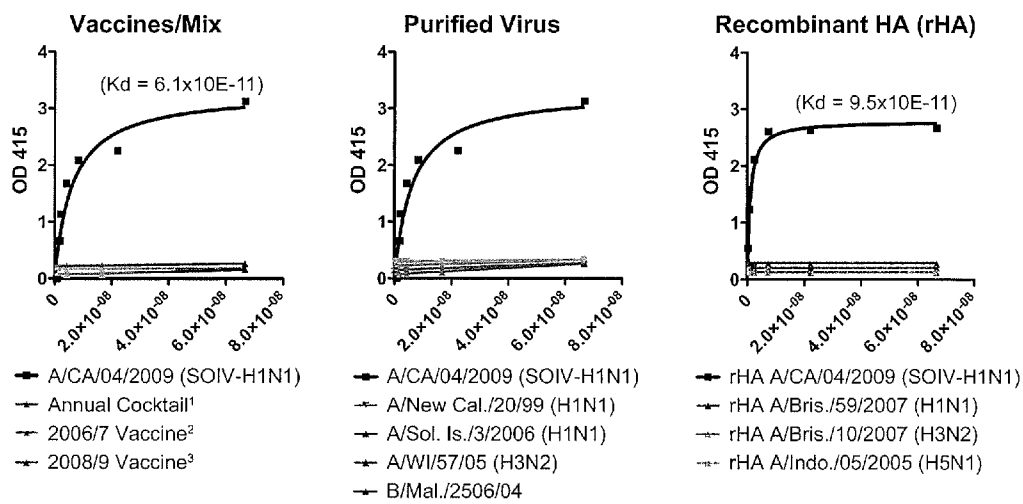
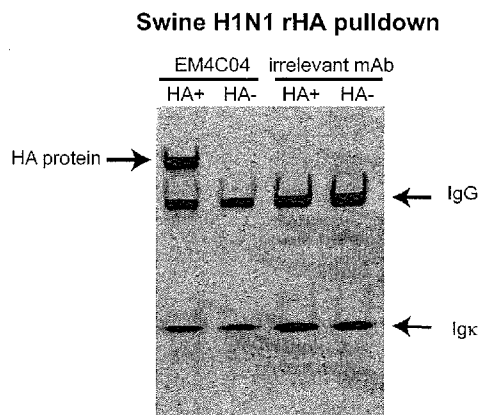


Figure 3

A.



B.



C.

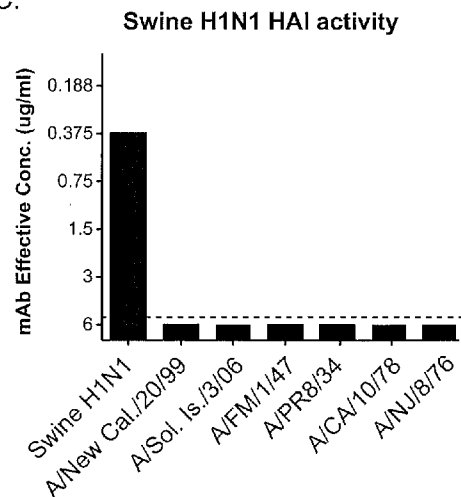
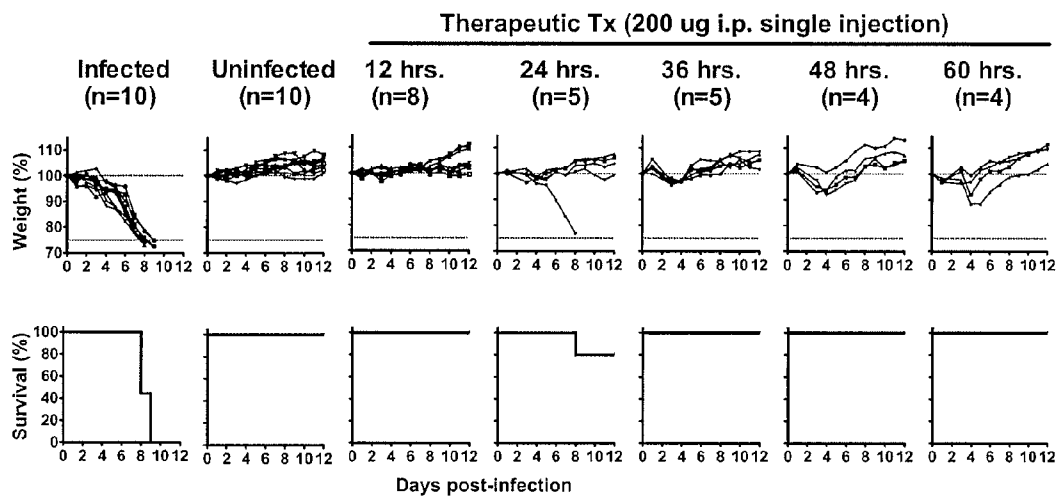
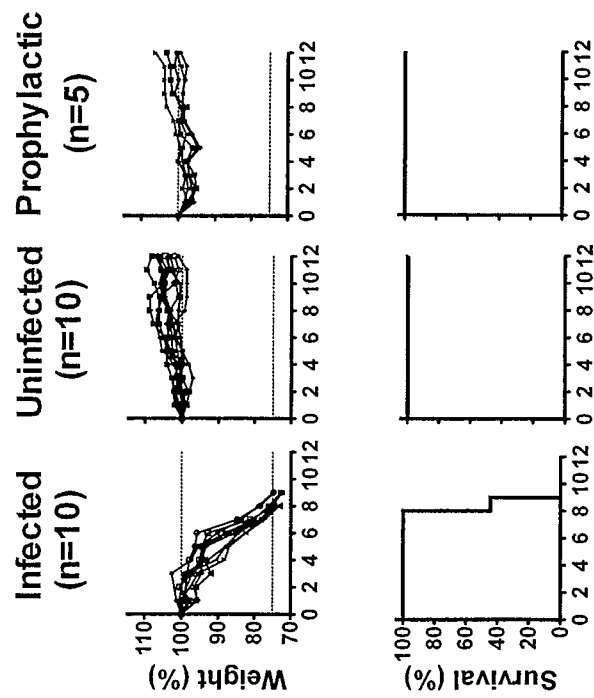


Figure 4



97% (30/31) of the mice lethally infected with pandemic swine H1N1 were rescued by EM4C04 treatment

Figure 6



RECOMBINANT ANTIBODIES AGAINST H1N1 INFLUENZA

CROSS REFERENCE TO RELATED APPLICATION

This application is the U.S. National Stage of PCT Application No. PCT/US2010/052274, filed Oct. 12, 2010, which was published in English under PCT Article 21(2), which claims the benefit of U.S. Provisional Application No. 61/260,650, filed on Nov. 12, 2009 and U.S. Provisional Application No. 61/250,479, filed on Oct. 9, 2009.

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BACKGROUND

The swine H1N1 influenza virus is currently causing a world-wide pandemic associated with substantial morbidity and mortality¹⁻⁵. This newly emergent strain is immunologically distinct from other influenza viruses including recent H1N1 strains⁶ thus leaving a large population of the world highly susceptible to infection by this pandemic virus⁷. Although there is some B cell cross-reactivity with the seasonal influenza viruses the protective epitopes of the swine H1N1 virus appear to be quite distinct.

SUMMARY

Described herein are recombinant antibodies (e.g., human monoclonal antibodies) against the swine H1N1 influenza virus.

Described herein are antibodies derived from plasmablasts isolated from patients during (or shortly after) infection with the novel influenza virus. Among the antibodies described herein is an antibody that binds with particularly high affinity, is highly specific to swine H1N1 virus, and is able to mediate hemagglutination-inhibition at low concentrations. In vivo experiments showed that this antibody is able to fully protect mice challenged with a lethal dose of swine H1N1 virus. The antibody is also able to cure mice in a therapeutic setting when treated as late as up to 60 hours (2.5 days) after infection with swine H1N1 virus. Such antibodies have great potential as a human therapeutic or prophylactic agent against the novel swine H1N1 influenza.

In one aspect, the recombinant antibodies described herein include all or part of the amino acid sequence of SEQ ID NO:1 (light chain) and/or all or part of the amino acid sequence of SEQ ID NO:2 (heavy chain). Within the light chain, the variable domain includes all or part of the sequence of SEQ ID NO:9 and can include one or more of CDR1-light (SEQ ID NO:3), CDR2-light (SEQ ID NO:4) and CDR3-light (SEQ ID NO:5). Within the heavy chain, the variable domain includes all or part of the sequence of SEQ ID NO:10 and can include one or more of CDR1-heavy (SEQ ID NO:6), CDR2-heavy (SEQ ID NO:7) and CDR3-heavy (SEQ ID NO:8).

Described herein is an isolated antibody or an antigen-binding fragment thereof that specifically binds the antigen bound by an H1N1 antibody having a light chain consisting of the amino acid sequence of SEQ ID NO:1 and a heavy chain consisting of the amino acid sequence of SEQ ID

NO:2. In various embodiments: the antibody or antigen-binding fragment thereof binds H1N1 (e.g., A/CA/04/2009 H1N1) with a Kd of equal to or less than 10^{-9} , 10^{-10} or 6×10^{-11}); the antibody or antigen-binding fragment thereof binds recombinant HA from H1N1 (e.g., A/CA/04/2009 H1N1) with a Kd equal to or less than 10^{-9} , 10^{-10} or 9×10^{-11}); the antibody comprises a light chain variable region comprising the amino acid sequences of SEQ ID NOs: 3, 4, and 5; the antibody comprises a heavy chain variable region comprising the amino acid sequences of SEQ ID NOs: 6, 7, and 8; the antibody is a human antibody; the antibody is an IgG antibody; the antibody is an IgG1 antibody; the antibody is an IgG1, kappa antibody; the antibody is an IgG1, lambda antibody; the antibody is selected from an IgM, IgA, IgD and IgE antibody; the antigen-binding fragment is selected from a Fab, a F(ab')₂ fragment, a Fd fragment, an Fv fragment, and a dAb fragment; the antibody is a scFv.

Also described is an isolated antibody or antigen-binding fragment thereof wherein the antibody comprises: (a) polypeptide comprising the amino acid sequences of one or more of SEQ ID NOs: 3, 4, and 5; and (b) polypeptide comprising the amino acid sequences of one or more of SEQ ID NOs: 6, 7, and 8. In various embodiments: the isolated antibody or antigen-binding fragment thereof comprises: (a) polypeptide comprising the amino acid sequences of two or more of SEQ ID NOs: 3, 4, and 5; and (b) polypeptide comprising the amino acid sequences of two or more of SEQ ID NOs: 6, 7, and 8; the isolated antibody or antigen-binding fragment thereof comprises: (a) polypeptide comprising the amino acid sequences of SEQ ID NOs: 3, 4, and 5; and (b) polypeptide comprising the amino acid sequences of SEQ ID NOs: 6, 7, and 8; the isolated antibody or antigen-binding fragment thereof comprises a first polypeptide comprising, in the amino terminal to carboxy terminal direction amino acid sequences of two or more of SEQ ID NOs: 3, 4, and 5, wherein there are 10-20 amino acids between SEQ ID NOs: 3 and 4 and between SEQ ID NOs: 4 and 5; and a second polypeptide comprising, in the amino terminal to carboxy terminal direction amino acid sequences of two or more of SEQ ID NOs: 6, 7, and 8, wherein there are 10-20 amino acids between SEQ ID NOs: 6 and 7 and between SEQ ID NOs: 7 and 8; the antibody or antigen-binding fragment thereof binds H1N1 (e.g., A/CA/04/2009 H1N1) with a Kd of equal to or less than 10^{-9} , 10^{-10} or 6×10^{-11}); the antibody or antigen-binding fragment thereof binds recombinant HA from H1N1 (e.g., A/CA/04/2009 H1N1) with a Kd equal to or less than 10^{-9} , 10^{-10} or 9×10^{-11}); the antibody comprises a light chain variable region comprising the amino acid sequences of SEQ ID NOs: 3, 4, and 5; the antibody comprises a heavy chain variable region comprising the amino acid sequences of SEQ ID NOs: 6, 7, and 8; the antibody is a human antibody; the antibody is an IgG antibody; the antibody is an IgG1 antibody; the antibody is an IgG1, kappa antibody; the antibody is an IgG1, lambda antibody; the antibody is selected from an IgM, IgA, IgD and IgE antibody; the antigen-binding fragment is selected from a Fab, a F(ab')₂ fragment, a Fd fragment, an Fv fragment, and a dAb fragment; the antibody is a scFv.

Also described is an isolated antibody or antigen-binding fragment thereof comprising a light chain variable region comprising SEQ ID NOs: 3, 4, and 5 and a heavy chain variable region comprising SEQ ID NOs: 6, 7, and 8. In various embodiments: In various embodiments: the antibody or antigen-binding fragment thereof binds H1N1 (e.g., A/CA/04/2009 H1N1) with a Kd of equal to or less than 10^{-9} , 10^{-10} or 6×10^{-11}); the antibody or antigen-binding

fragment thereof binds recombinant HA from H1N1 (e.g., A/CA/04/2009 H1N1) with a Kd equal to or less than 10^{-9} , 10^{-10} or 9×10^{-11} ; the antibody comprises a light chain variable region comprising the amino acids sequences of SEQ ID NOs: 3, 4, and 5; the antibody comprises a heavy chain variable region comprising the amino acids sequences of SEQ ID NOs: 6, 7, and 8; the antibody is a human antibody; the antibody is an IgG antibody; the antibody is an IgG1 antibody; the antibody is an IgG1, kappa antibody; the antibody is an IgG1, lambda antibody; the antibody is selected from an IgM, IgA, IgD and IgE antibody; the antigen-binding fragment is selected from a Fab, a F(ab')₂ fragment, a Fd fragment, an Fv fragment, and a dAb fragment; the antibody is a scFv.

Also described is a composition comprising an antibody or antigen binding fragment thereof described herein and a pharmaceutically acceptable carrier.

Also described is a method for treating or reducing one or more symptoms of infection with H1N1 in a human subject, the method comprising administering an antibody or antigen binding fragment thereof described herein.

Also described is a method of reducing the risk of becoming infected with H1N1, the method comprising administering an antibody described herein.

Naturally-occurring antibodies are immunoglobulin molecules comprised of four polypeptide chains, two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds. Each heavy chain is comprised of a heavy chain variable region (VH) and a heavy chain constant region. The heavy chain constant region is comprised of three domains, CH1, CH2 and CH3. Each light chain is comprised of a light chain variable region (VL) and a light chain constant region. The light chain constant region is comprised of one domain, CL. The VH and VL regions can be further subdivided into regions of hypervariability, called complementarity determining regions (CDR), interspersed with regions that are more conserved, called framework regions (FR). Each VH and VL is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4.

CDRs and FRs may be defined according to Kabat (Sequences of Proteins of Immunological Interest (National Institutes of Health, Bethesda, Md., 1987 and 1991)). Amino acid numbering of antibodies or antigen binding fragments is also according to that of Kabat.

Each CDR can include amino acid residues from a complementarity determining region as defined by Kabat (i.e. about residues 24-34 (CDR-L1), 50-56 (CDR-L2) and 89-97 (CDR-L3) in the light chain variable domain (SEQ ID NO:1) and 31-35 (CDR-H1), 50-65 (CDR-H2) and 95-102 (CDR-H3) in the heavy chain variable domain (SEQ ID NO:2); Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)) and/or those residues from a hypervariable loop (i.e. about residues 26-32 (CDR-L1), 50-52 (CDR-L2) and 91-96 (CDR-L3) in the light chain variable domain (SEQ ID NO:1) and 26-32 (CDR-H1), 53-55 (CDR-H2) and 96-101 (CDR-H3) in the heavy chain variable domain (SEQ ID NO:2); Chothia and Lesk J. Mol. Biol. 196:901-917 (1987)). In some instances, a complementarity determining region can include amino acids from both a CDR region defined according to Kabat and a hypervariable loop.

Framework regions are those variable domain residues other than the CDR residues. Each variable domain typically has four FRs identified as FR1, FR2, FR3 and FR4. If the CDRs are defined according to Kabat, the light chain FR

residues are positioned at about residues 1-23 (LCFR1), 35-49 (LCFR2), 57-88 (LCFR3), and 98-107 (LCFR4) of SEQ ID NO:1 and the heavy chain FR residues are positioned about at residues 1-30 (HCFR1), 36-49 (HCFR2), 66-94 (HCFR3), and 103-113 (HCFR4) of SEQ ID NO:2. If the CDRs comprise amino acid residues from hypervariable loops, the light chain FR residues are positioned about at residues 1-25 (LCFR1), 33-49 (LCFR2), 53-90 (LCFR3), and 97-107 (LCFR4) in the light chain (SEQ ID NO:1) and the heavy chain FR residues are positioned about at residues 1-25 (HCFR1), 33-52 (HCFR2), 56-95 (HCFR3), and 102-113 (HCFR4) in the heavy chain (SEQ ID NO:2). In some instances, when the CDR comprises amino acids from both a CDR as defined by Kabat and those of a hypervariable loop, the FR residues will be adjusted accordingly.

An Fv fragment is an antibody fragment which contains a complete antigen recognition and binding site. This region consists of a dimer of one heavy and one light chain variable domain in tight association, which can be covalent in nature, for example in scFv. It is in this configuration that the three CDRs of each variable domain interact to define an antigen binding site on the surface of the VH-VL dimer. Collectively, the six CDRs or a subset thereof confer antigen binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although usually at a lower affinity than the entire binding site.

The Fab fragment contains a variable and constant domain of the light chain and a variable domain and the first constant domain (CH1) of the heavy chain. F(ab')₂ antibody fragments comprise a pair of Fab fragments which are generally covalently linked near their carboxy termini by hinge cysteines between them. Other chemical couplings of antibody fragments are also known in the art.

Single-chain Fv or (scFv) antibody fragments comprise the VH and VL domains of antibody, wherein these domains are present in a single polypeptide chain. Generally the Fv polypeptide further comprises a polypeptide linker between the VH and VL domains, which enables the scFv to form the desired structure for antigen binding.

Diabodies are small antibody fragments with two antigen-binding sites, which fragments comprise a heavy chain variable domain (VH) connected to a light chain variable domain (VL) in the same polypeptide chain (VH and VL). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites.

Linear antibodies comprise a pair of tandem Fd segments (VH-CH1-VH-CH1) which, together with complementary light chain polypeptides, form a pair of antigen binding regions. Linear antibodies can be bispecific or monospecific.

The antibodies herein specifically include chimeric antibodies (immunoglobulins) in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity.

An antigen binding portion of an antibody specifically binds to an antigen (e.g., H1N1). It has been shown that the antigen-binding function of an antibody can be performed by portions of a full-length antibody, all of which are

encompassed by the general term antibody, including: (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a F(ab')₂ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody, (v) a dAb fragment (Ward et al. (1989) *Nature* 341:544-546), which consists of a VH domain; and (vi) an isolated complementarity determining region (CDR). Furthermore, although the two domains of the Fv fragment, VL and VH, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent molecules (known as single chain Fv (scFv); see e.g., Bird et al. (1988) *Science* 242:423-426; and Huston et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883). Single chain Fv and other forms of single chain antibodies, such as diabodies are also encompassed by the general term antibody. Diabodies are bivalent, bispecific antibodies in which VH and VL domains are expressed on a single polypeptide chain, but using a linker that is too short to allow for pairing between the two domains on the same chain, thereby forcing the domains to pair with complementary domains of another chain and creating two antigen binding sites (see e.g., Holliger et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:6444; Poljak et al. (1994) *Structure* 2:1121).

An antibody or antigen-binding portion thereof may be part of a larger immunoadhesion molecules, formed by covalent or noncovalent association of the antibody or antibody portion with one or more other proteins or peptides. Examples of such immunoadhesion molecules include use of the streptavidin core region to make a tetrameric scFv molecule (Kipriyanov et al. (1995) *Human Antibodies and Hybridomas* 6:93) and use of a cysteine residue, a marker peptide and a C-terminal polyhistidine tag to make bivalent and biotinylated scFv molecules (Kipriyanov et al. (1994) *Mol. Immunol.* 31:1047). Antibody portions, such as Fab and F(ab')₂ fragments, can be prepared from whole antibodies using conventional techniques, such as papain or pepsin digestion, respectively, of whole antibodies. Moreover, antibodies, antibody portions and immunoadhesion molecules can be obtained using standard recombinant DNA techniques.

Human antibodies include antibodies having variable and constant regions derived from (or having the same amino acid sequence as those derived from) human germline immunoglobulin sequences. Human antibodies may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo), for example in the CDRs and in particular CDR3.

Recombinant antibodies are prepared, expressed, created or isolated by recombinant means, such as antibodies expressed using a recombinant expression vector transfected into a host cell, antibodies isolated from a recombinant, combinatorial human antibody library, antibodies isolated from an animal (e.g., a mouse) that is transgenic for human immunoglobulin genes (Taylor et al. (1992) *Nucl. Acids Res.* 20:6287) or antibodies prepared, expressed, created or isolated by any other means that involves splicing of human immunoglobulin gene sequences or variants thereof to other DNA sequences. Such recombinant human antibodies have variable and constant regions derived from human germline immunoglobulin sequences or variants thereof. In certain embodiments, however, such recombinant human antibodies

are subjected to in vitro mutagenesis (or, when an animal transgenic for human Ig sequences is used, in vivo somatic mutagenesis) and thus the amino acid sequences of the VH and VL regions of the recombinant antibodies are sequences that may not naturally exist within the human antibody germline repertoire in vivo.

DESCRIPTION OF THE DRAWINGS

FIG. 1. Generation of human monoclonal antibodies against swine H1N1 influenza virus from plasmablasts of infected patients. (a) Antibody-secreting B cells in the PBMC of swine influenza virus infected patients were isolated by flow cytometry sorting based on their cell surface phenotype (CD19⁺, CD20⁻, CD3⁻, CD38^{high} and CD27^{high}). RT-PCR was used to isolate the variable genes from sorted single plasmablasts, which were then cloned into expression vectors and expressed in 293 cells as we have previously described^{11, 12}. (b) Forty-seven percent (25/53) of the monoclonal antibodies generated bound to purified swine H1N1 (A/CA/04/2009) virus as determined by ELISA. (c) Five of 53 antibodies bound to recombinant swine H1N1 hemagglutinin (rHA), but only one of these mAbs (EM4C04) could inhibit hemagglutination (HAI+) of erythrocytes by the swine H1N1 influenza strain (d).

FIG. 2. A majority of the antibodies induced by swine H1N1 infection are crossreactive to seasonal influenza strains. Antibodies generated during active infection with the swine H1N1 strain (top line) were screened by ELISA for reactivity to various influenza antigens (indicated within the figure). Bars indicate the area under the curve, thus providing insight into both the maximal binding (B_{max}) and persistence of binding with decreasing dilutions (affinity or K_d). Note that only a few antibodies were specific just to the swine H1N1 strain alone and that a number of antibodies bound to annual influenza vaccine strains either solely or with higher affinity (indicated with asterisks). In total 47% (25/52) bound swine H1N1 and 58% (30/52) bound influenza antigens at levels detectable by ELISA assay¹². The mAb EM4C04 (bold) had the highest and most specific affinity against swine H1N1. Cocktail: A/Sal. Is./3/2006 (H1N1), A/WI/57/05 (H3N2), and B/Mal./2506/04, 2006/7 Vaccine: A/New Cal./20/90 (H1N1), A/WI/57/05 (H3N2), and B/Mal./2506/04, 2008/9 Vaccine: A/Brisb./59/2007 (H1N1), A/Brisb./10/2007 (H3N2), and B/FL/4/2006.

FIG. 3. The monoclonal antibody EM4C04 is highly specific for the swine H1N1 influenza hemagglutinin and displays HAI activity only to the swine H1N1 virus. (a) ELISA binding curves of the mAb EM4C04, comparing binding to whole virus with reactivity to viral mixtures or to the annual vaccines as indicated, to purified virions or to recombinant hemagglutinin (rHA) from swine H1N1 versus other influenza strains. Calculated K_d values are shown in parenthesis above the graphs. Cocktail: A/Sal.Is./3/2006 (H1N1), A/WI/57/05 (H3N2), and B/Mal./2506/04, 2006/7 Vaccine: A/New Cal./20/90 (H1N1), A/WI/57/05 (H3N2), and B/Mal./2506/04, 2008/9 Vaccine: A/Brisb./59/2007 (H1N1), A/Brisb./10/2007 (H3N2), and B/FL/4/2006. (b) EM4C04 is able to immuno-precipitate recombinant from swine H1N1 HA protein. (c) EM4C04 displays HAI activity toward swine H1N1 but not to several other H1N1 strains tested as indicated.

FIG. 4. EM4C04 has therapeutic efficacy in mice challenged with a lethal dose of mouse-adapted 2009 swine H1N1 influenza. 6-8 week old Balb/c mice were infected with a 3xLD₅₀ dose of highly pathogenic, mouse-adapted 2009 swine H1N1 influenza (A/California/04/09). Subse-

quently, they were treated with 200 mg (10 mg/kg of body weight) EM4C04 human monoclonal antibody intraperitoneally at various time points (12, 24, 36, 48 and 60 hours) after infection. All mice were monitored daily for body weight changes and any signs of morbidity and mortality. Infected, untreated mice showed clear signs of sickness around day 4-5 post infection and perished by day 8-9. Upper panels show body weight change and the lower panels show survival curves.

FIG. 5. Plasmablasts expressing antibodies that cross-react to annual influenza strains have accumulated more somatic hypermutations. The higher frequency of mutations in the more crossreactive antibodies indicate that they were derived from a recall response of memory B cells, originally induced by annual influenza viruses. It is also notable that a number of IgG+ plasmablasts that had no detectable binding to influenza by ELISA were from cells that had no mutations of the variable genes. The origin and specificity of these cells is unknown but they may be cells activated during a primary response against swine H1N1 epitopes that had affinities below the threshold of detection. The frequency of point mutations was determined from the variable gene sequences of the VH and VK sequences that were generated for the cloning and expression of the antibodies. Points represent the sum of heavy and light chain mutations. Statistical significance was determined by students t test.

FIG. 6. Prophylactic treatment with EM4C04 can protect mice from a lethal challenge with mouse-adapted swine H1N1 influenza. 6-8 week old Balb/c mice were treated with 200 µg (10 mg/kg of body weight) EM4C04 human monoclonal antibody intraperitoneally 12 hours prior to infection with a 3xLD50 dose of highly pathogenic mouse adapted swine H1N1 influenza. All mice were monitored daily for body weight changes and any signs of morbidity and mortality. Upper panels show body weight change and the lower panels show survival curves.

SEQUENCE LISTING

The Sequence Listing is submitted as an ASCII text file [86975-88879-05_Sequence_Listing.txt, Mar. 30, 2012, 41.2 KB], which is incorporated by reference herein.

DETAILED DESCRIPTION

The studies described below analyzed the B cell responses in patients infected with swine H1N1 virus. As part of these studies we generated a panel of virus specific human monoclonal antibodies. These antibodies were isolated from plasmablasts that were activated by infection providing a means to directly evaluate the breadth and repertoire of the antibody response elicited by swine H1N1 virus. Interestingly, a majority of these antibodies also reacted with seasonal influenza viruses. In fact, several of the antibodies bound with higher affinity to past influenza strains than to the current swine H1N1 virus. These findings suggest that the swine H1N1 virus predominantly activated memory B cells previously generated against cross-reactive but non-protective epitopes present in annual influenza strains. Of the influenza specific antibodies generated five bound to recombinant hemagglutinin (HA) protein and of these only one antibody showed hemagglutination-inhibition (HAI) activity against the swine H1N1 influenza virus. In contrast to most of the other antibodies generated, this neutralizing antibody was highly specific for the swine H1N1 virus and did not cross-react with the other H1N1 influenza viruses, confirming that the critical HA active-site epitopes in this

new virus are quite unique. In vivo experiments showed that this antibody was able to protect mice challenged with a lethal dose of mouse-adapted swine H1N1 influenza virus. Moreover, it was effective therapeutically even when administered 60 hours after infection and could thus potentially be developed as a therapeutic agent against the swine H1N1 influenza virus pandemic.

The novel 2009 pandemic swine H1N1 influenza virus is characterized by a unique genetic make-up^{1,2,8} that results in little or no pre-existing serum antibody mediated protection against infection^{7,9}. It is currently unclear what effect this has on the repertoire of responding B cells in infected patients and whether infection with this novel virus leads to activation of cross-reactive memory B cells or if the response is dominated by newly induced naive B cells. To analyze the repertoire of the responding B cells after infection and to generate monoclonal antibodies (mAbs) against the swine H1N1 influenza strain, we examined the B cell responses in five patients infected with swine H1N1 virus. The clinical details about these patients are given in the supplemental methods section. Blood samples were taken 1-2 weeks after onset of clinical symptoms and were used to isolate infection-induced plasmablasts (CD19⁺, CD20⁻, CD3⁻, CD38^{high} and CD27^{high} cells) by flow cytometry based cell sorting (FIG. 1a shows a representative donor). Using an adapted single cell multiplex RT-PCR approach^{10, 11,12}, we then identified the heavy and light chain immunoglobulin genes from each individual plasmablast from two of the five patients. These heavy and light chain fragment pairs were then used to express fully human monoclonal antibodies. In total, 25 out of the 53 (47%) antibodies generated in this fashion bound to purified whole swine H1N1 influenza (A/CA/04/2009) virus by ELISA (FIG. 1b). It is notable that the majority of antibodies induced by infection were low affinity; only five of the 53 isolated antibodies, had affinities $>^{10-9}$ by non-linear regression analysis of ELISA data. Further, as indicated in FIG. 1c, five of the 53 antibodies bound to recombinant hemagglutinin (rHA) from swine H1N1 influenza by ELISA, but only one of these mAbs (EM4C04) displayed HAI activity (FIG. 1d). We conclude from this analysis that a large proportion of virus specific plasmablasts in these patients were not producing neutralizing antibodies, and that the majority of the B cell response was in fact directed at non-HA proteins.

In order to determine how specific the antibody response was to the swine H1N1 virus strain, the 53 monoclonal antibodies were screened by ELISA for reactivity to various influenza antigens (FIG. 2). The bars in FIG. 2 indicate the area under the curve of ELISA binding data (FIG. 1a), thus providing an overview of both the maximal binding (B_{max}) and the persistence of binding with decreasing dilutions (affinity or K_d), allowing a relative comparison of each antibody to all antigens by column. It is notable that most of the antibodies were indeed cross-reactive with past strains of influenza virus, suggesting that they arose through the activation of cross-reactive memory B cells. In total, 47% ($^{25}/_{52}$) of the antibodies bound to swine H1N1 and 58% ($^{30}/_{52}$) bound to antigens from any of the influenza strains tested. In fact, 23% of the antibodies bound to past annual influenza strains with higher affinity than to the swine H1N1 strain (FIG. 2, asterisks). The plasmablasts expressing antibodies that were cross-reactive to past annual influenza strains had also accumulated significantly more mutations in the variable genes on average than the swine H1N1-specific B cells (FIG. 5). These findings suggest that the swine H1N1 strain predominantly activated memory B cells previously gener-

ated against cross-reactive but non-protective epitopes present in annual influenza virus strains.

It is worth noting that the sole HAI⁺mAb, EM4C04 (FIG. 2) was also the most specific against swine H1N1, demonstrating that the critical HA active-site epitopes are quite unique, as predicted by analyses of the HA amino acid sequences by several other groups^{1,2,7,13}. The high specificity of EM4C04 demonstrates that this antibody could be valuable for diagnostic purposes for the pandemic swine H1N1 influenza virus (FIG. 3a). This antibody was also able to immuno-precipitate recombinant HA protein derived from swine H1N1 (FIG. 3b). In addition, while EM4C04 efficiently inhibited the agglutination of red blood cells by swine H1N1 virus, it had no HAI activity against several other influenza strains (FIG. 3c). The high affinity (6.1×10^{-11} to purified virus and 9×10^{-11} to rHA) for the HA active site suggested that this antibody could be used for passive immunization to treat swine H1N1 influenza infection. We therefore tested the prophylactic and therapeutic potential of EM4C04 in mice infected with a lethal dosage of highly pathogenic, mouse-adapted swine H1N1 strain.

As indicated in FIG. 4 (and FIG. 6), the EM4C04 antibody is highly effective at either providing prophylactic protection against infection or to treat and facilitate clearance of a lethal dose of mouse-adapted swine H1N1 from 6-8 week old Balb/c mice. For the prophylactic experiments mice were pretreated with 200 μ g EM4C04 human monoclonal antibody intraperitoneally and then challenged 12 hours later with a 3xLD₅₀ dose of mouse-adapted novel H1N1 influenza (FIG. 6). To determine the therapeutic potential of EM4C04, mice were first challenged and then treated with antibody at various times after infection (FIG. 4). While untreated mice died 8-9 days after the infection, mice treated even as late as 60 hours after challenge survived. Infected mice treated at later time points were already showing measurable weight loss that was reversed by administration of the antibody, demonstrating therapeutic potential even after the onset of symptoms. Overall, 30 of 31 infected mice that were treated with EM4C04, irrespective of when they were treated, made a complete recovery from infection. It is likely that the therapeutic effects of EM4C04 treatment involve both direct viral neutralization as well as facilitation of endogenous cell-mediated immunity¹⁴. It is possible that the antibody treatment may reduce viral titers and thus allow the endogenous immune responses to catch up and subsequently clear the infection.

The studies show that the antibody responses induced in patients infected with the novel swine H1N1 influenza appear to be dominated by a recall response of non-protective memory B cells that are cross-reactive to annual influenza strains. Of the 25 virus-specific monoclonal antibodies generated herein only one displayed HAI activity against the swine H1N1 virus. This low frequency of cells producing protective antibodies after infection differs significantly as compared to previous work on seasonal influenza vaccines¹², where 40% of the virus specific antibodies bound with high affinity to HA and half of those antibodies had HAI activity against the influenza vaccine viral strains. As the novel swine H1N1 vaccine is now becoming widely available¹⁵⁻¹⁸, it will be of interest to compare the vaccine induced antibody responses to the responses induced by infection as described herein. Finally, the *in vivo* protection experiments presented here demonstrate that the human monoclonal antibody EM4C04 has impressive prophylactic and therapeutic activity in mice and shows potential for development as a therapeutic agent against the pandemic swine H1N1 influenza virus in humans.

Patients were recruited with IRB approval and had ongoing or recent verified swine H1N1 infections. HAI titers, inhibiting antibody concentrations, and viral neutralization were determined by standard procedures as previously described^{12,19}. The ASCs were identified herein as CD3⁻/CD20^{-low}/CD19⁺/CD27^{hi}/CD38^{hi} cells as previously described^{11,12}. The single cell RT-PCR methods and the procedures for production of recombinant mAbs were as previously described¹⁰⁻¹². Monoclonal antibodies were screened against fresh influenza virions grown in chicken eggs. ELISA was performed on starting concentrations of 10 μ g/ml of virus or rHA and on 1:20 dilution of the vaccines and antibody affinities (Kd) were calculated by nonlinear regression analysis as previously described¹². For immunoprecipitation, 1 μ g each of recombinant HA protein and antibody were incubated at 4° C. overnight in 100 μ l NP40 Buffer prior to precipitation with Protein G-Sepharose. The samples were denatured for 5 min at 95° C. in Laemmli gel sample buffer followed by centrifugation to remove the Protein G-Sepharose and analysis on 12% Tris-Glycine polyacrylamide gels. Precipitated protein bands were identified by staining with Sypro-orange and Fluorescence imaging. For the challenge experiments, female Balb/c mice (8 weeks old) were challenged intra-nasally with 3xLD₅₀ of a highly pathogenic, mouse-adapted swine H1N1 influenza virus (A/California/04/09) that was passaged in mice for five generations. Mice were treated intraperitoneally with 200 μ g (10 mg/kg of body weight) of the specific mAb EM4C04 at all time points. All mice were monitored daily for morbidity and body weight changes.

Patients

All studies were approved by the Emory University, University of Chicago and Columbia University institutional review boards (Emory IRB#22371 and 555-2000, U of C IRB#16851E, CU IRB#AAAE1819). Patient 1 (EM) is a 30-year old healthy woman who developed fever, cough and progressive dyspnea over 8 days prior to hospital admission. She was diagnosed with acute respiratory syndrome (ARDS), which required mechanical ventilation. Her nasopharyngeal swab on admission was positive for influenza by RTPCR. She continued shedding virus (hospital day 13) despite treatment with oseltamivir, but had cleared the virus by day 15 with continued treatment. Her course was further complicated by bacterial pneumonia, pulmonary embolism, and a requirement for prolonged oscillatory ventilator support and tracheostomy. She gradually recovered and was discharged to home two months after becoming ill. Blood samples for PBMC preparation were collected 19 days and 29 days after the onset of symptoms. Patient 2 (SF) is a 37-year old man with a history of hypertension and interstitial lung disease of unknown etiology who was hospitalized with symptoms of fever, cough, shortness of breath, nausea and vomiting for 3 days. He was diagnosed with pneumonia, acute sinusitis and acute renal failure. His nasopharyngeal swab on admission was positive for influenza virus by culture and was confirmed as the swine H1N1 influenza virus by RTPCR. He was initially treated with oseltamivir for 5 days but was continuing to shed influenza virus and was discharged with a course of zanamivir. He was hospitalized for a total of 8 days and recovered. PBMCs were collected 18 days after the onset of symptoms. Patient 3 is a 25 year old male who developed cough and fever to 103° F. The diagnosis of 2009 H1N1 influenza was con-

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firmed by RT-PCR. He was treated with oseltamivir and his symptoms lasted for 4 days. He recovered completely and blood samples were collected 9 days after the onset of symptoms. Patient 4 is a previously healthy, 40-year old man who developed symptoms consistent with mild upper respiratory tract illness, including cough, rhinorrhea, and fever. MassTag PCR analysis of a nasopharyngeal swab specimen obtained 6 days after symptom onset identified H1N1 influenza virus; the presence of swine H1N1 influenza virus was subsequently confirmed by RT-PCR. Blood samples for PBMC isolation were obtained 13 days after the onset of symptoms. Patient 5 is a 52 year old female whose diagnosis of 2009 H1N1 influenza A was confirmed by RT-PCR. Her symptoms included fever, cough, pharyngitis, myalgias, nausea, headache, and gastrointestinal symptoms. She was treated with oseltamivir and her symptoms resolved after 6 days and she recovered completely. Blood samples were collected 10 days after the onset of symptoms.

Cell and Serum Isolation

All work with samples from infected patients was performed in a designated BSL2+ facility at Emory University. Peripheral blood mononuclear cells (PBMC) were isolated using Vacutainer tubes (Becton Dickinson, BD), washed, and resuspended in PBS with 2% FCS for immediate use or frozen for subsequent analysis. Plasma samples were saved in -80C.

Viruses and Antigens

The Swine H1N1 influenza virus (A/California/04/2009) was kindly provided by Dr. Richard J Webby at St. Jude Childrens Hospital. Influenza virus stocks used for the assays were freshly grown in eggs, prepared and purified as described¹⁹ and the hemagglutination activity (HA) was determined using turkey red blood cells (Lampire Biological Laboratories, Pipersville, Pa.) as previously described^{12,19} or purchased as inactivated preparations (ProSpec-Tany TechnoGene Ltd., Rehovot, Israel) and included: A/California/04/2009 (H1N1), A/FM/1/47 (H1N1), A/PR8/34 (H1N1), A/New Jersey/76 (H1N1), A/New Caledonia/20/9 (H1N1), A/Solomon Island/3/2006, A/Wisconsin/67/2005 (H3N2), and B/Malaysia/2506/2004. Vaccines tested included the 2006/7 vaccine from Chiron Vaccines Limited (Liverpool, UK) and the 2008/9 formulation from Sanofi Pasteur Inc. (Swiftwater, Pa.). Recombinant HA proteins were provided by the influenza reagent resource (IRR; influenza reagent resource.org) of the CDC (rHA from A/California/04/2009 (H1N1) (#FR-180), A/Brisbane/10/2007 (H1N1) (#FR-61), A/Brisbane/59/2007 (H3N2) (#FR-65)) or by Biodefense & Emerging Infections research repository (BEI; www.beiresources.org) (rHA from A/Indonesia/05/2005).

Flow Cytometry Analysis and Cell Sorting

Analytical flow cytometry analysis was performed on whole blood following lysis of erythrocytes and fixing in 2% PFA. All live cell sorting was performed on purified PBMCs in the BSL-3 facility at the Emory Vaccine Center. All antibodies for both analytical and cell sorting cytometry were purchased from Pharmingen, except anti-CD27 that was purchased from ebiosciences. Anti-CD3-PECy7 or PerCP, anti-CD20-PECy7 or PerCP, anti-CD38-PE, anti-CD27-APC and anti-CD19-FITC. ASCs were gated and isolated as

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CD19⁺CD3⁻CD20^{low}CD27^{high}CD38^{high} cells. Flow cytometry data was analyzed using FlowJo software.

Generation of Monoclonal Antibodies

Identification of antibody variable region genes were done essentially as previously described^{10,11}. Briefly, single ASCs were sorted into 96-well PCR plates containing RNase inhibitor (Promega). VH and Vκ genes from each cell were amplified by RT-PCR and nested PCR reactions using cocktails of primers specific for both IgG and IgA as previously described^{10,11} and then sequenced. To generate recombinant antibodies, restriction sites were incorporated by PCR with primers to the particular variable and junctional genes. VH or Vκ genes amplified from each single cell were cloned into IgG1 or Igκ expression vectors as previously described^{10,11}. Heavy/light chain plasmids were co-transfected into the 293A cell line for expression and antibodies purified with protein A sepharose.

ELISA and HAI Assays

Whole virus, recombinant HA or vaccine-specific ELISA was performed on starting concentrations of 10 ug/ml of virus or rHA and on 1:20 dilution of the vaccine as previously described¹². The hemagglutination inhibition (HAI) titers were determined as previously described^{11,19}. Affinity estimates were calculated by nonlinear regression analysis of curves from 8 dilutions of antibody (10 to 0.125 μg/ml) using GraphPad Prism.

Immunoprecipitation

For immunoprecipitation, 100 μl NP40 Buffer (20 mM Tris-HCl PH8.0, 137 mM NaCl, 10% Glycerol, 1% NP-40, 2 mM EDTA) containing complete Protease Inhibitors (Roche) was mixed with 1 μg of recombinant HA protein and incubated on ice for 30 min. One microgram of monoclonal antibody was then added. The antibody and HA mixture was incubated at 4° C. overnight with constant agitation. On the next day, Protein G-Sepharose (GE Healthcare) was prepared in NP40 buffer at a volume of 10 μl/sample. Protein G-Sepharose was incubated with the antibody and HA mixture at 4C for 4 hrs with constant agitation. The protein G-Sepharose was centrifuged for 3 min at 3000 rpm and the pellet was washed with 400 μl of NP40 buffer for 3 times. Finally the pellet was resuspended into 25 μl of Laemmli gel sample buffer (Bio-Rad). The samples were then boiled for 5 min at 95 C. The protein G was pelleted and 15 μl of supernatant was loaded onto 12% Tris-Glycine polyacrylamide gels. The gels were run in 1xTGS at 70V for 30 min, followed by 120V till the frontline ran out of the gel. The gels were stained with 1x Sypro-orange (Invitrogen) in 7.5% acetic acid for 1 hr, and then gels were destained with 7.5% acetic acid for 3 min. Gels were finally scanned in a Typhoon 9410 Fluorescence imaging system (GE Healthcare).

In Vivo Protection Experiments

Female Balb/c mice 6-8 weeks old were used for the challenge studies. Mice were inoculated intra-nasally with 3xLD₅₀ of a highly pathogenic, mouse-adapted swine H1N1 influenza virus (A/California/04/09) that was passaged in mice five generations. The LD₅₀ was determined by the method of Reed and Muench. The experiments were conducted in accordance with ethical procedures and policies

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approved by the Emory University's Institutional Animal Care and Use Committee. In order to determine the prophylactic efficacy of the mAb, mice were treated intraperitoneally with 200 µg (10 mg/kg of body weight) of the specific mAb EM4C04. Twelve hours later mice were challenged with 3xLD₅₀ of the mouse adapted H1N1 virus. All mice were monitored daily for any signs of morbidity and mortality. Body weight changes were registered daily for a period of 14 days. All mice that lost more than 25% of their initial body weight were sacrificed according to the IACUC guideless. In order to determine the therapeutic efficacy of the EM4C04 mAb, mice were challenged with 3xLD₅₀ of the mouse-adapted swine H1N1 virus. At various times post infection (12, 24, 36, 48, 60 hours) mice were treated intraperitoneally with 200 µg (10 mg/kg of body weight) of

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the specific mAb EM4C04. All mice were monitored daily and the body weight changes were registered daily as described above.

Statistical Analysis

Data was collected and graphed using MS Excel and Graphpad Prism software. Efficacy of the therapeutic and challenge experiments was evaluated by ANOVA using Graphpad Prism software.

Sequences of Antibodies

Described below are the sequences of the EM4C04 heavy chain and light chain

EM4C04 Heavy Chain Variable Region:
DNA

(SEQ ID NO: 11)

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCT
GTTACGCCCTCTGGATTACACCTTCAATATCTATGCCATGAACTGGTCCGCCAGGTTCCAGGAAA
GGGGCTGGATTGGGTCTCATCCATTAGTAGTAGGGGTGATTACATATACTACGCAGAGTCAGTG
GAGGGCCGATTACCATCTCCAGAGACAACGCCAAGAAGTCACTGTATCTGGAAATGAACAGCC
TGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCTGGGCTGGGTACAGTGGATTTAAG
GTGGGGGGGGCCTTCGACCACTGGGGCAAGGGAATCCTGGTCACCGTCTCCTCA

Amino Acid:

(SEQ ID NO: 2)

EVQLVESGGGLVQPKGSLRSLCSASGFTFNIIYAMNWRVQVPGKLDWVSSISSRGGDIYYAESS
GRFTISRDNAKNSLYLEMNLSRAEDTAVYYCARAGLGTVDLRWGGAFDHWGKGLVTVSS

Alignment:

Ig Sequence Name:EM-Swine1-4C04H-

V gene: Z14073_IGHV3-21*01
D Gene: None Found
D Gene 2: None Found
J Gene: X86355 IGHJ5*02
Clonal Pool: 0
CDR3 Length: 17
CDR3 AA: RAGLGTVDLRWGGAFDH (SEQ ID NO: 12)

> Z14073_IGHV3-21*01 20 30 40
E V Q L V E S G G G L V K P G
Germline GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC CTG GTC AAG CCT GGG
EM-Swine1-4C04H- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

50 60 70 80 90
G S L R L S C A A S G F T F S
Germline GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT
EM-Swine1-4C04H- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
S N

100 110 120 130
S Y S M N W V R Q A P G K G L
Germline AGC TAT AGC ATG AAC TGG GTC CGC CAG GCT CCA GGG AAG GGG CTG
EM-Swine1-4C04H- -T- --- GC- --- --- --- --- --- --- --- --- --- ---
I A V

140 150 160 170 180
E W V S S I S S S S Y I Y Y
Germline GAG TGG GTC TCA TCC ATT AGT AGT AGT AGT TAC ATA TAC TAC
EM-Swine1-4C04H- -T- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
D R G D

-continued

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                190          200          210          220
Germline      A D S V K G R F T I S R D N A
EM-Swine1-4C04H- --G-----G-----TCC AGA GAC AAC GCC
                E          E
                230          240          250          260          270
Germline      K N S L Y L Q M N S L R A E D
EM-Swine1-4C04H- ---AAG AAC TCA CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC
                G
                280          290          300          310
Germline      T A V Y C A ? ? ? ? ? ? ? ?
EM-Swine1-4C04H- ---ACG GCT GTG TAT TAC TGT GCG AGN NNN NNN NNN NNN NNN NNN
                R A G L G T V D
                320          330 |> X86355 IGHJ5*02          350          360
Germline      ? ? ? ? ? ? F D P W G Q G T L
EM-Swine1-4C04H- TTA AGG TGG GGG GGG GCC --- --A- --- --A- --- -T- ---
                L R W G G A H K I
                370
Germline      V T V S S ? (SEQ ID NO: 14)
EM-Swine1-4C04H- ---GTC ACC GTC TCC TCA G (SEQ ID NO: 13)
                (SEQ ID NO: 15)
                (SEQ ID NO: 2)

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EM4C04 kappa Variable Domain:
DNA
(SEQ ID NO: 16)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGAGACAGAGTCACCATCT
CTTGCCAGGCGAGTCAGGATATTACCAACTTTTTAAATTGGTACCAGCAGAAATCTGGGAAGC
CCCTAAGCTCCTGATCTACGATGCATCCGATTTGGAACAGGGGTCCCATCAAGGTTTCAGTGGA
AGTGGATCTGGGACAGATTTTACTTTCCACATCAGCAGGCTGCAGCCTGAAGACACTGCAACAT
ATTACTGTCAACAGTATGACGATCTCCCGTATACTTTTGGCCAGGGACCAAGGTGGAGATCAA
Amino acid
(SEQ ID NO: 1)
DIQMTQSPSSLSASVGRVITISCSQASQDITNFLNHWYQQKSGEAPKLLIYDASDLETGVPSTRFSGS
GSGTDFFTTISRLLQPEDTATYYCQQYDDLPLYTFGQGTKVEIK

Alignment:
Ig Sequence Name:EM-Swine1-4C04K-

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V gene:      M64855_IGKV1D-33*01
D Gene:      None Found
D Gene 2:    None Found
J Gene:      J00242 IGKJ2*01
Clonal Pool: 0
CDR3 Length: 8
CDR3 AA:     QYDDLPLYT (SEQ ID NO: 17)
                |> M64855_IGKV1D-33*01    20          30          40
Germline      D I Q M T Q S P S S L S A S V
EM-Swine1-4C04K- ---GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA
                50          60          70          80          90
Germline      G D R V T I T C Q A S Q D I S
EM-Swine1-4C04K- ---GGA GAC AGA GTC ACC ATC ACT TGC CAG GCG AGT CAG GAC ATT AGC
                T-- --- --- --- --T --- -C-
                S          T
                100          110          120          130
Germline      N Y L N W Y Q Q K P G K A P K
EM-Swine1-4C04K- ---AAC TAT TTA AAT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG
                -T- --- --- --- -C- --- --- T-T --- G-- --- ---

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-continued

FW3 : (SEQ ID NO: 30)
RFTISRDNAKNSLYLEMNSLRAEDTAVYYCAR

CDR3 : (SEQ ID NO: 8)
AGLGTVDLRWGGAFDH

FW4 : (SEQ ID NO: 31)
WGKGILVTVSS

CDR and FR of EM4C04 Light Chain:
Nucleotide:
FW1 : (SEQ ID NO: 32)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGAGACAGAGTCACCATCT
CTTGCCAGGCGAGT

CDR1 : (SEQ ID NO: 33)
CAGGATATTACCAACTTTTTAAAT

FW2 : (SEQ ID NO: 34)
TGGTACCAGCAGAAATCTGGGGAAGCCCCTAAGCTCCTGATCTAC

CDR2 : (SEQ ID NO: 35)
GATGCATCCGATTTGGAAACA

FW3 : (SEQ ID NO: 36)
GGGGTCCCATCAAGGTTTCAGTGGAGTGGATCTGGGACAGATTTTACTTTCACCATCAGCAGGC
TGCAGCCTGAAGACACTGCAACATATTACTGT

CDR3 : (SEQ ID NO: 37)
CAACAGTATGACGATCTCCCGTATACT

FW4 : (SEQ ID NO: 38)
TTTGCCAGGGGACCAAGGTGGAGATCAAA

Amino acids:
FW1 : (SEQ ID NO: 39)
DIQMTQSPSSLSASVGDRTVISC

CDR1 : (SEQ ID NO: 3)
QASQDIINFLN

FW2 : (SEQ ID NO: 40)
WYQQKSGEAPKLLIY

CDR2 : (SEQ ID NO: 4)
DASDLET

FW3 : (SEQ ID NO: 41)
GVPSRFSGSGSGTDFTFTISRRLQPEDTATYYC

CDR3 : (SEQ ID NO: 5)
QQYDDLPLYT

FW4 : (SEQ ID NO: 42)
FGQGTKVEIK

The CDR described herein can be grafted into the following vectors encoding human IgG and kappa chains, as well as others: Fully human IgG (GenBank® Accession No: FJ475055) and Fully human kappa (GenBank® Accession No: FJ475056).

GenBank ® FJ475055

(SEQ ID NO: 43)

RSTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSQVHTFPAV
 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPPC
 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKG
 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV
 LDDSDGSFFLYSKLTVDKSRWQQGNVFSQVMSHEALHNHYTQKSLSLSPGK

(SEQ ID NO: 44)

1 ttcgagctcg cccgacattg attattgact agttattaat agtaataat tacgggggtca
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 121 ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt tcccatagta
 181 acgccaatag ggactttcca ttgacgtcaa tgggtggagt atttacggta aactgccac
 241 ttggcagtac atcaagtgt tcatatgcca agtacgccc ctattgacgt caatgacggt
 301 aaatggccc cctggcatta tgcccagtac atgacctat gggactttcc tacttggcag
 361 tacatctacg tattagtcat cgctattacc atgggtgatgc ggttttggca gtacatcaat
 421 gggcgtgat agcggtttga ctcacgggga tttccaagtc tccaccccat tgacgtcaat
 481 gggagtttgt tttggacca aatcaacgg gactttccaa aatgtcgtaa caactccgcc
 541 ccattgacgc aaatggcgg taggcgtgta cgggtggagg tctatataag cagagctcgt
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 721 gccaagagtg acgtaagtac cgcctataga gtctataggc ccaccccctt ggcttcgta
 781 gaacgcggt acaattaata cataacctta tgtatcatac acatacgatt taggtgacac
 841 tatagaataa catccacttt gcctttctct ccacaggtgt ccaactccag gtccaactgc
 901 acctcggttc tatcgattga attccacct gggatggta tgtatcatcc tttttctagt
 961 agcaactgca accggtgtac actcgagcgt acggtcgacc aagggccat cggctctccc
 1021 cctggcacc tcctccaaga gcacctctgg gggcacagcg gcctgggct gcctggteaa
 1081 ggactacttc cccgaacctg tgacggtctc gtggaactca ggcgcccga ccagcggcgt
 1141 gcacaccttc ccggtgtcc tacagtcctc aggactctac tcctcagca gcgtggtgac
 1201 cgtgcctcc agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag
 1261 caacaccaag gtggacaaga aagttgagcc caaatcttgt gacaaaaactc acacatgccc
 1321 accgtgccc gcacctgaac tcctgggggg accgtcagtc tcctcttcc ccccaaaacc
 1381 caaggacacc ctcatgatct cccggacccc tgaggtcaca tcggtggtgg tggacgtgag
 1441 ccacgaagac cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc
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 1561 cgtcctgcac caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc
 1621 cctcccagcc cccatcgaga aaacctctc caaagccaaa ggcgagcccc gagaaccaca
 1681 ggtgtacacc ctgccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg
 1741 cctggtaaaa ggcttctatc ccagcgaat ccgctggag tgggagagca atgggcagcc

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1801 ggagaacaac tacaagacca cgcctcccggt gctggactcc gacggctcct tcttctctta
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1921 gatgcatgag gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa
1981 atgaagcttg gccgccatgg cccaacttgt ttattgcagc ttataatggt tacaataaaa
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2461 catggtgac taattttttt tttttatgca gaggccgagg ccgctcggc ctctgagcta
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2641 ttaatcgct tgcagcacat ccccccttcg ccagctggcg taatagcgaa gaggcccgca
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3181 gatattgccc atttggcct attggttaaa aaatgagctg attaacaaa aatttaacgc
3241 gaattttaac aaaatattaa cgtttacaat tttatggtgc actctcagta caatctgctc
3301 tgatgccgca tagttaagcc aactccgcta tcgctacgtg actgggtcat ggtgccc
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3481 ccgaaacgcg cgaggcagta ttctgaaga cgaagggcc tcgtgatacg cctattttta
3541 taggttaatg tcatgataat aatggtttct tagacgtcag gtggcacttt tcgggaaat
3601 gtgcgcgaa cccctatttg tttatttttc taaatacatt caaatatgta tccgctcatg
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GenBank[®] FJ475056

(SEQ ID NO: 45)

MSIQHFRVALIPFFAFLPVAHPETLVKVKDAEDQLGARVGYIELDLNSGKILE
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 DGMTVRELCSAAITMSDNTAANLLLTIGGPKELTAPLHNMGDVTLRDRWEPELN
 EAIPNDERDTMPAAMATLRKLLTGELLTLASRQQLIDWMEADKVAGPLLRSLP
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 SLIKHW

(SEQ ID NO: 46)

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 5041 acaggaaaca gctatgacca tgattacgaa ttaa

Use of Antibodies

Antibodies described herein can be used in any method that antibodies produced by other means can be used. Thus, they can be used in passive therapy and diagnosis. Passive

antibody immunization can provide a state of immediate immunity that can last for weeks and possibly months. Some human IgG isotypes have serum half-lives in excess of 30 days, which would confer long-lived protection to passively immunized persons. Where active vaccines are available,

they may be administered together with antibodies to both immediate and long-lasting protection. In addition, the antibodies can be administered in conjunction with one or more therapeutic drugs for treatment or prevention of infection or for treatment of infection. Administration of antibodies produced as described herein will follow the general protocols for passive immunization. Antibodies for administration be prepared in a formulation suitable for administration to a host. Aqueous compositions comprise an effective amount of an antibody dispersed in a pharmaceutically acceptable carrier and/or aqueous medium. The phrases “pharmaceutically and/or pharmacologically acceptable” refer to compositions that do not produce an adverse, allergic and/or other untoward reaction when administered to an animal, and specifically to humans, as appropriate.

As used herein, “pharmaceutically acceptable carrier” includes any solvents, dispersion media, coatings, antibacterial and/or antifungal agents, isotonic and/or absorption delaying agents and the like. The use of such media or agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions. For administration to humans, preparations should meet sterility, pyrogenicity, general safety and/or purity standards as required by FDA Office of Biologics standards.

Antibodies will generally be formulated for parenteral administration, e.g., formulated for injection via the intravenous, intramuscular, sub-cutaneous, intralesional, or even intraperitoneal routes. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation or in such amount as is therapeutically effective. Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject.

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SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 46

<210> SEQ ID NO 1
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 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide

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 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Gln Ala Ser Gln Asp Ile Thr Asn Phe
 20 25 30

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Leu Asn Trp Tyr Gln Gln Lys Ser Gly Glu Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Asp Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Arg Leu Gln Pro
 65 70 75 80

Glu Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asp Leu Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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 <211> LENGTH: 125
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 polypeptide

<400> SEQUENCE: 2

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Asn Ile Tyr
 20 25 30

Ala Met Asn Trp Val Arg Gln Val Pro Gly Lys Gly Leu Asp Trp Val
 35 40 45

Ser Ser Ile Ser Ser Arg Gly Asp Tyr Ile Tyr Tyr Ala Glu Ser Val
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ala Gly Leu Gly Thr Val Asp Leu Arg Trp Gly Gly Ala Phe
 100 105 110

Asp His Trp Gly Lys Gly Ile Leu Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 3
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 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 peptide

<400> SEQUENCE: 3

Gln Ala Ser Gln Asp Ile Thr Asn Phe Leu Asn
 1 5 10

<210> SEQ ID NO 4
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 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 peptide

<400> SEQUENCE: 4

Asp Ala Ser Asp Leu Glu Thr
 1 5

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<210> SEQ ID NO 5
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 5

Gln Gln Tyr Asp Asp Leu Pro Tyr Thr
1 5

<210> SEQ ID NO 6
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 6

Ile Tyr Ala Met Asn
1 5

<210> SEQ ID NO 7
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 7

Ser Ile Ser Ser Arg Gly Asp Tyr Ile Tyr Tyr Ala Glu Ser Val Glu
1 5 10 15

Gly

<210> SEQ ID NO 8
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 8

Ala Gly Leu Gly Thr Val Asp Leu Arg Trp Gly Gly Ala Phe Asp His
1 5 10 15

<210> SEQ ID NO 9

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<210> SEQ ID NO 10

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<210> SEQ ID NO 11
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 Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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<210> SEQ ID NO 14
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 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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 <220> FEATURE:
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 <222> LOCATION: (98)..(98)
 <223> OTHER INFORMATION: Arg or Ser
 <220> FEATURE:
 <221> NAME/KEY: MOD_RES
 <222> LOCATION: (99)..(111)
 <223> OTHER INFORMATION: Any amino acid

<400> SEQUENCE: 14

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe
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 Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 15
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 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(375)

<400> SEQUENCE: 15

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 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt tca gcc tct gga ttc acc ttc aat atc tat 96
 Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Asn Ile Tyr
 20 25 30
 gcc atg aac tgg gtc cgc cag gtt cca gga aag ggg ctg gat tgg gtc 144
 Ala Met Asn Trp Val Arg Gln Val Pro Gly Lys Gly Leu Asp Trp Val
 35 40 45
 tca tcc att agt agt agg ggt gat tac ata tac tac gca gag tca gtg 192
 Ser Ser Ile Ser Ser Arg Gly Asp Tyr Ile Tyr Tyr Ala Glu Ser Val
 50 55 60
 gag ggc cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg tat 240

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Glu	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	
65					70					75					80	
ctg	gaa	atg	aac	agc	ctg	aga	gcc	gag	gac	acg	gct	gtg	tat	tac	tgt	288
Leu	Glu	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90							95	
gcg	aga	gct	ggg	ctg	ggt	aca	gtg	gat	tta	agg	tgg	ggg	ggg	gcc	ttc	336
Ala	Arg	Ala	Gly	Leu	Gly	Thr	Val	Asp	Leu	Arg	Trp	Gly	Gly	Ala	Phe	
			100					105							110	
gac	cac	tgg	ggc	aag	gga	atc	ctg	gtc	acc	gtc	tcc	tca	g			376
Asp	His	Trp	Gly	Lys	Gly	Ile	Leu	Val	Thr	Val	Ser	Ser				
		115					120					125				

<210> SEQ ID NO 16
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 16

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ggggaagccc	ctaagctcct	gatctacgat	gcattccgatt	tggaaacagg	ggtcccatca	180
aggttcagtg	gaagtggatc	tgggacagat	tttactttca	ccatcagcag	gctgcagcct	240
gaagacactg	caacatatta	ctgtcaacag	tatgacgac	tcccgatac	tttggccag	300
gggaccaagg	tggagatcaa	a				321

<210> SEQ ID NO 17
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 17

Gln	Tyr	Asp	Asp	Leu	Pro	Tyr	Thr
1				5			

<210> SEQ ID NO 18
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(321)
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (285)..(288)
 <223> OTHER INFORMATION: a, c, t, g, unknown or other

<400> SEQUENCE: 18

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Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5						10				15		
gac	aga	gtc	acc	atc	act	tgc	cag	gcg	agt	cag	gac	att	agc	aac	tat	96
Asp	Arg	Val	Thr	Ile	Thr	Cys	Gln	Ala	Ser	Gln	Asp	Ile	Ser	Asn	Tyr	
			20					25						30		
tta	aat	tgg	tat	cag	cag	aaa	cca	ggg	aaa	gcc	cct	aag	ctc	ctg	atc	144

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Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
   35                               40                               45
tac gat gca tcc aat ttg gaa aca ggg gtc cca tca agg ttc agt gga      192
Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
   50                               55                               60
agt gga tct ggg aca gat ttt act ttc acc atc agc agc ctg cag cct      240
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
   65                               70                               75                               80
gaa gat att gca aca tat tac tgt caa cag tat gat aat ctc ccn nnn      288
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Xaa
   85                               90                               95
act ttt ggc cag ggg acc aag ctg gag atc aaa c                          322
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
   100                               105

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<210> SEQ ID NO 19
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (96)..(96)
<223> OTHER INFORMATION: Any amino acid

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<400> SEQUENCE: 19

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1                               5                               10                               15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
 20                               25                               30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35                               40                               45
Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
 50                               55                               60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65                               70                               75                               80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Xaa
 85                               90                               95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100                               105

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<210> SEQ ID NO 20
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(321)

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<400> SEQUENCE: 20

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gac atc cag atg acc cag tct cca tcc tcc ctg tct gca tct gtt gga      48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1                               5                               10                               15
gac aga gtc acc atc tct tgc cag gcg agt cag gat att acc aac ttt      96
Asp Arg Val Thr Ile Ser Cys Gln Ala Ser Gln Asp Ile Thr Asn Phe
 20                               25                               30
tta aat tgg tac cag cag aaa tct ggg gaa gcc cct aag ctc ctg atc      144
Leu Asn Trp Tyr Gln Gln Lys Ser Gly Glu Ala Pro Lys Leu Leu Ile

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-continued

35	40	45	
tac gat gca tcc gat ttg gaa aca ggg gtc cca tca agg ttc agt gga			192
Tyr Asp Ala Ser Asp Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly			
50	55	60	
agt gga tct ggg aca gat ttt act ttc acc atc agc agg ctg cag cct			240
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Arg Leu Gln Pro			
65	70	75	80
gaa gac act gca aca tat tac tgt caa cag tat gac gat ctc ccg tat			288
Glu Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asp Leu Pro Tyr			
	85	90	95
act ttt ggc cag ggg acc aag gtg gag atc aaa c			322
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys			
100	105		

<210> SEQ ID NO 21
 <211> LENGTH: 90
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 21

gaggtgcagc tgggtggatc tgggggagcc ctggtcaagc ctggggggtc cctgagactc	60
tectgttcag cctctggatt caccttcaat	90

<210> SEQ ID NO 22
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 22

atctatgcca tgaac	15
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<210> SEQ ID NO 23
 <211> LENGTH: 42
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 23

tgggtccgcc aggttccagg aaaggggctg gattgggtct ca	42
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<210> SEQ ID NO 24
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 24

tccattagta gtaggggtga ttacatatac tacgcagagt cagtggaggg c	51
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<210> SEQ ID NO 25
 <211> LENGTH: 96
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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oligonucleotide

<400> SEQUENCE: 25

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agagccgagg acacggctgt gtattactgt gcgaga 96

<210> SEQ ID NO 26

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 26

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<210> SEQ ID NO 27

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 27

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<210> SEQ ID NO 28

<211> LENGTH: 30

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide

<400> SEQUENCE: 28

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Asn

20 25 30

<210> SEQ ID NO 29

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 29

Trp Val Arg Gln Val Pro Gly Lys Gly Leu Asp Trp Val Ser

1 5 10

<210> SEQ ID NO 30

<211> LENGTH: 32

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide

<400> SEQUENCE: 30

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Glu

1 5 10 15

-continued

<400> SEQUENCE: 36

gggggcccat caaggttcag tggaagtgga tctgggacag attttacttt caccatcagc 60

aggctgcagc ctgaagacac tgcaacatat tactgt 96

<210> SEQ ID NO 37

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 37

caacagtatg acgatctccc gtatact 27

<210> SEQ ID NO 38

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 38

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<210> SEQ ID NO 39

<211> LENGTH: 23

<212> TYPE: PRT

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<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 39

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15Asp Arg Val Thr Ile Ser Cys
20

<210> SEQ ID NO 40

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 40

Trp Tyr Gln Gln Lys Ser Gly Glu Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> SEQ ID NO 41

<211> LENGTH: 32

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide

<400> SEQUENCE: 41

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Phe Thr Ile Ser Arg Leu Gln Pro Glu Asp Thr Ala Thr Tyr Tyr Cys

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290	295	300	
Val Phe Ser Cys Ser	Val Met His Glu Ala	Leu His Asn His Tyr Thr	
305	310	315	320
Gln Lys Ser Leu Ser	Leu Ser Pro Gly Lys		
	325	330	
<p><210> SEQ ID NO 44 <211> LENGTH: 5746 <212> TYPE: DNA <213> ORGANISM: Homo sapiens</p>			
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ttcagagctcg cccgacattg attattgact agttattaat agtaatcaat tacgggggtca			60
ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa tggcccgcct			120
ggctgaccgc ccaacgaccc ccgccattg acgtcaataa tgacgtatgt tcccatagta			180
acgccaatag ggactttcca ttgacgtcaa tgggtggagt atttacggta aactgcccac			240
ttggcagtac atcaagtgtg tcatatgcca agtacgcccc ctattgacgt caatgacggg			300
aaatggcccc cctggcatta tgcccagtac atgaccttat gggactttcc tacttggcag			360
tacatctacg tattagtcac cgctattacc atgggtgatgc ggttttggca gtacatcaat			420
gggcgtggat agcggtttga ctcacgggga tttccaagtc tccaccccat tgacgtcaat			480
gggagtttgt tttggcacca aaatcaacgg gactttccaa aatgtcgtaa caactccgcc			540
ccattgacgc aaatggggcg taggcgtgta cgggtgggagg tctatataag cagagctcgt			600
ttagtgaacc gtcagatcgc ctggagacgc catccacgct gttttgacct ccatagaaga			660
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gccaaagagt acgtaagtac cgcctataga gtctataggg ccacccccct ggettcggtta			780
gaacgcggct acaattaata cataacctta tgtatcatac acatacgatt taggtgacac			840
tatagaataa catccacttt gcctttctct ccacaggtgt ccactcccag gtccaactgc			900
acctcgggtc tatcagttga attccacat gggatgggtca tgtatcatcc tttttctagt			960
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cgtgccctcc agcagcttgg gcaccagac ctacatctgc aacgtgaatc acaagcccag			1260
caacaccaag gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc			1320
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gatgcatgag gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa	1980
atgaagcttg gccgccatgg cccaacttgt ttattgcagc ttataatggt taaaaataaa	2040
gcaatagcat cacaaatttc acaataaaag ctttttttc actgcattct agttgtgggt	2100
tgtccaaact catcaatgta tcttatcatg tctggatcga tcgggaatta attcggcgca	2160
gcaccatggc ctgaaataac ctctgaaaga ggaacttggg taggtacctt ctgaggcgga	2220
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 35             40             45
Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
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Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
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What is claimed is:

1. A non-naturally occurring chimeric monoclonal antibody, wherein the antibody comprises a heavy chain having a variable and constant region and a light chain having a variable and constant region, wherein the light chain variable region comprises CDR1 of SEQ ID NO: 3, CDR2 of SEQ ID NO: 4 and CDR3 of SEQ ID NO: 5 and wherein the heavy chain variable region comprises CDR1 of SEQ ID NO: 6, CDR2 of SEQ ID NO: 7 and CDR3 of SEQ ID NO: 8, and wherein the antibody specifically binds H1N1.
2. The non-naturally occurring chimeric monoclonal antibody of claim 1 wherein the antibody has Kd for purified H1N1 that is less than 1×10^{-9} .
3. A composition comprising a non-naturally occurring chimeric monoclonal antibody wherein the antibody comprises a heavy chain having a variable and constant region and a light chain having a variable and constant region, wherein the light chain variable region comprises CDR1 of SEQ ID NO: 3, CDR2 of SEQ ID NO: 4 and CDR3 of SEQ ID NO: 5 and wherein the heavy chain variable region comprises CDR1 of SEQ ID NO: 6, CDR2 of SEQ ID NO:

- 7 and CDR3 of SEQ ID NO: 8, and wherein the antibody specifically binds H1N1, and a pharmaceutically acceptable carrier.
4. A method for reducing the risk of infection with H1N1 in a human subject, the method comprising administering a non-naturally occurring chimeric monoclonal antibody comprising a heavy chain having a variable and constant region and a light chain having a variable and constant region, wherein the light chain variable region comprises CDR1 of SEQ ID NO: 3, CDR2 of SEQ ID NO: 4 and CDR3 of SEQ ID NO: 5 and wherein the heavy chain variable region comprises CDR1 of SEQ ID NO: 6, CDR2 of SEQ ID NO: 7 and CDR3 of SEQ ID NO: 8, specifically binds H1N1, to the human subject thereby reducing the risk of infection of H1N1 in the human subject.
5. A method for treating a patient infected with H1N1 virus, the method comprising administering a non-naturally occurring chimeric monoclonal antibody comprising a heavy chain having a

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variable and constant region and a light chain having a variable and constant region, wherein the light chain variable region comprises CDR1 of SEQ ID NO: 3, CDR2 of SEQ ID NO: 4 and CDR3 of SEQ ID NO: 5 and wherein the heavy chain variable region comprises CDR1 of SEQ ID NO: 6, CDR2 of SEQ ID NO: 7 and CDR3 of SEQ ID NO: 8, and wherein the antibody specifically binds H1N1, to the patient infected with the H1N1 virus, thereby treating the patient.

6. The non-naturally occurring chimeric monoclonal antibody of claim 1, or the antigen binding fragment thereof, wherein the heavy chain variable region consists of the amino acid sequence of SEQ ID NO: 2.

7. The non-naturally occurring chimeric monoclonal antibody of claim 1, or antigen binding fragment thereof, wherein the light chain variable region consists of the amino acid sequence of SEQ ID NO: 1.

8. The non-naturally occurring chimeric monoclonal antibody of claim 1, or the antigen binding fragment thereof, wherein the heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 2 and the light chain variable region comprises the amino acid sequence of SEQ ID NO: 1.

9. A non-naturally occurring chimeric monoclonal antibody, wherein the antibody comprises a heavy chain having a variable and constant region and a light chain having a variable and constant region,

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wherein the light chain variable region comprises CDR1 of SEQ ID NO: 3, CDR2 of SEQ ID NO: 4 and CDR3 of SEQ ID NO: 5 and wherein the heavy chain variable region comprises CDR1 of SEQ ID NO: 6, CDR2 of SEQ ID NO: 7 and CDR3 of SEQ ID NO: 8, wherein the heavy chain constant region comprises SEQ ID NO: 43, and wherein the antibody specifically binds H1N1.

10. A non-naturally occurring monoclonal antibody specifically binding influenza virus H1N1, having a heavy chain with a constant domain and variable domain, and light chain with a variable domain and constant domain wherein the light chain variable region comprises CDR1 of SEQ ID NO: 3, CDR2 of SEQ ID NO: 4 and CDR3 of SEQ ID NO: 5 and the heavy chain variable region comprises CDR1 of SEQ ID NO: 6, CDR2 of SEQ ID NO: 7 and CDR3 of SEQ ID NO: 8, and wherein the heavy chain comprises a sequence that is different from any sequences present in naturally derived antibodies for which the light chain variable region comprises CDR1 of SEQ ID NO: 3, CDR2 of SEQ ID NO: 4 and CDR3 of SEQ ID NO: 5 and the heavy chain variable region comprises CDR1 of SEQ ID NO: 6, CDR2 of SEQ ID NO: 7 and CDR3 of SEQ ID NO: 8.

* * * * *