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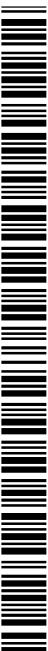
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(54) Title: PREVENTION AND TREATMENT OF HCV INFECTION EMPLOYING ANTIBODIES DIRECTED AGAINST CONFORMATIONAL AND LINEAR EPITOPE

(57) Abstract: Conformational epitopes of the envelope proteins E1 and E2 of the Hepatitis C virus (HCV) have been identified and characterized using a panel of monoclonal antibodies derived from patients infected with HCV. These conserved conformational and linear epitopes of the HCV protein E1 or E2 have been determined to be important in the immune response of humans to HCV and may be particularly important in neutralizing the virus. Based on the identification of these conformational epitopes, vaccines containing peptides and mimotopes with these conformational epitopes intact may be prepared and administered to patients to prevent and/or treat HCV infection. The identification of four distinct groups of monoclonal antibodies with each directed to a particular epitope of E1 or E2 may be used to stratify patients based on their response to HCV and may be used to determine a proper treatment regimen.

**PREVENTION AND TREATMENT OF HCV INFECTION EMPLOYING
ANTIBODIES DIRECTED AGAINST CONFORMATIONAL AND LINEAR EPITOPES**

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CROSS REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of co-pending patent application U.S.S.N. 09/728,720, filed December 1, 2000, which is a continuation-in-part of U.S.S.N. 09/430,489, filed October 29, 1999, which is a continuation-in-part of 15 patent application U.S.S.N. 09/187,057, filed November 5, 1998. Each of these applications is incorporated herein by reference.

INTRODUCTION

Technical Field

20 The field of this invention is related to the preparation of human monoclonal antibodies (HMAb) to structurally conserved epitopes of HCV. Such antibodies can be found in a high proportion of patients and are useful, for example, in the diagnosis and therapy of HCV infection, including being useful in the identification of patients expected to benefit from certain therapeutic strategies.

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Background

Hepatitis C virus (HCV) is an enveloped virus the genetic information for which is encoded in a 9.5 kb positive strand RNA genome. A highly conserved

noncoding region of 341 bp is localized at the 5'-end of this viral genome, which is followed by a long open-reading frame coding for a polyprotein of approximately 3,010 amino acids. Two putative envelope glycoproteins E1 (gp35) and E2 (gp72) have been identified with 5 or 6 and 11 N-linked glycosylation sites, respectively. A 5 high level of genetic variability is associated with the envelope genes. This variability is highly accentuated at the 5'-end of the E2 gene, where two hypervariable regions termed HVR1 and HVR2, have been described. Antibodies to HVR1 appear to mediate virus neutralization in cell culture and chimpanzee protection studies (Farci *et al.*, 1996 *Proc. Natl. Acad. Sci. USA* 93:15394-15399; 10 Shimizu *et al.*, 1994 *J. Virol.* 68:1494-1500; each of which is incorporated herein by reference). Unfortunately, antibodies to HVR1 tend to be isolate specific and over time drive the replication of new viral variants that the existing immune response does not recognize (Farci *et al.*, 1994 *Proc. Natl. Acad. Sci. USA* 91:7792-7796; Weiner *et al.*, 1992 *Proc. Natl. Acad. Sci. USA* 89:3468-3472; Kato *et al.*, 1993 *J. 15 Virol.* 67:3923-3930; each of which is incorporated herein by reference), although progress has been made at inducing a broader immune response to HVR1 related sequences (Puntoriero *et al.*, 1998 *EMBO Journal* 17:3521-3533; incorporated herein by reference). HCV envelope antigens appear to be highly immunogenic when expressed in glycosylated forms (da Silva Cardoso *et al.*, 1997 *Ann. Hematol.* 20 74:135-7; incorporated herein by reference). Preliminary data suggest the existence of conserved epitopes within the E2 protein (Lesniewski *et al.*, 1995 *J. Med. Virol.* 45:415-22; incorporated herein by reference). The existence of neutralizing antibodies in serum from infected patients has been proposed.

Studies using HCV E1-E2 proteins expressed in mammalian cells have 25 shown that infected individuals have an antibody response to HCV E2 composed in part to epitopes that are both conformational and linear in nature (Harada *et al.*, 1994 *J. Gen. Virol.* 76:1223-1231; incorporated herein by reference). Studies involving the isolation of human monoclonal or recombinant antibodies to HCV E2 protein showed that a substantial fraction of these antibodies recognize conformational 30 epitopes (da Silva Cordoso *et al.*, 1998 *J. Med. Virol.* 55:28-34; each of which is incorporated herein by reference). As to biological function of these domains,

investigators have employed surrogate assays to provide insights into virus neutralization since the virus cannot be grown, *in vitro* (Houghton, Hepatitis C viruses. In Fields, Knipe, Howley (eds) *Virology*. Lippincott-Raven, Philadelphia, pp. 1035-1058; incorporated herein by reference). One surrogate assay, the 5 neutralization of binding (NOB) assay, evaluates the ability of a given antibody or serum to prevent the association of HCV E2 protein with a human T-cell line (Rosa *et al.*, 1996 *Proc. Natl. Acad. Sci. USA* 93:1759-1763; incorporated herein by reference). The finding that serum antibodies obtained from chimpanzees protected 10 by vaccination were strongly positive in the NOB assay provides support for the relevance of the assay as a measure of virus neutralization activity (Rosa *et al.*, *supra*; Ishii *et al.*, 1998 *Hepatology* 28:1117-1120; each of which is incorporated herein by reference).

The human tetraspannin cell surface protein CD81 (TAPA-1, for review *see* Levy *et al.*, 1998 *Ann. Rev. Immunol.* 16:89-109; incorporated herein by reference) 15 is the target protein bound by HCV E2 in the NOB assay (Pileri *et al.*, 1998 *Science*. 282:938-941; incorporated herein by reference). Furthermore, human CD81 binds to free virions, and subsequently is a possible receptor for HCV (Pileri *et al.*, *supra*). However, little is known about the conservation of the epitopes recognized by the 20 NOB positive antibodies in HCV E2 proteins of different genotypes.

Other approaches to detection of and protection against HCV include the development of peptide mimetics. As an example, peptide mimetics of Hepatitis 25 type A and C viral proteins have been created through production of randomly generated synthetic and phage-display peptide libraries for use in detection assays and vaccination therapies (Mattioli *et al.*, 1995 *J. Virology* 69:5294-5299; Prezzi *et al.*, 1996 *J. Immunol.* 156:4504-4513; each of which is incorporated herein by reference). However, effective antibody binding of these mimotopes has only been compared to linearly defined viral epitopes. The sequential recombinant fusing of several linearly defined immunodominant HCV epitopes has been described for use 30 in diagnostic assays (Chein *et al.*, 1999 *J. Clin. Microbiol.* 37:1393-1397; incorporated herein by reference). However, this multiple-epitope fusion antigen designed from linear epitopes was not created to function in the same capacity as a

conformational mimetic: It was not designed to interfere with binding to a target receptor.

It is therefore of substantial interest to identify neutralizing antibodies in serum from infected patients, which may be used in diagnosis and passive immunotherapy, where the antibodies would originate from a human cell, and provide for neutralization of a broad spectrum of genotypes, particularly in a particular geographical area. Both breadth of reactivity to multiple HCV genotypes and the ability to interfere with the binding of HCV virions to susceptible cells would be key attributes for a therapeutically useful neutralizing antibody. Also of interest is the design of peptide and non-peptide (organic) structural mimetics of HCV envelope proteins.

Relevant Literature

References providing background information concerning HCV include Abrignani 1997 Springer *Semin. Immunopathology* 19:47-55; Simmonds, 1995 15 *Hepatology* 21:570:583; and Mahaney *et al.*, 1994 *Hepatology* 20:1405-1411; each of which is incorporated herein by reference.

Deleersnyder *et al.*, 1997 *J. of Virology* 71:697-704 describe an E2 reactive monoclonal antibody. Other references related to the use of antibodies to HCV include Akatsuka, *et al.*, 1993 *Hepatology* 18:503-510; DeLalla, *et al.*, 1993 *J. Hepatol.* 18:163-167; Mondelli, *et al.*, 1994 *J. Virol.* 68:4829-4836; Siemoneit, *et al.*, 1994 *Hybridoma* 13:9-13; and Moradpour, *et al.*, 1996 *J. Med. Virol.* 48:234-241; for producing human antibodies, Foung, *et al.*, 1990 *J. Immunol. Methods* 70:83-90; Zimmermann, *et al.*, 1990 *J. Immunol. Methods* 134:43-50; for producing modified antibodies using combinatorial libraries, Burton and Barbas, Dixon, FJ 25 (Ed.) *Advances in Immunology*, Vol. 57, Vi+391 p. Academic Press, Inc., San Diego, CA, 191-280, 1994; Plaisant, *et al.*, 1997 *Res. Virol.* 148-169; and Barbas and Burton, *Monoclonal Antibodies from Combinatorial Libraries. Cold Spring Harbor Laboratory Course Manual*, Cold Spring Harbor, NY, 1994. Modified antibodies can be produced by mutagenesis followed by in vitro selection for a 30 desirable property, such as increased affinity to a target antigen or broader or narrower specificity. The antibodies can also be modified by a toxin or other

bioactive molecule. Of course, antibodies to either E1 or E2 can be produced. Each of the references cited in this paragraph is incorporated herein by reference.

An assay for antibodies binding to HCV E2 is described by Rosa *et al.*, 1996 *Proc. Natl. Acad. Sci. USA* 93:1759-1763; incorporated herein by reference.

5 Vaccinia virus or baculovirus constructs having a portion of the HCV genome are described by Ralston *et al.*, 1993 *J. Virology* 67:6733-6761 and Lanford *et al.*, 1993 *Virology* 197:225-235; each of which is incorporated herein by reference.

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SUMMARY OF THE INVENTION

One aspect of the present invention provides monoclonal antibodies, including human monoclonal antibodies, which bind to the dominant HCV types in major geographical areas. Specifically, a family of monoclonal antibodies binding to conserved conformational and linear epitopes of the HCV E1 and E2 proteins is provided. Among the family are antibodies, which bind to the dominant genotypes found in the United States, so as to be substantially pan-monoclonal antibodies in being able to bind to almost all cases of HCV infection, which have been diagnosed in the United States, as well as at least a substantial proportion of the cases in other geographic locales. The monoclonal antibodies find use in a variety of diagnostic assays. In addition, conserved expression of recombinant HCV E1 and E2 proteins and fragments thereof are provided for use in assays, screening drugs, vaccines, diagnostic assays, and for other purposes. The inventive antibodies find use in passive immunotherapy strategies for reducing viral load of infected individuals and interfering with the infection of target cells. Antibodies recognizing conserved epitopes can also be used to provide a template for the rational design of peptide and conformationally defined epitope mimetics (*e.g.*, organic compounds, organometallic compounds, inorganic compounds, small molecules).

In a particularly preferred embodiment, the inventive antibodies are directed to both conformational and linear epitopes of the E2 or E1 protein of HCV.

Conformational and linear epitopes of E2 have been identified using a panel of monoclonal antibodies and a series of deletion constructs of E2. One group of antibodies has been found to bind to conformational epitopes between E2 amino acids 411-644 from HCV 1b. Antibodies of this group have been found to inhibit 5 the interaction of E2 with CD81. Another group of antibodies has been found to bind to conformational epitopes between HCV 1b E2 amino acids 470-644. A third group of antibodies binds to conformational epitopes between HCV 1b E2 amino acids 470-644 but fails to inhibit the binding of E2 to CD81. A fourth group binds to epitopes between HCV 1b E2 amino acids 644-661. A fifth group binds to 10 conformational epitopes between HCV 1b E1 amino acids 230-313. A sixth group binds to a linear HCV E1 epitopes derived from multiple genotypes. In a particularly preferred embodiment, the conformational epitopes to which the antibodies are directed are conserved among HCV strains. The antibodies of the present invention may be combined with pharmaceutically acceptable excipients to 15 provide pharmaceutical formulations.

Another aspect of the invention provides definition of conformational epitopes in HCV proteins, and further provided compositions and compounds containing such epitopes. For example, the present invention provides proteins, peptides, and small molecules comprising both conformational and linear epitopes of 20 HCV E1 or E2 protein. The peptides may be deletion constructs such as those in Figure 23. The peptides may contain one or more epitopes recognized by the antibodies of the present invention. In certain preferred embodiments, the proteins are strings of concatenated peptides at least one of which contains a conformational epitope of HCV. The peptides of the string may contain different conformational or 25 linear epitopes of HCV or the peptides may contain the same epitope. The peptides of the string should preferably fold properly in order to display the conformational epitope substantially as it appears in nature. Such proteins and peptides may be used in formulating vaccines or used in diagnostic tests.

The present invention also provides a method for stratifying patients based 30 on their immunological response to HCV and of identifying those patients likely to respond well to HCV immunotherapy. For example, a patient's serum may be used

to test for the presence of antibodies directed against a particular epitope of HCV. If the patient does not have adequate levels of antibodies directed to such an epitope, human monoclonal antibodies directed against the epitope may be administered to the patient.

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DEFINITIONS

“Animal”: The term animal, as used herein, refers to humans as well as non-human animals, including, for example, mammals, birds, reptiles, amphibians, and fish. Preferably, the non-human animal is a mammal (*e.g.*, a rodent, a mouse, a rat, 10 a rabbit, a monkey, a dog, a cat, a primate, or a pig). An animal may be a transgenic animal.

“Antibody”: The term antibody refers to an immunoglobulin, whether natural or wholly or partially synthetically produced. All derivatives and fragments thereof, which maintain specific binding ability, are also included in the term. The 15 term also covers any protein having a binding domain, which is homologous or largely homologous to an immunoglobulin-binding domain. These proteins may be derived from natural sources, or partly or wholly synthetically produced. An antibody may be monoclonal or polyclonal. The antibody may be a member of any immunoglobulin class, including any of the human classes: IgG, IgM, IgA, IgD, and 20 IgE. Derivatives of the IgG class, however, are preferred in the present invention.

“Peptide”: According to the present invention, a “peptide” comprises a string of at least three amino acids linked together by peptide bonds. Peptide may refer to an individual peptide or a collection of peptides. Inventive peptides 25 preferably contain only natural amino acids, although non-natural amino acids (*i.e.*, compounds that do not occur in nature but that can be incorporated into a polypeptide chain; see, for example,

<http://www.cco.caltech.edu/~dadgrp/Unnatstruct.gif>, which displays structures of non-natural amino acids that have been successfully incorporated into functional ion channels) and/or amino acid analogs as are known in the art may alternatively be 30 employed. Also, one or more of the amino acids in an inventive peptide may be modified, for example, by the addition of a chemical entity such as a carbohydrate

group, a phosphate group, a farnesyl group, an isofarnesyl group, a fatty acid group, a linker for conjugation, functionalization, or other modification, *etc.* In a preferred embodiment, the modifications of the peptide lead to a more stable peptide (*e.g.*, greater half-life *in vivo*). These modifications may include cyclization of the 5 peptide, the incorporation of D-amino acids, *etc.* None of the modifications should substantially interfere with the desired biological activity of the peptide.

“Polynucleotide” or “oligonucleotide”: Polynucleotide or oligonucleotide refers to a polymer of nucleotides. The polymer may include natural nucleosides (*i.e.*, adenosine, thymidine, guanosine, cytidine, uridine, deoxyadenosine, 10 deoxythymidine, deoxyguanosine, and deoxycytidine), nucleoside analogs (*e.g.*, 2-aminoadenosine, 2-thiothymidine, inosine, pyrrolo-pyrimidine, 3-methyl adenosine, 5-methylcytidine, 2-aminoadenosine, C5-bromouridine, C5-fluorouridine, C5-iodouridine, C5-propynyl-uridine, C5-propynyl-cytidine, C5-methylcytidine, 2-aminoadenosine, 7-deazaadenosine, 7-deazaguanosine, 8-oxoadenosine, 15 8-oxoguanosine, O(6)-methylguanine, and 2-thiocytidine), chemically modified bases, biologically modified bases (*e.g.*, methylated bases), intercalated bases, modified sugars (*e.g.*, 2'-fluororibose, ribose, 2'-deoxyribose, arabinose, and hexose), or modified phosphate groups (*e.g.*, phosphorothioates and 5'-
-N-phosphoramidite linkages).

“Small molecule”: As used herein, the term “small molecule” refers to organic compounds, whether naturally-occurring or artificially created (*e.g.*, via chemical synthesis) that have relatively low molecular weight and that are not proteins, polypeptides, or nucleic acids. Typically, small molecules have a molecular weight of less than about 1500 g/mol. Also, small molecules typically have multiple carbon-carbon bonds. Known naturally occurring small molecules include, but are not limited to, penicillin, erythromycin, taxol, cyclosporin, and rapamycin. Known synthetic small molecules include, but are not limited to, ampicillin, methicillin, sulfamethoxazole, and sulfonamides.

Figure 1 is a Western blot indicating the expression of HCV E2 proteins by some of the vaccinia virus constructs described in this application. Cytoplasmic extracts were prepared from CV1 cells infected with wild type vaccinia virus and then transfected with pVOTE (wt) or recombinant pVOTE expressing HCV E2 of 5 genotype 1a (Q1a) or 2b (Q2b). Cells were cultured for 24 hours in the presence (+) or absence (-) of the inducer IPTG. Extract corresponding to 2×10^5 cells was fractionated by SDS PAGE and blotted onto nitrocellulose. HCV E2 protein was revealed by incubation with 1/500 diluted ascites fluid of mMab E2G using the ECL detection system (Amersham). Migration of molecular weight standards is indicated 10 at right.

Figure 2 (SEQ ID NOS: 9-12) describes sequences amplified from the central region of the HCV E2 vaccinia virus clones. Shown are the sequences of the central fragment for HCV E2 vaccinia constructs Q1a, Q1b, Q2a, and Q2b as compared to representative sequences of the appropriate HCV genotypes. Accession 15 numbers for the representative sequences of each genotype are as follows HCV 1A = M62321, HCV 1B = D10750, HCV2A = D00944, HCV 2B = D10988. Phylogenetic analysis was performed with CLUSTALV and DNAPARS program of the PHYLIP package.

Figure 3 (SEQ ID NOS: 1-8) is a comparison of sequences of HCV: 1a, 20 Q1a-FR, -1b, 1Q1b-FR, 2a, Q2a-FR, -2b, -Q2b-FR, using the most parsimonious tree found.

Figure 4 shows a graph of the reactivity of HCV sera with HCV E2 proteins of different genotypes. HCV E2 protein expressed by 6×10^5 HeLa cells infected with vaccinia virus Q1a , Q1b , Q2a , Q2b , or non recombinant vaccinia 25 virus VWA was captured onto wells coated with 500 ng of GNA lectin. Wells were washed and blocked, and bound protein was incubated with increasing dilutions (x axis) of genotyped HCV sera or an HCV negative serum (indicated above the graph). Values are the mean absorbance of replicate wells. Error bars indicate one standard deviation from the mean.

Figure 5 is a bar graph indicating the reactivity of sera from individuals infected with HCV genotype 2b with HCV E2 proteins of multiple genotypes. Twelve sera from individuals infected with HCV genotype 2b (x axis) were titrated against HCV E2 proteins of genotypes 1a (dark blue bars), 1b (magenta bars), 2a (yellow bars), and 2b (light blue bars). The dilution of the serum that resulted in a mean specific absorbance (mean absorbance obtained with HCV E2 containing extract subtracted from the mean specific absorbence obtained with the VWA extract) of 0.5 is indicated on the y-axis. This value was calculated from titration curve data analogous to that presented in Figure 4.

Figure 6 depicts a schematic of a direct binding assay to assess for antibodies that recognize conformational epitopes of HCV E2 envelope proteins employed in the experiments described in Figures 7, 8, and 9. GNA lectin is coated onto a solid surface and then added E2-containing protein extracts are captured by the lectin. Test antibodies are allowed to bind to the captured E2, the excess unbound is removed, and bound antibody is detected with a labeled secondary antibody.

Figure 7 is a bar graph of the reactivity of HCV HMabs to HCV E2 captured by lectins. Proteins from cytoplasmic extracts of 6×10^5 cells infected with wild type (Bars labeled VWA) or HCV 1a E2 (HCV 1a) (bars labeled HCV) expressing vaccinia virus were applied to microtiter plates coated with 500 ng of *Galanthus nivalis* (GNA) or *Triticum vulgaris* (WGA). Captured proteins were incubated with 5 μ g/ml of the indicated HMabs (x axis). R04 is an isotype-matched control. Bound HMab was detected with anti-human antibody-alkaline phosphatase and appropriate substrate. Bars indicate the mean OD value of replicate wells. Error bars indicate one standard deviation from the mean.

Figure 8 shows graphs of HCV antibody reactivity with E2 protein of divergent HCV genotypes. HCV E2 proteins expressed by 6×10^5 HeLa cells infected with vaccinia virus Q1a, Q1b, Q2a, Q2b was captured onto wells coated with 500 ng of GNA lectin. Wells were washed and blocked, and bound protein was incubated with the indicated HCV HMabs (HMab identified above each of Figs. 9A-9J) and control HMab (R04) Fig. 9K to a CMV protein (Ward, *et al.*, 1995, *Proc Natl Acad Sci USA*. 92:6773-6777; incorporated herein by

reference). Values are the mean specific binding (extracts of cells infected with vaccinia virus expressing HCV E2 protein - wt vaccinia extracts) of replicate wells. Reactivity of HCV and control HMabs with proteins from wt vaccinia virus infected cells did not exceed an absorbance of 0.04. Error bars indicate one standard deviation from the mean.

Figure 9 is a bar graph showing the reactivity of HCV HMabs with native (NAT) and denatured (DNT) HCV 1b E2 protein. Cytoplasmic extract derived from 6×10^5 HeLa cells infected with vaccinia virus Q1b and VWA or VWA alone were either left untreated (blue bars) or denatured by incubation with 0.5% SDS and 5 mM dithiothreitol for 15 minutes at 56 °C (yellow bars). After treatment, proteins were diluted 1:5 in BLOTTO and captured onto wells coated with 500 ng of GNA lectin. Wells were washed and blocked, and bound protein was incubated with the indicated concentration of HCV HMabs and control HMAb (R04). Bound antibody was detected with anti-human IgG alkaline phosphatase conjugate and PNPP. Color development was allowed to proceed for 45 minutes. Values for native and denatured HCV 1b are the mean signal obtained from replicate wells. Signals from single wells of native and denatured proteins derived from VWA infected HeLa cells were indistinguishable and also averaged (red bars). Error bars indicate one standard deviation from the mean.

Figure 10 depicts a schematic of the competition binding analysis employed in the experiments described in Figures 11, 12, and 13. GNA lectin is coated onto a solid surface and then added E2-containing protein extracts are captured by the lectin. Competing antibodies are allowed to bind to the captured E2 before removing unbound excess and adding labeled test antibody.

Figure 11 is a bar graph of a competition analysis using HCV HMAb CBH-5. HCV E2 protein from cytoplasmic extracts of HeLa cells infected with vaccinia virus Q1a (blue bars) or Q1b (red bars) was captured with 500 ng of GNA. Bound HCV E2 was detected with 5 µg/ml of biotinylated CBH-5 in the presence of 25 µg/ml of the indicated HMabs (x axis). Results are compared to binding of biotinylated CBH-5 in the absence of any competitor. Bars indicate the mean value

obtained from replicate wells. Error bars indicate one standard deviation from the mean.

Figure 12 is a competition analysis showing the ability of the HCV HMabs to interfere with the binding of HMAb CBH-2 to HCV E2 proteins of multiple genotypes. HCV E2 protein from cytoplasmic extracts of HeLa cells infected with vaccinia virus Q1a (Blue bars), Q1b (red bars), Q2a (yellow bars), or Q2b (light blue bars) was captured with 500 ng of GNA lectin. The HMabs CBH-4D, -4B, and -17 were only evaluated with HCV 1a or 1b E2 protein due to their limited reactivity to genotype 2 E2 proteins. Bound HCV E2 was detected with 2 μ g/ml of biotinylated CBH-2 in the presence of 20 μ g/ml of the indicated HMabs (x axis). The bars indicate the binding observed in the presence of the indicated antibody relative to binding of biotinylated CBH-2 to HCV E2 in the absence of any competing antibody (y axis). R04 is a control HMAb that recognizes a cytomegalovirus protein. Bars indicate the mean value obtained from replicate wells. Error bars indicate one standard deviation from the mean.

Figure 13 is a competition analysis showing that HCV HMAb CBH-7 recognizes a unique epitope. HCV E2 protein from cytoplasmic extracts of HeLa cells infected with vaccinia virus Q1a (blue bars) or Q1b (red bars) was captured with 500 ng of GNA lectin. Bound HCV E2 was detected with 2 μ g/ml of biotinylated CBH-7 in the presence of 20 μ g/ml of the indicated HMabs (x axis). The bars indicate the binding observed in the presence of the indicated antibody relative to binding of biotinylated CBH-7 to HCV E2 in the absence of any competing antibody (y axis). R04 is a control HMAb that recognizes a cytomegalovirus protein. Bars indicate the mean value obtained from replicate wells. Error bars indicate one standard deviation from the mean.

Figure 14 depicts a schematic for assessing the ability of antibodies to block CD81 binding to E2 proteins as employed in the experiments described in Figure 1. Recombinant CD81 is coated onto a solid surface. E2-containing protein extracts are then either added directly, or after preincubation with the test antibody. Bound test antibody-E2 complexes are detected using an appropriate labeled secondary antibody.

Figure 15 is a bar graph that demonstrates that a subset of HCV HMAbs react with HCV E2 when bound to CD81-LEL. Extracts from BSC-1 cells infected with recombinant vaccinia virus expressing HCV E2 proteins were combined with 5 μ g/ml of the indicated HMAbs (x axis) in a total volume of 100 μ l and incubated in 5 microtiter plate wells coated with 100 ng of a GST CD81-LEL fusion protein or non-recombinant GST overnight. Wells were washed and bound antibody was detected using an appropriate alkaline-phosphate conjugated secondary antibody and PNPP substrate as further described in Example 6. Values are the mean OD value of antibody captured by CD81 divided by the mean OD value for antibody captured by 10 GST in the presence of 1a (purple bars), 1b (red bars), 2a (yellow bars), or 2b (green bars) E2 protein. OD values obtained from wells coated with GST ranged between 0.021 and 0.081.

Figure 16 depicts a schematic for assessing the ability of antibodies to block CD81 binding to HCV virions as employed in the experiments described in Figure 15. Recombinant CD81 is coated onto a solid surface. HCV virions are 17. Recombinant CD81 is coated onto a solid surface. HCV virions are preincubated with test antibodies, and then allowed to bind to immobilized CD81. Detection of bound HCV virions is measured by quantitative PCR.

Figure 17 shows a bar graph demonstrating that HMAbs CBH-2 and CBH-5 inhibit binding of HCV virions to CD81. The number of HCV RNA molecules 20 bound to polystyrene beads (x axis) after HCV 1a chimpanzee serum was combined with 10 μ g of the indicated antibodies (y axis) and then allowed to bind to beads coated with CD81-LEL.

Figure 18 is a bar graph that shows that HMAb CBH-4G can be employed to detect the presence of antibodies that inhibit binding of HCV E2 to CD81. HCV 1a 25 E2 protein derived from extracts of BSC-1 cells infected with vaccinia virus Q1a was incubated with 4 μ g/ml of a biotinylated preparation of HMAb CBH-4G for 20 minutes at 4°C. A 50 μ l aliquot of the E2-CBH-4G complexes was then added to wells coated with either 500 ng of GNA (blue bars) or 100 ng of GST-CD81-LEL (red bars) to which 50 μ l of a 40 μ g/ml of the indicated antibodies (x axis) was 30 added. R04 is a control HMAb that recognizes a cytomegalovirus protein. After an overnight incubation at 4°C the wells were washed and bound biotinylated CBH-4G

detected as described in Example 7. The bars indicate the mean signal obtained from duplicate wells in the presence of the indicated antibody relative to the signal obtained in the absence of any competing antibody. Error bars indicate one standard deviation from the mean.

5 Figure 19 is a bar graph that shows that HMAb CBH-4G can be employed to detect the presence of antibodies that inhibit binding of HCV E2 to CD81 in sera from HCV infected individuals. HCV 1a or 2b E2 protein derived from extracts of BSC-1 cells infected with vaccinia virus Q1a or Q2b was incubated with 4 µg/ml of a biotinylated preparation of HMAb CBH-4G for 20 minutes at 4°C. The four sera 10 at left were tested with HCV 1a E2 protein; the four sera at right were tested with HCV 2b E2 protein. The E2-CBH-4G complexes were then added to wells coated with either 500 ng of GNA (blue bars) or 100 ng of GST-CD81-LEL (red bars) in the presence of a 1/500 dilution of the indicated sera from genotyped HCV infected (1a or 2b) or uninfected (NEG) individuals (x axis). After an overnight incubation at 15 4 °C, the wells were washed, and bound biotinylated CBH-4G was detected as described in Example 7. The bars indicate the mean signal obtained from duplicate wells in the presence of the indicated serum (final dilution 1/1000) relative to the signal obtained in the absence of any competing serum. Error bars indicate one standard deviation from the mean.

20 Figure 20 is a cartoon of the competition assay. Plates are first coated with GNA lectin, which is used to capture full-length intracellular E2 onto microtiter plates by binding of CHO moieties to GNA lectin. Competing HMAb are contacted with the GNA-captured E2. Biotinylated test HMAb is added to the plates, and binding of the biotinylated test HMAb to E2 is detected using a streptavidin-AP 25 conjugate. Inhibition of binding of test HMAb suggests epitopes within same antibody binding domain.

Figure 21 shows competition analysis of four HCV human monoclonal antibodies. HCV Q1b E2 protein was captured onto GNA lectin coated microtiter plates. Biotinylated test antibody (indicated above each panel) at 2 µg/ml was added 30 to wells containing the indicated concentration (x-axis) of competing human monoclonal antibody. Bound biotinylated test antibody was detected using

streptavidin alkaline phosphatase conjugate. Signal obtained in the presence of competing antibody was expressed as the percent of signal obtained by the biotinylated test antibody relative to the signal obtained in the absence of competing antibody (y-axis). The points indicate the mean value obtained from two replicate wells. The bars indicate one standard deviation from the mean. Competing antibodies are identified in the key at left.

Figure 22 shows the results of a human monoclonal competition analysis. Results are the mean percent binding of test antibody relative to wells without any competing antibody. Results are the mean values obtained from 2-5 separate experiments. Both genotype 1a and 1b E2 proteins were tested. ND = not done.

Figure 23 depicts HCV E2 deletion constructs described herein. The names of the E2 constructs are provided at left. Sequences derived from the vector pDisplay are indicated as solid black bars. The positions of the HA epitope and the c-myc epitope present in the pDisplay vector are also indicated. Sequences derived from HCV 1b E2 are indicated as white boxes. Sequences derived from HCV 1b E2 are indicated as light gray boxes. Numbering of the X-axis (below) is according to the polyprotein of the HCV-1 isolate.

Figure 24 shows Western blot analysis of HCV E2 deletion constructs indicating that the constructs are efficiently expressed. The indicated HCV E2 constructs (above lanes) were transfected into HEK-293 cells. Twenty-four hours after transfection cytoplasmic extracts were prepared and fractionated via SDS-PAGE. The fractionated proteins were transferred to nitrocellulose membranes and incubated with either rat monoclonal antibody to the HA epitope (HA rMAB) or a control HMAb to a CMV protein (control). Bound antibody was detected with the appropriate AP conjugated antisera. HEK = mock-transfected HEK-293 cells. The migration of molecular weight markers is indicated at left.

Figure 25 shows reactivity of certain inventive human monoclonal antibodies with the various HCV E2 deletion constructs. HEK-293 cells were mock transfected (white bars) or transfected with the indicated HCV E2 constructs (see keys each graph). Twenty four hours post transfection cytoplasmic extracts were

prepared and equivalent aliquots were captured onto GNA lectin coated microtiter plates as described above. The captured E2 proteins were then incubated with the indicated HCV HMAb (x-axis) and the amount of bound antibody was determined. Bars represent the mean absorbance value obtained from duplicate wells. Error bars 5 indicate one standard deviation from the mean.

Figure 26 shows graphs demonstrating that sera from HCV infected individuals have variable levels of antibodies that inhibit CBH-2 and CBH-7. Homologous HCV E2 proteins were captured onto wells and incubated with the increasing dilutions of HCV 1a, 1b, 2a, or 2b sera. Values are the specific inhibition 10 of binding of biotinylated CBH-2 or CBH-7 obtained with individual sera. The mean percent inhibition (y-axis) obtained from duplicate determinations at a given dilution (x-axis) is plotted. The mean specific inhibition obtained for eight negative sera are also presented (genotypes of E2 proteins employed are indicated). Error bars on negative sera indicate one standard deviation from the mean.

Figure 27 shows scatterograms demonstrating that sera from HCV infected individuals have variable levels of antibodies that inhibit CBH-2 and CBH-7. Scattergram showing percentages of test HMAb inhibition. HCV sera of the indicated genotype (x-axis) or control sera (NEG) were diluted 1:200 and incubated 20 with biotinylated test HMAb (indicated above graph) in wells coated with genotyped matched E2 proteins. Binding of test HMAb was detected using streptavidin-conjugated-AP. Results obtained were compared to binding of test HMAb in absence of competitor. Each symbol indicates results obtained with an individual serum. The line indicates the median percent inhibition. The dotted line indicates the cutoff for calling a serum positive for the presence of the test HMAb.

Figure 28 is a histogram of CBH-2 inhibitory titers obtained from a panel of 74 individuals with chronic hepatitis. The CBH-2 inhibitory titers obtained with individual serum were segregated into 20 bins of 100 and 1 bind for all titers >2000. The bars indicate the number of sera having a CBH-2 inhibitory titer within a given bin. Numbers of HCV 1a/1b sera are indicated in black. Number of HCV 2a/2b 30 sera is indicated in gray. The number of sera with low (<200), intermediate (200-1000), and high (>1000) inhibitory titers is indicated below the graph.

Figure 29 is a histogram of CBH-7 inhibitory titers obtained from a panel of 74 individuals with chronic hepatitis. The CBH-7 inhibitory titers obtained with individual serum were segregated into 20 bins of 100 and 1 bin for all titers >2000. The bars indicate the number of sera having a CBH-7 inhibitory titer within a given bin. Numbers of HCV 1a/1b sera are indicated in black. Number of HCV 2a/2b sera is indicated in gray. The number of sera with low (<200), intermediate (200-1000), and high (>1000) inhibitory titers is indicated below the graph.

Figure 30 is a schematic representation of HCV E1 and E1E2 constructs.

Figure 31 shows an alignment of amino acid sequences of E1 constructs from HCV E1 1b (ZYK-E1); full-length HCV 1b (HPCJ491); and H isolate of HCV 1a (HPCST90). Conserved amino acids are indicated by dots and numbering is relative to the initiating methionine of the HCV polyprotein.

Figure 32 shows photocopies of Western blots of glycosylated and non-glycosylated E1 constructs. A. HEK-293 cells transfected with pDisplay vector (VEC) or the indicated HCV E1 construct. B. HEK-293 cells were transfected with pDisplay vectors (VEC) or the indicated HCV E1 construct in the presence (+) or absence (-) of tunicamycin.

Figure 33 is a graph representing a FACScan analysis of E1 recombinant proteins expressed in HKE293 cells transfected with E1 deletion constructs.

Figure 34 shows a panel of photographs representative of IFA data using HCV serum.

Figure 35 is a Table showing the immunoreactivity of E1 and E1/E2 constructs to human antibodies in HCV positive serum.

Figure 36 shows photographs of IFA data with HCV anti-E1 HMabs H-111 and H-114.

Figure 37 shows Western blots of E1 proteins with HMabs H-111 and H-114. A. Immunoprecipitation. B. Western Blot.

Figure 38 shows graphs representing FACScan analysis of HCV HMAbs H-111 and H-114 with E1-1 recombinant protein transiently expressed in HEK-293 cells.

Figure 39 is a chart showing epitope mapping experiments of E1 HMAbs.
5 Figure 40 is a graph illustrating a peptide competition analysis of HMAb H-111 epitope.

Figure 41 is a photograph of a Western blot of mutated E1 recognized by H-114.

Figure 42 is a graph illustrating a peptide competition analysis of HMAb
10 H-114.

Figure 43 shows graphs illustrating the effect of point mutations of amino and carboxy terminal regions of HMAb H-114 epitope. A. Mutational analysis of amino acids 206-211. B. Mutational analysis of amino acids 306 to 313.

Figure 44 shows photographs of immunoprecipitation analyses on binding
15 of HMAb H-114 to E1 in the presence and absence of DTT.

Figure 45 is a table showing the results of an alanine scanning experiment on internal E1 cysteine residues.

Figure 46 is a Western blot of different E1 mutants.

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DETAILED DESCRIPTION OF CERTAIN

PREFERRED EMBODIMENTS OF THE INVENTION

Monoclonal antibodies, particularly human monoclonal antibodies (“HMAbs”), are provided which bind to one or more hepatitis C virus genotypes, which antibodies find use for diagnosis, therapy, and vaccine development. A panel 25 of human monoclonal antibodies (HMAbs) from peripheral B-cells of an individual with asymptomatic HCV infection and having a high serum neutralization of binding titer were produced and characterized. Eleven HMAbs to HCV E2 and two HMAbs to

HCV E1 have been produced. One group of antibodies binds to the genotypes 1 and 2 of HCV, while other antibodies bind to fewer than this group of genotypes. HCV genotypes 1 and 2 together are the dominant virus types encountered in the western hemisphere and other geographic locations. The antibodies bind to conformational and linear epitopes, which are conserved across virus types and genotypes. The 5 antibodies binding to HCV E2 proteins of genotypes 1a, 1b, 2a, and 2b and a subset of these antibodies inhibit the interaction of these E2 proteins with human CD81. Additionally, one of two HMAbs to HCV E1 binds to multiple genotypes of HCV.

By virtue of the variety of binding profiles of the antibodies, diagnostic 10 assays may be employed which will detect a plurality of types and genotypes, so as to provide a pan-anti-HCV antibody for HCV encountered in the United States, while at the same time being able to dissect individual genotypes by subtractive analysis. In addition, the antibodies being human may be used for passive immunization, as protective therapy for individuals at risk for HCV or as a therapy for people who are 15 seropositive for HCV.

The HMAbs of the invention offer several advantages over existing HMAbs against HCV. Because non-homologous primary amino acid sequences may still define immunologically identical tridimensional protein structures, HMAbs binding to structurally conserved epitopes can recognize multiple, sequentially divergent HCV 20 genotypes in native conformation, whereas antibodies recognizing only linear or denatured epitopes may not. In particular, conformationally dependent and selected linear-dependent epitopes of anti-HCV E1 or E2 HMAbs may effectively interfere with the interaction of native HCV virus and its cellular target receptors. Using conformationally dependent and selected linear-dependent epitopes of HMAbs to 25 actively interfere with the ability of native HCV virus to bind to target cell receptors such as CD81 has specific therapeutic application for reducing viral load in infected individuals, and preventing infection or re-infection of organs in non-infected individuals (by, e.g., a) recognizing HCV E1 or E2 proteins encoded by different HCV genotypes; b) binding HCV particles; c) preventing attachment and entry of HCV viral 30 particles to their target cells), particularly in recent organ transplant recipients, individuals undergoing renal dialysis, and individuals undergoing treatment for

hemophilia or other blood clotting disorders. Other recipients include individuals recently exposed to HCV containing bodily fluids. Both individual HCV HMAbs and a cocktail of several HCV HMAbs recognizing several epitopes may be employed.

Certain subsets of the HMAbs interfere with E2-associated viral infection by 5 mechanisms other than preventing direct interaction with CD81. This subset of antibodies interferes with viral infectivity by a number of possible mechanisms, including preventing E2 binding to co-receptor proteins, conformational changes in E1 and/or E2 proteins necessary for target cell binding, E1 and E2-mediated viral fusion to target cells, and uncoating of HCV virions. Because they bind distinct epitopes, the 10 subset of HMAbs that directly interferes with E2 binding to CD81 complements HMAbs in the subset that interfere with infectivity by other mechanisms for both therapeutic, vaccine, and diagnostic applications.

HMAbs, which recognize viral epitopes and interfere with virus/target receptor interaction, and viral epitopes which bind to such HMAbs, may also serve as 15 templates for rationally designing peptide and other structural mimics of the viral epitopes. Structural molecular mimics defined by these anti-HCV HMAbs find use in their ability to block binding of the native virus to target receptors by binding to the target receptor themselves.

By producing human monoclonal antibodies, it is possible to directly analyze 20 the human immune response to HCV. Importantly, by using human monoclonal antibodies, immune responses against the antibodies themselves as foreign antigens are minimal, whereas vigorous immune responses are generated against monoclonal antibodies produced from non-human sources, because they are recognized as foreign antigens. Selecting for HMAbs that recognize conserved viral conformational 25 epitopes affords broader and more effective therapeutic application of these reagents for ameliorating or preventing HCV infection than antibodies able to bind only linear or denatured epitopes. All previous antibodies described as having the property of preventing HCV infection or uptake into target cells recognize a highly variable sequence of HCV E2 known as the hypervariable region. In contrast, the antibodies 30 described above recognize both conformational and linear epitopes, the majority of which are highly conserved HCV E2 proteins of multiple different genotypes. Thus

the antibodies described herein have the advantage that they are active against a much wider range of HCV isolates than previously described neutralizing antibodies. An additional advantage is that the high conservation of the epitopes recognized by the antibodies described herein indicates that these antibodies recognize sequences with 5 functional and/or structural significance within the HCV E1 or E2 protein. Thus peptides or small molecules isolated with these antibodies have a high probability of being targeted to functional regions within HCV E1 or E2. This is not true for other HCV antibodies described to date.

Of the detection antibodies described, CBH-4G has essentially equal 10 reactivity to HCV E2-CD81 complexes of multiple HCV genotypes, whereas CBH-4B recognizes HCV genotypes 1a and 1b. The level of interfering antibodies present in HCV antisera has also been shown to be quite low. Therefore they provide a straightforward means of assaying the level of neutralizing antibodies present in a sample in a microtiter plate format without resorting to multiple flow cytometric 15 analyses.

The overall strategy employed for the development of the subject HMAbs was as follows: (1) individuals with evidence of exposure to HCV were identified; (2) antigen specific B-cells from their peripheral blood were expanded and activated *in vitro*; (3) these cells were immortalized by electrofusion with a suitable mouse-human 20 heteromyeloma; (4) relevant human antibody secreting hybridomas were identified; and (5) the relevant hybridomas were stabilized by cloning. This strategy resulted in the identification of HMAbs that are specific to the HCV E2 protein, a number of which bound to conformation epitopes of E2 of HCV genotypes 1a and 1b and HCV genotypes 2a and 2b, so as to recognize the primary genotypes encountered in the 25 United States and elsewhere with a single antibody, while others bound to fewer of the indicated genotypes, so as to be useful in identifying an HCV type or genotype. The above strategy also resulted in the identification of HMAbs that are specific to HCV E1 protein, described herein.

As an example, peripheral B cells from an individual with asymptomatic 30 HCV infection and a high serum neutralization of binding titer were used to produce and characterize a panel of human monoclonal antibodies. The initial screening made

use of a genotype 1a E2 protein having an amino acid sequence with 98% homology to the same region of the HCV-1 isolate (Lanford *et al.*, 1993 *Virology* 197:225-235; incorporated herein by reference). This step biased the screening approach used to the selection of antibodies to epitopes conserved between genotypes 1a and 1b since the 5 donor was infected with a 1b isolate. All of the HMAbs also reacted with E2 from a heterologous HCV 1b isolate, Q1b, which was 79% homologous with the HCV 1a isolate employed in the selection of HMAbs. Denaturation of recombinant E2 completely abrogated the reactivity of 10 of 11 HCV HMAbs. Thus, the majority of the HMAbs recognized conformational epitopes.

10 Five HMAbs, CBH-4D, -4B, -4G, -9, and -17, were negative in the NOB assay and reacted with HCV E2-CD81 complexes. Two of these antibodies, CBH-4G and CBH-9, reacted with HCV E2 proteins of genotypes 1a, 1b, 2a, and 2b in both the GNA and CD81 capture assays. The other three antibodies, CBH-4B, -4D, and -17, exhibited restricted reactivity to E2 proteins of genotypes 1a and 1b. HMAbs CBH-15 4B and CBH-4D have kappa and lambda light chains, respectively, and probably recognize different epitopes. HMAb CBH-17 was the only antibody to recognize a denaturation insensitive epitope. Thus it is likely that each of the NOB negative antibodies recognizes a distinct epitope.

20 Six of the HMAbs recognizing conformational epitopes, CBH-2, -5, -7, -8C, -8E, and -11, were positive when tested with the neutralization of binding assay using HCV 1a E2 protein. Five of these antibodies HMAbs CBH-2, -5, -7, -8C, and -8E reacted with E2 proteins of all tested genotypes. The same six antibodies failed to bind to E2 of genotypes 1a, 1b, 2a, or 2b when complexed to CD81-LEL. Thus 25 epitopes that partially or fully overlap the CD81 binding site within HCV E2 are both conformational in nature and highly conserved. A high degree of sequence conservation in the CD81 binding site is consistent with the proposition that the interaction between HCV E2 and CD81 is biologically relevant. Two of the four NOB positive antibodies tested, HMAbs CBH-2 and CBH-5 were able to prevent the binding of intact HCV virions to CD81. The HMAbs CBH-7 and CBH-11 did 30 significantly inhibit binding of HCV virions to CD81, despite the antibodies having equivalent activity in the NOB assay. This may reflect the fact that HCV virions are

thought to have E1-E2 complexes at their surface, and that not all of the epitopes present in E2 may be exposed in such complexes. Testing of the HMabs with E1-E2 complexes may shed light on this issue. Alternatively, the differential results in the NOB and virion inhibition assays may reflect differences in the true affinity of the 5 HMabs for the E2 protein or E1-E2 complexes. In any event, a strong neutralization of binding activity in and of itself does not ensure that an antibody will bind to intact HCV virions. Thus it is probable that not all antibodies inhibiting the interaction of E2 protein with CD81-LEL *in vitro* will neutralize infectivity *in vivo*.

Five of these six NOB positive antibodies are to epitopes shared among the 10 five HCV isolates used in this study. The other antibody CBH-11 exhibited differential reactivity to two 1a isolates and probably recognizes an epitope distinct from the other antibodies. Indeed the variable reactivity of CBH-11 to different 1a isolates may have contributed to its negative result in the virion binding experiment. Both the differential reactivity of CBH-2 and CBH-7 with HCV virions and 15 competition experiments indicate that CBH-2 and CBH-7 recognize distinct epitopes. Competition experiments also suggest that the epitopes recognized by HMabs CBH-5 and CBH-2 are distinct. It remains possible that CBH-2 and CBH-8E recognize the same or very similar epitopes, however. Determining the total number of unique epitopes will require sequencing of the antibody genes produced by the hybridomas as 20 well as competition studies and testing with additional HCV isolates.

Competition analysis (Figure 22) has been employed to define antibodies with similar binding sites in HCV E2. Seven HMabs were biotinylated and the binding of the biotinylated antibodies to HCV E2 in the presence of increasing amounts of competing HCV HMabs was determined. Antibodies that cross-competed 25 significantly were grouped together. Regions of HCV E2 that contained the binding sites were localized using a series of HCV E2 deletion constructs (Figure 23). Four competition groups were defined. Group I consisted of five HMabs, CBH-2, -8E, -5, -8C, and -11. Antibodies from this group inhibit binding of HCV E2 to CD81 and recognize conserved epitopes localized to HCV E2 amino acids 411 to 644. Group II 30 consists of HMabs CBH-7, which recognize a highly conserved epitope located between HCV E2 amino acids 470-644. Antibodies from groups I and II exhibited

minimal cross-competition. Group III consisted of three antibodies, CBH-4G, -4B, and -4D, which do not inhibit binding of HCV E2 to CD81 and recognize epitopes between HCV E2 amino acids 470 to 644. Group IV consisted of one antibody, CBH-17, that recognized an epitope located between HCV E2 amino acids 644 to 661.

5 Antibodies in group I and II have been found to inhibit HCV replication in a small animal model and recognize two distinct conserved binding sites outside of the hypervariable region of E2. The low level of competition between antibodies of groups I and II should lead to additive virus neutralization activity and raises the possibility that these antibodies might act synergistically *in vivo*.

10 These results indicate that several conformational epitopes within HCV E2 are highly conserved among divergent HCV genotypes. The antibodies that recognize these epitopes are useful as reagents to better define the structure of HCV E2.

15 Furthermore, the antibodies that inhibited binding of HCV virions to human CD81, CBH-2 and CBH-5, are prime candidates to mediate virus neutralization. The absence of a true *in vitro* model for virus neutralization, however, will require that the fundamental proof be obtained by the ability of selected HMAbs to prevent or modify HCV infection in appropriate animal models. If successful, broadly reactive neutralizing antibodies will likely have therapeutic utility. Analogous to the success achieved with hepatitis B immunoglobulin in liver transplantation (Dickson, 1998

20 *Liver Transpl. Surg.* 4(5 Suppl 1):S73-S78; Markowitz *et al.*, 1998 *Hepatology* 28:585-589; each of which is incorporated herein by reference), one possible application is to suppress HCV infection in liver transplant recipients with broadly reactive neutralizing human monoclonal antibodies.

The above strategy for isolating HMAbs also resulted in the identification of 25 HMAbs that are specific to the HCV E1 protein. These HMAbs, like the HMAbs to E2, also bound both conformational and linear epitopes of HCV E1. One HMAb to E1 of HCV genotype 1b was identified, H-114. Another antibody to E1, H-111, recognized epitopes from four or more genotypes (genotypes 1a, 1b, 2b, and 3a). This broad specificity is particularly preferred in the diagnostic and therapeutic applications 30 described above. The isolation and characterization of the H-114 and H-111 HMAbs are described in Example 10.

The HMAbs to HCV E1 of the present invention recognize different epitopes than previously identified anti-E1 antibodies. H-114 recognizes a non-linear sequence of amino acids that may include the putative fusion peptide of E1. Since the fusion between the viral envelope and cellular membranes is a critical event in the initiation 5 of virus infection, the H-114 antibody that might interfere with this event and inhibit the HCV life cycle including the steps of cell entry, uncoating, and virion assembly. The antibody H-111 has the unique feature of recognizing individual amino acids across multiple genotypes.

The epitopes recognized by H-111 and H-114 provide new possibilities for 10 virus neutralization. E1 and E2 are believed to interact to form a heterodimeric nonvalent E1-E2 complex that ultimately constitutes the virion envelope. Due to the unique binding activities of H-111 and H-114, these antibodies can be used to gain insights on the interaction of E1/E2 and the formation of mature envelope on virions.

While human monoclonal antibodies are provided, other antibodies from 15 other sources may recognize the same epitopes recognized by the human antibodies described herein, and may also be employed. Generally antibodies from murine sources, mice and rats, lagomorpha and domestic animals find use. One may produce antibodies having the conserved regions of these mammalian sources using genetic engineering and replacing the constant regions of the HMAbs provided herein or may 20 use the proteins to be described below as immunogens for immunizing the animals and then immortalizing the resulting B cells and screening as described below for immortalized cells which produce monoclonal antibodies having analogous broad range binding specificity. By screening in competitive assays with the subject HMAbs, one can determine whether the non-human antibodies bind to the same 25 epitope.

For diagnosis, the antibodies may be used in a variety of ways, for capturing and/or identifying circulating HCV virions, E1 or E2 protein, or anti-E1 or anti-E2. The antibodies may be used for immunotherapy, prophylactic, or therapeutic. The antibodies may also be used for development of vaccines for HCV.

The isolated antibodies are of the IgG class. The following are the designations for the antibodies and the HCV genotypes, which the antibodies recognize. Some of the HMabs exhibited good affinity for HCV E2 proteins, with the antibodies exhibiting maximal signals at concentrations ranging between 1 to 20 5 μ g/ml. These antibodies are the IgG class, particularly IgG₁_K. The following are the designations for the antibodies and the HCV genotypes, which the antibodies recognize. The below HMabs exhibited good affinity for HCV E1 or E2 proteins,

Table 1		
HCV Genotypes bound by HMabs		
Antibody	Protein bound	Genotypes bound
CBH-2	E2	1a, 1b, 2a, 2b
CBH-4D	E2	1a, 1b
CBH-4B	E2	1a, 1b
CBH-4G	E2	1a, 1b, 2a, 2b
CBH-5	E2	1a, 1b, 2a, 2b
CBH-7	E2	1a, 1b, 2a, 2b
CBH-8C	E2	1a, 1b, 2a, 2b
CBH-8E	E2	1a, 1b, 2a, 2b
CBH-9	E2	1a, 1b, 2a, 2b
CBH-11	E2	-, 1b, 2a, 2b
CBH-17	E2	1a, 1b
H-111	E1	1a, 1b, 2b, 3a
H-114	E1	1b

10 The antibodies may be used in their native form or may be truncated to provide Fab or F(ab')₂ fragments. The genes encoding the heavy and light chains

may be isolated and modified in a number of different manners. Conveniently, using RT-PCR, the cDNA may be obtained for the genes in a convenient construction for further manipulation. The nucleotide sequences of the variable regions of the heavy and light chains may be isolated and joined, either directly or 5 indirectly or through a chain of $3n$ nucleotides, where n is at least 1 and not more than about 60, usually not more than about 40, to provide a linker of amino acids between the two variable regions. The length of the chain can be determined empirically to provide the optimum affinity and other properties, *e.g.*, linkage through mercapto, carboxy, or amino groups, for chelation, bonding to a surface or 10 other molecule, or the like. In addition, the genes, intact or portions thereof, including at least the variable regions, may be fused to other sequences to provide for each of attachment to a surface, labels or tags for identification, sequences for affinity isolation, and the like. Any of these reagents can be attached to the antibody with a cleavable arm, *e.g.*, a protease site or chemical linker.

15 Labels or tags may be attached to the gene encoding the antibody to provide for specific affinity isolation methods for the expressed antibody. The labels or tags may otherwise improve the utility of the isolated antibody gene. Some examples of tags include the biotinylation sequence of *E. coli* biotin carboxylase carrier protein; a sequence of six histidines or a sequence of alternating histidines and aspartic acids 20 that are suitable for allowing binding of the antibody to a column containing immobilized diivalent cations; the sequence of any one of several known high affinity antibody epitopes including the FLAG epitope DYKDDDDK, the T7 tag sequence MASMTGGQMG, the S-tag sequence KETAAAKFERQHMDS, or any other known sequence that confers binding to a specific antibody; a fusion protein 25 partner such as glutatione-S-transferase, streptavidin, or ligands to cell surface receptors found on a desirable cell target; and fluorescent, radioactive, luminescent or enzymatically detectable moieties.

Where labels are polypeptides, the sequence can be directly fused to a gene of one of the antibody chains. In any case, sequences may be provided which 30 provide a site for linking a label, such as cysteines for forming thioethers with maleimide groups, polyhistidine/cysteines or polyhistidines/aspartic acids for

chelating metals, which may be bonded to a variety of molecules, polylysines for reacting with aldehydes in reductive amination reactions, *etc.* Labels may include enzymes, chelating groups, ligands for binding to a ligand binding proteins, *e.g.*, biotin and streptavidin, digoxigenin and antidigoxigenin, *etc.*, green fluorescent protein, and the like. The biotinylation sequence of *E. coli* biotin carboxylase carrier protein (BCCP) can be used for *in vivo* biotinylation of proteins expressed in *E. coli* or introduced in a lysate of *E. coli*. A sequence of six histidines or a sequence of alternating histidines and aspartic acids that are suitable for allowing binding of the antibody to a column containing immobilized divalent cations can be used.

Sequences encoding high affinity epitopes may be employed, such as the FLAG epitope DYKDDDDK (SEQ ID NO: 13), the T7 tag sequence MASMTGGQMG (SEQ ID NO: 14), the S-tag sequence KETAAAKFERQHMDS (SEQ ID NO: 15), or any other sequence that confers high affinity binding to its correlative binding member or a protein reagent. Fusion proteins, besides the ones indicated above, include glutathione-S-transferase, luciferase, ligands to cell surface receptors found on hepatocytes, T-cells or other desirable cellular target, and the like. Such fusions are usually joined via a linker sequence of 3-50 amino acids that promotes the bi-functionality of the protein. These molecules can be linked to the antibodies via cleavable arms (protease sites) or other means. The antibodies may be chemically linked or fused to various toxins, such as diphtheria toxin, ricin, abrin, ribosome inactivating proteins, apoptosis signaling proteins, pore forming proteins, *e.g.*, perforin, and the like. Alternatively, the antibodies may be linked to chelated toxic heavy metals or radioactive isotopes, particularly technetium, radioactive iodine or the like. The antibodies may be chemically linked to fluorophores or chemiluminescent molecules. Chemical coupling may involve biotinylation using the activated carboxylic acid group or biotin-C11-hydroxysuccinimide ester, which will react with cysteines; coupling through the use of CNBr activation of various beads (sepharose, agarose, magnetic, polystyrene, *etc.*) or surfaces to link the antibodies, and the like; any number of other methods generally involving bridging the antibody to a useful chemical moiety, usually accomplished by modifying lysine or other basic residues or through use of reagents specific for free sulfhydryl groups.

Using the genes for the heavy and light chain variable regions, particularly the hypervariable regions of the variable region may be mutated in accordance with known ways to enhance the binding affinity of the antibody or to broaden reactivity. One may use *in vitro* selection to identify the optimum binding antibodies using 5 phage display methodologies, random or directed mutagenesis of sequences, or other similar methodologies. Alternatively, one may use an alanine or glycine walk of the hypervariable regions to identify essential amino acids and then vary the amino acids at those or other sites to identify improved binding of the epitope. Other techniques known in the art may be employed to provide the mutagenized 10 antibodies.

Instead of using the hybridomas as a source of the antibodies, the genes may be isolated and introduced into an appropriate mammalian host cell, *e.g.*, CHO, HeLa, CV1, or the like. Suitable expression plasmids are exemplified by pcDNA3.1 Zeo, pIND(SP1), pREP8 (all available from Invitrogen, Carlsbad, CA) (see Example 15 11), and the like. The antibody genes may be expressed via viral or retroviral vectors, which may be exemplified by MLV based vectors, vaccinia virus based vectors, *etc.* Similarly, the antibody genes may be expressed using the pCOMB series of vectors on the surface of M13 phage, as two independent chains, which may be renatured to form the intact antibody. Alternatively, the antibodies may be 20 expressed as a single chain, including at least the variable regions. The genes may be used for gene therapy by introducing the genes into appropriate cells, such as lymphocytes, muscle cells, fibroblasts, and the like, where the antibodies may be expressed and secreted, either constitutively or inductively, to provide a continuous or intermittent source of the antibodies over a predetermined period of time, based 25 on the lifetime of the host cell. The genes in conjunction with a marker gene, *e.g.*, antibiotic resistance, may be introduced in cell cultures of cells taken from a subject, the modified cells selected by means of the marker and the marked cells returned to the host. The DNA may be introduced into the cells using various plasmid DNA, naked DNA, DNA virus constructs, such as adenovirus, adeno- associated virus, or 30 vaccinia virus or RNA viruses such as Vesicular stomatitis virus, sindbis virus, and semiliki forest virus to name but a few. The DNA would have a construct having a

promoter for which transcription factors are present in the subject cells or can be induced or introduced and the genes under the transcriptional control of such promoter. Other regulatory sequences may also be present, such as leaders for secretion, enhancers, RNA stabilizing sequences, and the like.

5 For diagnostic purposes, the antibodies may be used in a wide variety of formats for detecting the E1 or E2 protein, discerning HCV genotypes, detecting virions and antibodies, *see* for example U.S. Patent No. 5,695,390, incorporated herein by reference. The antibodies may be used individually or in combination with other of the subject group or other antibodies or with lectins which bind to the 10 glycosyl groups present on E1 or E2, the virion envelope proteins, or other proteins with which HCV E1 or HCV E2 complexes, *e.g.*, a HCV E1:HCV E2 complex. For diagnostic purposes, a wide variety of labels may be employed, which for the most part have been mentioned previously. These include, but are not limited to, fluorophores, chemiluminescers, radioisotopes, enzymes, particles, *e.g.*, colloidal 15 carbon and gold, latex particles, *etc.*, ligands for which there are high affinity receptors, and prolabeled, which can be activated to provide a detectable signal.

In one embodiment, a surface is coated with a protein, which will bind to HCV antigens as free, or circulating proteins or as part of an intact or partially intact virion. One may use antibodies of the subject invention which bind to both type 1 20 and 2 HCV, or lectins, such as *Galanthus nivalis* lectin. One may also use antibodies of the subject invention, which bind to types 1, 2, and 3. In particularly preferred embodiments, the antibodies of the invention bind to at least four genotypes. In particularly preferred embodiments, the antibodies of the invention bind to E1 of the genotypes HVC 1a, 1b, 2b, and 3a. The assay involves contacting 25 the surface with a medium, which may contain free or virion involved protein, where the medium may be the sample or a solution of known E1 or E2 of one or more genotypes. After incubation and washing to remove non-specifically bound protein, the assay may proceed in various manners depending upon what is being assayed. Where a blood sample suspected of being seropositive is being assayed, the sample 30 is applied to the layer of E1 or E2 protein, incubated, and washed, and the presence of human antibodies bound to the protein layer determined. One may use labeled

anti-(human antibodies) (other than against the isotype of the subject antibodies, where the subject antibodies have been initially used). In assays for antibodies in seropositive subjects, the subject antibodies may be used as controls with the same reagent used to detect any human anti-HCV in the sera of such subjects. The 5 specificity of the antibodies in the sample can be confirmed by using the subject antibodies, which are differentially labeled from the anti-(human antibodies) and determine whether they are blocked by the antibodies in the sample.

Where the sample is assayed for HCV E1 or HCV E2 protein, detection employs labeled subject antibodies, the selection depending upon whether one is 10 interested in genotyping or detection of E1 or E2 protein. After washing away non-specifically bound antibody, the presence of the labeled antibodies is determined by detecting the presence of the label in accordance with known techniques. Alternatively, where the subject antibodies are bound to the surface, a labeled lectin for E1 or E2 may be employed to detect the presence of the E1 or E2 protein.

15 The subject antibodies can be used to measure the reactivity of other antibodies, including antibodies in sera, monoclonal antibodies, antibodies expressed as a result of genetic engineering. Desirably, intact virions are used, rather than HCV proteins, although conformationally conserved envelope proteins may also find use. For virion capture, see, for example, Kimura *et al.*, 1998 *J. Med. Virology* 56:25-32; Morita *et al.*, 1996 *Hepato-Gastroenterology* 43:582-585; Sata *et al.*, 1993 *Virology* 196:354-357; and Hijikata *et al.*, 1993 *J. Virology* 67:1953-1958, 20 each of which is incorporated herein by reference. One protocol is to coat a solid support with a lectin, *e.g.*, GNA, and then contact the surface with a medium, *e.g.*, serum of a seropositive patient, comprising intact HCV virions. Additives which might destroy the virions should be avoided, *e.g.*, detergents. After incubating the 25 medium and washing to remove non-specifically bound components of the medium, the virions may be contacted with the antibodies of the subject invention and the antibodies of the sample. This may be performed concurrently or consecutively, where the sample is added first. An amount of the subject antibody is used which is sensitive to displacement by another antibody. Such amount may be determined 30 empirically, and one may wish to use different amounts of the subject antibody in a

series of tests. By knowing the signal, which is obtained in the absence and presence of the sample, one can determine the reactivity or binding affinity of the antibodies in the sample. Various techniques may be used to determine the amount of a subject antibody bound to the virions. Where the subject antibodies are labeled, 5 *e.g.*, biotin or digoxigenin, streptavidin or anti(digoxigenin) labeled with a fluorophore or enzyme whose substrate produces a detectable signal can serve to determine the amount of the subject antibodies.

Where the receptor (antibody or lectin) is labeled with a DNA sequence, either directly or indirectly (indirectly intends a ligand-nucleic acid sequence 10 conjugate which can bind to empty sites of the receptor bound to the virion), by using primers homologous to the label sequence and standard conditions of the PCR, the sequence may be expanded. The DNA may then be detected in a separate hybridization reaction or by agarose gel electrophoresis. Alternatively, the Taqman approach may be used, using an internal labeled oligonucleotide probe homologous 15 to the amplified sequence, having a light emitting label, fluorophore or luminescer, at one end and a quenching moiety at the other end. As the fragment is amplified, the 5'-3' exonuclease activity of the Taq polymerase degrades the hybridizing oligonucleotide freeing the fluorophore from the quencher, so that the fluorophore 20 may now be detected by irradiation of the medium with light of an appropriate wavelength.

One may also use a labeled oligonucleotide probe appropriate for performing cycling probe technology. An oligonucleotide is constructed of about 15-20 deoxynucleotides homologous to the label and having a TM 45°C, a sequence of about 5 or more ribonucleotides homologous to the label and having a TM 45°C. 25 The intact oligonucleotide will have a TM > 60°C. The oligonucleotide is further modified as described above with a light emitting label and a quencher label. After adding an excess of the oligonucleotide construct to the bound label and allowing it to hybridize to the bound label at a temperature of about 55°C, RNase H, active at 55°C is added to degrade the ribonucleotides. Upon denaturation the light-emitting 30 label will be released and free of the quencher, and upon irradiation or activation its light emission determined.

Alternatively, transcription mediated amplification (TMA) may be employed. In this case, the bound oligonucleotide label contains a promoter recognized by T7 polymerase or other convenient polymerase. Addition of T7 or other appropriate polymerase and rNTPs under appropriate conditions results in the transcription of the bound oligonucleotide to oligoribonucleotides, which can then be detected by any convenient means, *e.g.*, electrophoresis.

Labeled subject antibodies may be used in assaying for the presence of HCV from biopsy material. Labeled antibody may be incubated with immobilized biopsy material, such as a liver slice, with a solution of one or more of the subject labeled antibodies. After washing away non-specifically bound antibodies, the presence of the antibodies bound to the cells of the biopsied tissue may be detected in accordance with the nature of the label.

Conformationally conserved E2 genotype proteins 1a, 1b, 2a, and 2b, the latter two being novel expression compositions are provided as proteins expressed from vaccinia virus constructs. Their preparation is described in the experimental section. The proteins are obtained free of amino acids of E1 proteins, although they can be prepared from genes encoding both E1 and E2, where the resulting fusion protein is processed to provide the two proteins which are no longer covalently joined, but may exist as a complex. Conformationally conserved E1 genotype proteins can similarly be prepared by any mammalian expression vector such as pDisplay by Invitrogen (Carlsbad, California) described in the experimental section. The proteins may be isolated from a lysate. The protein may be readily purified using affinity chromatography, HPLC or non-denaturing gel electrophoresis. The proteins may be obtained in purities exceeding 95 wt. %, usually at least 99 wt. %. The proteins may be used in assays for genotyping sera from HCV infected patients, in screening monoclonal antibodies for affinity and specificity, for evaluating drugs where the proteins are the target of the drugs, for immunizing mammalian hosts for the production of antisera and monoclonal antibodies, and the like. Their use in diagnostic assays has already been discussed.

The antibodies may be used to identify the structural epitopes on E1 or E2 proteins that they bind. Two basic approaches may be employed using the

monoclonal antibodies for identifying conformational epitopes. In the first, natural variants or mutation analysis of HCV isolates may be used to identify regions, and ultimately individual amino acids that are involved in the epitopes recognized by the monoclonal antibodies (Schwartz *et al.*, 1999 *J. Mol. Biol.* 287:983-999; 5 incorporated herein by reference). The antibodies are screened against a number of different HCV E1 or E2 isolates, identifying isolates that are selectively non reactive with individual antibodies. For example, HMAb CBH-11 reactivity with HCV E2 protein Q1a is reduced compared to its reactivity with HCV E2 Q2a (Figure 9). “Chimeric” E2 envelope proteins are then constructed in which portions of the 10 chimera are derived from E2 proteins from one HCV genotype and other portions are derived from E2 proteins of another HCV genotype. These chimeric E2 proteins are constructed by PCR amplifying overlapping fragments, and/or by using restriction sites common to both E2 proteins. An alternative method is DNA shuffling as pioneered by the biotechnology company Maxy-Gen. By surveying the 15 observed binding reactivities of different chimeric E2 proteins with different monoclonal antibodies, amino acid regions in the E2 proteins critical in forming conformational epitopes are identified. Once the critical regions are identified, individual amino acids that differ between the different genotypes are mutated to compose a reactive E2 sequence. Mutants that restore full reactivity identify amino 20 acids that are involved in forming the epitope.

A second basic approach to defining a conformational epitope is to synthesize a series of overlapping peptides 10-15 residues in length that encode the desired sequence of HCV E1 or E2. The peptides are then screened against the antibodies using high concentrations of antibody (often 100 µg/ml or higher). 25 Individual regions that comprise the full conformational epitope often retain residual binding activity with the antibody that can be detected. Once these regions are identified, they can be confirmed using mutational studies involving the 10-15 residues of the peptide, either in the context of the peptide or by substituting into a conformationally intact HCV E1 or E2 protein. A variation of this methodology is 30 described in (Reineke *et al.*, 1999 *Nature Biotechnology*, 17:271-275; incorporated herein by reference).

The subject antibodies also may be used for screening for mimotopes.

Mimotopes may be prepared using phage display, and the peptides screened with the subject antibodies (Livnah *et al.*, 1996 *Science* 273:464-471; Prezzi *et al.*, 1996 *J. Immunol.* 156:4504-4513; each of which is incorporated herein by reference).

5 Antibodies that recognize conformationally conserved HCV epitopes may be used as templates for the rational design of peptide or non-peptide structural mimics of the conformational epitope or mimotopes.

The generation of mimotopes is biologically significant. By mimicking the structure of the conformationally defined viral epitope, the mimotope can interfere 10 with the ability of the virus to bind its target receptor by binding to the receptor itself. For example, analysis of a solved crystal structure defining the interface between a monoclonal antibody and tumor necrosis factor (TNF) enabled the rational design of a non-peptide mimetic capable of antagonizing the biological function of TNF by binding to the TNF receptor (Takasaki *et al.*, 1997 *Nat. Biotech.* 15:1266-1270; incorporated herein by reference). Computational techniques that 15 may be employed to rationally deduce protein folding from a primary amino acid sequence for use in designing a peptide structural mimetic are reviewed in Teichmann *et al.*, 1999 *Curr. Opin. Struct. Biol.* 9:390-399; incorporated herein by reference. The practical application of computer programs for use in structurally 20 modeling conformationally conserved epitopes is described by Schwartz *et al.*, 1999 *J. Mol. Biol.* 287:983-999; incorporated herein by reference. An alternative method for rationally creating a peptide structural mimic of an antibody epitope involves systematic permutations of synthetic peptides designed to be a linear representation 25 of a discontinuous antibody binding site (Reineke *et al.*, 1999 *Nat. Biotech.* 17:271-275; incorporated herein by reference).

Peptides, or other small molecules having specific affinity for a monoclonal antibody and competitive with an epitope of a conformationally intact E1 or E2 protein. Alternatively, peptides or other small molecules may have specific affinity for a monoclonal antibody and competitive with an epitope of E1 complexed with 30 E2 or E2 complexed with E1. Such peptides may be used as vaccines, in diagnostic assays, for immunization for the production of antibodies to a specific HCV epitope,

in competitive assays for defining genotype, and the like. See, for example, Puntoriero *et al.*, 1998 *EMBO J.* 17:3521-3533; Meola *et al.*, 1995, *J. Immunol.* 154:3162- 3172; Tafi *et al.*, 1997 *Biol. Chem.* 378:495-502.

Another approach to effectively create structural mimetics of 5 conformationally conserved HCV epitopes is to produce anti-idiotypic antibodies to the conformationally dependent anti-HCV HMAbs. Anti-idiotypes may effectively block the binding of native virus with its target receptor (Chanh *et al.*, 1987 *Proc. Natl. Acad. Sci. USA* 84:3891-3895; Kopecky *et al.*, 1999 *Intervirol.* 42:9-16; Xue *et al.*, 1993 *J. Gen. Virol.* 74:73-79; each of which is incorporated herein by 10 reference). Anti-idiotypic antibodies recognizing the conformational binding sites of any one of the anti-HCV HMAbs CBH-2, 5, 4B, 4D, 4G, 7, 8C, 8E, 9, or 11 could prevent viral infectivity by interfering with E2 binding to a target cellular protein, or even by interfering with virion attachment to the target cell. Similarly, anti-idiotypic antibodies recognizing the conformational binding sites of either of 15 the HCV HMAbs H-114 or H-111 could also prevent viral infectivity by interfering with E2 binding to a target cellular protein, or even by interfering with virion attachment to the target cell.

The subject antibodies find use for prophylactic therapy or for treating HCV 20 infection, by reducing viral load, by inhibiting binding of the virus to its target proteins, by inhibiting virus mediated fusion with a target cell, and by interfering with conformational changes in the viral envelope proteins necessary for cell infectivity. The composition used can be a monoclonal antibody directed to a single conformational epitope, or a mixture of complementary monoclonal antibodies that 25 recognize distinct conformational epitopes on one or more viral envelope proteins, thereby simultaneously interfering with multiple mechanisms in the infectious process.

For reducing viral load of a body component, particularly a body component 30 of a patient infected with HCV, patient blood is passed through a device comprising the antibodies bound to a surface for capturing the HCV. See, for example, U.S. Patent Nos. 5,698,390 and 4,692,411; each of which is incorporated herein by reference. Various other devices found in the literature can be used with the subject

antibodies to achieve a similar result. A body component can be a biological fluid, a tissue, an organ, such as the liver, and the like.

The antibodies also may be used for passive immunization therapies or other *in vivo* therapies. See, for example, Piazzi *et al.*, 1997 *Arch Intern Med.* 157:1537-5 1544; Farci *et al.*, 1996 *Proc. Natl. Acad. Sci. USA.* 93:15394-15399; al-Hemsi *et al.*, 1996 *Clin. Transplant.* 10:668-675; Krawczynski *et al.*, 1996 *J. Infect. Dis.* 173:822-828; each of which is incorporated herein by reference. For such therapeutic use, the antibodies may be formulated in any convenient way for injection or intravenous administration. Various media may be used such as 10 phosphate buffered saline, saline, or the like. The amount of the antibodies may be varied depending on the level of infection, the affinity of the antibodies, the manner of administration, the frequency of administration, the response of the patient, the use of other therapeutics, and the like. Generally the amount of antibody administered will be in the range of about 0.1 to 5 mg/kg. See, for example, Andrus 15 *et al.*, 1998 *J. Infect. Dis.* 177:889-97 and Kreil *et al.*, 1988 *J. Virology* 72:3076-3081; each of which is incorporated herein by reference.

The chimpanzee is an accepted animal model for screening HCV vaccines and therapeutics. See, for example, Farci *et al.*, 1996 *Proc. Natl. Acad. Sci. USA* 93:15394-15399; Farci *et al.*, 1994 *Proc. Natl. Acad. Sci. USA* 91:7792-7796; Farci 20 *et al.*, 1992 *Science* 258:135-140; Krawczynski *et al.*, 1996 *J. Infect. Dis.* 173:822-828; Bassett *et al.*, *J. Virology* 72:2589-2599; each of which is incorporated herein by reference. The effectiveness of the antibodies can be determined by monitoring for the presence and titer of HCV RNA using quantitative PCR methods. A 25 successful reduction of viral load, or prevention of infection in a test animal or subject is reflected as a reduction or elimination of HCV RNA in serum. Enzymatic tests such as measurement of alanine aminotransferase and/or use of sequential punch needle liver biopsies also is used to test effectiveness, where improvement in the rating of either would indicate a reduction in viral-induced liver damage.

In formulating vaccines to HCV, any agent that mimics at least one conformational epitope of the HCV E1 or HCV E2 protein may be used. For example, the agent may be a peptide, protein, small molecule, mimotope, organic compound, organometallic compound, or inorganic compound, *etc.* In a preferred embodiment, the epitopes represented in the vaccine include those against which antibodies known to prevent infection are directed. In another preferred embodiment, the epitopes represented in the vaccine include ones that are conserved among different genotypes of the virus or among different strains of the virus. In a particularly preferred embodiment of the present invention, peptides or proteins that contain the conformationally-defined epitopes of E1 or E2 of HCV are used in the formulation of a vaccine to prevent an infection by HCV or to treat an HCV infection. In other particularly preferred embodiments, peptides or proteins that contain conformationally defined epitopes of at least one conformationally defined epitope of E1 and at least one conformationally defined epitope of E2 of HCV are used in the formulation of a vaccine. Alternatively, the E1 and E1 epitopes may be linear epitopes. In yet another preferred embodiment, the E1 and E2 epitopes may be a mixture of linear and conformational epitopes. The peptides or proteins are preferably less than 100 amino acids in length, and more preferably less than 50 amino acids in length. In a particularly preferred embodiment, the peptides to be used in formulating a vaccine are peptide fragments of the E1 or E2 protein of HCV. Preferably the peptide folds in a manner similar to its fold in the native E1 or E2 protein thus preserving the three-dimensional structure of the conformational epitope.

The vaccine may also contain proteins that represent concatenated peptides that have the conformational epitope to which antibodies are desired. Several different peptides making up the multimer may be used so that each peptide contains a different epitope, or the same peptide may be used more than once in the multimer.

Peptides of the invention may be synthesized using any method known in the art including Merrifield solid phase chemistry. The peptides may also be obtained by cleavage of E1 or E2 protein and purification. The peptides may be made recombinantly and produced in *E. coli*, yeast (*e.g.*, *S. cerevisiae*), insect cells (*e.g.*,

Sf9 cells), or mammalian cells (e.g., CHO cells) using any available techniques in the art (Sambrook *et al.*; Miller & Calos, eds., *Gene Transfer vectors for Mammalian Cells*, 1987; Ausubel *et al.*, eds., *Current Protocols in Molecular Biology*, 1987; each of which is incorporated herein by reference). The peptides 5 may be modified to increase their immunogenicity, solubility in aqueous solution, or to increase their propensity to fold correctly. For example, peptides may be glycosylated, farnesylated, hydroxylated, reduced, oxidized, *etc.*

In a particularly preferred embodiment, the peptide comprises amino acids 411 through 644 of the E2 protein of HCV genotype 1b. In another embodiment, 10 the peptide comprises amino acids 470 through 644 of the E2 protein of HCV genotype 1b. In yet another embodiment, the peptide comprises amino acids 644 through 661 of the E2 protein of HCV genotype 1b. As would be appreciated by one of ordinary skill in this art, analogous amino acid sequences of E2 proteins from other genotypes of HCV may be used. Analogous sequences may be determined by 15 aligning multiple sequences of the E2 protein from different strains or genotypes of HCV. Homologous sequences that preserve the desired epitope may also be used in the formulation of vaccines. Preferably, the sequences are at least 50% homologous to the native sequence from HCV 1b E2 protein, more preferably at least 60% homologous, and most preferably at least 70% homologous.

20 In a particularly preferred embodiment, the peptide comprises amino acids 192 through 383 of the E1 protein of HCV genotype 1b. In another embodiment, the peptide comprises amino acids 192 through 340 of the E1 protein of HCV genotype 1b. In yet another embodiment, the peptide comprises amino acids 192 through 352 of the E1 protein of HCV genotype 1b. In yet another embodiment, the 25 peptide comprises amino acids 192 through 366 of the E1 protein of HCV genotype 1b. In yet another embodiment, the peptide comprises amino acids 192 through 370 of the E1 protein of HCV genotype 1b. As would be appreciated by one of ordinary skill in this art, analogous amino acid sequences of E1 proteins from other genotypes of HCV may be used. Analogous sequences may be determined by aligning 30 multiple sequences of the E1 protein from different strains or genotypes of HCV. Homologous sequences that preserve the desired epitope may also be used in the

formulation of vaccines. Preferably, the sequences are at least 50% homologous to the native sequence from HCV 1b E1 protein, more preferably at least 60% homologous, and most preferably at least 70% homologous.

In a particularly preferred embodiment, the peptide or collection of peptides
5 is mixed with an adjuvant and optionally other pharmaceutically acceptable
excipients before administration to an individual.

Adjuvants

Compositions utilized in the practice of the present invention may include, or
10 may be administered as part of a protocol that includes one or more adjuvants or cytokines. Any adjuvant may be used in accordance with the present invention. A large number of adjuvant compounds is known; a useful compendium of many such compounds is prepared by the National Institutes of Health and can be found on the world wide web (<http://www.niaid.nih.gov/daids/vaccine/pdf/compendium.pdf>,
15 incorporated herein by reference; see also Allison *Dev. Biol. Stand.* 92:3-11, 1998; Unkeless *et al. Annu. Rev. Immunol.* 6:251-281, 1998; and Phillips *et al. Vaccine* 10:151-158, 1992, each of which is incorporated herein by reference). Hundreds of different adjuvants are known in the art and could be employed in the practice of the present invention.

20

Administration

Those of ordinary skill in the art will appreciate that antibodies or vaccines to
25 be administered to individuals according to the present invention may be administered via any of a variety of routes, protocols, and dosing regimens. Known routes of administration include, for example, intravenous (IV), intraperitoneal (IP), intragastric (IG), subcutaneous (SQ), intramuscular (IM), oral (PO), rectal (PR), intrathecal, vaginal, intranasal, transdermal, intradermal, *etc.* Intravenous, 30 intramuscular, transdermal, intradermal, intranasal, and oral deliveries are generally preferred.

Pharmaceutical Compositions

Pharmaceutical compositions for use in accordance with the present invention may include a pharmaceutically acceptable excipient or carrier. As used herein, the term "pharmaceutically acceptable carrier" means a non-toxic, inert solid, semi-solid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. Some examples of materials which can serve as pharmaceutically acceptable carriers are sugars such as lactose, glucose, and sucrose; starches such as corn starch and potato starch; cellulose and its derivatives such as sodium carboxymethyl cellulose, ethyl cellulose, and cellulose acetate; powdered tragacanth; malt; gelatin; talc; excipients such as cocoa butter and suppository waxes; oils such as peanut oil, cottonseed oil; safflower oil; sesame oil; olive oil; corn oil and soybean oil; glycols such as propylene glycol; esters such as ethyl oleate and ethyl laurate; agar; buffering agents such as magnesium hydroxide and aluminum hydroxide; alginic acid; pyrogen-free water; isotonic saline; Ringer's solution; ethyl alcohol, and phosphate buffer solutions, as well as other non-toxic compatible lubricants such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, releasing agents, coating agents, sweetening, flavoring and perfuming agents, preservatives and antioxidants can also be present in the composition, according to the judgment of the formulator. The pharmaceutical compositions of this invention can be administered to humans and/or to animals, orally, rectally, parenterally, intracisternally, intravaginally, intranasally, intraperitoneally, topically (as by powders, creams, ointments, or drops), buccally, or as an oral or nasal spray.

Liquid dosage forms for oral administration include pharmaceutically acceptable emulsions, microemulsions, solutions, suspensions, syrups and elixirs. In addition to the active compounds, the liquid dosage forms may contain inert diluents commonly used in the art such as, for example, water or other solvents, solubilizing agents and emulsifiers such as ethyl alcohol, isopropyl alcohol, ethyl carbonate, ethyl acetate, benzyl alcohol, benzyl benzoate, propylene glycol, 1,3-butylene glycol, dimethylformamide, oils (in particular, cottonseed, groundnut, corn, germ,

olive, castor, and sesame oils), glycerol, tetrahydrofurfuryl alcohol, polyethylene glycols and fatty acid esters of sorbitan, and mixtures thereof. Besides inert diluents, the oral compositions can also include adjuvants such as wetting agents, emulsifying and suspending agents, sweetening, flavoring, and perfuming agents.

5 Injectable preparations, for example, sterile injectable aqueous or oleaginous suspensions may be formulated according to the known art using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation may also be a sterile injectable solution, suspension, or emulsion in a nontoxic parenterally acceptable diluent or solvent, for example, as a solution in 1,3-butanediol. Among 10 the acceptable vehicles and solvents that may be employed are water, Ringer's solution, U.S.P. and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil can be employed including synthetic mono- or diglycerides. In addition, fatty acids such as oleic acid are used in the preparation of injectables.

15 The injectable formulations can be sterilized, for example, by filtration through a bacteria-retaining filter, or by incorporating sterilizing agents in the form of sterile solid compositions which can be dissolved or dispersed in sterile water or other sterile injectable medium prior to use.

20 In order to prolong the effect of an agent, it is often desirable to slow the absorption of the drug from subcutaneous or intramuscular injection. This may be accomplished by the use of a liquid suspension of crystalline or amorphous material with poor water solubility. The rate of absorption of the agent then depends upon its rate of dissolution, which, in turn, may depend upon crystal size and crystalline form. Alternatively, delayed absorption of a parenterally administered drug form is 25 accomplished by dissolving or suspending the drug in an oil vehicle. Injectable depot forms are made by forming microencapsulated matrices of the drug in biodegradable polymers such as polylactide-polyglycolide. Depending upon the ratio of agent to polymer and the nature of the particular polymer employed, the rate of release of the agent can be controlled. Examples of other biodegradable polymers 30 include poly(orthoesters) and poly(anhydrides). Depot injectable formulations are

also prepared by entrapping the drug in liposomes or microemulsions, which are compatible with body tissues.

Compositions for rectal or vaginal administration are preferably suppositories which can be prepared by mixing the compounds of this invention 5 with suitable non-irritating excipients or carriers such as cocoa butter, polyethylene glycol, or a suppository wax which are solid at ambient temperature but liquid at body temperature and therefore melt in the rectum or vaginal cavity and release the active compound.

Solid dosage forms for oral administration include capsules, tablets, pills, 10 powders, and granules. In such solid dosage forms, the active compound is mixed with at least one inert, pharmaceutically acceptable excipient or carrier such as sodium citrate or dicalcium phosphate and/or a) fillers or extenders such as starches, lactose, sucrose, glucose, mannitol, and silicic acid, b) binders such as, for example, carboxymethylcellulose, alginates, gelatin, polyvinylpyrrolidinone, sucrose, and 15 acacia, c) humectants such as glycerol, d) disintegrating agents such as agar-agar, calcium carbonate, potato or tapioca starch, alginic acid, certain silicates, and sodium carbonate, e) solution retarding agents such as paraffin, f) absorption accelerators such as quaternary ammonium compounds, g) wetting agents such as, for example, cetyl alcohol and glycerol monostearate, h) absorbents such as kaolin 20 and bentonite clay, and i) lubricants such as talc, calcium stearate, magnesium stearate, solid polyethylene glycols, sodium lauryl sulfate, and mixtures thereof. In the case of capsules, tablets, and pills, the dosage form may also comprise buffering agents.

Solid compositions of a similar type may also be employed as fillers in soft 25 and hard-filled gelatin capsules using such excipients as lactose or milk sugar as well as high molecular weight polyethylene glycols and the like.

The solid dosage forms of tablets, dragees, capsules, pills, and granules can be prepared with coatings and shells such as enteric coatings and other coatings well known in the pharmaceutical formulating art. They may optionally contain 30 opacifying agents and can also be of a composition that they release the active ingredient(s) only, or preferentially, in a certain part of the intestinal tract,

optionally, in a delayed manner. Examples of embedding compositions, which can be used, include polymeric substances and waxes.

Solid compositions of a similar type may also be employed as fillers in soft and hard-filled gelatin capsules using such excipients as lactose or milk sugar as 5 well as high molecular weight polyethylene glycols and the like.

The compounds can also be in micro-encapsulated form with one or more excipients as noted above. The solid dosage forms of tablets, dragees, capsules, pills, and granules can be prepared with coatings and shells such as enteric coatings, release controlling coatings, and other coatings well known in the pharmaceutical 10 formulating art. In such solid dosage forms the active compound may be admixed with at least one inert diluent such as sucrose, lactose, or starch. Such dosage forms may also comprise, as is normal practice, additional substances other than inert diluents, *e.g.*, tableting lubricants and other tableting aids such a magnesium stearate and microcrystalline cellulose. In the case of capsules, tablets, and pills, the dosage 15 forms may also comprise buffering agents. They may optionally contain opacifying agents and can also be of a composition that they release the active ingredient(s) only, or preferentially, in a certain part of the intestinal tract, optionally, in a delayed manner. Examples of embedding compositions that can be used include polymeric substances and waxes.

20 Dosage forms for topical or transdermal administration of an inventive pharmaceutical composition include ointments, pastes, creams, lotions, gels, powders, solutions, sprays, inhalants, or patches. The active component is admixed under sterile conditions with a pharmaceutically acceptable carrier and any needed preservatives or buffers as may be required. Ophthalmic formulation, ear drops, and 25 eye drops are also contemplated as being within the scope of this invention.

The ointments, pastes, creams, and gels may contain, in addition to an active compound of this invention, excipients such as animal and vegetable fats, oils, waxes, paraffins, starch, tragacanth, cellulose derivatives, polyethylene glycols, silicones, bentonites, silicic acid, talc, and zinc oxide, or mixtures thereof.

30 Powders and sprays can contain, in addition to the compounds of this invention, excipients such as lactose, talc, silicic acid, aluminum hydroxide, calcium

silicates, and polyamide powder, or mixtures of these substances. Sprays can additionally contain customary propellants such as chlorofluorohydrocarbons.

Transdermal patches have the added advantage of providing controlled delivery of a compound to the body. Such dosage forms can be made by dissolving 5 or dispensing the compound in the proper medium. Absorption enhancers can also be used to increase the flux of the compound across the skin. The rate can be controlled by either providing a rate controlling membrane or by dispersing the compound in a polymer matrix or gel.

10 *Treatment of Patients*

The present invention also provides a method of stratifying and optionally treating patients infected with HCV. In a particularly preferred embodiment, the treatment regimen is particularly suited for an individual. A patient to be treated is provided, and a sample of serum is taken from the patient. The serum is then 15 analyzed for the presence of particular antibodies such as neutralizing antibodies or antibodies that bind to a particular region or epitope of a protein of HCV. Any method known in the art including those described in this application may be used to determine the presence of the antibodies to be detected (e.g., ELISA, competition assay). Based on the level of antibodies in the patient's serum, a treatment can be 20 designed for the patient. For example, a patient who does not have antibodies known to interfere with the binding of virions to their natural receptor may be treated with monoclonal antibodies of this type. In one particularly preferred embodiment, the sera from the HCV-infected patient is considered positive for the presence of a competing antibody if 50% or greater inhibition of E2 binding was 25 obtained at a dilution of 1/200 or greater of the patient's serum, more preferably of 1/500 or greater, and most preferably of 1/1000 or greater.

One of the advantages of this method is that the treatment is tailored to the particular individual being treated. Only those antibodies that are needed and not produced naturally by the patient are administered. This avoids or reduces the risk 30 of adverse reactions from administering therapeutics that are not needed. This method would also eliminate the expense of treating patients who would not benefit

from such treatment. For example, if a patient were already producing an antibody to a particular epitope of E2, there would be no need to administer a human monoclonal antibody directed against the epitope exogenously.

Those skilled in the art will further appreciate that a patient may receive infusions of one or several HCV HMabs that can reduce the amount of HCV virions circulating that are capable of infecting new cells. This antibody treatment may be given alone, during the course of another treatment, or after the cessation of treatment of other antiviral compounds. Additionally, the HCV HMabs may be linked to known toxins or proteins capable of inducing apoptosis or other cell death processes. These modified HCV HMabs can be administered to individuals suffering from HCV mediated liver disease as a means of killing HCV infected cells.

In another particularly preferred embodiment, the treatment may include administering a vaccine designed to induce the production of antibodies that have been found to be lacking in the patient. The most effective vaccines are preferably composed of antigens that have a native conformation, mediate a protective response (such as complement activation or virus neutralization) or can induce a strong antibody response. In a particularly preferred embodiment, the vaccine contains an epitope or mimotope thereof, to which antibodies are not being produced naturally in the individual. For example, synthetic peptide mimotopes isolated with HCV HMabs, especially HCV HMabs recognizing multiple genotypes, have the potential to induce a potent immune response similar to the antibody used in the original isolation of the mimotope. The administration of such a vaccine would induce the patient's immune system to start producing a set of antibodies directed against the administered epitope. It will be appreciated that the mimotopes (or epitopes) of the invention can be used alone or in combination with recombinant proteins or as a cocktail of several different mimotopes.

In the present invention, pharmaceutical compositions are provided that include HMabs to one of either HCV E1 or HCV E2 protein. In certain preferred embodiments, the pharmaceutical compositions include antibodies to both HCV E1 and E2. In other preferred embodiments, the pharmaceutical compositions include two or more antibodies to HCV E1 and HCV E2. As described herein the HCV E1

and E2 antibodies can be directed to E1 or E2 epitopes of a single HCV genotype or multiple HCV genotypes. It will also be appreciated that the antibodies can be directed to either linear or conformational epitopes, as described herein. Particularly preferred combinations of antibody include H-111 with any anti-E2 human monoclonal antibody. Some particularly preferred combinations of antibodies include combinations of the H-111 HMAb with any one or more of CBH-5, CBH-7, CBH-4G, CBH-8C, CBH-17, or CBH-2.

Applications

10 The HCV antibodies of the present invention can be used to identify HCV receptors. Those skilled in the art will appreciate the multitude of ways this can be accomplished (Sambrook J., Fritsch E. and Maniatis T. *Molecular Cloning: A Laboratory Manual*. Cold Spring Harbor Press, Cold Spring Harbor, NY, 1989; Ausubel *et al.*, eds., *Current Protocols in Molecular Biology*, 1987; each of which is incorporated herein by reference). Typically, protein and peptide receptors, and in the case of the present invention, receptors for HCV proteins and peptides, preferably E1 and E2, can be identified by determining whether an antibody to E1 or E2 can inhibit HCV virions attachment to a cell susceptible to HCV infection. A susceptible cell can be incubated in the presence of HCV and anti-HCV E1 or E2 antibody and use a cell binding assay to determine whether attachment is decreased in the presence of the antibody.

25 Cells expressing putative receptors for HCV or libraries of putative receptors for HCV may also be screened for their ability to bind HCV. For example, cells expressing a putative HCV receptor (e.g. a receptor for HCV E1 or E2) can be contacted with an HCV protein or peptide in the presence of an antibody for a time and under conditions sufficient to allow binding of the HCV protein or peptide to putative receptor on the surface of the cell. Alternatively, the HCV protein or peptide, or HCV virions, can be pre-incubated with the antibody prior to contacting the putative receptor on the cell surface. Binding can be detected by any means known in the art, e.g., flow cytometry etc. (see Ausubel *et al.* or Sambrook *et al.*, *supra*). A decrease in binding to the surface of the cell in the presence of antibody

compared to binding in the absence of the cell in the absence of the antibody indicates the identification of an HCV receptor.

Other methods of identifying HCV receptors, such as E1 or E2 receptors, include the use of solid supports, such as beads, columns and the like. For example, 5 receptors for HCV proteins and peptides, or HCV virions, can be identified by attaching an HCV antibody to a solid support and then contacting the antibody with an HCV protein or peptide for a time sufficient for the HCV protein or peptide to bind to the antibody. This provides an HCV protein ligand for putative HCV receptors that can be contacted with the antibody:ligand complex on the solid 10 support for a time and under conditions sufficient to allow binding of a receptor to the HCV protein or peptide. The proteins can be expressed from a library or provided as a cell extract or purified protein preparation from natural or recombinant cells. Once specific binding complexes between the HCV protein or peptide are formed, unbound HCV proteins or peptides, e.g., library proteins or peptide that did 15 not bind specifically to the HCV proteins or peptides, are removed, e.g., by standard washing steps. The bound proteins are then eluted and identified, e.g. by gel electrophoresis.

These and other aspects of the present invention will be further appreciated 20 upon consideration of the following Examples, which are intended to illustrate certain particular embodiments of the invention but are not intended to limit its scope, as defined by the claims.

EXAMPLESExample 1Production of HCV E2 proteins from multiple genotypes in *vaccinia* virus

5 To analyze the reactivity of HCV sera and test the breadth of HCV-HMAbs reactivity, the complete coding sequence of HCV were cloned from isolates of HCV genotypes 1a, 1b, 2a, and 2b, were PCR amplified from HCV positive sera and expressed with vaccinia virus using the pVOTE (Ward *et al.*, 1995 *Proc. Natl. Acad. Sci. USA* 92:6773-6777; incorporated herein by reference) transfer vector (constructs 10 Q1a, Q1b, Q2a, and Q2b for HCV genotypes 1a, 1b, 2a, and 2b, respectively). Genotype selection was based on its divergence and frequency among HCV infected individuals in the United States (Mahaney *et al.*, 1994 *Hepatology* 20:1405-1411; incorporated herein by reference). Oligonucleotide primers were designed to amplify fragments that expressed the final 39 amino acids of E1, all of E2/p7, and 15 the N-terminal 98 amino acids of NS2. See Table 2. SEQ ID NOS: 18-27).

Accordingly, aliquots of plasma from individuals PCR positive for HCV RNA were obtained and genotyped using the InnoLipa HCV genotyping assay performed according to manufacturer's instructions (Innogenetics, Ghent, Belgium). RNA was prepared from 125 µl of plasma from individuals infected with HCV 20 genotypes 1a, 1b, 2a, and 2b using the Puerescript RNA kit, according to manufacturer's instructions (Gentra Systems, Minneapolis, MN). RNA pellets were re-suspended in 25 µl of RNase free H₂O and 10 µl was subjected to reverse transcriptase PCR. Reverse transcription reactions were performed using MMLV 25 reverse transcriptase employing the reverse HCV specific primer HCV E2-R1 5'- CGC GCA CrA AGT AsG GyA CT-3' (SEQ ID NO: 16). Reverse transcription was for 60 minutes at 40°C. Reverse transcribed cDNA was denatured by a 5 minute incubation at 98°C followed by cooling to 4°C and the addition of PCR mix containing 0.15 mM dNTPs, 3 µl 10X PCR buffer, 3 units of AmpliTaq polymerase, and the forward primer HCV E2-F1 5'-CGC ATG GCi TGG GAY ATG ATG-3' 30 (SEQ ID NO: 17). Amplification was for 30 cycles of 94°C for 1 minute, 55°C for 3

minutes, and 72°C for 3 minutes. Between 2 and 8 µl of amplified product was then subjected to a second round of PCR amplification with using the forward primer appropriate for cloning each genotype and an internal reverse primer INT-Reverse (Table 2, SEQ ID NOS: 18-27) or the reverse primer appropriate for each genotype and INT-Forward. PCR amplifications were for 30 cycles of 94°C for 1 minute, 5

60°C for 2.5 minutes, and 72°C for 2 minutes. Appropriately sized bands (~820 nucleotides for the genotype specific forward primer and INT-Reverse and ~1080 nucleotides for INT forward and the genotype specific reverse primer) and were excised from ethidium-bromide stained agarose gels and purified using a

10 commercially available resin (Qiagen, Valencia, CA). Approximately 50 ng of each band were combined and re-amplified with the forward and reverse primers appropriate for each genotype (Table 2). PCR amplifications were for 30 cycles of 94°C for 1 minute, 55°C for 2.5 minutes, and 72°C for 2 minutes. The amplified products were then excised from ethidium bromide stained agarose gels, purified, 15 and digested with the appropriate restriction enzymes. This three-step amplification procedure resulted in a much higher yield of full-length insert than standard two-step procedures. The digested DNAs were then ligated into a similarly digested pVOTE 1 or pVOTE 2 vector (Ward *et al.*, 1995 *Proc. Natl. Acad. Sci. USA* 92:6773-6777; incorporated herein by reference). The ligated plasmids were transfected into 20 competent *E. coli* and insert-containing clones were identified and propagated using standard methods (Sambrook J., Fritsch E. and Maniatis T. *Molecular Cloning: A Laboratory Manual*. Cold Spring Harbor Press, Cold Spring Harbor, NY, 1989; incorporated herein by reference). The clones obtained were designated Q1a, Q1b, Q2a, and Q2b for constructs expressing full length E2 and p7 of HCV genotypes 1a, 25 1b, 2a and 2b, respectively.

Table 2: Primers* employed in cloning HCV E2 protein

	Gty	Forward Primer	SEQ ID NO.	Reverse Primer ID NO.	SEQ ID NO.	SEQ ID NO.
P						
1a	CG AGG CTT <u>CAT</u> <u>ATG</u> ATC GCT GGT GCT TGG	Nde I	18	CG GAA TCC <u>CTG</u> <u>CAG</u> CTA CAA ACT GGC TTG AAG AAT	19	
1b	CG CAT ATG <u>GAG</u> <u>CTC</u> GCG GGG GCC CAC TGG GGA GT	Sac I	20	GCTCT AGA <u>CTG</u> <u>CAG</u> CTA TAT GCC AGC CTG GAG CAC	21	
2a	C GCT CGA <u>GCC</u> <u>ATG</u> GTT GGC GGG GCT CAT TGG GGC	Nco I	22	TC GAA TTC <u>GGA</u> <u>TCC</u> TAC AAA GCA CCT TTT AGG AGA	23	
2b	C GCT CGA <u>GCC</u> <u>ATG</u> GTT TTC GGC GGC CAT TGG GTG	Nco I	24	TC GAA TTC <u>GGA</u> <u>TCC</u> TAC AGA GAC GCT TTA AGG AGG	25	
INT	TG GTT CGG BTG YWC ITG GAT GAA		26	TAA TGC CAi ARC CKR Tai GGG TAG TC		27

*Inner nested primers employed in cloning of vaccinia virus E2 constructs. The restriction sites employed in the cloning are underlined. The primers contained additional restriction sites in their 5' ends. The primers contain other restriction sites. Gtyp = HCV genotype. The primers INT-F and INT-R contain degenerate nucleotides and were used for all genotypes. PCR amplification conditions are described in Example 1.

Expression of intact E2 protein by vaccinia virus constructs Q1a and Q2b was verified in a transient expression assay. CV-1 cells were infected with 5 plaque-forming units (pfu) of wild type vaccinia virus strain VWA (Ward *et al. supra*) and then transfected with pVOTE plasmid using Transfectam (Promega, Madison, WI), 5 according to the manufacturer's instructions. Cells were cultured in media supplemented with 1 mM Isopropyl-B-D-thiogalactopyranoside (IPTG) to induce expression of HCV proteins (Ward *et al. supra*). Forty eight hours after transfection the cells were harvested by washing cultured cells with PBS and resuspending the cells in lysis buffer (150 mM NaCl, 20 mM Tris (pH 7.5), 0.5% deoxycholate, 1.0% 10 Nonidet-P40, 1 mM EDTA) to which the protease inhibitors Pefbloc (Boehringer Mannheim, Indianapolis, IN), Aprotinin, Leupeptin, and Pepstatin were added to final concentrations of 0.5 mg/ml, 2 µg/ml, 2 µg/ml, and 1 µg/ml, respectively. One hundred microliters of lysis buffer was added for every 3 x 10⁶ cells harvested. Nuclei were pelleted by centrifugation at 18,000 x g at 4 °C for 10 minutes and 15 the supernatant was either used directly or stored at 4 °C for not more than two days prior to use.

For Western blot analysis, 10 µl of lysis buffer extract was combined with 10 µl of 2X SDS sample buffer (20% glycerol, 10% β-mercaptoethanol, 4.8% SDS, 0.125 mM Tris (pH 6.8), heated to 95 °C for 5 minutes, and fractionated by sodium 20 dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) (Laemmli *et al.*, 1970 *Nature* 227:680-685; incorporated herein by reference) employing 12% polyacrylamide gels. The fractionated proteins were then electrotransferred to nitrocellulose and incubated overnight with murine monoclonal antibody (mMab) 2C8 that recognizes Western blotted HCV E2 (available from Dr. H. Greenberg, 25 Stanford University). mMab 2C8 was diluted 1:500 in BLOTTO (2.5% non fat dry milk, 2.5% normal goat serum, 0.1% Tween-20 (Sigma, St. Louis, MO), 0.02% sodium azide in TBS: 150 mM NaCl, 20 mM Tris, pH 7.5). Purified HCV or control antibodies or HMAb-containing culture media diluted to an IgG concentration of 5 µl/ml in BLOTTO. The blots were washed 3 times with TBS, 30 and bound antibody was detected with the ECL Western blot kit, according to manufacturer's instructions (Amersham, Arlington Heights, IL).

The constructs Q1a and Q2b produced an approximately 70 kdal protein that was immunoreactive with mMAb 2C8 (Figure 1). As expected with the pVOTE system (Ward *et al.*, 1995 *Proc. Natl. Acad. Sci. USA* 92:6773-6777; incorporated herein by reference) the expression of the HCV E2 proteins was highly dependent on 5 the presence of the inducer IPTG. Expressed protein was also detected from all 4 constructs by IFA with a panel of 10 genotyped HCV sera (data not shown). None of the constructs were reactive with HCV-negative sera nor did any of the HCV antisera react with cells infected with wild type vaccinia virus.

The genotypes of the cloned E2 proteins were confirmed by DNA 10 sequencing of either a 160 bp internal fragment (nts. 2009 to 2168 of HCV-1) from the center of HCV E2 from each of the four clones. See Figure 2 (SEQ ID NOS: 9-12), or the entire insert (construct Q1b) employing dye terminator methodologies and an automated DNA sequencer (Applied Biosystems, Foster City CA). The inserts were highly homologous to the appropriate sequences of HCV E2 available 15 in various databases with no frame shift or termination mutations. See FIG. 3 (SEQ ID NOS: 1-8). Thus, this is good evidence that HCV E2 of all 4 genotypes was accurately expressed by the pVOTE constructs. Plasmids that produced intact HCV were then used to generate recombinant vaccinia virus by homologous recombination into the hemagglutinin locus of the vaccinia virus strain VWA (Ward 20 *et al.*, *supra* as described Moss and Earl, *In* F. Ausubel and R Brent and R Kingston (ed.), *Current Protocols in Molecular Biology*, Vol. 2, John Wiley & Sons, New York, NY, 1994; each of which is incorporated herein by reference). Recombinant vaccinia viruses were identified via infection of BSC-1 cells followed by selection for guanine phosphoribosyl transferase containing virus with media containing 25 mycophenolic acid, xanthine, and hypoxanthine, using standard methods (Moss *et al.*, *supra*). Purified viral stock was obtained for each recombinant virus and titers measured using BSC-1 cells ranged between 5-10x10⁸ pfu/ml.

Example 2**Antibody Screening of potential HCV E2 positive B-cell donors**

Since HCV cannot be reliably propagated *in vitro*, it is necessary to use recombinant envelope proteins expressed in eukaryotic cells to identify individuals with strong titers to HCV proteins. In such screening it is necessary to use methods that preserve the native structure of the envelope proteins thus allowing the detection of antibodies to conformational epitopes. In the identification of sera for the generation of HCV HMAbs an immunofluorescent assay (IFA) was employed. This assay uses acetone-fixed cells and is analogous to methods used in the production of neutralizing HMAbs to conformational epitopes on human T-lymphotropic virus envelope protein (Hadlock *et al.*, 1997 *J. Virology* 71:5828-5840; incorporated herein by reference). For HCV, acetone-fixed cells expressing HCV E2 envelope proteins were used. At various points the E2 proteins were expressed using recombinant baculovirus in Sf9 cells, recombinant vaccinia virus in HeLa cells, as described above, or in Chinese hamster ovary (CHO) cells using a commercially available vector (pDisplay, In Vitrogen, Carlsbad, CA). Since insect derived cells may not express viral envelope proteins in a truly native conformation (Rosa *et al. supra*; Arp *et al.*, 1996 *J. Virology*, 70:7349-7359; each of which is incorporated herein by reference) the use of vaccinia virus or mammalian cell expression systems is preferred. The fluorescence observed with a given serum was scored visually via fluorescence microscopy, and in some cases increasing dilutions of the sera were evaluated to obtain an end point dilution titer of the potential donor sera.

To confirm results obtained with immunofluorescence a microtiter plate assay for evaluating the reactivity of sera to HCV E2 was developed. Monolayers of HeLa cells were grown to 80% confluence and infected with 5 pfu/cell of VWA and 5 pfu/cell of recombinant vaccinia virus or 5 pfu of VWA only. HCV recombinant viruses were mixed with wild type vaccinia with an intact hemagglutinin gene to minimize the vaccinia virus induced cytopathic effect observed with hemagglutinin minus virus (Seki *et al.*, 1990 *Virology* 175:372-384; incorporated herein by reference). Twenty-four hours after infection cells were harvested. Extracts were prepared by washing the cells with PBS and then resuspending 30×10^6 cells in 1 ml

of lysis buffer (150 mM NaCl, 20 mM Tris (pH 7.5), 0.5% deoxycholate, 1.0% Nonidete-P40, 1 mM EDTA, 0.5 mg/ml Pefablock (Boehringer Mannheim, Indianapolis, IN), 2 µg/ml Aprotinin, 2 µg/ml Leupeptin, and 1 µg/ml Pepstatin).
5 Nuclei were pelleted by centrifugation at 18,000 x g at 4°C for 10 minutes. Extracts were stored at 4 °C and used for ELISA within 24 hours of preparation. Microtiter plates (Maxisorp, Nalge Nunc International, Rochester, NY) were prepared by coating individual wells with 500 ng of purified *Galanthus nivalis*, lectin (obtained from SIGMA, St. Louis, MO.) in 100 µl of PBS for 1 hour at 37°C. Wells were then washed with TBS (150 mM NAC1, 20 mM Tris-HCL, pH 7.5), and blocked by 10 incubation for 1 hour at room temperature with 150 µL BLOTO (TBS plus 0.1% Tween-20, 2.5% normal goat sera, 2.5% non fat dry milk). Plates were washed two times with TBS followed by the addition of 20 µl of extract from vaccinia virus infected HeLa cells 1:5 with BLOTO. After incubation for 1.5 hours at room temperature, plates were washed three times with TBS followed by addition of HCV sera at various dilutions in 95 µl of BLOTO supplemented with 5 µL of soluble 15 extract from HeLa cells infected with vaccinia virus VWA. The inclusion of the soluble extract served to suppress reactivity to vaccinia virus proteins that might also be captured by GNA lectin. Plates were incubated for 1.5 hours, wells were washed three times with TBS and 100 µl of anti-human alkaline-phosphatase conjugate (Promega, Madison, WI) diluted 1/5000 in BLOTO was added. After incubation 20 for 1 hour at RT, the plates were then washed four times with TBS followed by incubation with a 1 mg/ml solution of *p*-nitrophenyl phosphate (PNPP). Substrate development was allowed to proceed for 30 to 45 minutes, then the absorbance of the wells at 405 nm was determined using a multiwell plate reader (Du Pont Co., 25 Wilmington, DE).

Typical results are presented in Figure 4. In this experiment five genotyped HCV sera and one serum from an HCV negative blood donor were titrated against HCV E2 proteins of genotypes 1a, 1b, 2a, and 2b, as well as proteins captured from extracts infected with non-recombinant vaccinia virus VWA. Minimal reactivity to 30 the HCV E2 was observed with a serum from an uninfected individual (Graph labeled Negative Serum). Additionally all five sera from HCV infected individuals

exhibited little or no reactivity to proteins captured from extracts infected with wild type vaccinia virus (thin black lines, all graphs). It can be appreciated that a wide variation in seroreactivity to HCV E2 proteins was obtained with the five sera tested, with the HCV 2a individual exhibiting the highest overall reactivity.

5 The results obtained with 12 sera from individuals infected with HCV genotype 2b are presented in Figure 5. In this graph the dilution of sera that resulted in a specific OD of 0.5 for all four of the HCV E2 proteins is compared (Specific OD is the OD obtained from wells coated with extract of HCV E2 construct - OD of wells coated with extract of non-recombinant vaccinia virus). For all 12 sera, 10 reactivity to HCV 2b or 2a E2 protein was significantly greater than that obtained with HCV 1a or 1b E2 protein. This indicates the superiority of HCV genotype 2 E2 proteins for the detection of antibodies recognizing the HCV envelope in individuals infected with HCV genotype 2a or 2b. Also, the individuals presented on the right side of the graph would be more promising donors for the isolation of HCV HMAbs 15 specific for epitopes present in genotype 2a or 2b E2 proteins.

The donor employed to generate the HCV HMAbs was identified as HCV seropositive with the first generation HCV screening assay during a course of autologous donation. Alanine aminotransferase (ALT) testing of the donated units resulted in 6 out of 7 of the donations being within the normal range (<45 IU). One 20 donation had an ALT value of 49, which is just over the normal cutoff. Otherwise the donor exhibited no outward symptoms of hepatitis. This individual was later confirmed to be HCV positive by PCR using the Roche amplicor HCV assay (Roche Diagnostics, Branchburg, NJ) and was determined to be infected with HCV of the 1b genotype by the InnoLipa probe assay (Innogenetics, Ghent, Belgium). This 25 individual was found to have a high titer of antibodies capable of recognizing HCV E2 using IFA. Testing with the neutralization of binding assay (see below) also indicated this donor had a high titer of potentially neutralizing antibodies. Peripheral blood B-cells were isolated from this individual and successfully used to generate HCV antibody secreting human hybridomas (described below).

Example 3**Production of E2 antigen-specific human monoclonal antibodies**

Peripheral B-cells were purified from donor T-cells by T-cell rosetting as described (Foung *et al.*, 1984 *J. Immunol. Methods* 134:35-42; incorporated herein by reference) which disclosure is incorporated by reference. Individual cultures of 1x10⁴ B-cells were EBV-activated in microtiter plates. HCV specific antibodies were detected with an immunofluorescence assay (IFA). Cells infected with recombinant vaccinia virus expressing HCV E2 proteins, recombinant baculovirus expressing HCV E2, and/or mammalian cell lines that have been engineered to express HCV E2 from their DNA were fixed onto HTC supercured 24-spot slides. The cells were fixed with 100% acetone for 10 minutes at room temperature. Fixed cells were incubated with undiluted culture media from EBV activated B cells or hybridomas for 30 minutes at 37°C and washed for 5 minutes with phosphate buffered saline (PBS), pH 7.4. Slides were then incubated for 30 minutes at 37°C with 0.001% solution of Evan's blue counterstain and fluorescein isothiocyanate (FITC) conjugated goat-anti-human IgG (Zymed, South San Francisco, CA). Bound antibody was revealed by fluorescence microscopy.

Out of 540 cultures, 99 wells showing significant immunofluorescence to HCV E2 were identified (yield ~18%) and 30 of the EBV-activated cultures with different immunofluorescence patterns were selected for electrofusion to mouse-human heteromyelomas as described (Found *et al.*, 1990 *J. Immunol. Methods* 134:35-42; Zimmerman, *et al.*, 1990 *J. Immunol. Methods* 134:43-50; Perkins *et al.*, 1991 *Hum. Antibod. Hybridomas* 2:155-159; each of which is incorporated herein by reference). Out of 12 fusions (some fusions contained more than one positive EBV activated culture), 182 out of 456 initial hybridoma cultures exhibited reactivity with HCV E2 by IFA (yield 40% overall). Six additional fusions were performed on two of the original EBV-activated cultures that showed reactivity to HCV-E2 by Western blot. Hybridomas secreting HCV E2 antibodies reactive by Western blot (in addition to being IFA reactive) were isolated from two of the fusions. Overall, 30 human hybridomas were frozen. Limiting dilution clones were isolated from 12 parent hybridomas and HCV-HMAbs from 11 of the hybridomas

were produced in bulk for subsequent studies. eight of the HCV HMabs were IgG₁ with kappa light chains and two were IgG₁ with lambda light chains. HMab CBH-9 was IgG₁ but it is not known whether it uses a lambda or kappa light chain. PCR and DNA sequence analysis of 10 of the HMabs (the lone exception was HMab 5 CBH-9) confirmed that all of the HMabs expressed distinct heavy and light chains. The fusion partners, IgG subtypes, and results obtained in IFA with the hybridomas are described in Table 3.

Example 4

10

HCV E2 ELISA

Previous studies indicated that the HCV E2 protein is highly glycosylated and can be bound by any one of several lectins including *Galanthus nivalis* (GNA), *Tiriticum vulgaris* (WGA), and *Ricinus communis* (Ralston *et al.*, 1993, *supra*; da Silva Cardosa, 1998, *supra*; Sato *et al.*, 1993 *Virology* 196:354-357; each of which 15 is incorporate herein by reference). Therefore, the utility of the two lectins GNA and WGA as reagents was evaluated for capturing HCV E2 protein onto a microtiter plate. A schematic of this assay is depicted in Figure 6.

Monolayers of HeLa cells were grown to 80% confluence and infected with 5 pfu/cell of VWA and 5 pfu/cell of recombinant vaccinia virus or 5 pfu of VWA 20 only. HCV recombinant viruses were mixed with wild type vaccinia with an intact hemagglutinin gene to minimize the vaccinia virus induced cytopathic effect observed with hemagglutinin minus virus (Seki *et al.* 1990, *Virology* 175:372-384; incorporated herein by reference). Twenty-four hours after infection cells were harvested. Extracts were prepared by washing the cells with PBS and then 25 resuspending 30 x 10⁶ cells in 1 ml of lysis buffer (150 mM NaCl, 20 mM Tris pH 7.5, 0.5% deoxycholate, 1.0% Nonidet-P40, 1 mM EDTA, 0.5 mg/ml Pefabloc (Boehringer Mannheim, Indianapolis, IN), 2 µg/ml Aprotinin, 2 µg/ml Leupeptin, and 1 µg/ml Pepstatin). Nuclei were pelleted by centrifugation at 18,000 x g at 4°C for 10 minutes. Extracts were stored at 4°C and used for ELISA within 24 hours of 30 preparation.

Table 3
Characteristics and IFA reactivity of HCV HMAbs

Antibody ^a	Hetero Myeloma	Subtype		Immunofluorescence			
		<i>Heavy</i>	<i>Light</i>	1a	1b	2a	2b
CBH-2	K ₆ H ₆ /B5	IgG1	Kappa	++	++	++	++
CBH-4D	K ₆ H ₆ /B5	IgG1	Lambda	+	+	-	-
CBH-4B	K ₆ H ₆ /B5	IgG1	Kappa	++	++	+/-	-
CBH-4G	K ₆ H ₆ /B5	IgG1	Kappa	+	+	+/-	+/-
CBH-5	H73C11	IgG1	Kappa	++	++	++	++
CBH-7	K ₆ H ₆ /B5	IgG1	Kappa	++	++	++	++
CBH-8C	K ₆ H ₆ /B5	IgG1	Kappa	++	++	++	++
CBH-8E	K ₆ H ₆ /B5	IgG1	Kappa	++	++	++	++
CBH-9	H73C11	IgG1	Unknown	+	+	+/-	+/-
CBH-11	K ₆ H ₆ /B5	IgG1	Kappa	+	++	++	++
CBH-17	K ₆ H ₆ /B5	IgG1	Lambda	+	++	-	-
R04		IgG1	Lambda	-	-	-	-

^aReactivity by IFA of HCV HMAbs with HeLa cells infected with recombinant vaccinia virus expressing HCV E2 of the indicated genotype. Reactivity was scored ++ strongly positive; + positive; +/- weakly positive; - negative. The heavy and light chain subtypes of the antibodies are provided. R04 is an isotype matched control antibody. Antibodies were tested at 10 µg/ml.

10 Microtiter plates (Maxisorp, Nalge Nunc International, Rochester, NY) were prepared by coating individual wells with 500 ng of purified lectin in 100 µl of PBS for 1 hour at 37°C. Wells were then washed with TBS (150 mM NAC1, 20 mM Tris-HCL, pH 7.5), and blocked by incubation for 1 hour at room temperature with 150 µL BLOTTO (TBS plus 0.1% Tween-20, 2.5% normal goat sera, 2.5% non fat dry milk). Plates were washed two times with TBS followed by the addition of 20 µl of extract from vaccinia virus infected HeLa cells 1:5 with BLOTTO. After

incubation for 1.5 hours at room temperature, plates were washed three times within TBS followed by addition of unlabeled antibodies at various concentrations in 100 μ l of BLOTTO. Plates were incubated for 1.5 hours, wells were washed three times with TBS and 100 μ l of anti-human alkaline phosphatase conjugate (Promega, 5 Madison, WI) diluted 1/5000 in BLOTTO was added. After incubation for 1 hour at RT, the plates were then washed four times with TBS followed by incubation with a 1 mg/ml solution of *p*-nitrophenyl phosphate (PNPP). Substrate development was allowed to proceed for 30 to 45 minutes, then the absorbance of the wells at 405 nm was determined using a multiwell plate reader (Du Pont Co., Wilmington, DE).

10 HCV 1a E2 produced by recombinant Q1a vaccinia virus was employed as a source of HCV E2 and six HCV HMabs were employed as detection reagents (Figure 7). No reactivity was observed to proteins captured with either lectin with a control monoclonal and only background levels of reactivity were observed for all HCV HMabs with proteins captured by WGA. In contrast, HCV HMabs CBH-2, 15 CBH-5, CBH-7 all exhibited strong reactivity to proteins captured by GNA. Additionally HCV HMabs CBH-17 and CBH-4D had lower levels of reactivity with GNA captured proteins. This suggests that HCV HMAb CBH-11 does not recognize this particular E2. However it is clear that the GNA capture ELISA is extremely useful for analyzing the reactivity of HMabs with HCV E2.

20 Therefore the reactivity of the HCV HMabs was then evaluated with recombinant vaccinia virus expressing E2 proteins of divergent genotypes (Figure 8). All 11 HCV HMabs bound to two or more of the HCV E2 constructs and no specific signal was obtained with a control HMAb (Panel marked R04). The HMabs with the highest relative affinity and levels of reactivity to E2 proteins of all 25 four genotypes were CBH-7 and CBH-8C followed by HMabs CBH-5, -2, and -8E. HMabs CBH-4G and CBH-9 exhibited significantly greater reactivity to HCV E2 proteins of genotypes 2a and 2b, while HMAb CBH-11 was markedly less reactive with Q1a E2 protein. HMAb CBH-17, and to a lesser extent CBH-4D and CBH-4B, exhibited preferential binding to E2 proteins of genotype 1a and 1b relative to E2 30 proteins of genotypes 2a or 2b. These variations were not a result of varying efficiencies of capture of the different E2 proteins since the maximum signals

obtained with the different E2 proteins since the maximum signals obtained with the different E2 proteins were very comparable in all experiments. These results were consistent with the results obtained in IFA with the same constructs (See Table 3, above). Seven antibodies, CBH-2, -4G, -5, -7, -8C, -8E, and -9, exhibited 5 significant reactivity with all tested HCV E2 constructs and can be considered broadly reactive.

The reactivity of all tested HMabs with at least two HCV genotypes suggested that the epitopes recognized by the HCV HMabs would be highly conserved (See Figure 9). It was of interest to determine whether the epitopes 10 recognized by the HMabs would be conformational or linear in nature. This was addressed directly by comparing the reactivity of the HCV HMabs to both native and denatured HCV E2 proteins (See Figure 9). As expected all 11 HCV HMabs recognize HCV 1b E2. Treatment of HCV E2 by heating to 56°C in the presence of 0.5% SDS and 5 mM dithiothreitol results in complete abrogation of reactivity for 15 10 of the 11 HCV HMabs. The sole exception is HMAb CBH-17, which retains approximately 90% of its reactivity with the denatured E2 protein. Western Blot analysis of the HMAb CBH-17 confirmed it was weakly reactive with HCV envelope proteins expressed by vQ1a, or vQ1b (data not shown). No reactivity with Western blotted vQ1a was observed with any of the remaining 10 HMabs (data not 20 shown). Thus 10 of the 11 HCV HMabs recognize conformational epitopes.

Lastly, competition analyses were employed to define which HCV HMabs recognize the same (or very spatially close) epitopes. A schematic of this assay is depicted in Figure 10. The HCV HMabs CBH-5, CBH-2, and CBH-7 were biotinylated using standard methods and the reactivity of the biotinylated HMabs to 25 HCV type 1 or type 2 E2 in the presence of an excess of selected HMabs was compared to those seen in samples without any added antibody. As seen in Figure 11, the control HMAb R04 and the HCV HMabs CBH-4D, -4B, -4G, -7, -9, and -17 all exhibited essentially no inhibition of HMAb CBH-5 binding. In contrast HMAb CBH-5 was inhibited 85% by an excess of itself and approximately 75% by HMAb 30 CBH-8E. HMAb CBH-5 was inhibited more variably by HMabs CBH-8C and CBH-11 and only inhibited to approximately 50% by HMAb CBH-2. In particular,

the competition seen with HMAb CBH-2 is relatively equivocal, and it is not clear whether CBH-2 recognizes the same epitope as CBH-5 at a reduced affinity, or recognizes a separate spatially close epitope.

Analysis of the antibody competition with HMAb CBH-2 (Figure 12), 5 indicated that HMAb CBH-2 binding was inhibited to greater than 75% by itself and HMAbs CBH-5, -8C, and -8E. In contrast, CBH-7 inhibited binding to only Q1a proteins by 60%, and CBH-11 inhibited binding only to Q1b and Q2a proteins. As with HMAb CBH-5, no competition was observed with HMAbs CBH-4G, -4D, -4B, -9, or -17. Analysis of competition results with HMAb CBH-7 (Figure 13) indicate 10 that the only HMAb that significantly inhibited binding of CBH-7 was itself. These data demonstrate that among the broadly reactive HMAbs, CBH-2, -5, -11, and -7 all recognize distinct epitopes. The possibility remains that CBH-2, -8C, and -8E may recognize either the same epitope or two distinct epitopes. Additionally CBH-9, and CBH-4G may recognize the same epitope or two distinct epitopes, but their failure 15 to compete with CBH-2, -5 etc. ensures that they do not recognize the same epitope(s) as the other broadly reactive HMAbs. Thus, minimally the broadly reactive HMAbs recognize five distinct epitopes.

Example 5

20 Assessment of E2-specific HMAb activity in the Neutralization of Binding

Assay

The neutralization of binding (NOB) assays tests whether a given antibody or serum can prevent the binding of HCV E2 protein to a putative receptor, expressed 25 on human T cell lines. The NOB assays were performed using methods and HCV E2 proteins previously described (Rosa *et al.*, *supra*; Ishii *et al.*, *supra*). Briefly, 1 μ g of the HCV E2 1a protein produced in mammalian cells (Rosa *et al.*, *supra*) was mixed with serial dilution of antibodies (from 0.1 to 300 μ g/ml) and incubated for 30 min. at 37°C. Molt-4 cells (10^5) were added to the mixture and incubated on ice 30 for 1 hour. After washing, the amount of HCV-E2 bound to Molt-4 cells was

assessed by flow cytometry as described previously (Rosa *et al.*, *supra*). The NOB titer is defined as the serum dilution that shows 50% neutralization of E2 binding.

The ability of HMAbs to inhibit binding of HCV 1a E2 to CD81 expressing target cells was assessed with the neutralization of binding (NOB) assay (Rosa *et al.*, *supra*). HMAbs CBH-4D, 4B, 4G, and 17 did not block the binding of E2 to target cells at concentrations of less than 25 µg/ml. HMAbs CBH-2, -5, -7, -8C, -8E, and -11 achieved 50% inhibition at concentrations of 1 to 10 µg/ml in multiple experiments (Table 4).

10

Example 6

Effect of HCV HMAbs on E2 binding to CD81: Microtiter plate assays

Recently, the human tetraspannin protein CD 81 has been identified as a potential receptor for HCV and the cellular target protein for HCV E2 in the NOB assay. The binding site for HCV E2 within CD81 has been localized to the large extracellular loop, CD81-LEL (Pileri *et al.*, 1998 *Science* 282:938-941; incorporated herein by reference), previously referred to as extracellular loop 2 or LEL. To prevent confusion between E2 and LEL we have opted to refer to this region as the Large Extracellular Loop (LEL). The large extracellular loop of human CD81 (CD81-LEL) was expressed as a fusion protein with glutathione-S-transferase employing the pGEX vector (GST-2T). Construction and purification of the protein were as described (Flint *et al.*, 1999 *J. Virology* 73:6235-6244; incorporated herein by reference). This CD81-LEL-GST fusion protein was used to determine which HMAbs could recognize CD81-HCV E2 complexes. A schematic of this assay is provided in Figure 14. Microtiter plate wells were coated with 100 ng of purified CD81-LEL or non-recombinant GST diluted in PBS. After 2 hours at 37°C, wells were washed one time with TBS and blocked by incubation with 150 µl of BLOTTO for 1 hour at RT. Extract from BSC 1 cells infected with HCV E2 expressing vaccinia virus was combined with test antibody in 100 µl of BLOTTO in coated plates that were incubated overnight with gentle agitation at 4°C. Wells were then washed three times with TBS followed by adding appropriate alkaline-phosphate conjugated secondary antibody and PNPP substrate as described in Example 4.

To confirm the NOB results using E2 proteins of multiple genotypes, we assessed whether the HCV HMAbs could inhibit the interaction of HCV E2 with CD81. Microtiter plates were first coated with purified CD81-LEL glutathione-S-transferase fusion protein to which an excess HCV E2 was added in the presence of 5 the HCV HMAbs. Because HCV E2 binds specifically to human CD81 but not CD81 proteins of most other primates (Rosa *et al.*, *supra*), the E2 proteins were produced in the green monkey kidney cell line BSC-1 to minimize the effect of endogenous CD81. Both anti-HCV and control antibodies were not captured by purified non-recombinant glutathione-S-transferase. Nor were the HCV or control 10 antibodies captured by CD81 when combined with extracts of BSC-1 cells infected with wild type vaccinia virus (data not shown).

The NOB negative HMAb CBH-4G was captured onto CD81 coated plates to equivalent extents with E2 proteins of all four genotypes tested. The HMAbs CBH-4B, -4D and -17, were captured to variable extents onto CD81 coated plates by 15 HCV 1a or 1B E2 proteins but not HCV 2A or 2B E2 proteins, consistent with the reactivity of these HMAbs with GNA captured E2 protein (Figure 15). Titration analysis of the four NOB negative HMAbs confirmed that they all bound to HCV 1b E2 protein with 50% of maximum binding is obtained at concentrations between 1 and 10 µg/ml (Table 4). None of the NOB positive antibodies, CBH-2, -5, -7, -8C, -20 -8E, and -11 were captured by CD81 and E2 proteins of any of the our genotypes tested (Figure 15). Similar results were obtained when the HCV antibodies were added to wells on which HCV 1b E2 protein was already bound to CD81-LEL (data not shown) indicating that the results obtained were independent of each other of addition of the E2 protein and the HCV HMAbs. Titration analysis of HMAbs 25 CBH-2 and 7, which are strongly reactive with GNA captured E2 but negative with CD81 bound E2, confirmed that these antibodies did not bind to CD81-LEL E2 complex at concentrations of up to 25 µg/ml (data not shown). Thus, six HMAbs inhibited the binding of HCV E2 of multiple genotypes to CD81-LEL.

Table 4: Inhibition of HCV E2-CD81
Binding by Anti-HCV HMAbs

		CD81	
	HMAb	NOB 1a ^a	1b E2 ^b
10	CBH 2	5 µg/ml	-
	CBH 5	2 µg/ml	-
	CBH 7	7 µg/ml	-
	CBH 8C	10 µg/ml	-
	CBH 8E	8 µg/ml	-
	CBH 11	3 µg/ml	-
15	CBH 4G	-	3 µg/ml
	CBH 9	-	1 µg/ml
	CBH 4B	-	0.4 µg/ml
	CBH 4D	-	2 µg/ml
	CBH 17	-	3 µg/ml
20	R04	-	-

^aHMAb reactivity in representative NOB assays are presented as µg/ml of antibody that results in 50% inhibition of E2 binding to CD81 expressing T cells. Antibodies were tested at concentrations that ranged from 0.1 to 300 µg/ml. (-) = negative.

^bHMAb reactivity is presented as the concentration of antibody (in µg/ml) that results in 50% of maximum binding to E2 captured by GNA or E2 captured by a CD81-LEL. (-) = negative.

Example 7**Microtiter plate assay for HCV neutralizing antibodies**

To assist in the treatment and management of individuals with HCV infection, it would be desirable to know whether they have a potent anti-viral immune response. Although several assays that can measure neutralizing antibody titers have been described, including the neutralization of binding assay described above and *ex vivo* neutralization prior to inoculation of chimpanzees these assays are all cumbersome and are not suited to testing large numbers of samples. Therefore we employed HMAb CBH-4G, which is equivalently reactive to HCV E2-CD81 complexes with E2 proteins of multiple genotypes in an inhibition assay to determine the level of neutralizing of binding like antibodies in human sera.

Individual wells of microtiter plates were coated with either 500 ng of purified GNA lectin or 100 ng of GST-CD81-LEL fusion protein for one hour at 37°C. Wells were then washed one time with TBS and blocked for one hour with 150 µl of BLOTTO at room temperature. The wells are then washed one time with TBS, and various dilutions of test sera or monoclonal antibodies were added to the appropriate wells in a total volume of 50 µl. At the same time 15 µl of HCV E2 protein containing extract was combined with 4 µg/ml of a biotinylated preparation of HMAb CBH-4G in a total volume of 50 µl of BLOTTO for each well. After incubation for 20 minutes at 4°C the E2 CBH-4G mixture was added to microtiter plate wells already containing the test antibody. The entire plate was then incubated overnight at 4°C with gentle agitation. The next morning the contents of the wells were discarded and the wells washed three times with TBS. This was followed by the addition of 100 µl of strepavidin conjugated alkaline phosphatase (Amersham-Pharmacia, Piscataway NJ) diluted 1/1000 in PBS plus 0.1% Tween-20 (Sigma, St Louis MO). The plates were then incubated for one hour at room temperature after which time the wells were washed four times with TBS and bound biotinylated antibody detected by incubation with PNPP substrate as described in examples 2 and 4 above.

The results obtained when the panel of 11 HCV HMAs was used as test antibodies are presented in Figure 18. In this experiment the ability of a 20 µg/ml concentration of the HCV HMAs to inhibit the binding of HCV genotype 1a E2

protein to human CD81-LEL was evaluated. Inhibition of binding observed in CD81-LEL coated wells are compared to results obtained with the same antibody in GNA lectin coated wells. Inhibition observed of E2 binding in GNA coated wells reflects inhibition of the interaction between the CBH-4G detection antibody and the 5 competing antibody. Inhibition observed specifically in the CD81-LEL coated wells reflects inhibition of the interaction between CD81 and E2. None of the 11 HCV HMAbs or the control antibody, R04 exhibited more than 50% inhibition of CBH-4G binding to E2 captured by GNA. In contrast five of the six HCV HMAbs previously shown to be neutralization of binding positive strongly inhibited binding 10 of CBH-4G-E2 complex to CD81-LEL. The lone exception was HMAb CBH-11, which does not efficiently recognize the Q1a isolate of genotype 1a E2 protein. The HMAbs CBH-4b, -4G, -4D, -9 and -17, which recognize CD81-LEL-E2 complexes all minimally effected binding of CBH-4G bound E2 to CD81-LEL. Thus HMAb CBH-4G can effectively discriminate between antibodies that can or cannot inhibit 15 the interaction of HCV E2 with CD81.

Table 5: Preliminary epitope analysis of HCV HMabs

Epitope	Type ¹	HMab	Inhibits E2-CD81 ²	Binds to HCV Virion	Comp w CBH 2	1a	1b	2a	2b
1	CONF	CBH 2	+	+	+	+	+	+	+
		CBH 8Ec	+	ND	+	+	+	+	+
2	CONF	CBH 5	+	+	+/- ³	+	+	+	+
3	CONF	CBH 7	+	-	-	+	+	+	+
4	CONF	CBH 11	+	-	+	-	+	+	+
5	CONF	CBH 8C	+	NDn	+	+	+	+	+
6	CONF	CBH 4G	-	ND	-	+	+	+	+
		CBH 9	-	ND	-	+	+	+	+
7	CONF	CBH 4B	-	ND	-	+	+	-	-
		CBH 4D	-	ND	-			-	-
8	LIN	CBH 17	-	ND	-	+	+	-	-

¹ CONF = recognizes a conformational epitope; LIN = recognizes a linear epitope

² Summarizes results obtained in NOB assay and CD81-E2 binding assays described

5 above

³ Non-reciprocal partial competition is observed. CBH-2 inhibits binding of CBH-5 to HCV 1a or 1b E2 protein at a level of ~ 50%. CBH-5 inhibits binding of CBH-2 to HCV E2 of genotypes 1a, 1b, 2a, or 2b to ~80%.

10 Accordingly this experiment was then repeated using HCV and control sera in place of the HCV HMabs (Figure 19). Six genotyped HCV sera (three genotype 1a sera and three genotype 2b sera) and two HCV negative sera were tested against the homologous E2 protein at a dilution of 1/1000. As seen with the HCV HMabs little or no inhibition of HCV E2 binding to GNA was observed. Nor did either of 15 the negative sera significantly affect binding of HCV E2 to CD81-LEL. In contrast a wide variation of inhibition of E2 binding to CD81-LEL was observed with the

HCV sera. Thus HMAb CBH-4G binding to a putative receptor, CD81, in a microtiter plate format.

It is evident from the above results that the monoclonal antibodies are an important addition in the development of diagnostics and therapies for the treatment 5 of patients having HCV. By virtue of recognizing genotypes 1 and type 2, HCV assays can be performed with a higher expectancy of fewer false negatives and fewer antibodies are required for performing the assays to identify HCV infection. The antibodies will find use in a wide variety of protocols. In addition, the antibodies may be used to identify genotypes, isolate virion particles, isolate HCV 10 RNA, capture antigen from serum or other samples, and identify and isolate mimotopes (e.g., by screening random peptide phage libraries). By virtue of their being human, they may be used in therapy, either prophylactic, to protect a subject who may be exposed to the virus, or therapeutic, to reduce the effective viral load of a patient.

15

Example 8

Competition analysis and epitope localization of human monoclonal antibodies to HCV E2 that inhibit HCV replication in a small animal model of HCV

20

infection

MATERIALS AND METHODS

Cell lines and viruses. HeLa cells were grown in minimal essential media (MEM, Life Technologies, Bethesda, MD) supplemented with 10% fetal calf serum (FCS) and 2 mM glutamine. Human embryonic kidney (HEK-293) cells were maintained in Dulbecco's modified minimal essential medium (DMEM, Life Technologies, Gaithersburg, MD) supplemented with 10% fetal calf serum (GIBCO) and L-glutamine (2 mM) (GIBCO) in 5% CO₂. Recombinant vaccinia virus expressing HCV envelope proteins were constructed and grown as described (HCV JoV). 25 Vaccinia virus 1488 expressing the structural proteins of HCV 1a strain H was obtained from Dr Charles Rice.

Monoclonal antibodies. The production, purification, and biotinylation of the HCV HMabs were performed as described (HCV JoV). Rat monoclonal antibody 3/11 to HCV E2 was cultured as described previously and was obtained from Dr. Jane 5 McKeating. Rat monoclonal antibody to the influenza hemagglutinin (HA) epitope was obtained from Roche Diagnostics (Indianapolis, IN). Murine monoclonal antibody to the c-myc epitope was obtained from Santa Cruz Biotechnology (Santa Cruz, CA).

10 **Competition Assays.** Monolayers of HeLa cells were grown to 80% confluence, infected with recombinant vaccinia virus expressing HCV E2, and cytoplasmic extracts prepared as described (HCV JoV). Microtiter plates were prepared by coating wells with 500 ng of purified *Galanthus nivalis* (GNA) lectin (SIGMA, St Louis, MO) in 100 μ l of PBS for 1 hour at 37°C. Wells were washed with TBS (150 15 mM NaCl, 20 mM Tris-HCl, pH 7.5), and then blocked with 150 μ l BLOTTO (TBS plus 0.1% Tween-20, 2.5% normal goat sera, 2.5% non fat dry milk) by incubation for 1 hour at room temperature. Plates were washed twice with TBS followed by the addition to each well of 15 μ l of extract in 100 μ l BLOTTO. After 1.5 hours at RT, plates were washed 3 times with TBS followed by the addition of competing 20 antibodies at various concentrations in a total volume of 50 μ l/well. Plates were incubated for 30 minutes at which point 50 μ l/well of a 8 μ g/ml (CBH-4G) or 4 μ g/ml solution (all other HMabs) of biotinylated test antibody was added. After 25 incubation for 1.5 hours at room temperature, the plates were washed 3 times with TBS, and 100 μ l of 1/1000 diluted alkaline-phosphatase conjugated streptavidin (Amersham-Pharmacia Biotech, Piscataway, NJ) was added. After 1 hour at room temperature, the plates were washed 4 times with TBS followed by 30 minutes 30 incubation with a 1 mg/ml solution of *p*-nitrophenyl phosphate (PNPP). Absorbance was measured at 405 nm with a multi-well plate reader (BioTek Instruments, Winooski VT). Signals obtained with biotinylated test antibody and E2 in the presence of competing antibody were compared to signals obtained from test antibody and E2 in the absence of any competing antibody.

Isolation and cloning of HCV E2 deletion constructs. HCV 1b RNA was isolated from serum from an individual infected with HCV genotype 1b using the PureScript (Gentra systems, Minneapolis, MN) according to the manufacturer's instruction.

5 Both the vaccinia virus recombinant Q1b and all of the HCV 1b deletion constructs were derived from the same individual. HCV RNA was converted into cDNA using random primers and reverse transcriptase (Perkin-Elmer Applied Biosystems, Foster City, CA) according to manufacturer's protocol at 42°C for 30 min. Fragments of HCV E1 were amplified by polymerase chain reaction (PCR) using *pfu* taq 10 polymerase (Stratagene, La Jolla, CA) from cDNA with appropriate oligonucleotide primers (obtained from Integrated DNA Technologies, Corlville, IA) that contained flanking *Bgl* II or *Pst* I restriction sites. HCV strain H constructs were amplified by PCR from viral stocks of vaccinia virus construct vv1488. Amplified DNAs were subsequently ligated into the *Bgl* II and *Pst* I digested pDisplay plasmid (Invitrogen, 15 Carlsbad, CA). All plasmids were constructed using standard procedures (28). The presence of in-frame HCV inserts was confirmed by DNA sequencing using ABI PRISM Dye terminator cycle sequencing on an automated sequencer (PE-Applied Biosystems, Foster City CA).

20 **Expression of HCV E2 deletion constructs.** Human embryonic kidney (HEK) 293 cells were seeded to obtain 60-70% confluence by the following day. For transfection of a T-75 flask, a mixture of μ g of the appropriate plasmid DNA and μ g of PerFect Lipid Pfx-2 (InVitrogen, Carlsbad CA) were combined in ml of serum free media at a DNA:lipid ratio of 1:6 (w/w). After four hours incubation at 25 37°C the transfection solution is replaced with 2.5 ml of complete medium and cells were grown for an additional 24 hours. Cell extracts were prepared by washing cells with PBS and resuspending them in 1 ml of lysis buffer (150 mM NaCl, 20 mM Tris pH 7.5, 0.5% deoxycholate, 1.0% Nonidet-P40, 1 mM EDTA, 0.5 mg/ml Pefabloc (Boehringer Mannheim, Indianapolis, IN), 2 μ g/ml Aprotinin, 2 μ g/ml Leupeptin, 30 and 1 μ g/ml Pepstatin). Nuclei were pelleted by centrifugation at 18,000 x g at 4°C for 10 minutes. For Western blot analysis, extracts were combined 1 to 1 with 2X

sodium dodecyl sulfate polyacrylamide electrophoresis sample buffer (SDS-SB; 20% glycerol, 10% β -mercaptoethanol, 4.8 % SDS, 0.125 mM Tris pH 6.8). Proteins were denatured via heating to 95°C for five minutes followed by sodium dodecyl sulfate polyacrylamide electrophoresis (SDS-PAGE) in 12% polyacrylamide gels of 20 μ l aliquots of the denatured extracts. SDS-PAGE and subsequent Western blotting were performed using standard methods.

For microtiter plate assays, microtiter plates were prepared by coating wells with 500 ng of purified *Galanthus nivalis* (GNA) lectin (SIGMA, St Louis, MO) in 100 μ l of PBS for 1 hour at 37°C. Wells were washed with TBS (150 mM NaCl, 20 mM Tris-HCL, pH 7.5), and then blocked with 150 μ l BLOTO (TBS plus 0.1% Tween-20, 2.5% normal goat sera, 2.5% non fat dry milk) by incubation for 1 hour at room temperature. Wells were washed twice with TBS followed by the addition of 25 μ l of extract from HEK-293 cells transfected with E2 deletion constructs 15 diluted in 75 μ l of BLOTO. After 1.5 hours at room temperature, plates were washed 3 times with TBS followed by the addition of monoclonal antibodies at various concentrations. Plates were incubated for 1.5 hours, washed 3 times with TBS, and then 100 μ l of appropriate alkaline-phosphatase conjugated secondary antibody, diluted in BLOTO as recommended by the manufacturer, was added (for 20 anti-human and anti-mouse, Promega, Madison, WI, for anti-rat, Kirkegaard and Perry, South San Francisco CA). After 1 hour at room temperature, the plates were washed 4 times with TBS followed by incubation for 30 minutes with a 1 mg/ml solution of *p*-nitrophenyl phosphate (PNPP). Absorbance was measured at 405 nm with a multi-well plate reader (Du Pont Co, Wilmington, DE).

25

Flow cytometric analysis. Various dilutions of test antibody in a total volume of 100 μ l of staining solution (PBS plus 1% FCS and 0.1% sodium azide) were combined with 10^6 viable HCV E1 expressing or control HEK-293 cells, resuspended in 100 μ l of staining solution, and incubated at 4°C for 45 minutes. 30 After adding an additional 3 ml of staining solution, the cells were pelleted by

centrifugation for 10 minutes at 500 x g at room temperature. The pellet was reserved and resuspended in 100 μ l of FITC conjugated secondary antibody diluted as recommended by the manufacturer (Jackson Immunoresearch laboratories, West Grove, PA) in staining solution. After 45 minutes at 4°C, 900 μ l of staining solution
5 was added, and the cells were pelleted as above. The cells were then resuspended in 1 ml of fixative solution (3.8% formaldehyde in PBS), and the amount of HMAb bound to the surface of cells was analyzed on a FACScalibur (Becton-Dickinson, San Jose, CA). For two color staining secondary antibodies were conjugated to R-phycoerythrin and fluorescence monitored at 606 nm while EGFP fluorescence was
10 monitored at 545 nm.

RESULTS

Human monoclonal antibodies recognizing HCV E2 were obtained from two sources. Ten HMabs (CBH-2, CBH-4B, CBH-4D, CBH-4G, CBH-5, CBH-7,
15 CBH-8C, CBH-8E, CBH-11, and CBH-17) were obtained from an individual who had an asymptomatic infection with HCV of genotype 1b. The antibodies varied in the breadth of their reactivity with different genotypes of HCV E2 and in their ability to inhibit the interaction of HCV E2 with human CD81. The designations, reactivity, and properties of the HCV HMabs are summarized in Table 6.

20

Table 6: HCV HMABs

HMAB ¹	HCV E2 Antibodies			E2 Reactivity ³			Functional Assays		
	Heavy ²	Light	Gtyp 1	Gtyp 2	Inhibit CD81 ⁴	Bind Virions ⁵	Trimera ⁶		
CBH-2	VH5-51	V _k III A27	7 (8)	2 (2)	++	++	++		
CBH-8E	VH1-69	V _k J O12	8 (8)	2 (2)	++	ND	ND		
CBH-5	VH1-69	V _k J L12	8 (8)	2 (2)	++	+	+-		
CBH-8C	VH4-59	V _k III L6	5 (8)	2 (2)	++	ND	ND		
CBH-11	VH1-69	V _k J L12	4 (8)	2 (2)	++	-	ND		
CBH-7	VH1-69	V _k J O12	8 (8)	2 (2)	++	-	++		
CBH-4G	VH1-9	V _k J A20	8 (8)	2 (2)	-	ND	ND		
CBH-4B	VH1-9	V _k III A27	8 (8)	0 (2)	-	ND	ND		
CBH-4D	VH1-9	V _k λ 2a2	8 (8)	0 (2)	-	ND	ND		
CBH-17	VH3-73	V _k λ 3h	7 (8)	0 (2)	-	ND	ND		
3/11	rat MAb		8 (8)	2 (2)	ND	ND	ND		
HA	rat MAb		2 (2)	0 (0)	-	ND	ND		
R04	IgG1		0 (8)	0 (2)	-	-	ND		

¹CBH Antibodies are further described in Hadlock *et al. J. Virol. 74:10407-10416, 2000*; incorporated herein by reference. HA recognizes a synthetic epitope present in some HCV E2 constructs. rMAB 3/11 was generously provided by Jane McKeating, Ph.D.

²Antibody sequences are from Chan HC, *et al. In Press Blood*.

³The number of reactive E2s is followed by the total number tested (in parentheses).

⁴++ = inhibits binding of E2 to CD 81. - = no inhibition. ND = not done.

⁵++ = binds to HCV virions in immunoprecipitation and/or CD 81 inhibition assays.

⁶++ = significantly inhibits serum HCV levels in Trimer mice. Test HMAb is pre-incubated with HCV inoculum prior to exposure to human liver and transplantation into Trimer mice. HCV serum viral loads are determined at 15-20 days post transplantation. Sequence analysis of the IgG1 genes of 10 of the 11 HMABs confirmed that they were derived from independent B cells. Of note, HMAB CBH-4B, CBH-4G, CBH-4D, and CBH-17 all failed to inhibit the binding of E2 to CD81-LEL (Table 6).

Competition assays were employed to determine the number of distinct sites within E2 that were reactive with the HMabs. Individual HMabs were purified, biotinylated, and the binding of the antibodies in the presence of increasing 5 concentrations of competing antibody was determined. Representative binding curves are presented in Figure 21. Binding of HMabs CBH-2, CBH-5, CBH-8C, and CBH-11 to HCV 1b E2 were all significantly inhibited by an excess of HMabs CBH-2, -8E, -5, -8C, and -11. In general HMAb CBH-5 exhibited the highest level of inhibition, and CBH-2 and CBH-8E exhibited the weakest inhibition. For 10 HMabs CBH-2, -5, -8C, and -11 and no significant inhibition was observed with a control HMAb, R04, or HCV HMabs CBH-7, CBH-4B, and CBH-4G. In contrast, HMAb CBH-7 was strongly inhibited by itself, very weakly inhibited by HMAb CBH-4B, and unaffected by the presence of HMabs CBH-2, -5, -8C, -8E, -11, -4G, or the control antibody. Similarly HMAb CBH-4B showed intermediate levels of 15 inhibition with HMabs CBH-7, CBH-4B, and CBH-4G. HMabs CBH-2, -5, -8C, -11, and 8E recognized epitopes that were in close proximity to each other and potential define an antibody-binding site within HCV E2

The results from the full series of inhibition experiments are presented in Figure 22. Five antibodies CBH-2, -8E, -5, -8C, and -11 that recognize 20 conformational epitopes and can inhibit the binding of E2 with CD81-LEL all significantly cross competed and formed one competition group (Group I). A second competition group (Group II) contains HMAb CBH-7. A third competition group is formed by HMabs CBH-4G, CBH-4B, and CBH-4D, and a fourth competition group is formed by CBH-17, the only antibody in the panel to recognize 25 a linear epitope. The binding of antibodies from group I was only marginally affected by antibodies from group II and not affected at all by antibodies from groups III or IV. The binding of antibodies from group II to E2 was not affected by the presence of antibodies from any other group. Antibodies from group III were unaffected by the presence of antibodies from group I and either strongly inhibited, 30 or in the case of CBH-4G binding in the presence of CBH-7, stimulated by the presence of antibodies from group III. HMAb CBH-17 did not influence the binding

of any of the other antibodies. Thus the eleven HCV HMabs defined four relatively distinct antibody binding sites within HCV E2.

Currently there is no efficient culture system for the propagation of HCV. When HCV structural proteins are expressed in mammalian derived cells the 5 proteins are usually retained intracellularly. Recently, however several groups have reported the successful expression of HCV E2 on the surface of mammalian cells. Since HCV E2 expressed on the surface of cells might more closely mirror the structure of HCV E2 on the surface of infectious virions, we expressed the extracellular domain of HCV 1b E2 (amino acids 384-661) in a the pDisplay vector. 10 The HCV E2 sequences were expressed in-frame with the transmembrane domain of platelet derived growth factor receptor (PDGFR). The signal sequence at the carboxy terminal of the HCV E1 protein was replaced with the murine IgK leader sequence. Strong linear epitopes from influenza virus hemagglutinin (HA) and c-myc are located immediately in front and behind the HCV sequences, respectively. The 15 expected molecular weight of the HCV 1b construct sf1b (expressing amino acids 384-661 of HCV 1b E2) was 42 KD, prior to glycosylation. Two different immunoreactive proteins were produced by the sf1b-E2 cell line when protein expression was analyzed by Western blot. The first is a relatively discreet band migrating at 68-70 kdal. This species was efficiently purified by affinity chromatography with GNA lectin and is an intracellular form of E2 with mannose-rich carbohydrate chains. The second immunoreactive protein is a heterogeneous smear, which ranged in size from 70 to 98 kD. This species was not efficiently purified by GNA lectin chromatography and is assumed to have complex carbohydrate chains and be the major species present on the surface of the cells. 20 DNA sequencing confirmed cloning of the expected insert with no frame shifts or terminations.

The HCV E2 construct sf1b-E2 was introduced into CHO cells and a cell line expressing the protein was obtained. The sf1b-E2 expressing cells were then combined with the HCV HMabs or control antibodies, and the ability of the 30 HMabs to bind to cell-surface expressed HCV E2 was determined. When stained with the monoclonal antibody to the HA epitope, a strong signal was obtained from

greater than 95% of the cells. No specific signal was obtained from the parent CHO cells nor was any signal obtained with the sf1b-E2 expressing cell line and control antibody. The HCV HMAbs CBH-2, CBH-7, and CBH-4B all exhibited staining of the sf1b-E2 cell line that was equivalent to that observed with the HA epitope. In 5 contrast the HMAbs CBH-11 and CBH-17, although also reactive with the cell surface expressed E2 protein, exhibited 10 fold reduced staining relative to the other HMAbs (Table 7). Thus 9 of the 11 HCV HMAbs reacted strongly with cell-surface expressed E2 protein, and two of the HMAbs exhibited significant reductions in reactivity when E2 was expressed on the cell surface.

Table 7: Reactivity of HCV HMAbs with intra & extracellular E2 proteins

HMAb	Sf-1b	pDN-411	pDN-447	pDN-470	pDC-644	pDC-579
	GNA ¹	Flow ²	GNA	Flow	GNA	Flow
CBH 2	++	338	+	-	+	-
CBH 8E	++	408	+	-	+	-
CBH 5	++	546	++	17	2	28
CBH 8C	++	282	++	-	++	-
CBH 11	++	43	++	-	++	-
CBH 7	++	303	++	19	26	14
CBH 4G	++	175	++	++	++	-
CBH 4B	++	241	++	17	21	9
CBH 4D	++	173	++	++	+	++
CBH 17	++	23	+	++	++	-
HA	++	375	++	42	++	40
c-myc	++	68	++	++	++	++
R04	-	3	-	2	-	2

¹Results in GNA capture assays are expressed as ++ strongly positive (OD > 0.5), + positive (~ OD 0.1 to 0.5), - negative.

²Mean Fluorescence obtained with 10 ug/ml of indicated HMAb staining CHO cells permanently expressing the sf1b-E2 construct.

³Mean Fluorescence obtained with 10 ug/ml of indicated HMAb staining HEK-293 cells transiently transfected with the indicated HCV E2 constructs. A blank cell indicates the HMAb was not tested by flow cytometry.

Next we were interested in localizing the regions of HCV E2 that contained the binding sites recognized by antibodies from the four different groups. To that end deletions were made from the amino terminal and carboxy terminal ends of 5 sf1b-E2. One of the deletions pDN411 removed the hypervariable region of HCV sf1b-E2. The other deletions removed larger portions from the amino or carboxy terminals of sf1b-E2. The deleted E2s were then re-cloned into the vector pDisplay, which allows for the cell surface expression of inserts. HCV E2 deletion constructs expressing sequences from genotype 1b and the H isolate of HCV 1a were 10 constructed (SEQ ID NO: 28-35) (Figure 23). The expression of the E2 deletion constructs was verified by transfection into HEK-293 cells followed by Western blot analysis of cytoplasmic extracts using a monoclonal antibody to the HA epitope (Figure 24). No reactivity was observed with a control antibody to a CMV protein (data not shown). As seen with sf1b-E2, both a faster migrating discreet band and a 15 slower migrating heterogenous smear were observed with all constructs. Similar results were obtained with sfH1a-E2 and pDNH-411 (data not shown). DNA sequencing confirmed that each of the constructs expressed the expected sequences with no frame shifts or terminations.

Therefore, the HCV E2 deletion constructs were transfected into HEK-293 20 cells, cytoplasmic extracts prepared, and intracellular forms of E2 captured onto microtiter plates using GNA lectin. The reactivity of the HCV HMAbs with the GNA captured E2 was then determined. As expected, all of the HCV HMAbs reacted with sf1b E2 protein and none reacted with proteins captured from extracts of mock-transfected HEK-293 cells (Figure 25). Also all of the HCV HMAbs were 25 strongly reactive with E2 produced by pDN-411, indicating that the epitopes recognized by the HMAbs did not include HVR-1. Next, the same panel of antibodies was tested against the extracellular domain of HCV E2 derived from strain H both with (sfH1a-E2) (SEQ ID NO: 29) or without (pDNH-411) HVR1 (SEQ ID NO: 30). HCV HMAbs CBH-8C and CBH-11 did not recognize either 30 sfH1a-E2 or pDNH-411, suggesting that the epitopes recognized by these two HMAbs were mutated in strain H derived E2 protein. Significant reductions in the reactivity of HMAbs CBH-2, CBH-8E , and CBH-5 with strain H E2 protein were

also noted. These HMAbs retained reactivity with the HVR1 construct pDNH-411, confirming that the epitope recognized by these HMAbs was outside of HVR1. The other HCV HMAbs and control antibodies exhibited equivalent reactivity with the strain H derived E2 proteins and the genotype 1b E2 proteins. Thus nine of the 11 5 HCV HMAbs recognized an epitope conserved between sf1b-E2 and sfH1a-E2.

Further deletion of amino acids 384-446 (pDN-447) (SEQ ID NO: 31) or 384-469 (pDN-470) (SEQ ID NO: 32) from the sequences of sf1b-E2 abrogated the reactivity of all Group I HMAbs (CBH-2, -8E, -5, -8C, and -11). Also rat MAb 3/11 which was previously determined to recognize a linear epitope consisting of amino 10 acids 384 to 445 of HCV E2 was non-reactive with pDN-447 and pDN-470. In contrast, HCV HMAbs of group II, III, and IV retained their reactivity with both constructs. PDN-447 and pDN-470, indicating that the epitopes recognized by HMAbs from these groups were located in the central to carboxy terminal regions of HCV E2. Finally, E2 proteins with deletions in the carboxy terminal region were 15 evaluated with the HCV HMAbs. All of the HCV HMAbs, except for CBH-17, were reactive with E2 proteins expressing amino acids 384-644 of HCV E2 (pDC-644) (SEQ ID NO: 33). In contrast, none of the HCV HMAbs were reactive with constructs expressing amino acids 384-579 of HCV E2 (pDC-579) (SEQ ID NO: 34). The rat MAb 3/11 retained reactivity with both carboxy terminal deleted E2 20 proteins as did MAbs to the HA or c-myc epitopes. Thus deletion of HCV E2 sequences between amino acids 644 to 579 is sufficient to abrogate reactivity of all 10 HCV HMAbs that recognize conformational epitopes.

Use of the GNA assay confirmed reactivity of the HCV HMAbs with the intracellular forms of the deletions. To verify the reactivity of the HCV HMAbs 25 with the cell surface expressed E2 of the same deletion constructs the binding of the HMAbs with cells expressing the E2 deletion constructs was evaluated by flow cytometry. Constructs were evaluated with CBH-5 from HMAb group I, CBH-7 of HMAb Group III, and HMAb CBH-4B of HMAb group III. Control antibodies included rat MAb 3/11 and HA. Representative results with E2 deletion constructs 30 pDN411 and pDN447 are presented in Figure 25. Results with all of the E2 deletions are included in Table 7. Because the E2 deletions were introduced into the

HEK-293 cells via transient transfection only about 50-60% of the cells took up plasmid and expressed E2 proteins. Thus the geometric means of the fluorescence observed are notably reduced relative to those obtained with the cloned CHO cell line. Nevertheless, results obtained with HMAbs CBH-5, CBH-7, and CBH-4B by 5 flow cytometry were in complete concordance with the results of the GNA capture assay (Table 7). Thus HMAbs from groups II and III recognize epitopes located between amino acids 470 to 644 of HCV E2. HMAbs from group I recognize an epitope located between amino acids 411-644 of HCV E2.

10

Example 9

High levels of antibodies that can neutralize HCV infection are rare in HCV infected individuals

PATIENTS AND METHODS

Patients. Sera evaluated were from individuals undergoing nucleic acid testing to 15 confirm or follow up a diagnosis of hepatitis C infection between 1991 and 1999. All individuals were being seen for their hepatitis at clinics in the San Francisco bay area. The subjects were positive for HCV RNA by polymerase chain reaction, negative for the presence of hepatitis B virus surface antigen, genotyped, and not receiving antiviral therapy at the time the sample was obtained. Demographic 20 information was obtained from medical records and included age, sex, date of diagnosis, previous interferon therapy, alanine transaminase (ALT) value, and potential route of exposure. The majority of the subjects reported at least one risk-factor for HCV infection. Not all information was available from all subjects. Liver biopsies, when performed, were scored using the histologic activity index (HAI). 25 Genotype analysis was performed using the InnoLIPA assay according to manufacturer's instructions (Innogenetics, Leuven, Belgium). HCV viral load determinations were performed with the COBAS Amplicor HCV monitor kit (Roche molecular systems, Alameda, CA). HCV negative control sera were obtained from plasma of blood donors to the Stanford Medical School blood center, and were 30 negative for the presence of transfusion-transmitted viruses by standard antibody-based screening assays.

E2 Antibody Screening of HCV sera. Monolayers of HeLa cells were grown to 80% confluence and infected with HCV E2 expressing vaccinia virus. Twenty-four hours after infection cells were harvested and extracts were prepared as described (Hadlock *et al.*, 2000). ELISA assay for HCV E2 reactivity were performed as outlined below. Microtiter plate wells were coated with 500 ng of purified *Galanthus nivalis*, lectin in 100 ml of PBS for 1 hour at 37° C. Wells were then washed with TBS and blocked by incubation with BLOTTO (TBS plus 0.1% Tween-20, 2.5% normal goat sera, 2.5% non fat dry milk). Plates were washed and each well received 15 ml HCV E2 containing extract diluted in BLOTTO. After 10 incubation for 1.5 hours at 25 ° C, wells were washed with TBS followed by addition of increasing dilutions of sera from HCV infected or uninfected individuals diluted in BLOTTO. After incubation for 30 minutes biotinylated test HMAb was added to a final concentration of 2 mg/ml. The plates were incubated for 1.5 hours at 25 ° C, wells were washed three times with TBS and 100 ml of streptavidin-AP 15 conjugate added for 1 hour at 25 ° C. Wells were washed 4 times with TBS followed by incubation with PNPP. Substrate development was allowed to proceed for 30 minutes, then the absorbence of the wells at 405 nm was determined using a multiwell plate reader.

For each dilution of competing serum the optical density (OD) reading 20 obtained was compared to the OD obtained from wells without competing antibody. The resulting percentages of bound antibody were plotted versus the dilution and employed to calculate the dilution of sera that resulted in 50% inhibition of test HMAb binding. Sera that did not achieve 50% inhibition were assigned a titer of 40, which was less than the lowest dilution tested. Individuals evaluating sample 25 seroreactivity were blinded to the viral load and clinical status of the samples they were testing. Statistical analysis was performed using InStat and Prism software packages (Graph Pad Software Inc, San Diego, CA).

RESULTS

30 In this study, sera from HCV-infected individuals were evaluated for the presence of antibodies capable of inhibiting the binding of CBH-2 and CBH-7 to

HCV E2. Human monoclonal antibodies CBH-2 and CBH-7 were purified and biotinylated, and the dilution of serum that resulted in 50% inhibition of CBH-2 or CBH-7 binding to a genotype-matched E2 protein was determined. Sera from HCV-negative individuals were used to measure nonspecific binding and to establish a 5 cutoff value. Sera from HCV-infected individuals were considered positive for the presence of competing antibody if 50% or greater inhibition of E2 binding was obtained at a dilution of 1/200 or greater (Figures 26 and 27). Among 74 sera from HCV-infected individuals positive for viral RNA, 35 (47%) were positive for antibodies inhibiting CBH-2 binding, and 32 (43%) were positive for antibodies 10 inhibiting CBH-7 binding (Figures 28 and 29). Fifteen sera (20%) were negative for the presence of antibodies that inhibited both CBH-2 and CBH-7. Nineteen (27%) individuals has high titers (>1/1000) of antibodies that inhibited binding of CBH-2 or CBH-7 (see Table 8). These individuals had a significantly reduced median viral load (2.4×10^6 vs. 4.7×10^6 , $p=0.035$), but were not otherwise different than other 15 HCV infected individuals. Thus, most HCV infected individuals are characterized by low levels of serum antibodies with putative neutralization activity. Individuals with low levels of CBH-2 or CBH-7 like HMAbs can be identified using a simple inhibition assay. Therapeutic use of HCV-neutralizing human monoclonal antibodies, such as CBH-2 and CBH-7, has the potential to be of value in these 20 individuals.

Table 8: Distribution of CBH-7 inhibitory titers in HCV Sera

Characteristic	N / Value	CBH'2 / CBH'7 Inhibitory Titer	
		< 1000	> 1000
HCV Sera	74	55 (73%)	19 (27%)
Genotype 1a/1b	36	26 (72%)	10 (28%)
Genotype 2a/2b	38	29 (76%)	9 (24%)
Male / Female	47 / 26	35 / 19	12 / 7
Age	Median (N) Range	45 (54) 31 - 70	48 (20) 40 - 73
Years HCV + estimated	Median (N) Range	5.0 (31) 0.5 - 28	5.0 (13) 1 - 32
Previous Interferon	18	14 (78%)	4 (22%)
Viral Load (GEq / ml)	Median (N) Range	4.7 x 10 ⁶ (36) 1.8 x 10 ⁴ - 2.5 x 10 ⁷	2.4 x 10 ⁶ (16) 1.1 x 10 ⁵ - 6.7 x 10 ⁶
ALT	Median (N) Range	97 (43) 19 - 4480	124 (15) 26 - 301
Disease Severity (HAI)	Median (N) Range	7.5 (31) 1 - 11	7.0 (11) 3 - 13
Cirrhosis	9	8 (86%)	1 (14%)

* Significantly different than <1000 group, p=0.035. Significance testing was performed using the Mann Whitney test.

Example 10**Preparation of HCV E1 and E2 antigens as screening targets and generation of human monoclonal antibodies targeting HCV E1 protein****MATERIAL AND METHODS**

5 **Cell lines and Reagents.** HEK-293 cells were maintained in Dulbecco's modified minimal essential medium (DMEM) (GIBCO, Grand Island, N.Y.) supplemented with 10% fetal calf serum (GIBCO) and L-glutamine (2 mM) (GIBCO) in 5% CO₂. CHO- K1 cells were maintained in Ham's F12 medium supplemented with 10% fetal calf serum and L-glutamine (2 mM) Clinical serum samples containing HCV 10 viruses in different genotypes were collected by Dr. Gish. Oligonucleotide primers were synthesized by IDT (Corlville, IA).

15 **Antibodies and Patient sera.** Monoclonal antibody to the influenza hemagglutinin (HA) epitope was raised in rat and obtained from Roche Diagnostics (Indianapolis, IN). Monoclonal antibody to HCV E1 (HCM-E1) was obtained from Austral Biologicals (San Ramon, CA). Monoclonal antibody to the c-myc epitope was obtained from Santa Cruz Biotechnology (Santa Cruz, CA). Eight HCV plasma samples were obtained from blood donors who tested positive for the presence of HCV using standard antibody-based screening assays. Genotype analysis was performed using the 20 InnoLIPA assay according to manufacturer's instructions (Innogenetics, Leuven, Belgium). Sixteen additional HCV 1b plasma samples were obtained from individuals undergoing nucleic acid testing to confirm or follow up a diagnosis of hepatitis C infection between 1996 and 1998. The subjects were positive for HCV RNA by polymerase chain reaction, negative for the presence of hepatitis B virus surface antigen, HCV genotyped, and 25 not receiving antiviral therapy at the time the sample was obtained. Genotype analysis was performed using the InnoLIPA assay according to manufacturer's instructions (Innogenetics, Leuven, Belgium). HCV negative samples consisted of plasma from blood donors to the Stanford Medical School Blood Center, and were negative for the presence of HCV, hepatitis 30

B virus, human immunodeficiency virus and human T-cell lymphotropic virus type1 by standard antibody-based screening assays.

HCV RNA isolation, amplification, and plasmid construction. HCV RNA was isolated from human serum (genotype 1b) using the PureScript (Gentra systems, Minneapolis, MN) according to manufacture's instruction. The reverse transcription of HCV RNA was performed with random primers and RT (Perkin-Elmer, Norwalk, Conn.) according to manufacture's protocol at 42⁰C for 30min. Fragments of HCV E1 or E2 were amplified by PCR (*pfu*, Stratagene) from cDNA with appropriate oligos flanked with *Bgl* II or *Pst* I restriction sites. All plasmids were constructed using standard procedures (Maniates *et al.*, 1982). The parent plasmid pDisplay (Invitrogen, Carlsbad, CA) contains sequences encoding the murine Ig kappa chain V-J2-C signal peptide and the platelet-derived growth factor receptor transmenbrane domain (PDGFR-TM) with multiple cloning sites in between with transcription driven by the CMV promoter. *Bgl* II and *Pst* I cloning sites were used to generate HCV E1 and E2 plasmids where the ORFs are inframe with sequences encoding hemagglutinin A and *myc* epitopes. Plasmid #38 containing the HCV E2 sequence was constructed by inserting E2 fragments corresponding to amino acids 384 – 661 into *Bgl* II and *Pst* I (New England Nuclear, Boston, Mass.) cloning sites. Plasmids 46, 115, 113, 107, 102 and 98 containing HCV E1 of various lengths were generated by introducing E1 fragments corresponding to amino acids 192 – 383, 192 – 370, 192 – 366, 192 – 352, 192 – 340 and 192 – 321 into *Bgl* II and *Pst* I cloning sites. Sequences were confirmed using ABI PRISM Dye terminators cycle sequencing kit (Beckman center, Stanford).

CD81 construct was made using the same method as described above except total RNA was isolated from HEK293. Fragment of CD81 was amplified by PCR (*pfu*, Stratagene) from cDNA with oligos flanked with *Xho* I and *EcoR* I restriction sites. Plasmid CD81 was constructed by inserting the fragment corresponding to nucleotides 239-950 into *Bgl* II and *Pst* I (New England Nuclear, Boston, MA) cloning sites.

Transfection. HEK 293 cells were seeded prior to transfection to reach a cell density of 50-60% confluence by the following day. Transient transfection was performed using PerFect Lipids™ (Invitrogen) according to manufacturer's protocol. For 6-well plate transfection, a mixture of 5 ug DNA and lipid (Pfx-2) at 1:6 ratio (w/w) in serum-free medium was used. Cells were switched to complete medium after 4 hours transfection. Assays for cell surface expression was performed between 24 to 48 hours post-transfection. EGFP (Clontech, Palo Alto, CA) was used as an internal control for transfection efficiency.

10 **Creation of Stable Cell Line (Drug Selection).** CHO-K1 cells at 50-60% confluence one day after plating were transfected with PerFect Lipid Pfx-8™ (Invitrogen) according to manufacturer's protocol. For 100 mm plate transfections, 29 ug DNA was mixed with Lipid Pfx-8 at 1:6 ratio (w/w) in serum-free Ham's F12-K medium and added to cells. After 5 hours, the cells were switched to 15 complete medium. After incubation overnight at 37°C in 5% CO₂, selection medium consisting of complete medium plus G418 (Gibco BRL, Rockville, MD) at 450 ug/ml was used to replace the complete medium. After 2 weeks in selection medium, the numerous selected clones were harvested as one population. Subsequently, cells were replated in 100 mm plates with selection medium at 20 various cell densities to enhance the growth of well isolated clones. Ten days later, isolated clones were transferred to 24-well plates by standard technique (Ausubel, Current Protocols in Molecular Biology 2000, John Wiley & Sons INC.) Sterile, 1/8th inch cloning disks (PGC Scientific, Gaithersburg, MD) saturated with equal parts 0.2% trypsin and Versene 1:5000 (Gibco BRL) were placed on top of clones 25 chosen for transfer. After several minutes at room temperature, each trypsin/Versene soaked filter with harvested cells was transferred to a well containing selection medium in a 24-well plate. When cells were nearly confluent, they were harvested, transferred to 12-well plates, and again harvested when nearly confluent. Harvested cells were put onto slides and IFA was performed as described elsewhere. The strongest IFA positive clones were expanded and carried in culture. 30 It was noted that over time the level of protein expression dropped and therefore,

cloning by limiting dilution was done by standard method. Briefly, cells were plated at 5, 2, 0.5 and 0.1 cells/well in multiple 96-well, flat-bottom plates in selection medium. Cells from wells containing single clones were transferred to 24-well plates, grown to near confluence and harvested for IFA staining as above. The 5 strongest IFA positive clones were also tested by flow cytometric analysis using standard methods as described below. In summary, cells were stained with CBH-5 and CBH-4G at 10 ug/ml, two anti-E2 HCV human monoclonal antibodies as primary antibodies and with FITC goat anti-human IgG (H & L chain) (Jackson Immunoresearch Laboratories, Inc., West Grove, PA) as secondary antibody. One 10 of the strongest positive clones, designated 38-19/5G3, was expanded for assays and has continued to express high levels of HCV E2 protein for several months.

Western blotting. HEK-293 cells were grown on six well tissue culture plates and transfected with various HCV E1 constructs as described above. Twenty-four hours 15 later the cells were washed with PBS and resuspended in 0.5 ml of lysis buffer (150 mM NaCl, 20 mM Tris pH 7.5, 0.5% deoxycholate, 1.0% Nonidet-P40, 1 mM EDTA, 0.5 mg/ml Pefabloc (Boehringer Mannheim, Indianapolis, IN), 2 μ g/ml Aprotinin, 2 μ g/ml Leupeptin, and 1 μ g/ml Pepstatin). Nuclei were pelleted by centrifugation at 18,000 x g at 4°C for 10 minutes and resulting cytoplasmic extracts 20 were combined 1 to 1 with 2X sodium dodecyl sulfate polyacrylamide electrophoresis sample buffer (SDS-SB; 20% glycerol, 10% β -mercaptoethanol, 4.8 % SDS, 0.125 mM Tris pH 6.8). Alternatively, 24 hours after transfections cells were washed with PBS, resuspended in 100 μ l of PBS to which 100 μ l of 2X SDS-SB was added. Proteins were denatured via heating to 95°C for five minutes 25 followed by sodium dodecyl sulfate polyacrylamide electrophoresis (SDS-PAGE) in 12% polyacrylamide gels of 20 μ l aliquots of the denatured extracts.

Flow Cytometry. Transient transfected cells were removed from the wells or flasks with Versene 1:5000 (Gibco BRL), washed with staining solution (PBS with 1% 30 FCS and 0.1% sodium azide) and suspended at about 10(10^6) cells/ml. Various dilutions of test antibody in a total volume of 100 μ l of staining solution were

combined with 10^6 viable transfected or control cells resuspended in 100 μ l of staining solution, and incubated at 4°C for 45 minutes. All dilutions and washes were done in staining solution. Primary test antibodies utilized were anti-HA (Boehringer-Mannheim), anti-E2 (Austral Biologicals) all at 5 μ g/ml plus control antibodies anti-T7 RNA polymerase (Novagen, Madison, WI) and purified whole rat IgG (Jackson ImmunoResearch Laboratories, Inc.) both at 10 μ g/ml. After adding an additional 3 ml of staining solution, the cells were pelleted by centrifugation for 10 minutes at 500 x g at room temperature. The pellet was reserved and resuspended in 100 μ l of FITC conjugated goat-anti human IgG diluted 1 to 50 in staining solution. After 45 minutes at 4°C, 3 ml of staining solution was added and the cells were pelleted as above. Second step antibodies included R-phycoerythrin (R-PE) conjugated anti-rat, anti-mouse, and anti-human IgG (H+L) (all from Jackson ImmunoResearch Laboratories). Surface expression of target antigens was analyzed on a FACSCalibur flow cytometer (Becton-Dickinson, San Jose, CA). The cells were then resuspended in 1 ml of fixative solution (3.8% formaldehyde in PBS) and the amount of HMAb bound to the surface of cells was analyzed on a Becton-Dickinson FACS Vantage flow cytometer (Becton-Dickinson, San Jose CA).

Immunofluorescence assay. HEK-293 cells were transfected with various HCV E1 constructs, as described above and were fixed onto HTC Super Cured 24-spot slides (Cel-Line Associates, Newfield, NJ) with 100% acetone for 10 minutes at room temperature. Fixed cells were incubated with between 3 to 5 μ g/ml purified monoclonal antibodies or human serum diluted 1 to 40 in PBS for 30 minutes at 37°C. Slides were then washed for 5-10 minutes with phosphate buffered saline (PBS), pH 7.4 and incubated for 30 minutes at 37°C with 0.001% solution of Evan's blue counterstain and appropriate fluorescein isothiocyanate (FITC) conjugated secondary antibody (Jackson Immunoresearch laboratories, West Grove, PA). Bound antibody was detected by fluorescence microscopy employing a Zeiss Universal microscope.

RESULTS

Construction of HCVE1 and E1E2 recombinant proteins. Since HCV cannot be reliably propagated *in vitro*, we used differential binding of antibodies to

5 mammalian cells expressing HCV E1 and E2 envelope proteins to screen antiE1 antibodies from donor plasma. Typically, mammalian cells expressed HCV E1 proteins are in a more native conformation when they expressed on the cell surface. A map of the structural proteins of the HCV genome indicating protein sequences expressed by the HCV constructs employed in these studies is presented in Figure 10 30. A series of amino and carboxyl-terminal deletion mutations of the E1& E2 gene were synthesized by PCR and fused to the 3' end of the sequence encoding hemagglutinin A and the 5' end of the sequence encoding *myc* epitopes. Sequences were confirmed by sequencing. The plasmid vector pDisplay (Invitrogen, Carlsbad, California) contains sequences encoding the murine Ig kappa chain V-J2-C signal 15 peptide and the platelet-derived growth factor receptor transmembrane domain (PDGFR-TM). Expression of the constructs were confirmed by Western blot and cell surface expression of the constructs were confirmed by flow cytometric analysis after each plasmid was transient transfected into HEK 293 cells.

HCV sequences were amplified from plasma obtained from an individual 20 infected with HCV genotype 1b. DNA sequencing of the E1 region (Figure 31) revealed 92% identity at the amino acid level with the sequence of the HPCJ491 isolate of HCV 1b (2) and 81% identity with the sequence reported for the HCV 1a strain H (Ogata et al., Proc. Natl. Acad. Sci. USA (1991) 88:3392-3396), on which a majority of previous studies of HCV E1/E2 expression and processing have been 25 performed (Cocquerelet al., *J. Virol.* (1999) 73:2641-2649.; Deleersnyder et al. *J. Virol.* (1997) 71: 697-704.; Dubuisson et al., *J. Virol.* (1994) 68:6147-6160; Duvet et al., *J. Biol. Chem.* (1998) 273: 32088-32095; Flint et al., *J. Virol.* (1999) 73:6782-6790; Flint et al., *J. Gen. Virol.* (1999) 80:1943-1947; Meunie et al., *J. Gen. Virol.* (1999) 80: 887-896). The E1 sequence contained five potential N-linked 30 glycosylation sites and a sixth site with the sequence NWSP, which has been previously demonstrated to not be glycosylated (Meunie et al., *J. Gen. Virol.* (1999)

80: 887-896). The internal hydrophobic domain (amino acids 265 – 287) and the carboxy terminal hydrophobic domain (amino acids 354 – 377) can clearly be identified.

The vector pDisplay was employed to express six constructs E1-321, E1-340, E1-352, E1-366, E1-370, and E1-383 that expressed HCV amino acids 192-321, 192-340, 192-352, 192-366, 192-370, and 192-383, respectively. All HCV sequences were expressed in-frame with the transmembrane domain of platelet derived growth factor receptor (PDGFR, see Table 9). Constructs E1-321, E1-340, and E1-352 excluded the carboxy terminal hydrophobic domain of E1; the other constructs included all or part of it (Table 9). The signal sequence at the carboxy terminal of the HCV capsid was replaced with the murine IgK leader sequence. Strong linear epitopes from influenza virus hemagglutinin HA epitope and c-myc epitope are located immediately at N-terminus and C-terminus of the HCV sequences, respectively. All of the constructs were DNA sequenced and contained the expected inserts with no frame shifts or terminations.

Table 9. Characteristics of HCV E1 constructs

Construct	Leader ¹			HCV E1 ²			TM Domain ³			Protein ⁴			
	IgK	HA	Link	Fus Pep	Gly (N)	TM (AA)	E1 (AA)	PDGFR	Lin k	My c	TM	Total AA	Calc MW
E1 321	21	9	7	+	5	-	130	4	10	53		234	25
E1 340	21	9	7	+	5	-	149	4	10	53		253	28
E1 352	21	9	7	+	5	-	161	4	10	53		265	29
E1 366	21	9	7	+	5	14	175	4	10	53		279	30
E1 370	21	9	7	+	5	18	179	4	10	53		283	31
E1 383	21	9	7	+	5	31	192	4	10	53		296	32

1> Indicates presence and size (in amino acids) of IgK signal peptide (METDTLLLWVPGSTGD), hemagglutinin (HA) epitope (YPYDVPDYA), and linker amino acids

2> Indicates presence of putative E1 fusion peptide (Flus. Pep., (Flint, M., Thomas, J.M., Maidens, C.M., Shotton, C., Levy, S., Barclay, W.S., and McKeating, J.A. (1999). Functional analysis of cell surface-expressed hepatitis C virus E2 glycoprotein. *J. Virol.* 73:6782-6790), number of N-linked glycosylation sites (Gly), size of the carboxy terminal transmembrane domain (- = not present or number of amino acids), and total size (in amino acids) of E1 portion of construct.

3> Indicates presence and size (in amino acids) of linker sequence, c-my epitope (EQKLISEEDL), and PDGFR transmembrane domain (AVGQDTQEVTYVPPHSILPFKVVVVISALLAVVLTISLLTLLWQKKRPR).

Indicates total size of protein produced by construct and calculated molecular weight (in kdal) of non-glycosylated protein.

Characterization of HCVE1 and E1E2 recombinant proteins.

Protein expression analysis. Human embryonic kidney (HEK-293) cells were transfected with each of the HCV E1 pDisplay constructs or HCV E1 vector alone as negative control. After 24 hours, cytoplasmic extracts were prepared and equivalent aliquots were fractionated by SDS PAGE and blotted onto nitrocellulose and Western blotted analyzed upon overnight incubation with 1 µg/ml of the HCM-E1 murine monoclonal antibody to HCV 1a E1 protein (Figure 32, panel A). Similar results were obtained with a rat monoclonal antibody to the influenza hemagglutinin (HA) epitope. All of the E1 constructs produced multiple immunoreactive bands that migrated with an apparent molecular weight of between 40 to 46 kd. No reactive proteins were observed in cells transfected with the vector alone. Nor were any of the constructs reactive with a control monoclonal antibody that recognized a CMV protein (data not shown). The observed sizes were approximately 12-15 kd larger than the sizes predicted from the amino acid composition of the protein suggesting that the proteins were heavily glycosylated. Surprisingly, the largest of the constructs, E1-383 had the smallest apparent molecular weight of approximately 38 kd. A previous report also indicated that HCV E1 constructs ending at amino acid 384 could migrate faster than shorter constructs (Fournillier-Jacob et al., *J. Gen. Virol.* (1996) 77: 1055-1064). Alternatively, the E1-383 construct may have undergone proteolytic cleavage at or near glycine 383, the site of cleavage between HCV E1 and E2 when the two proteins are expressed co-linearly (Dubuisson et al. *J. Virol.* (1994) 68:6147-6160; Lanford et al. *Virology* (1993) 197:225-235; Matsuura et al. *Virology* (1994) 205: 141-150; Ralston et al. *J. Virol.* (1993) 67:6753-6761; Spaete et al. *Virology* (1992) 188: 819-830).

Glycosylation of HCV E1 constructs. To confirm the presence of glycosyl moieties, HEK-293 cells were transfected with the E1 constructs and cultured for 24 hours in the presence or absence of tunicamycin, which inhibits the initial step of N-linked glycosylation (Kornfield and Kornfield *Ann. Rev. Biochem.* (1985) 54:631-664). HEK-293 cells were transfected with pDisplay vector or the indicated HCV

E1 construct and grown in the absence or presence of 2 μ g/ml tunicamycin. Twenty-four hours post transfection whole cell extracts were prepared and aliquots were fractionated by SDS-PAGE and blotted onto nitrocellulose. HCV E1 protein was detected by Western blot analysis after overnight incubation with 1 μ g/ml HA 5 rMAb to the HA epitope. (Figure 33, panel B).

E1 constructs produced in the absence of tunicamycin had molecular weights of 40 to 46 kd, as above, although the expression of multiple immunoreactive bands was less noticeable with the HA monoclonal antibody. Inhibition of glycosylation resulted in the appearance of reactive proteins with molecular weights of 25 to 32 kd 10 for E1-321, E1-340, E1-352, E1-366, and E1-370, which were in good agreement with the predicted molecular weights of the predicted unglycosylated forms of 25, 28, 29, 30 and 31 kd of the five constructs respectively (Table 9). In the absence of tunicamycin, E1-383 was poorly expressed and had an apparent molecular weight of approximately 38 kd. In the presence of tunicamycin, no unglycosylated protein 15 was detectable for construct E1-383. This result indicates that the non-glycosylated E1-383 might be unstable.

Cell surface expression of HCV E1 constructs. The ability of the HCV E1 and E1E2 constructs to be expressed on the cell surface was determined by FACScan 20 analysis. HEK-293 cells were transfected with the HCV E1 or E1E2 constructs. Twenty-four hours post-transfection the cells were harvested, incubated with various monoclonal antibodies and the amount of cell surface staining determined by flow cytometry. Transfection efficiency was monitored by co-transfection of cells with a plasmid expressing green fluorescent protein (data not shown).

Figure 33 shows a FACScan analysis of E1 recombinant proteins expressed 25 in HEK293 cells transfected with E1 deletion constructs. The x axis shows fluorescence intensity and the y axis shows the number of fluorescing cells. HEK293 and R04 (anti-CMV) represent fluorescence obtained in the absence of 30 specific primary antibody. A shift of the area to the right side indicates protein expression on the cell surface. The marker (M1) was used to indicate the range (0-

100%) of fluorescence considered above background. The recombinant peaks were detected with HCM-E1 murine MAb.

As shown in Figure 33, only background levels of staining were observed with a control antibody R04 (anti-CMV). With the mouse HCV E1 antibody (HCM-E1 mMAb) to the recombinant E1 proteins, high levels of cell surface expression were obtained with the constructs E1-321, E1-340, E1-352 and E1-366. An intermediate level of surface expression was seen with the constructs E1-370, no cell surface expression was observed with E1-383. The transfection efficiency obtained with all constructs was similar (~40%) thus suggesting that the reduced levels of cell surface expression seen with E1-370 and E1-383 were not due to variations in transfection efficiency. In addition, intracellular expression of the constructs as measured by fixed cell immunofluorescence was comparable (Figure 34).

15 Immunoreactivity to E1 human antibodies in HCV positive serum. Having achieved significant cell surface expression with 5 of 6 E1 constructs, the immunoreactivity of the E1 constructs with a panel of sera from individuals infected with genotype 1 HCV was evaluated (Table 10). HEK-293 cells were transfected with each of the E1 constructs and fixed onto glass slides for IFA. The approximate transfection efficiency was determined by incubating the fixed cells with HA 20 monoclonal antibody.

Figure 34 shows representative IFA data with HCV serum. HEK293 cells transfected with the indicated constructs or untransfected HEK293 cells were fixed onto slides with acetone and stained with rat monoclonal antibody to HA at 5 mg/ml or an HCV serum at dilution 1:50. Slides were counterstained with 0.001% solution of Evan's blue counterstain and bound antibody was detected with fluorescein isothiocyanate (FITC) conjugated goat-anti-human or anti-rat IgG. Strong staining was observed in approximately 50% of the transfected cells for each of the constructs. No staining was observed with eight sera from HCV negative blood donors with any of the E1 constructs (Table 10). When cells transfected with the E1 25 constructs were tested with sera from HCV 1b infected individuals at a dilution of 1

to 40, a moderate level of positive staining was observed. Staining obtained with a representative serum is presented in Figure 34.

One of the sera had strong reactivity to non-transfected HEK-293 cells (Table 10). Five of the six HCV E2 constructs were reactive with 54 to 71% of the HCV 1b sera tested (Figure 35 ADDED). Construct E1-383 was the least reactive at 33% (8 of 24 sera). Excluding E1-383, reactivities of the E1 constructs with HCV genotype 1 antisera are comparable to the reactivity observed in a study using secreted E1 protein (Gane et al. *Transplantation*. (1999) 67: 78-84.). E1-352 was selected as an antigen for E1 HMAbs screening since it showed highest reactivity (71%) to HCV positive sera.

Selection of the blood donor for HCV E1 HMAbs screen. Among the 17 HCV 1b positive sera tested (Table 10), donor HC29 showed high titer serum antibodies to HCV E1 constructs. Peripheral blood B-cells were isolated from this individual and successfully used to generate HCV E1 antibody secreting human hybridomas.

Table 10 Summary. Reactivity of HCV Sera with E1 constructs

Sera	N	HEK 293 ^a	E1-321	E1-340	E1 352	E1 366	E1 370	E1 383
HCV 1b	17	1	12	13	14	12	13	8
HCV 1a	7	0	2	2	3	1	2	0
Total HCV	24	1 (4%)	14 (58%)	15 (63%)	17 (71%)	13 (54%)	15 (63%)	8 (33%)
HCV Neg	8	0	0	0	0	0	0	0

20 Indicates number of positive sera (%). A serum was considered positive if greater than 5% of the transfected cells were judged to exhibit clear immunofluorescence, similar to that exhibited by the HCV 1b serum of Figure 34.

25 **Production of antigen-specific human monoclonal antibodies.** Having achieved significant cell surface expression with two of the E1 constructs, the larger protein, E1-352, was employed to evaluate the seroreactivity of HCV infected individuals to

E1. Accordingly, the plasmid expressing E1-352 was introduced into HEK-293 cells and a cell line expressing E1-352 was obtained. The E1-352 expressing cells were then fixed onto glass slides for Indirect Fluorescence Assay (IFA). The reactivity of the cells with a panel of sera from blood donors, which were found to be PCR positive for HCV genotype 1, was determined. Eleven out of 23 (48%) blood donors with HCV genotype 1 infection were reactive with the E1-352 protein. This contrasted with zero out of eight HCV negative blood donors and six out of nine (67%) patients with HCV hepatitis. The donor with the strongest antibody response to E1-352 (Figure 34, panel HCV 1b) was used as the source of peripheral B cells for hybridoma isolation. Accordingly, a second aliquot of blood was obtained from this individual and both plasma and mononuclear cells were isolated. The donor was an asymptomatic, 51 year old, Hispanic male who was not aware of his HCV status prior to the donation. Testing of a second sample drawn 11 months later confirmed that the donor retained a strong antibody response to E1-352.

15 Peripheral B cells were then isolated, activated with Epstein Barr virus, and cultured for 16 to 30 days. IFA with E1-352 expressing cells resulted in the identification of 7 out of 417 wells (~2%) with antibodies to E1-352. EBV activated cells ($2-13 \times 10^5$) from the 7 E1-reactive wells were then fused to K₆H₆/D5, a mouse-human heteromyeloma fusion partner, at a ratio of 1 EBV-activated cell : 2 K₆H₆/D5 cells in hypo-osmolar (125 L3 or 180 L3), or iso-osmolar (300 L3) fusion medium. 20 Two hybridomas were isolated that, after cloning, secreted 1 to 80 ug human IgG per ml. Both antibodies were strongly reactive with E1-352 by IFA (Figure 36). In the experiments shown in Figure 36, HEK293 cells transfected with E1-3 construct or CD4 construct in the same parent vector were fixed onto slides at a ratio of 1 to 2 with acetone and stained with H-111, H-114, R04 (anti-CMV HMAb) at 10 ug/ml or rat monoclonal antibody to HA at 5 ug/ml. Slides were counterstained with 0.001% solution of Evan's blue counterstain and bound antibody was detected with fluorescein isothiocyanate (FITC) conjugated goat-anti-human or anti-rat IgG. 25 Hybridoma H-111 expressed an IgG1 (K1) with heavy chain sequencing revealing greatest homology to the VH3-30 germline sequence. Hybridoma 114 (H-114) 30

expressed an IgG1 (K2) whose heavy chain was most homologous with the VH1-3 germline sequence.

Reactivity of E1 HMAbs with HCV envelope proteins. To confirm the results obtained by IFA with fixed cells, the HMAbs H-111 and H-114 were tested for reactivity with various E1 proteins / E1-352 by Western blot and immunoprecipitation assay (Figure 37). HEK-293 cells were mock transfected (0) or transfected with the indicated HCV E1 constructs or pDisplay E2 (optional) and 24 hours post transfection cytoplasmic extracts were prepared. Aliquots of the extracts were then subjected to immunoprecipitation with 5 ug of the H-111 or H-114 HMAb, as described in the Materials and Methods. Bound protein was then eluted with SDS sample buffer and subjected to SDS-PAGE and Western blot. Blotted E1 protein was detected with 2 ug/ml of the ECM E1 murine antibody. For the Western Blot, HEK-293 cells were transfected with the indicated HCV E1 construct or mock transfected. Twenty-four hours post transfection, cytoplasmic extracts were prepared and equivalent aliquots were fractionated by SDS PAGE and blotted onto nitrocellulose. HCV E1 protein was detected by overnight incubation with 5 μ g/ml of HMAb H-111 or H-114.

As shown in Figure 37, HMAb H-111 was strongly reactive with E1-352, E1-340, and E1-321 by both Western blot and immunoprecipitation. HMAb H-114 was strongly reactive with the E1 proteins by Immunoprecipitation but was weakly positive by Western blot. No reactivity was observed with an isotype control HMAb with any of the E1 constructs by Western blot or immunoprecipitation. Thus, HMAb H-111 recognizes a denaturation insensitive epitope within E1-321. HMAb H-114 recognized an epitope within E1-321 that appeared to be partially susceptible to denaturation.

The E1 HMAbs were isolated using an E1 construct that exhibited a significant level of expression on the surface of cells. However, IFA was used to identify the HMAbs; raising the possibility that the HMAbs were specific for intercellular forms of the E1-352 protein. To confirm that the HCV HMAbs also recognized E1-352 on the surface of cells the reactivity of the E1 HMAbs with

HEK-293 cells expressing E1-352 was determined by flow cytometry. Figure 38 shows a FACScan analysis of HCV HMAbs H-111 and H-114 with E1-1 recombinant protein transient expressed in HEK293 cells. The *x* axis shows fluorescence intensity and the *y* axis shows the number of fluorescent cells. R04 (anti-CMV) represents fluorescence obtained in the absence of specific primary antibody. A shift of the area to the right side indicates antibody binding and anti-HA represents HA tag expression as fusion protein. The marker (M1) was used to indicated the range (0-100%) of fluorescence considered above background. The data in Figure 38 indicates that both H-111 and H-114 recognized cell surface expressing E1-352.

Reactivity of HCV HMAbs with HCV envelope protein isolates from multiple genotypes. To test conservation of HMAb epitopes, HCV RNA isolated from various HCV genotypes was reverse transcribed and amino acids 192 - 352 region was amplified and cloned into the pDisplay vector. Recombinant plasmids were transfected into HEK-293 cells and the reactivity of the HMAbs with the constructs was assessed by IFA and confirmed by Western blot analysis. HEK293 cells were transfected with HCV E1 constructs comprising E1 genes cloned from indicated HCV genotypes and analyzed by an immunofluorescence assay (IFA). The protein extracts of the transfected cells prepared twenty-four hours post-transfection were fixed onto slides with acetone and stained with rat monoclonal antibody to HA at 2 ug/ml, HMAbs at 5 ug/ml or an human monoclonal antibody to CMV at 5 ug/ml. Slides were counterstained with 0.001% solution of Evan's blue counter stain and bound antibody was detected with fluorescein isothiocyanate (FITC) conjugated goat-anti-human or anti-rat IgG. Results obtained with the entire panel of E1 proteins are presented in Table 11 and Table 12.

Table 11 Summary Reactivity of HMAs with HCV E1 protein isolates from multiple genotypes

HCV E1 Protein	anti-HA (positive control)	HC-111 (HMAb)	HC-114 (HMAb)	anti-CMV (negative control)
HCV 1b	+++	+++	+++	-
HCV 1a	+++	+++	-	-
HCV 2b	+++	+++	-	-
HCV 2a	+++	-	-	-
HCV 3a	+++	++	-	-
HCV 4	+++	-	-	-

HCVE1 Protein	anti-HA (positive control)	HC-111 (HMAb)	HC-114 (HMAb)	anti-CMV (negative control)
HCV 1b	+++	+++	+++	-
HCV 1a	+++	+++	-	-
HCV 2b	+++	+++	-	-
HCV 2a	+++	-	-	-
HCV 3a	+++	++	-	-
HCV 4	+++	-	-	-

Table 12 HCV positive sera employed in genotype study

Genotype	Serum
HCV 1b	HC-29
	HC-03
HCV 1a	HC-06
	HC-16
	V5704
HCV 2b	V6674
	V3551
	189
HCV 2a	V3402
	V2238
	S0208
	S0223
	2180
HCV-3a	1966
	2255
	S0126
	S0236
	S0159
HCV-4a	S0652

5 The presence of transfected proteins was verified with the HA MAb. Typically between 20 to 40 percent of the cells were positive with the HA MAb. Both HMAbs were reactive with E1 protein isolated from the B cell donor (HC-29). HMAb H-111 was reactive with 17 of the 19 E1 proteins from different infected individuals, including all proteins of genotypes 1a, 1b, 2b, and 3a. HMAb H-111 was not reactive with 10 E1 proteins represent genotype 2a isolated from 5 different infected individuals. Thus the epitope recognized by HMAb H-111 might be mutated in genotype 2a. HMAb H-111 was also non reactive with an E1 protein of genotype 4. HMAb H-114 did not react with any E1 protein except that it was

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isolated against (E1-352) and that of the B cell donor (HC-29). Thus HMAb H-114 expresses an HCV 1b specific epitope.

5 Epitope localization of E1 HMAbs. A series of deletions were introduced into the carboxyl and amino terminals of E1-352 to localize the epitopes recognized by the two HMAbs. The E1 deletion constructs were then transfected into HEK-293 cells and extracts containing the proteins were subjected to Western blot and IFA with HMAbs H-111 and H-114. Expression of the proteins was verified using the HMAb. The results obtained are summarized in Figure 39. HMAb H-111 was reactive all of the carboxy terminal deletion constructs including a construct limited to the amino terminal 20 amino acids of E1-352. In contrast HMAb H-114 was reactive with E1-321 and a construct expressing amino acids 192-313 but not any of the other carboxy terminal constructs. Deletion of as little as five amino acids from the amino terminal of E1-352 was sufficient to abrogate reactivity of HMAb H-111.

10 Thus the epitope of HMAb H-111 was located proximal to the amino terminal of E1-352. In contrast HMAb H-114 was reactive with constructs expressing amino acids 192-313, 199-321, and 206-321, but not constructs expressing amino acids 212-313, 244-313, and 262-313. Thus the epitope of HMAb H-114 is located between amino acids 206 – 313 of E1-352 but could not be further defined.

15

20 **Peptide competition analysis of HMAb H-111 epitope.** The HCV E1 epitope bound by HMAb H-111 (amino acids 192- 211) contains two glycosylation sequences. This epitope is also conserved in many of the HCV subtypes, despite a comparatively high degree of variation in the amino acid sequences of the E1 amino terminal. This raised the possibility that the glycosyl moieties of the E1 amino terminal might be involved in the epitope recognized by HMAb H-111. To address this possibility synthetic peptides comprising the amino terminal 7 and 14 amino acids of HCV E1 were synthesized (Table 13).

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Table 13. Amino acid sequence of the synthetic peptides for epitope binding competition.

Peptide code	Peptide	Amino Acids Sequence
H-111-7	192-198	YEVRNVS
H-111-14	192-205	YEVRNVSGVYHVTN
H-114-12	304-315	CNCSIYPGHHVYVG
H-114-6 N	206-211	DCSNSS

Since the synthetic peptides would not be glycosylated, successful competition for HMAb binding would indicate that glycosylation was not required for antibody binding. E1-352 produced from transfected HEK-293 cells was captured onto microtiter plates using GNA lectin. Then binding of HMAb H-111 was assessed in the presence of increasing amounts of the various synthetic peptides. HEK-293 cells were transfected with E1-352 and E1 glycoproteins were captured onto microtiter plates coated with 500 ng of GNA lectin. Wells were washed and blocked and bound protein was incubated with 10 ug/ml of HMAb H-111 in the presence of increasing amounts (x axis) of control synthetic peptides. μ control HTLV peptide; σ E1 peptide YEVRNVS; ν E1 peptide YEVRNVSGYHVTN). The y axis indicates the mean OD values derived from replicate wells. The error bars indicate one standard deviation from the mean.

In the absence of peptide HMAb H-111 was strongly reactive with GNA captured E1-321 (Figure 40). The addition of an irrelevant peptide from HTLV-1 gp46 had no affect on binding of HMAb H-111 to E1-321. Nor did the 7 amino acid peptide affect binding of HMAb H-111. In contrast, addition of the 14 amino acid peptide resulted in a dose dependent inhibition of binding of HMAb H-111 to E1-321. Thus, the HMAb H-111 epitope does not require glycosylation to be recognized.

Epitope mapping of HMAb H-111 with alanine scanning. To obtain a fine map of the HMAb H-111 epitope on the 14-mer peptide spanning amino acids 192-204 of E1 glycoprotein, we introduced conservative (Alanine) amino acid substitution over 11 positions in this 14-mer competing peptide (position 192-Tyr, 193-Glu, 194-Val, 5 195-Arg, 196-Asn, 197-Val, 198-Ser, 199-Gly, 200-Val, 201-Tyr, and 202-His) (Table 14).

Table 14. Epitope mapping.

Y E V R N V S G V Y H V T N

Constructs	Mutations	IFA & comments		
		HA	H-111	R04
107	E1-352 WT	+	+	--
783	E1-192 Y/A	+	+	--
784	E1-192 Y/A	+	+	--
787	E1-193 E/A	+	+	--
789	E1-193 E/A	+	+	--
792	E1-194 V/A	+	Weak+	--
793	E1-194 V/A	+	Weak+	--
796	E1-195 R/A	+	+-	--
797	E1-195 R/A	+	+-	--
798	E1-195 R/A	+	+-	--
799	E1-195 R/A	+	+-	--
800	E1-196 N/A	+	--	--
801	E1-196 N/A	+	--	--
802	E1-196 N/A	+	--	--
803	E1-196 N/A	+	--	--
804	E1-197 V/A	+	+	--
805	E1-197 V/A	+	+	--
808	E1-198 S/A	+	Weak <5%	--
810	E1-198 S/A	+	Weak <5%	--
811	E1-198 S/A	+	Weak <5%	--
812	E1-198 S/A	+	Weak <5%	--
813	E1-199 G/A	+	Weak <5%	--
814	E1-199 G/A	+	Weak <5%	--
815	E1-199 G/A	+	Weak <5%	--
816	E1-199 G/A	+	Weak <5%	--
886	E1-200 V/A	+	+	--
887	E1-200 V/A	+	+	--
890	E1-201 Y/A	+	--	--
891	E1-201 Y/A	+	--	--
894	E1-202 H/A	+	+	--
895	E1-202 H/A	+	+	--

5 The amino acid sequence of H-111 epitope on E1 glycoprotein is indicated on top of Table 14 in single letter-code. R at position four, N at position five, and Y at position ten are essential amino acids and VSG at positions three, seven and eight are crucial amino acids for HMAb H-111 binding to E1 glycoprotein. Numbers at the mutation site indicate amino acid expressed by each construct and are relative to the entire HCV polyprotein. The reactivity to each protein with the HA mMAb

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(positive control), HMAb R04 (negative control) or the H-111 HMAb by IFA is indicated as positive (+) or negative (-). The mutated E1 was expressed in CHO cells and analyzed by both IFA (Table 14) and Western Blotting (Figure 41) using HMAb H-111, mMAb HA as positive control and R04, which is anti-CMV human monoclonal antibody as negative control. All of the mutants were expressed in CHO cells in approximately equal amounts and at approximate molecular weight of the wild type E1-352 glycoprotein (see Figure . Amino acid substitution occurring at 195-Arg, 196 Asn, and 201-Tyr profoundly affected binding activity of HMAb H-111 to E1 glycoprotein and at 194-Val, 198-Ser, and 199-Gly remarkably weakened binding activity of HMAb H-111 to E1 glycoprotein, but did not completely diminished the binding, indicating that the central region on the 14-mer competing peptide is important for the interaction between antibody and HCV E1 envelope protein. Substitution corresponding to amino acids 192-Tyr, 193-Glu, 197-Val, 200-Val, and 202-His did not affect the binding activity of HMAb H-111 to E1 glycoprotein. These results suggest that epitope for HMAb H-111 consists at least five amino acid residues Val (194), Arg (195), Asn (196), Ser (198), Gly (199), and 201-Tyr, and is within amino acid 194 to 204.

Peptide competition analysis of HMAb H-114 epitope. The two discontinuous HMAb H-114 epitopes, CSIYPGHV at C-terminus and DCSNSS at N- terminus, were defined by deletion mapping presented above, consist of one glycosylation sequence (209-NSS) and two Cysteine residues (Cys-306 and Cys-207) located approximate 100 amino acid apart. This raised the possibility that the glycosyl moieties of the E1 amino terminal might be involved in the epitope recognized by HMAb H-114 and/or intramolecular disulfide bond formation is required for HMAb H-114 epitope recognition. To address these possibilities two synthetic peptides comprising the amino terminal 6 or 12 amino acids of HCV E1 were synthesized (Table 13). Since the synthetic peptides would not be glycosylated, successful competition for HMAb binding would indicate that glycosylation was not required for antibody binding.

Truncated E1-352 and E1 glycoproteins glycoproteins produced from transfected HEK-293 cells was captured onto microtiter plates using 500 ng GNA lectin. Binding of HMAb H-114 was assessed in the presence of increasing amounts of the two synthetic peptides. Specifically, wells were washed and, blocked, and 5 bound protein was incubated with 10 ug/ml of HMAb H-114 in the presence of increasing amounts (x axis) of control synthetic peptides. (Peptide H-114-12-C corresponding to the C terminus region from amino acids 304 to 315 on the E1 glycoprotein and peptide H-114-14-N corresponding to the N terminus region from amino acids 206 to 211 on the E1 glycoprotein). The addition of these two synthetic 10 peptides had no apparent effect on the binding activity of HMAb H-114 to truncated E1-352 protein (Figure 42), nor did control peptide, which correspond to immunodominant region on HTLV-1 gp46. These data indicate that (i) the two 15 discontinuous HMAb H-114 epitopes may require glycosylation to be recognized; (ii) the two discontinuous HMAb H-114 epitopes may not be the antibody binding sites but instead the epitope is between the two epitopes where amino acids spanning from 216 to 303; and (iii) the 108 amino acid sequence defined by the deletion constructs may contain structural features, such as a compact domain or disulfide bonds that are required for presentation of the epitope recognized by HMAb H-114.

20 **Serine or alanine scan of amino and carboxyl terminal regions of HMAb H-114 epitope.** To discriminate between these possibilities a series of serine or alanine substitutions were introduced into amino acids 206 – 211 and 306 – 313. The modified E1s were then transfected into HEK-293 cells and the E1 proteins were captured onto microtiter plates with GNA lectin. The reactivity of HMAb H-114 25 with the bound E1 proteins was then determined by mutational analysis of amino terminal amino acids 206 to 211 or carboxy terminal amino acids 306-313 (Figure 43). HEK-293 cells were transfected with E1 proteins with the substitutions indicated in Figure 43 and E1 glycoproteins were captured onto microtiter plates coated with 500 ng of GNA lectin. Wells were washed and blocked and bound 30 protein was incubated with 5 ug/ml of the HA mMAb (solid bars) or 10 ug/ml of HMAb H-114. Bound antibody was detected with the appropriate alkaline

5 phosphatase conjugated secondary antibody and PNPP substrate. The x axis indicates the signal obtained with each mutant expressed as a percentage of the signal obtained with wild type E1 sequence. The error bars indicate one standard deviation from the mean. To adjust for variation in protein expression that might result from the point mutations, the reactivity of the constructs with the HA MAb was also determined. The signal obtained was compared to that of the unmodified protein E1-321.

10 As shown in Figure 43, substitution of the cysteine residue in the amino terminal sequence DCSNSS specifically abrogated binding of HMAb H-114 but not the HA antibody. In contrast, mutation of the asparagine or serine residues of the glycosylation site NSS resulted in equivalent reductions in signal in both the HA and H-114 antibodies. Thus, the amino-terminal glycosylation site is probably not implicated as contributing to the HMAb H-114 epitope. Similarly, for the sequence 15 CSIYPGHV, mutation of the cysteine residue also abrogated binding of HMAb H-114 without affecting binding of HA. The reason for the stimulation of HA binding by the sequence CSISPGHV is not known. However the binding of HMAb H-114 was unaffected, suggesting that Y-309 is not part of the H-114 epitope.

20 **Binding of HMAb H-114 to E1 is disulfide dependent.** The requirement for two cysteines to maintain the HMAb H-114 epitope, suggests that disulfide bond formation is required for presentation. Under these conditions disulfide bonds should also abrogate HMAb H-114 binding. This was confirmed by pre-treating cell lysates of E1-321 with DTT prior to immunoprecipitation with HMAb H-114 (Figure 44). HEK-293 cells were transfected with E1-321 and 24 hours after 25 transfection cytoplasmic extracts were prepared. Aliquots of the extract were either left untreated or incubated with 5 mM dithiothreitol for 15 minutes at 56°C. Extracts were diluted 1:5 in ice-cold BLOTO and subjected to immunoprecipitation with various antibodies (indicated above lanes). Bound protein was then eluted with SDS sample buffer and subjected to SDS-PAGE and Western 30 blot.

No precipitation of E1-321 was observed with a control HMAb. In the absence of DTT pre-treatment, both HMAbs H-111 and H-114 precipitate a 46 kdal protein that reacts with a monoclonal antibody to E1. After pre-treatment with 5 mM DTT at a temperature of 56 C, binding of HMAb H-111 to E1 is unaffected. In 5 contrast, binding of HMAb H-114 is completely abrogated. Thus the epitope recognized by HMAb H-114 depends on the formation of disulfide bonds that involve C-207 and C-306.

Alanine scanning on internal E1 cysteine residues. E1 glycoprotein contains 8 10 cysteine residues at positions 207, 226, 229, 238, 272, 281, 304 and 306 that could form intramolecular disulfide bonds. Expression of 6 of E1 mutants substituted C to A was analyzed (Figure 45) to determine whether the cysteine residues internal of 207-cys and 306-cys are involved in structure formation of the epitope recognized by HMAb H-114. First, E1 mutants were expressed in CHO cells following 15 transient transfection with the corresponding plasmids and analyzed by IFA. As shown in Figure 45, all mutated proteins were expressed and recognized by a mouse MAb HA targeting the tag epitope as positive control. All mutated proteins were recognized by HMAb H-111 targeting an epitope located between amino acid 192-211 as described above. Among the E1 C/A mutants, 207C, 229C 238C and 304C 20 eliminated essentially all of binding activity of HMAb H-114, while 272C and 281C showed no effect on the binding activity of HMAb H-114 to E1 mutated protein.

Immunoprecipitation analysis of alanine mutations of the HMAb H-114 25 binding site on HCV E1 was performed. HEK-293 cells were transfected with the mutations and 24 hours after transfection cytoplasmic extracts were prepared. Extracts were subjected to immunoprecipitation with HMAb H-114. Bound protein was eluted with SDS sample buffer and subjected to SDS-PAGE and Western blot. Blotted E1 protein was detected with 2 μ g/ml of the ECM E1 murine antibody. As shown in Figure 46, the number on the top of each lane indicates the location of cysteine residues on the E1 glycoprotein that were substituted with Alanine. 30 Migration of molecular weight standards are as indicated at the left. Protein expression was evaluated with HA-tagged expression by Western Blot. These

immnoprecipitation studies confirmed that mutants 207C, 229C 238C and 304C were not able to be detected by H-114, while 272C and 281C showed no effect on the binding activity of HMAb H-114 to E1 mutated protein (Figure 46).

5

Example 11

Antibody Production

The following Example provides a variety of methods by which to produce HCV HMAbs.

Expression and purification of antibody from a plasmid vector. The gene encoding the entire antibody molecule can be amplified from its parent hybridoma by RT-PCT and cloned into a heterologous expression cassette capable of driving expression of the antibody in a constitutive or inducible manner in a eukaryotic cell line. For example, the antibody genes can be expressed in an expression plasmid such as pcDNA3.1 Zeo, pIND(SP1), or pREP8, (all from 10 Invitrogen, Carlsbad, California) and equivalents. Alternatively, the antibody genes can be expressed via viral or retroviral vectors such as MLV based vectors, vaccinia virus-based vectors or Adenovirus-based vectors. Similarly, the antibody genes can be expressed in insect virus vectors such as baculovirus vectors. Other vectors, such 15 as the pCOMB series of vectors allow for expression of an antibody heavy and light chain pair or a single chain antibody on the surface of M13 phage or bacteria.

20

Once expressed, the antibody can be purified using, e.g., protein-A or protein-G sepharose, and the purified antibody can be chemically or enzymatically modified in any of the following ways: biotinylation using, e.g., biotin-C11-hydroxysuccinimide ester; coupling to beads of various formats, e.g., sepharose, 25 agarose, magnetic, polystyrene, through the use of cyanogen bromide; or bridging the antibody to a useful chemical moiety, e.g., by modifying a lysine or other basic residues or through the use of reagents specific for free sulphydryl groups.

Other Embodiments

30 Those of ordinary skill in the art will readily appreciate that the foregoing represents merely certain preferred embodiments of the invention. Various changes

and modifications to the procedures and compositions described above can be made without departing from the spirit or scope of the present invention, as set forth in the following claims.

5 What is claimed is:

CLAIMS

1. An antibody directed to a conformational epitope within amino acids 206 to 313 of the E1 protein of the HCV virus 1b.
5
2. An antibody directed to a linear epitope within amino acids 194 to 204 of the HCV E1 protein derived from multiple HCV genotypes.
3. An antibody directed to the epitope recognized by H-114.
10
4. An antibody directed to the epitope recognized by H-111.
5. A cell line expressing the antibody of claim 1 or claim 2.
15
6. The cell line of claim 5, wherein the cell line is a B cell line.
7. The cell line of claim 5, wherein the cell line is a human cell line.
8. The cell line of claim 5, wherein the cell line is a mammalian cell line.
20
9. The cell line of claim 6, wherein the cell line is a eukaryotic cell line.
10. The cell line of claim 5, wherein the cell line is a hybridoma.
25
11. The cell line of claim 5, wherein the cell line has been transformed with Epstein-Barr virus (EBV).
12. The cell line of claim 5, wherein the cell line has been infected with a virus.
30
13. The cell line of claim 5, wherein the cell line has been infected with a phage.

14. A virus displaying the antibody of claim 1 or claim 2.

15. The antibody of claim 1, 2, 3, or 4, wherein the antibody is a monoclonal antibody.

5

16. The antibody of claim 1, 2, 3, or 4, wherein the antibody is a humanized antibody.

17. The antibody of claim 1, 2, 3, or 4, wherein the antibody is a mammalian antibody.

18. A method of identifying receptors for HCV E1 protein or peptide comprising the steps of:

15 contacting a HCV E1 protein or peptide with an antibody of claim 1, 2, 3, or 4 for a time sufficient for the antibody to bind the HVC E1 protein or peptide;

 contacting a cell expressing a putative receptor for E1 with the HCV E1 protein or peptide and the antibody for a sufficient time to allow binding of the protein or peptide to a putative receptor;

20 detecting binding of the protein or peptide to the cell, a decrease in binding to the surface of the cell compared to binding in the absence of the antibody indicating identification of the receptor as an HCV E1 receptor.

19. A method of identifying receptors for HCV E1 protein or peptide comprising the steps of

25 attaching an antibody of claim 1, 2, 3, or 4 to a solid support;

 contacting the antibody with an HCV E1 protein or peptide for a time sufficient for the HCV E1 protein or peptide to bind to the antibody to form a protein or peptide:antibody complex;

30 contacting the complex with a library of proteins or peptides for a time sufficient for the library proteins or peptides to bind to the complex;

 removing the unbound library proteins or peptides from the complex;

identifying the library proteins or peptides that are bound to the complex, the bound library proteins or peptides being putative HCV E1 receptors.

20. A pharmaceutical composition comprising the antibody of claim 1, 2, 3, or 4
5 and a pharmaceutically acceptable excipient.

21. A pharmaceutical composition comprising a combination of two or more monoclonal antibodies, wherein the antibodies are directed to E1 and E2 proteins of HCV.

10

22. The pharmaceutical composition of claim 21, wherein the antibodies are directed to E1 and E2 proteins of a single HCV genotype.

15

23. The pharmaceutical composition of claim 21, wherein the antibodies are directed to E1 and E2 proteins of multiple HCV genotypes.

24. The pharmaceutical composition of claim 21, wherein the antibodies are directed to linear epitopes.

20

25. The pharmaceutical composition of claim 21, wherein the antibodies are directed to conformational epitopes.

26. The pharmaceutical composition of claim 21, wherein the antibodies are directed to linear and conformational epitopes.

25

27. The pharmaceutical composition of claim 21, comprising H-111 and CBH-5.

28. The pharmaceutical composition of claim 21, comprising H-111 and CBH-7.

30

29. The pharmaceutical composition of claim 21, comprising H-111 and CBH-4G.

30. The pharmaceutical composition of claim 21, comprising H-111 and CBH-8C.

5 31. The pharmaceutical composition of claim 21, comprising H-111 and CBH-17.

32. The pharmaceutical composition of claim 21, comprising H-111 and CBH-2.

10 33. A method of treating a patient infected with HCV, the method comprising steps of:

providing a patient infected with HCV or susceptible to HCV infection; and administering to the patient the antibody of claim 1, 2, 3, or 4.

15 34. A method of treating a patient exposed to HCV, the method comprising steps of:

providing a patient infected with HCV or susceptible to HCV infection; and administering to the patient the antibody of claim 1, 2, 3, or 4.

20 35. The method of claim 33 or 34, wherein the method comprises administering more than one different antibody.

36. The method of claim 35, wherein the method comprises administering to the patient two or more monoclonal antibodies, wherein the antibodies are directed to 25 E1 and E2 protein of HCV.

37. The method of claim 35, wherein the antibodies are directed to E1 and E2 proteins of a single HCV genotype.

30 38. The method of claim 35, wherein the antibodies are directed to E1 and E2 proteins of multiple HCV genotypes.

39. The method of claim 35, wherein the antibodies are directed to linear epitopes.

5 40. The method of claim 35, wherein the antibodies are directed to conformational epitopes.

41. The method of claim 35, wherein the antibodies are directed to linear and conformational epitopes.

10 42. The method of claim 35, comprising H-111 and CBH-5.

43. The method of claim 35, comprising H-111 and CBH-7.

15 44. The method of claim 35, comprising H-111 and CBH-4G.

45. The method of claim 35, comprising H-111 and CBH-8C.

46. The method of claim 35, comprising H-111 and CBH-17.

20 47. The method of claim 35, comprising H-111 and CBH-2

48. A peptide comprising a conformational epitope of E1 protein of HCV comprising amino acids 206 to 313 of the E1 protein of the HCV virus 1b.

25 49. A peptide comprising an amino acid sequence of HCV, E1 wherein the amino acids are analogous to amino acids 206 to 313 of the E1 protein of HCV 1b.

30 50. A non-HCV protein or peptide comprising amino acids analogous to amino acids 206-313 of HCV 1b E1 protein.

51. The non-HCV protein or peptide of claim 50, wherein amino acids 206-313 of HCV 1b E1 protein are in native conformation.
52. A peptide wherein the peptide is at least 60% identical to a peptide of claim 5 49.
53. A peptide wherein the peptide is at least 70% identical to a peptide of claim 10 49.
54. A peptide wherein the peptide is at least 80% identical to a peptide of claim 49.
55. A peptide wherein the peptide is at least 90% identical to a peptide of claim 15 49.
56. An agent having sufficient three-dimensional structural similarity to conformational epitope of the HCV E1 1b genotype comprising amino acids 206-313 to compete for binding of the epitope to an antibody in the presence of the agent versus in the agent's absence.
- 20 57. The agent of claim 56, wherein the agent is a peptide.
58. The agent of claim 56, wherein the agent is a small molecule.
- 25 59. The agent of claim 56, wherein the agent is a chemical compound.
60. The agent of claim 56, wherein the agent is an organic molecule.
61. The agent of claim 56, wherein the agent is an inorganic molecule.
- 30 62. The agent of claim 56, wherein the agent is a mimotope.

63. A vaccine comprising a peptide fragment of HCV E1 that contains a conformational epitope within amino acids 206 to 313 of the E1 protein of the HCV virus 1b.

5

64. A vaccine comprising a peptide fragment of HCV E1 that contains an epitope recognized by the antibody of claim 1 or 3.

65. A vaccine comprising a peptide fragment of HCV E1 that contains an epitope recognized by a human monoclonal antibody selected from the group 10 consisting of H-114 and H-111.

66. A vaccine comprising the peptide of claim 48.

15 67. A vaccine comprising the agent of claim 56.

68. A vaccine comprising a combination of at least one peptide fragment of HCV E1 that contains an epitope recognized by a human monoclonal antibody and 20 at least one peptide fragment of HCV E2 that contains an epitope recognized by a human monoclonal antibody.

69. The vaccine of claim 68, wherein the peptide fragments are of a single HCV genotype.

25 70. The vaccine of claim 68, wherein the peptide fragments of HCV E1 and E2 are of multiple HCV genotypes.

71. The vaccine of claim 68, wherein the epitopes are linear epitopes on peptide fragments of HCV E1 and E2.

30

72. The vaccine of claim 68, wherein the epitopes are conformational epitopes on peptide fragments of HCV E1 and E2.

73. The vaccine of claim 68, wherein the epitopes are a combination of linear
5 and conformational epitopes on peptide fragments of HCV E1 and E2.

74. The vaccine of claim 68, comprising H-111 and CBH-5.

75. The vaccine of claim 68, comprising H-111 and CBH-7.

10 76. The vaccine of claim 68, comprising H-111 and CBH-4G.

77. The vaccine of claim 68, comprising H-111 and CBH-8C.

15 78. The vaccine of claim 68, comprising H-111 and CBH-17.

79. The vaccine of claim 68, comprising H-111 and CBH-2.

80. A method of classifying patients infected with HCV, the method comprising
20 steps of:

providing serum from a patient infected with HCV;
measuring inhibition by the patient's serum of binding of an anti-HCV monoclonal antibody of claim 1 or 2 to its epitope; and
identifying patient as candidate for administration of a treatment.

25 81. The method of claim 44, the method comprising additional step of:
administering to the patient an antibody.

82. A method of detecting HCV infection, the method comprising steps of:
30 providing an individual;

contacting a body fluid from the individual with an antibody of claim 1 or 2 under suitable conditions for binding of antibody to its antigen; and detecting the binding of an antibody to the peptide.

5 83. A method of identifying the genotype of HCV, the method comprising steps of:

providing an individual;
contacting a body fluid from the individual with at least two antibody of claim 1 under conditions suitable for antibody/antigen binding;
10 detecting binding of antibody to the peptides; and
analyzing the profile of antibody binding to determine the genotype of HCV.

84. The method of claim 82 or 83, wherein the body fluid is blood.

15

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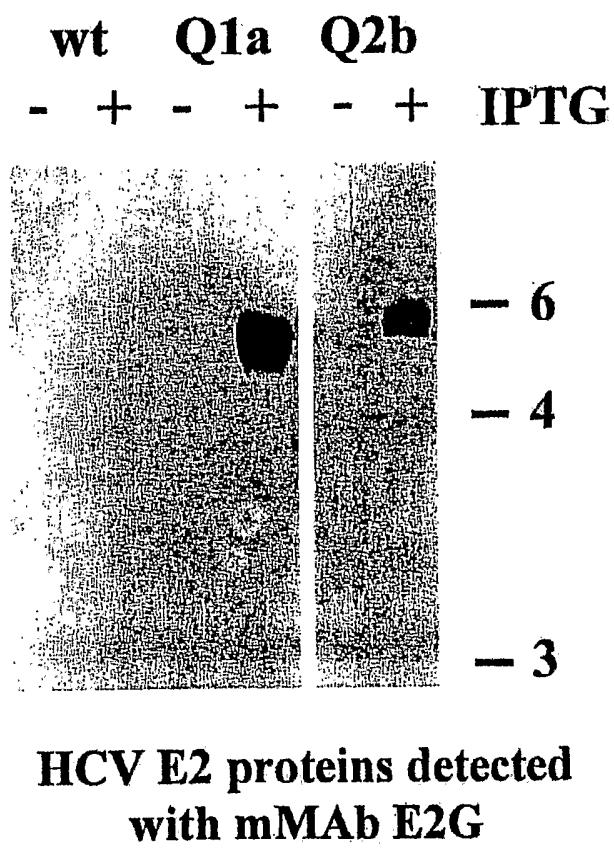


FIG. 1

Sequences amplified from central region of HCV E2 vaccinia virus clones

>hcv-1a3, (Q1a)
 CTCAACTGGATTCAACCAAAGTGTGGAGGGCCCCCTGTGTCAATCGGGAGGGGGCGGG
 CAACAAACACCTT
 GTACTCTCGGTGGCTCCGGTCCCTGGATTACGCCAGGTGGCTGGTc

>hcv-1b8, (Q1b)
 TGGCACAGGTTCACCAAGAACGTTGTTGGGGCCCCCATGTAAACATGGGGGGTGG
 CAATAACACCTT
 TTACACCAAAATGTGGTTGGGGCTTGGCTGACACCTAGGTGGCATAGTt

>hcv-2a-25, (Q2a)
 CTCCCACTGT TTCAACAAAAACTTGGGGCACCCCTGCCGCATCAGAGCTGACTT
 TAATGCCAGCACggacCTGCTGGCCCCACGGACTGTTTCAGGAAGGCATCCTGAAGCCAC
 TTACATCAAATGTGGCTCTGGGCCctgtgacgccaaggccctgtgata

>HCV-2B-1, (Q2b)
 TGGGACTGGGGTTCACTAACAGACATGGGGTGCACCCCTGCCGCATTAGGAGGGACTG
 CAACGGAACCCCTcgacCTATTGTGGCCCCACAGACTGTTCAAGAACCCAGATACTAC
 CTACCTTAAGTGTGGAGGGGGCTTGGTTGACCCCCAAATGCATGGTa

FIG. 2

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Name	Sequences	Sequences	Sequences
HCV-1a	CTCAACTGGA	TTCACCAAAG	TGTGCGGAGC
HCV-Q1a-FR	...G...T...	...T...GA	...G...
HCV-1b	...G...T...	...G...T...	...G...
HCV-Q1b-FR	...G...T...	...GA	...G...
HCV-2a	...A...G...	...GA	...G...
HCV-Q2a-FR	...C...C...	...GA	...G...
HCV-2b	...-T...A...	...CT	...G...
HCV-Q2b-FR	...G...G...	...A	...G...
HCV-1a	CAACACC---	----CTGCACT	GCCCCACTGA
HCV-Q1a-FR	...T...G...	...T...G...	...T...
HCV-1b	...T...G...	...T...AT	...G...
HCV-Q1b-FR	...T...G...	...T...ACT	...G...
HCV-2a	...T...G...	...GACT	...G...
HCV-Q2a-FR	...G...G...	...GACT...TTG	...G...
HCV-2b	...G...G...	...GAC...TG	...G...
HCV-Q2b-FR	...G...G...	...TATC	...A...

FIG. 3A

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Name	Sequences
HCV-1a	CTCTCGGTGC
HCV-Q1a-FR	GGCTCCGGTC
HCV-1b	CCTGGATCAC
HCV-Q1b-FR	ACCCAGGTGC
HCV-2a	CTGGTC
HCV-Q2a-FR	
HCV-2b	
HCV-Q2b-FR	
	+--HCV-2B-1.C
	+----7
	!
	+--hcv-2B,
	! !
	+----6
	!
	+--hcv-2a-25.
	! !
	+----5
	+
	+--4
	! !
	+--HCV-2A,
	! !
	+--hcv-1b8.se
	+----2
	! !
	+--HCV-1B,
	-1 !
	+----3
	! !
	+--HCV-Q1a

One most parsimonious tree found:

FIG. 3B

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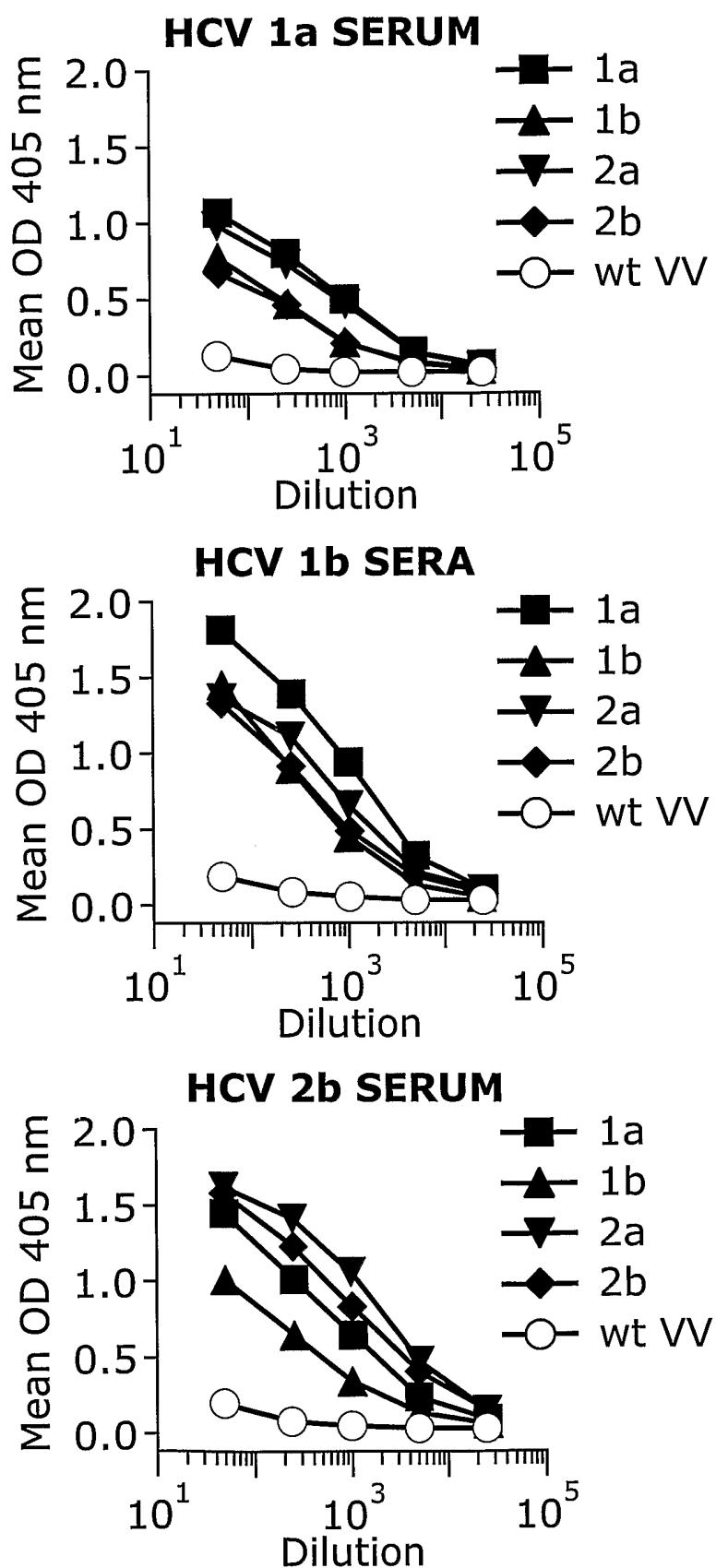


FIG. 4A

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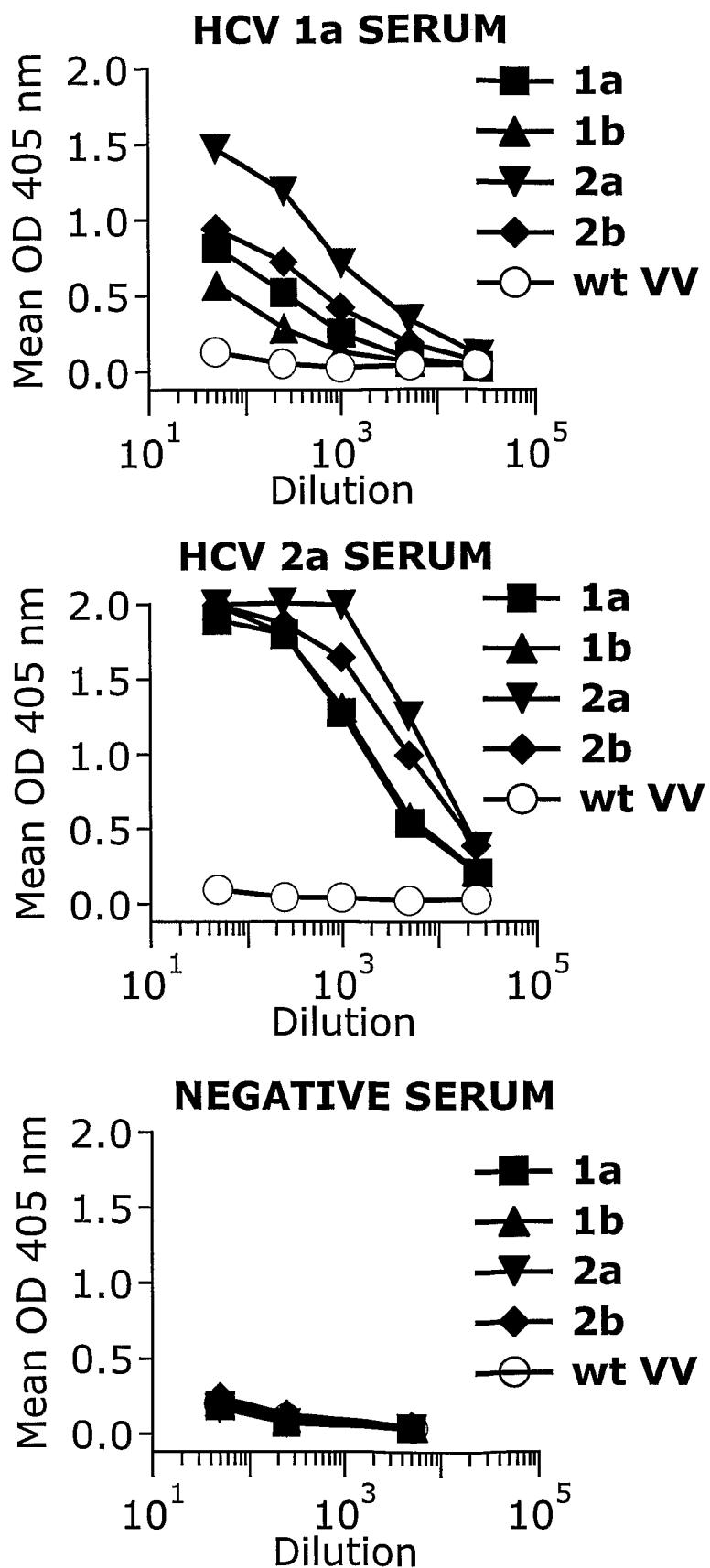


FIG. 4B

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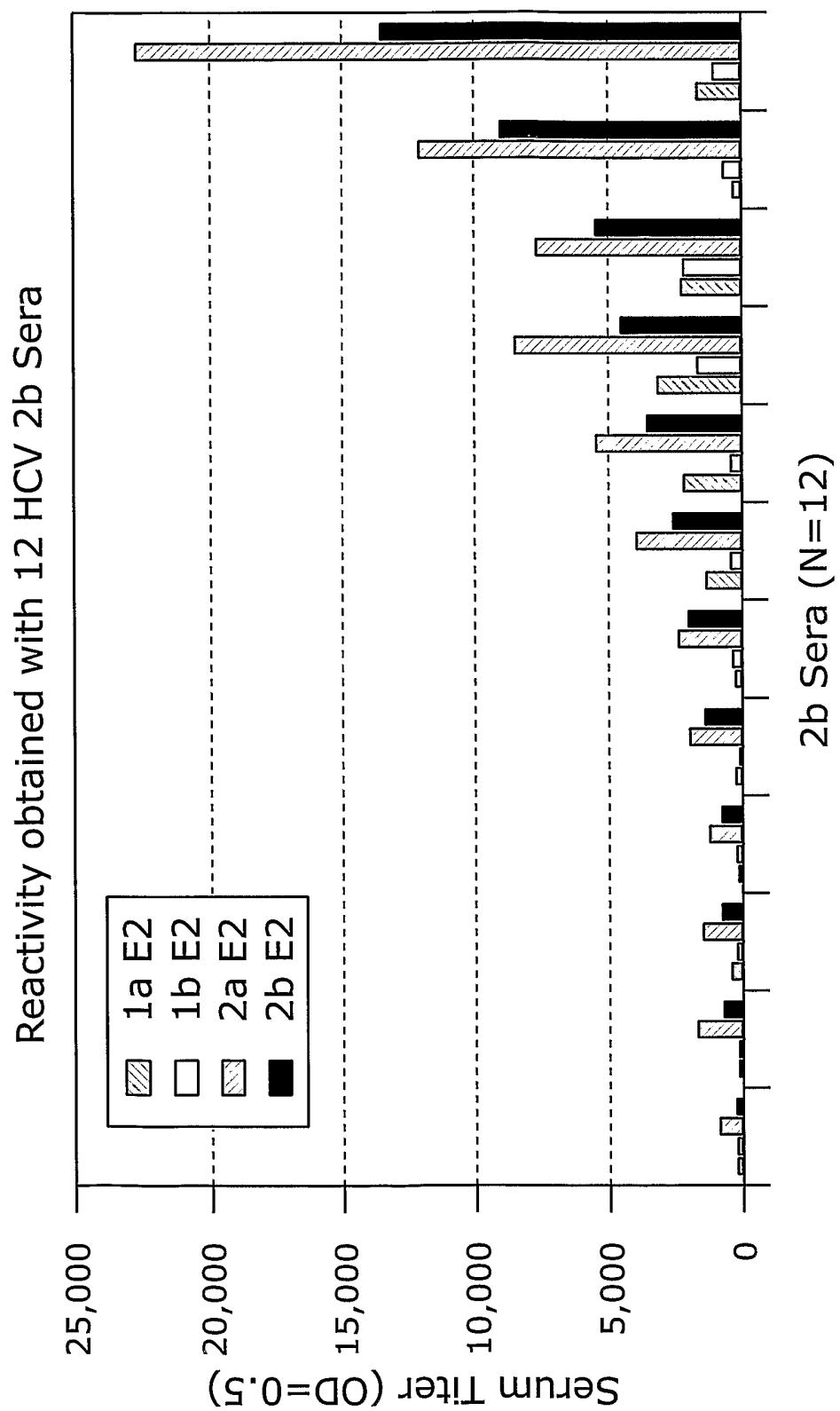


FIG. 5

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Binding Analysis of HCV HMabs

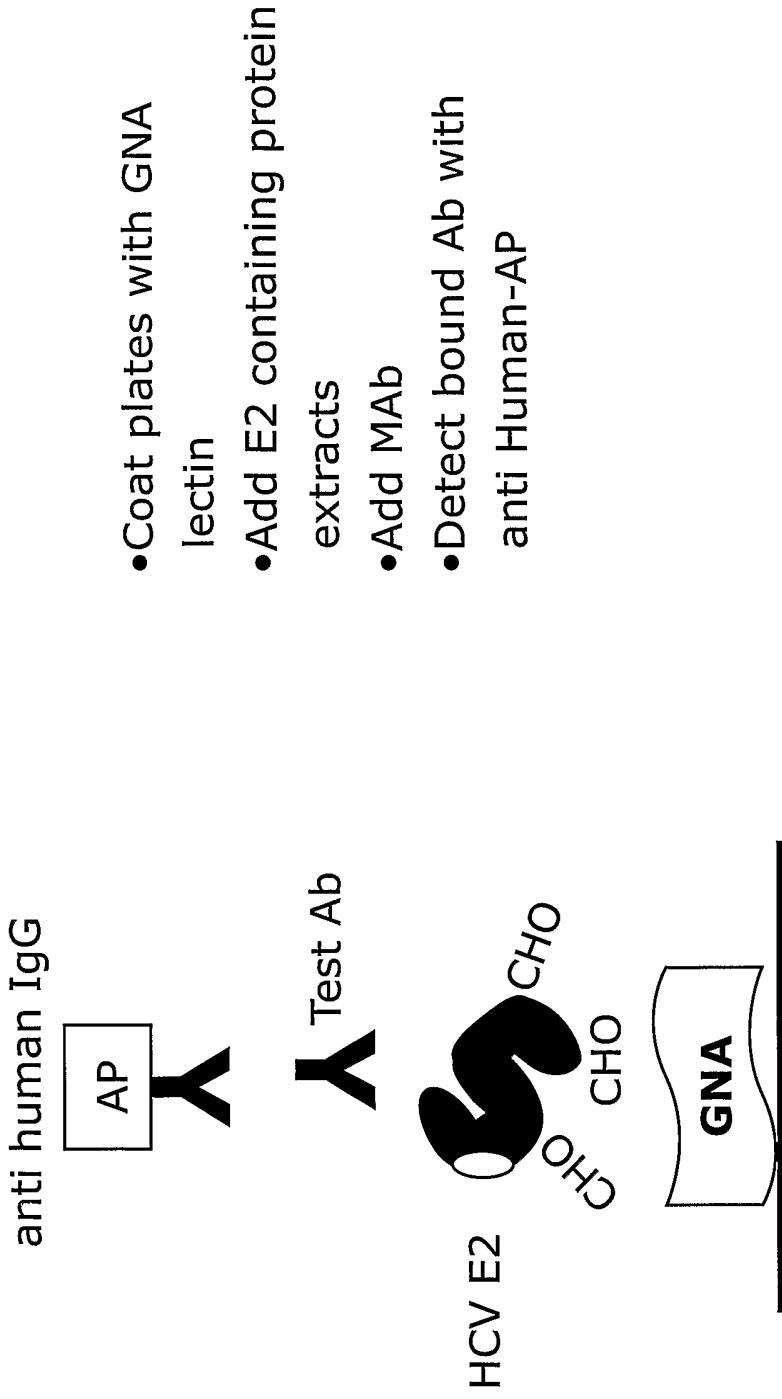


FIG. 6

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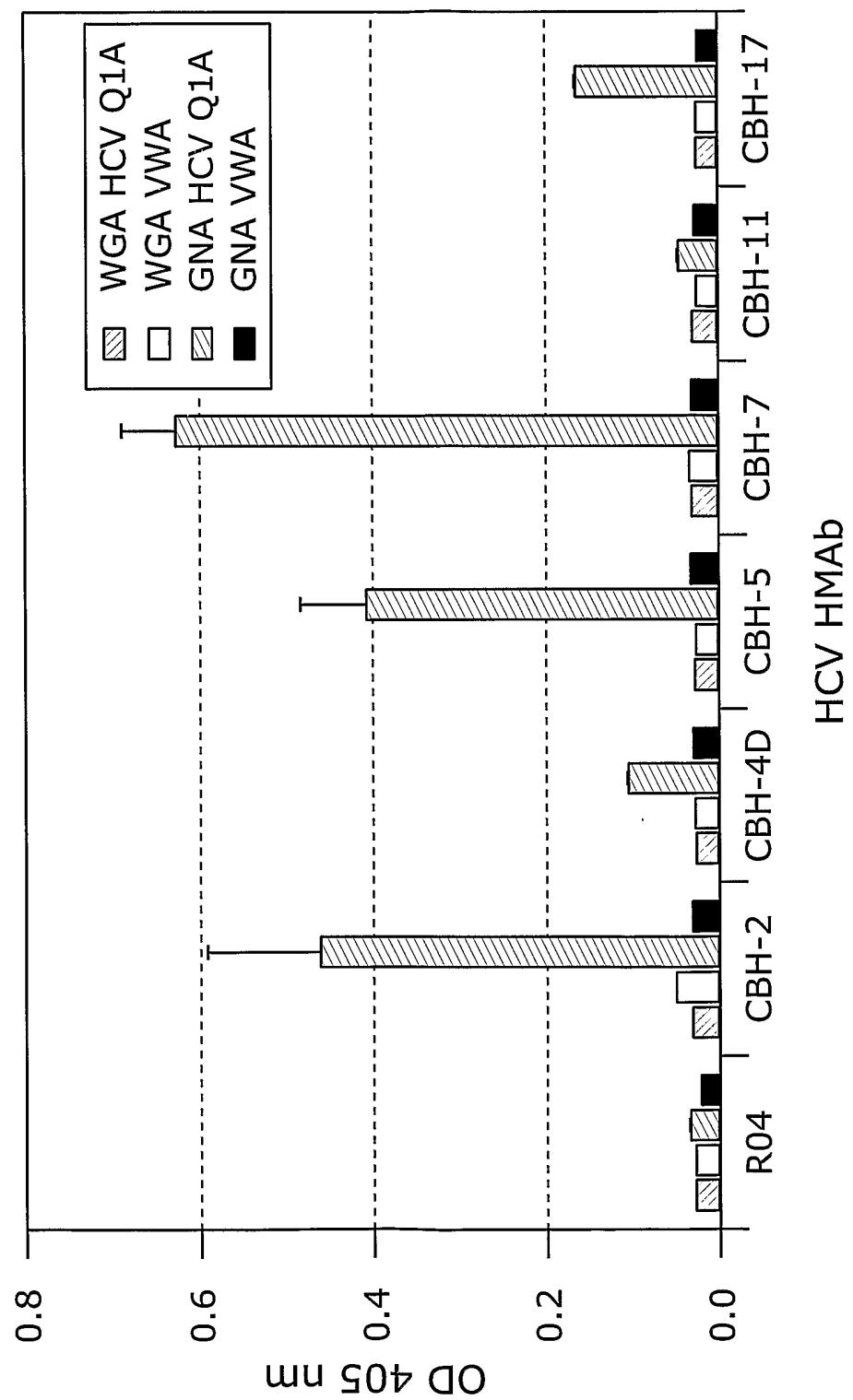


FIG. 7

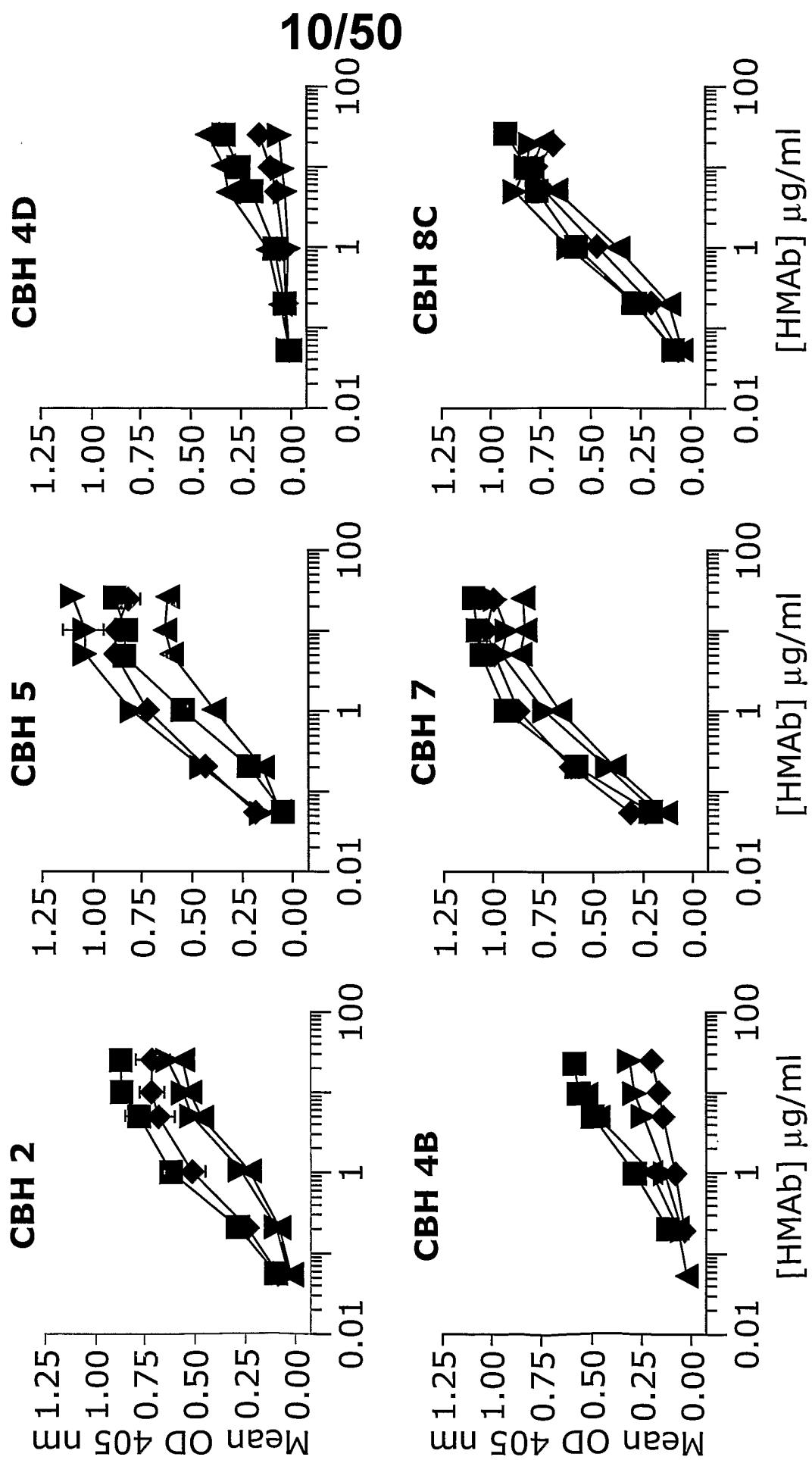


FIG. 8A

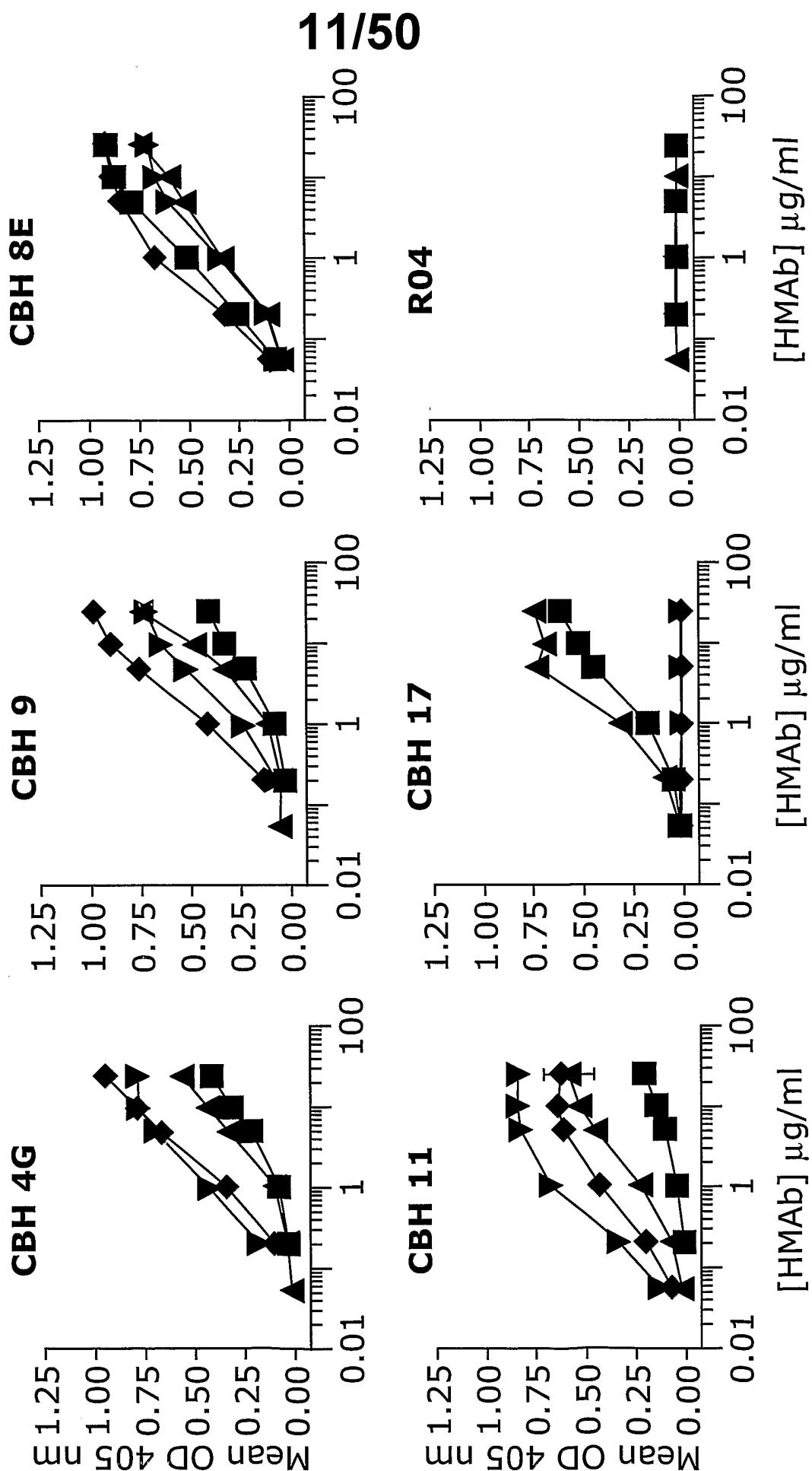


FIG. 8B

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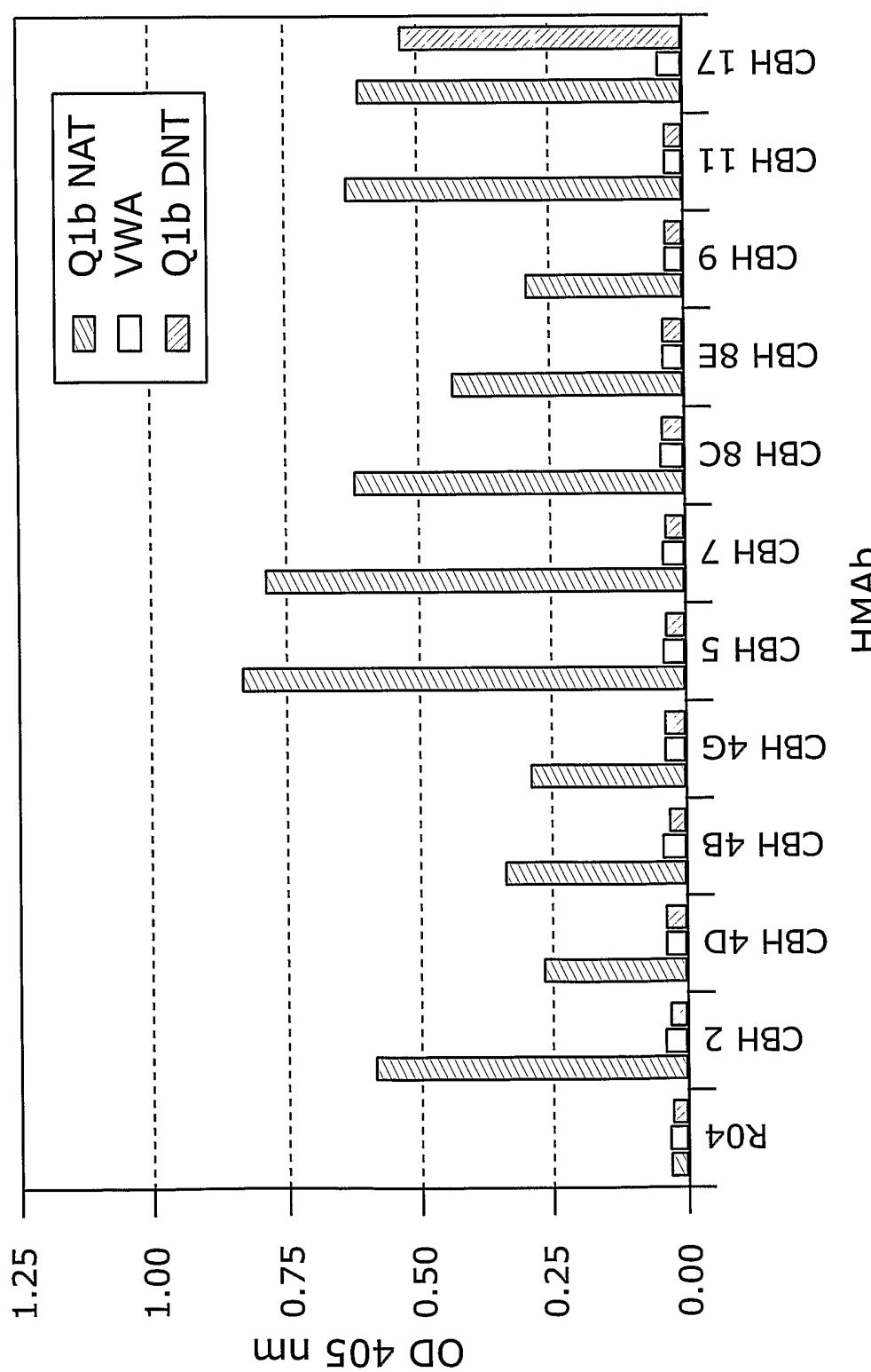


FIG. 9

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Competition Analysis

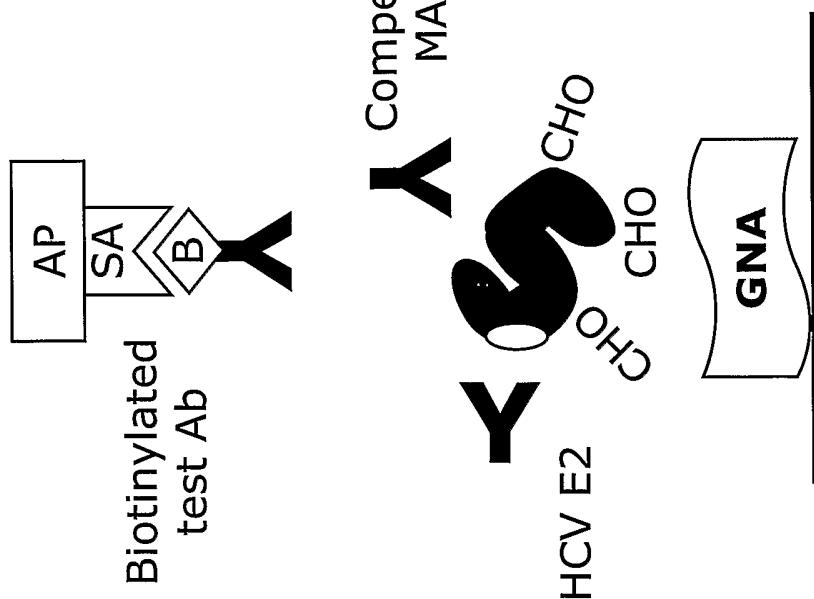


FIG. 10

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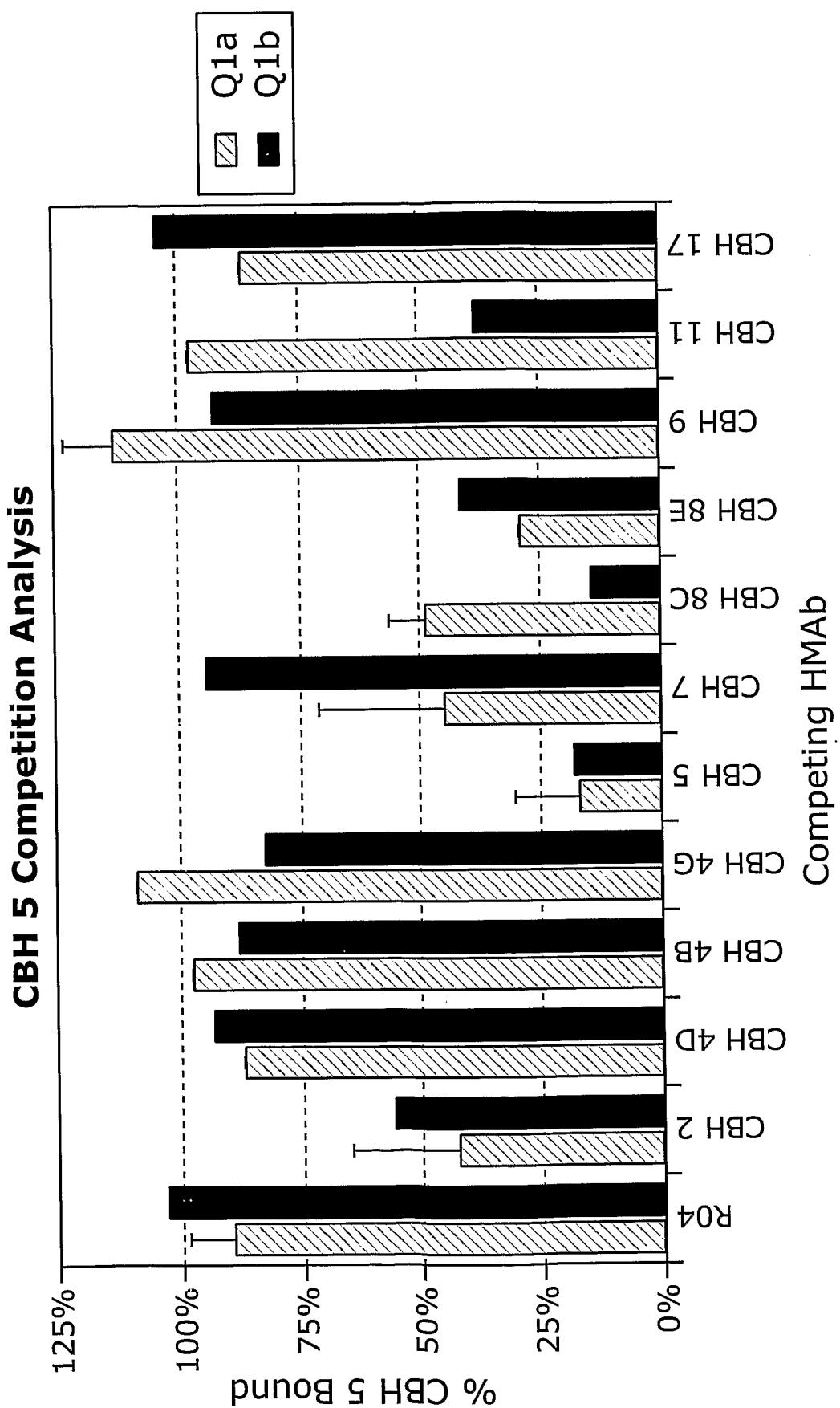


FIG. 11

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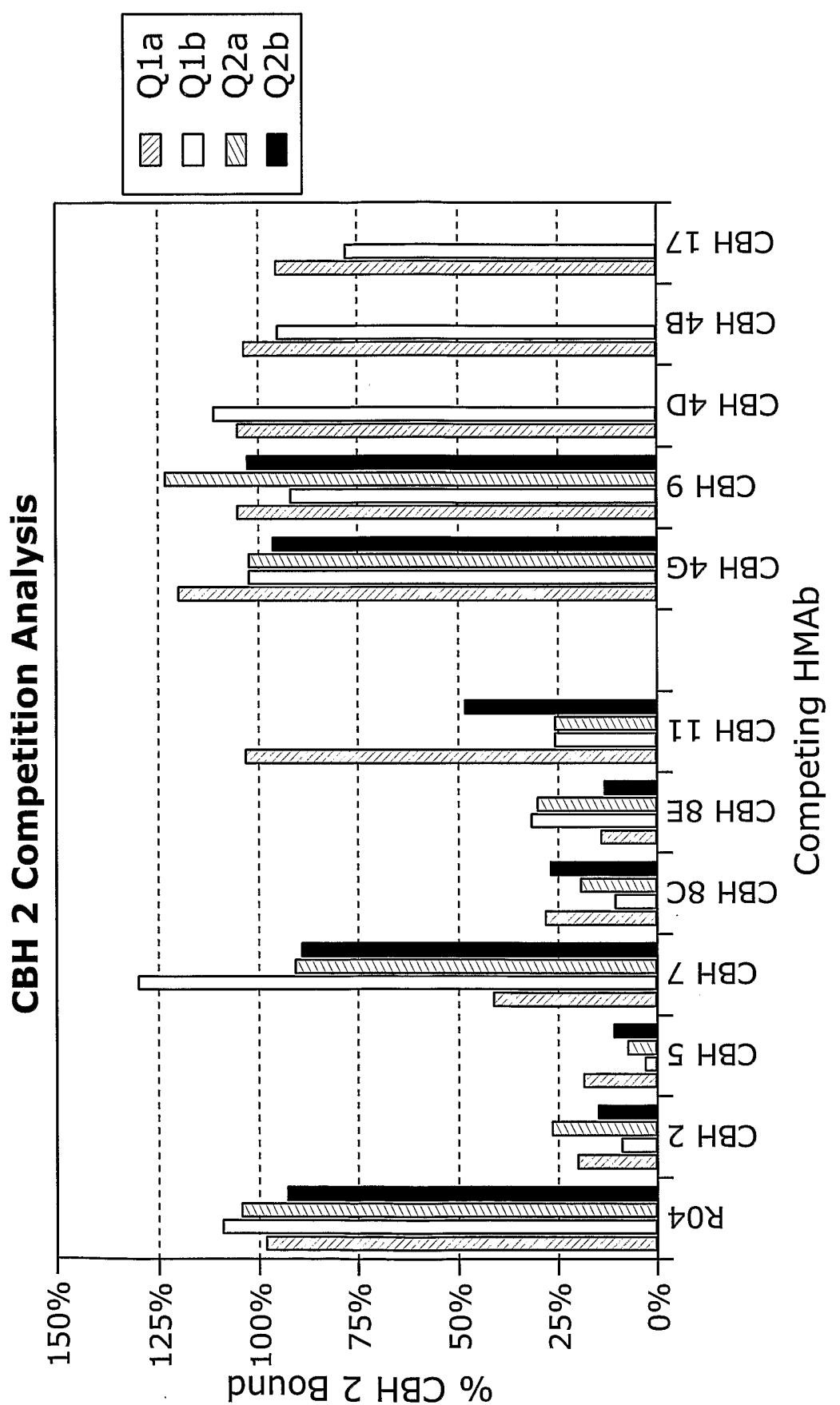


FIG. 12

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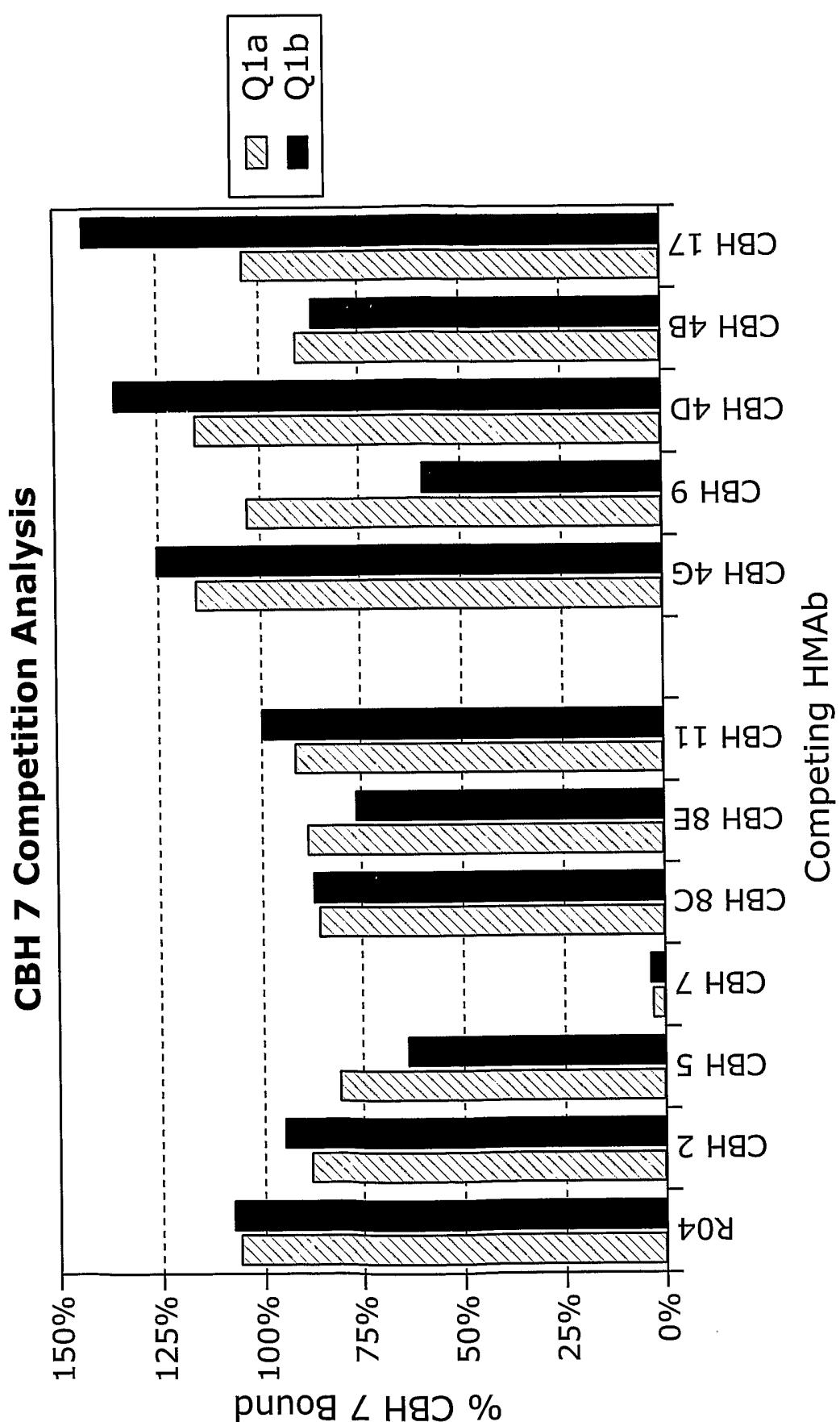


FIG. 13

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Binding to CD81-E2 complex

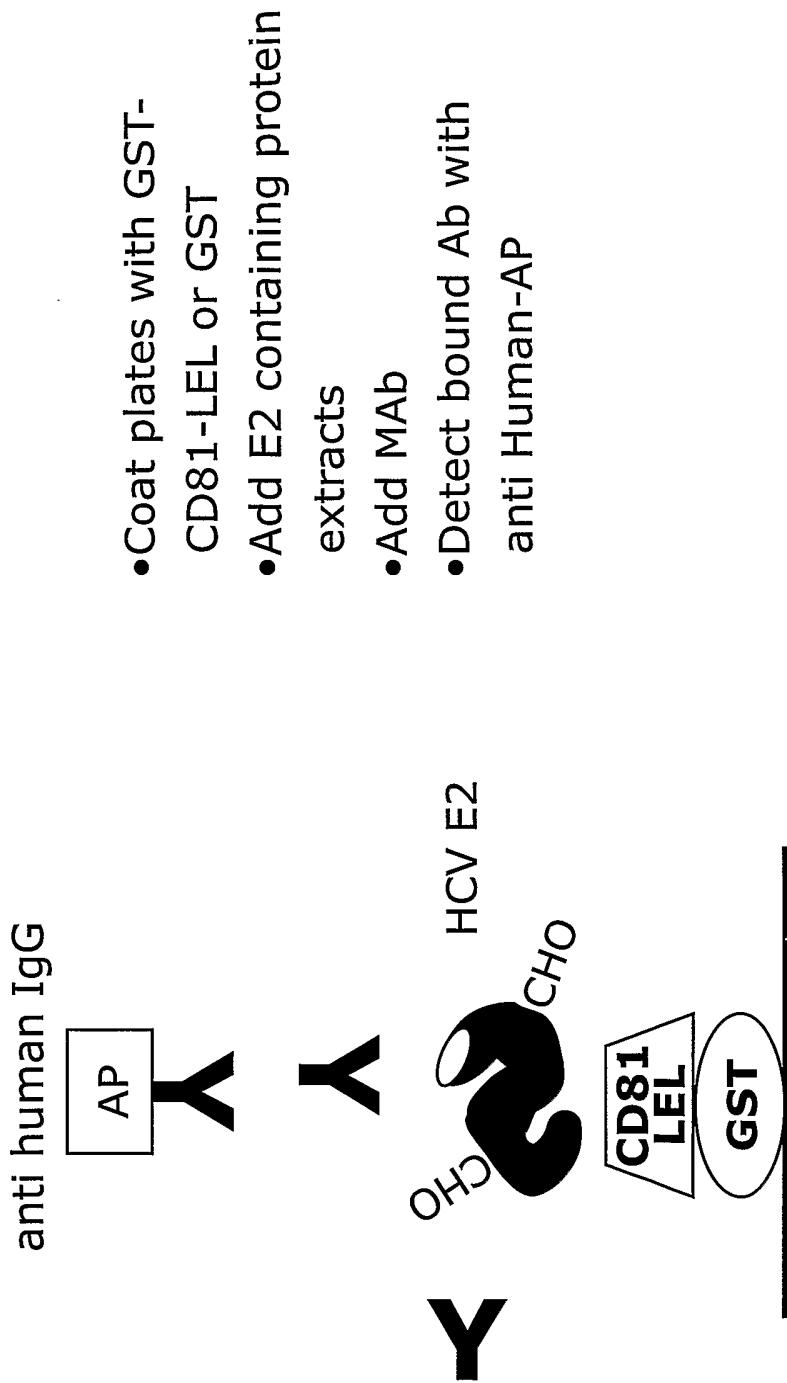


FIG. 14

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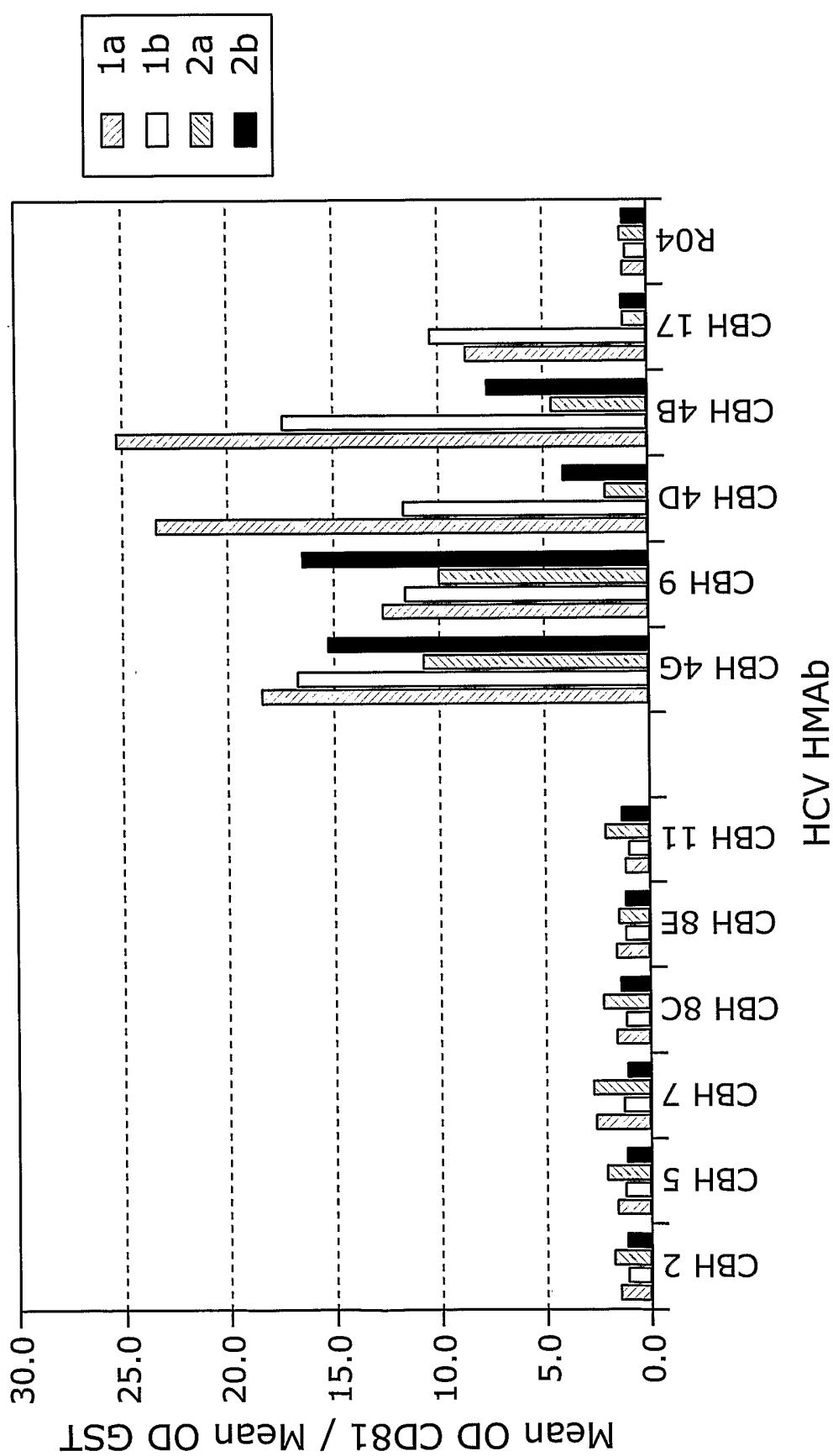


FIG. 15

Inhibition of HCV virion binding to CD81

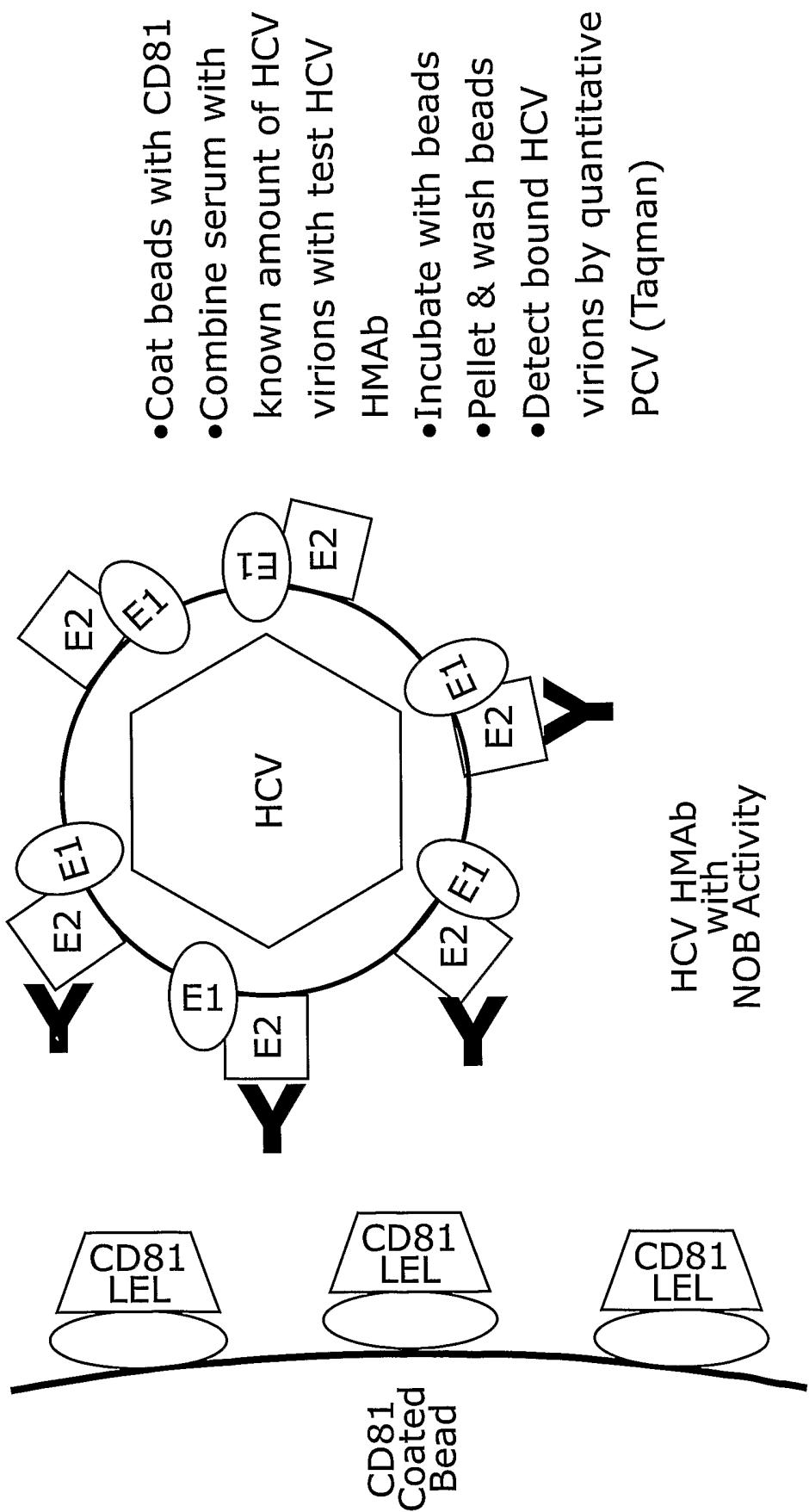


FIG. 16

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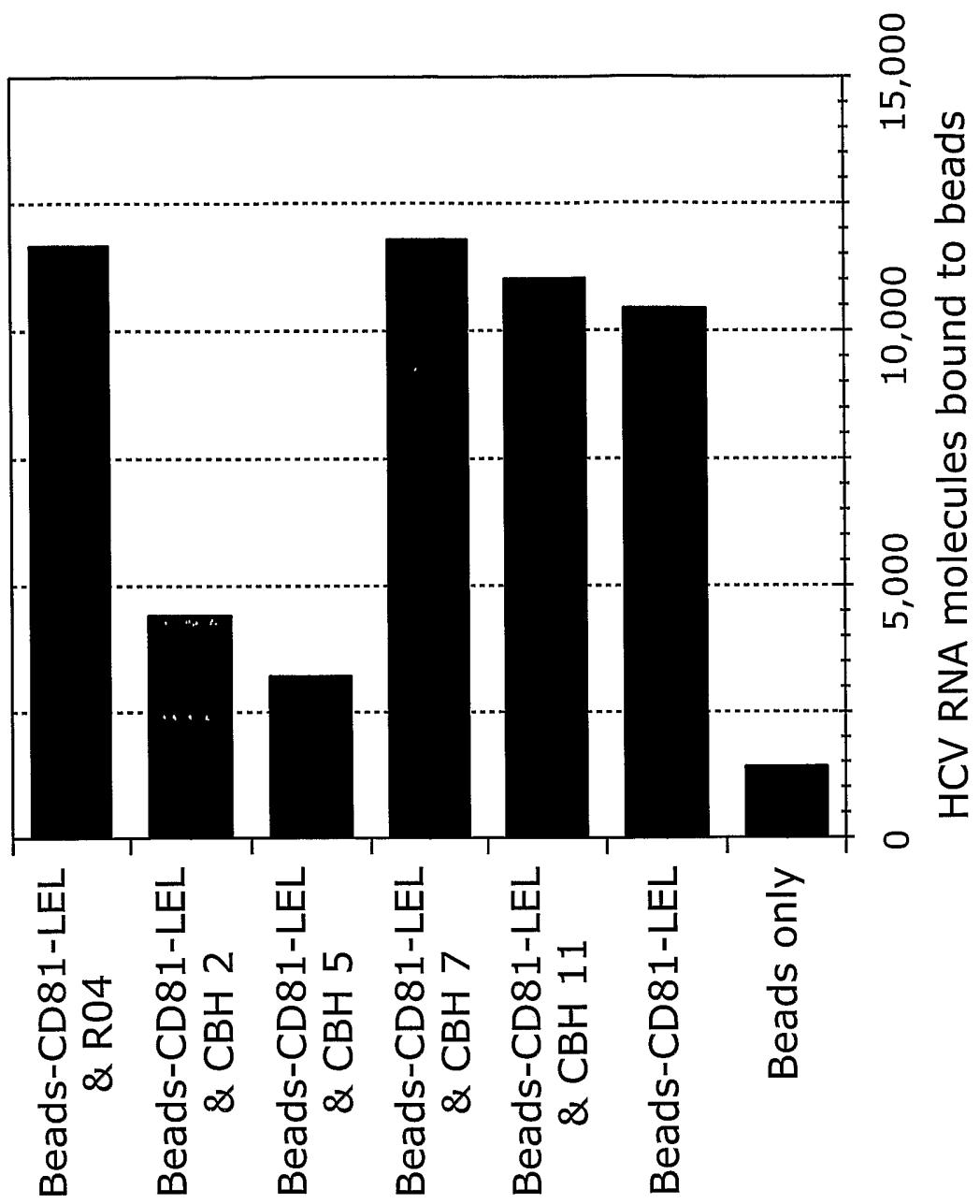


FIG. 17

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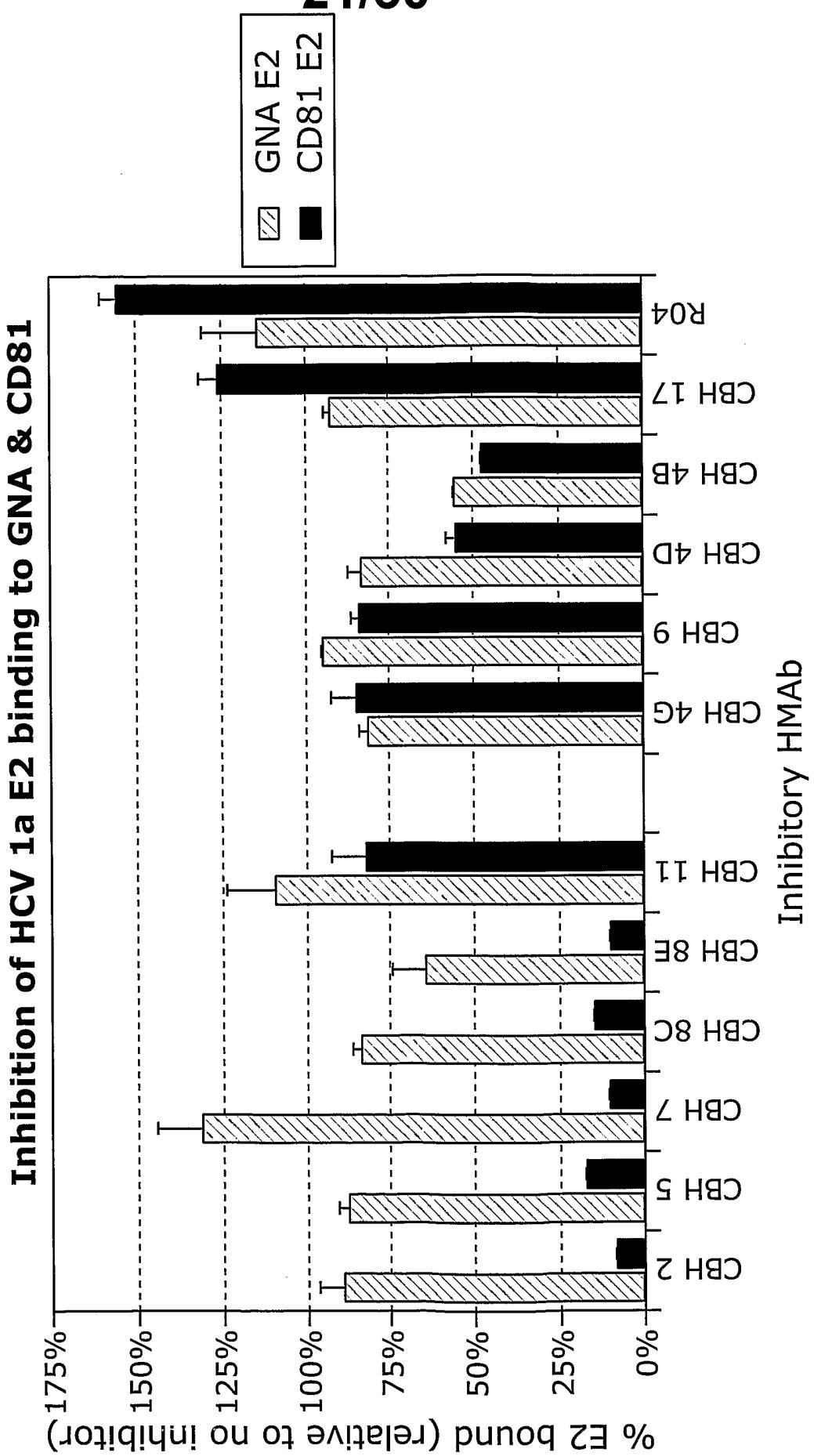


FIG. 18

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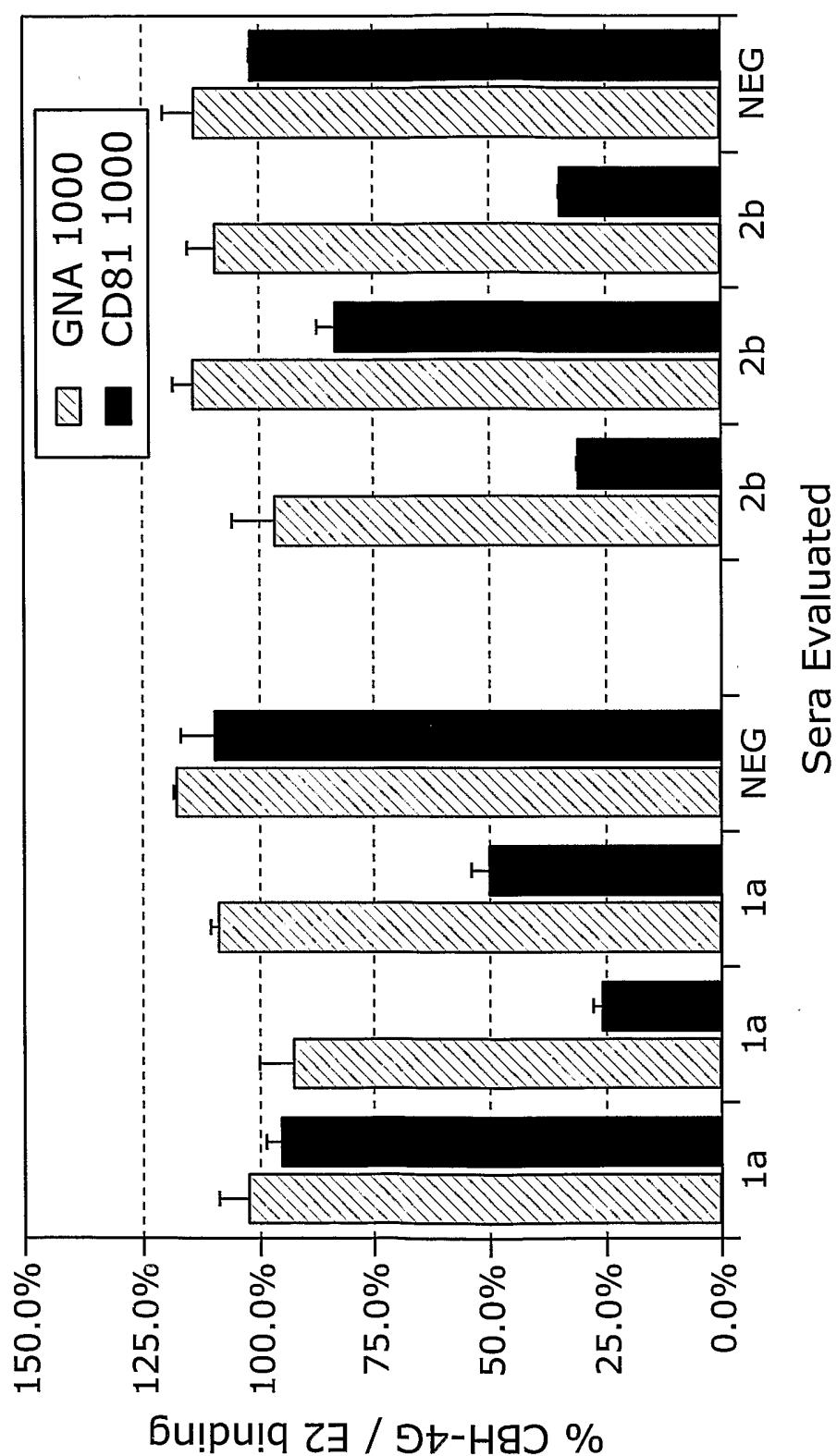
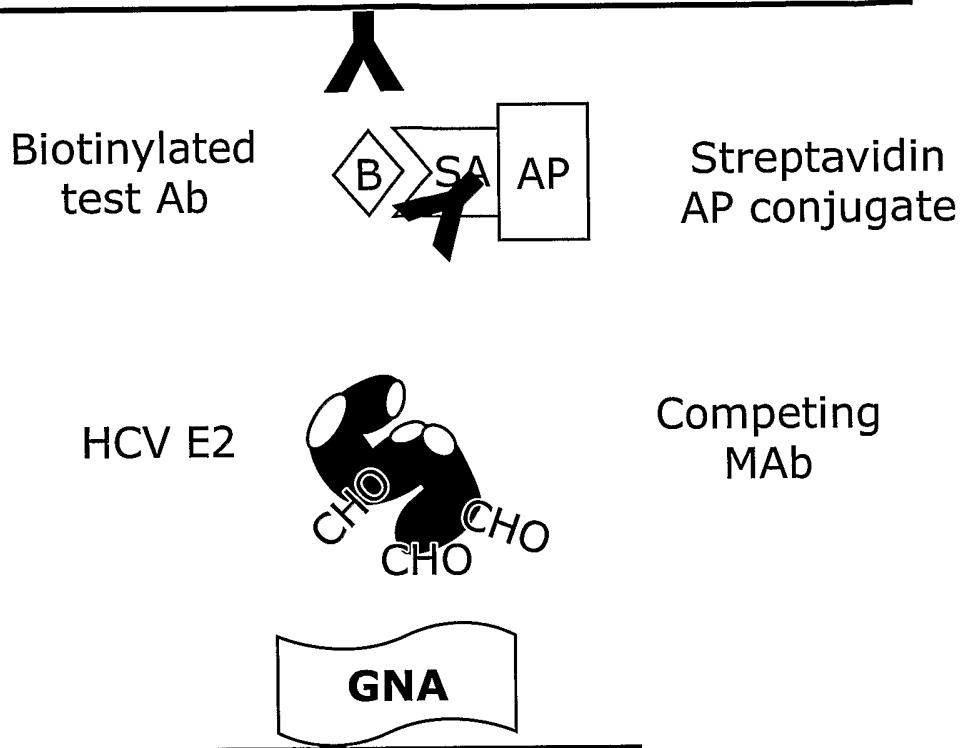


FIG. 19

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Competition Assays



- Coat plates with GNA lectin
- Capture full-length intracellular E2 onto microtiter plate by binding CHO moieties to GNA lectin
- Mix competing HMAb with GNA-captured E2
- Add biotinylated test HMAb. Detect binding of biotinylated test HMAb to E2 with streptavidin-AP conjugate
- Inhibition of binding of test HMAb suggests epitopes within same antibody binding domain

FIG. 20

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Competition Analysis of 4 HCV HMAbs

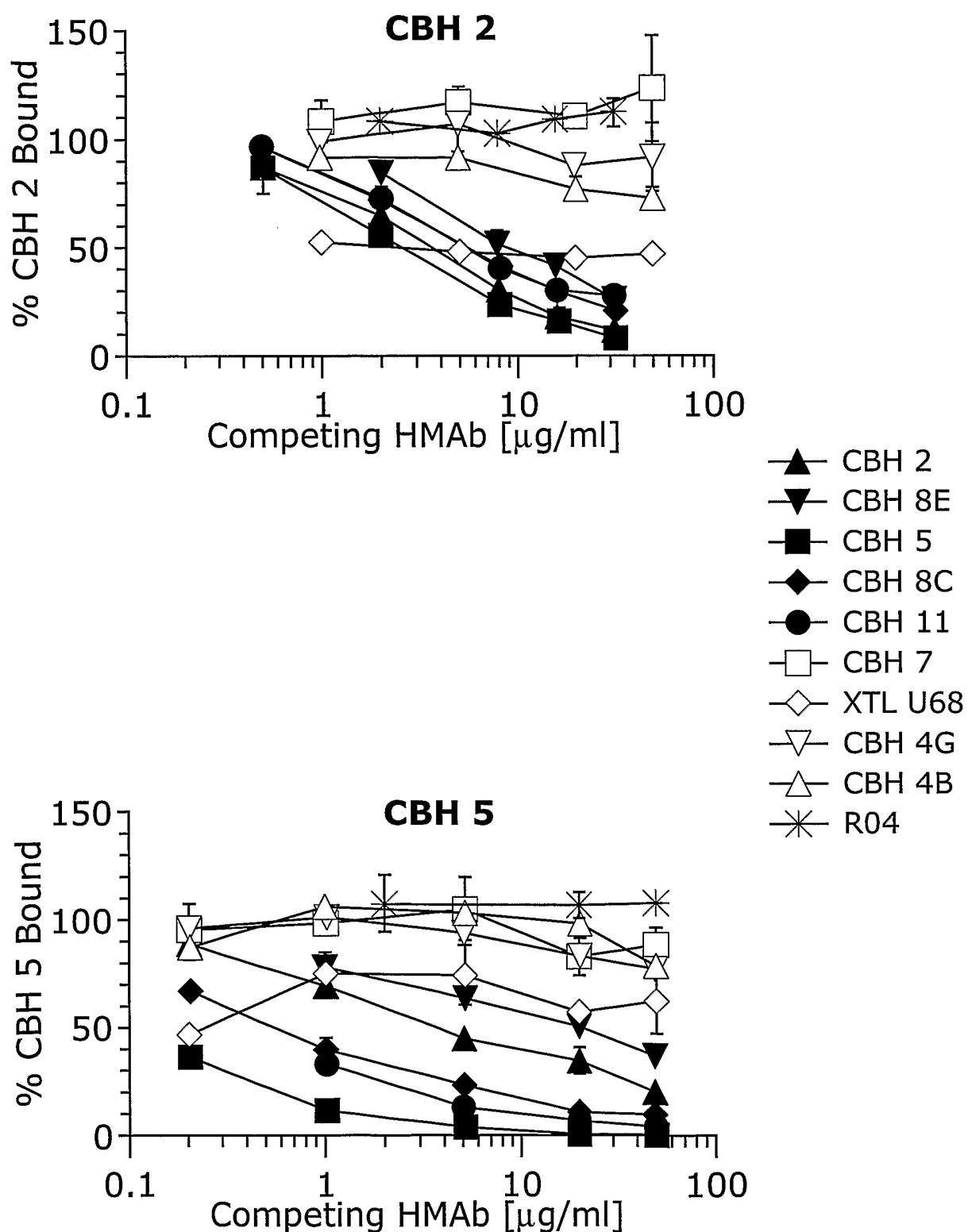


FIG. 21A

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Competition Analysis of 4 HCV HMAbs

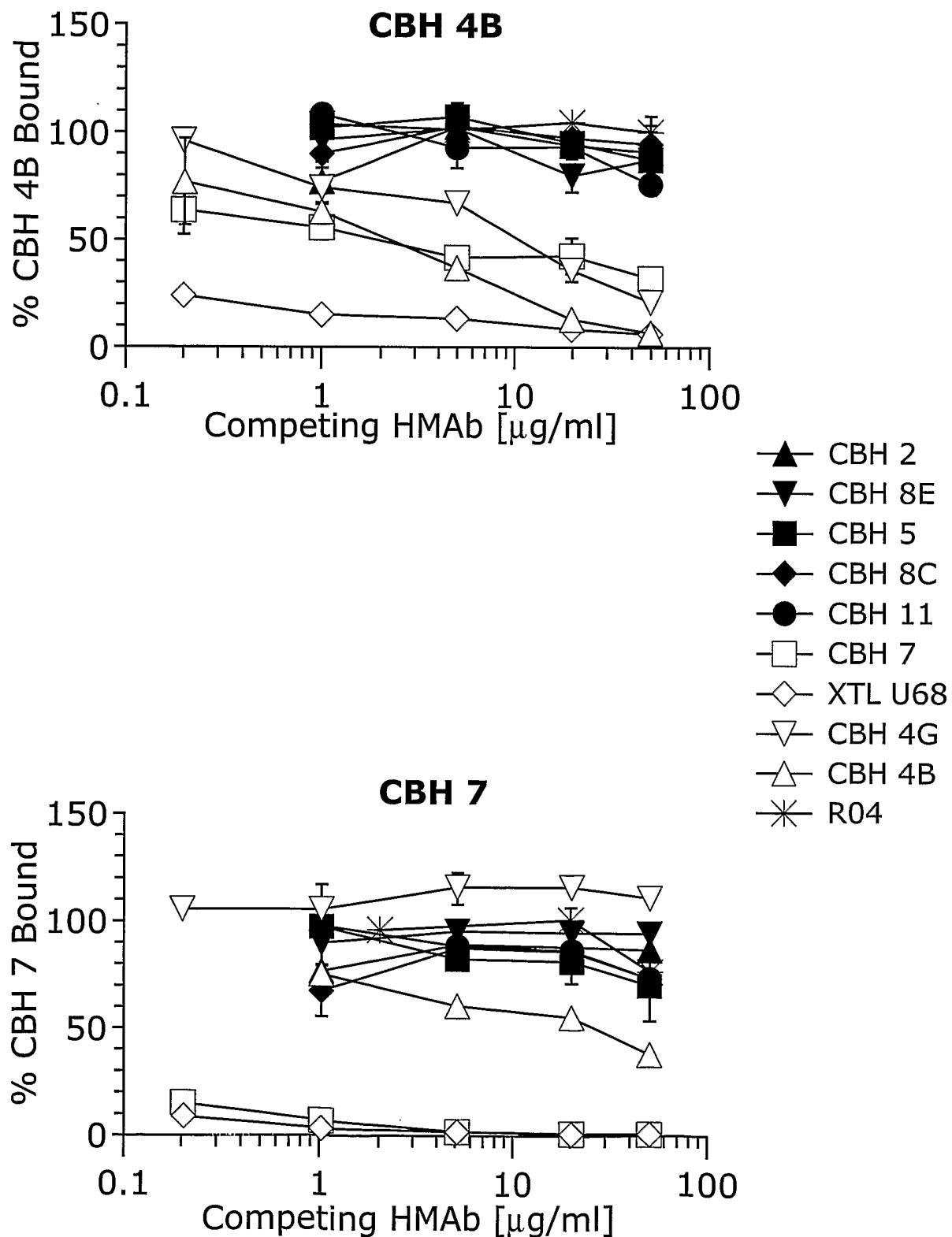


FIG. 21B

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Summary of HMAb Competition Analysis

Competitor Grp	HMAb	E2	GROUP I					GRP II CBH 7	GROUP III		
			CBH 2	CBH 2	CBH 5	CBH 8C	CBH 11		CBH 4G	CBH 4B	
I	CBH 2	1a	18	39	51	ND	93	66	76		
		1b	17	50	50	48	91	84	84		
	CBH 8E	1a	13	39	48	ND	79	63	80		
		1b	23	45	57	51	91	87	78		
	CBH 5	1a	17	9	22	ND	71	60	74		
		1b	4	7	24	9	77	76	80		
	CBH 8C	1a	27	48	25	ND	85	74	84		
		1b	11	23	33	23	84	87	86		
	CBH 11	1a	96	93	84	ND	97	72	87		
		1b	24	25	43	25	82	97	97		
II	CBH 7	1a	40	42	45	ND	2	251	11		
		1b	104	104	89	92	2	146	36		

FIG. 22A

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XTL U68		1a	60	63	108	ND	2
		1b	39	57	73	66	9
III	CBH 4G	1a	107	95	85	ND	112
		1b	87	83	81	87	114
	CBH 4B	1a	92	92	87	ND	85
		1b	78	93	66	81	63
	CBH 4D	1a	98	86	90	ND	135
		1b	91	82	76	87	102
IV	CBH 17	1a	94	87	87	ND	114
		1b	73	101	88	95	92
C	R04	1a	98	91	92	ND	101
		1b	96	104	104	101	99
Scale		>140%		60%-140%		30%-59%	
		10%-29%		10%-29%		<10%	

Results are the mean percent binding of test antibody relative to wells without any competing antibody. Results are the mean values obtained from 2-5 separate experiments. Both genotype 1a and 1b E2 proteins were tested. ND = not done.

FIG. 22B

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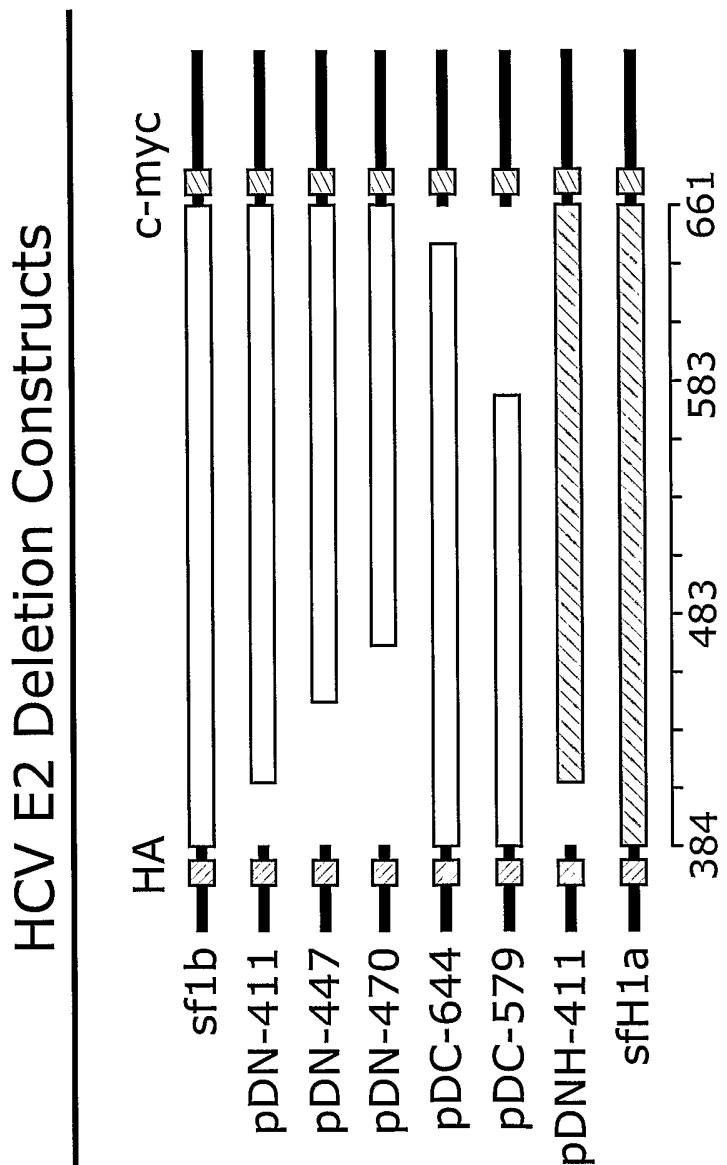


FIG. 23

HCV E2 Deletion Constructs
are efficiently expressed

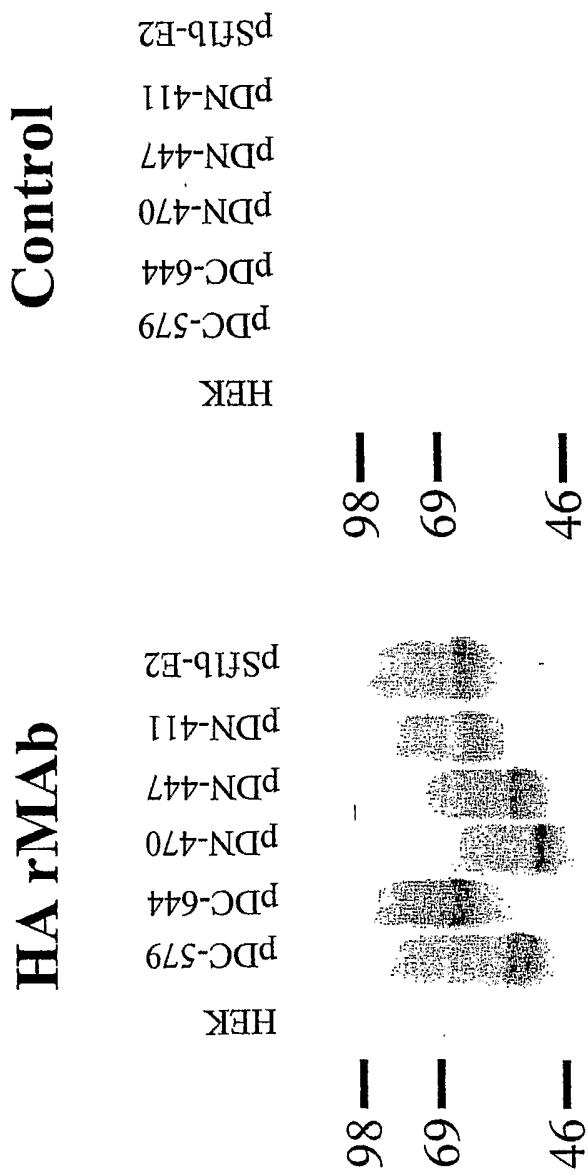
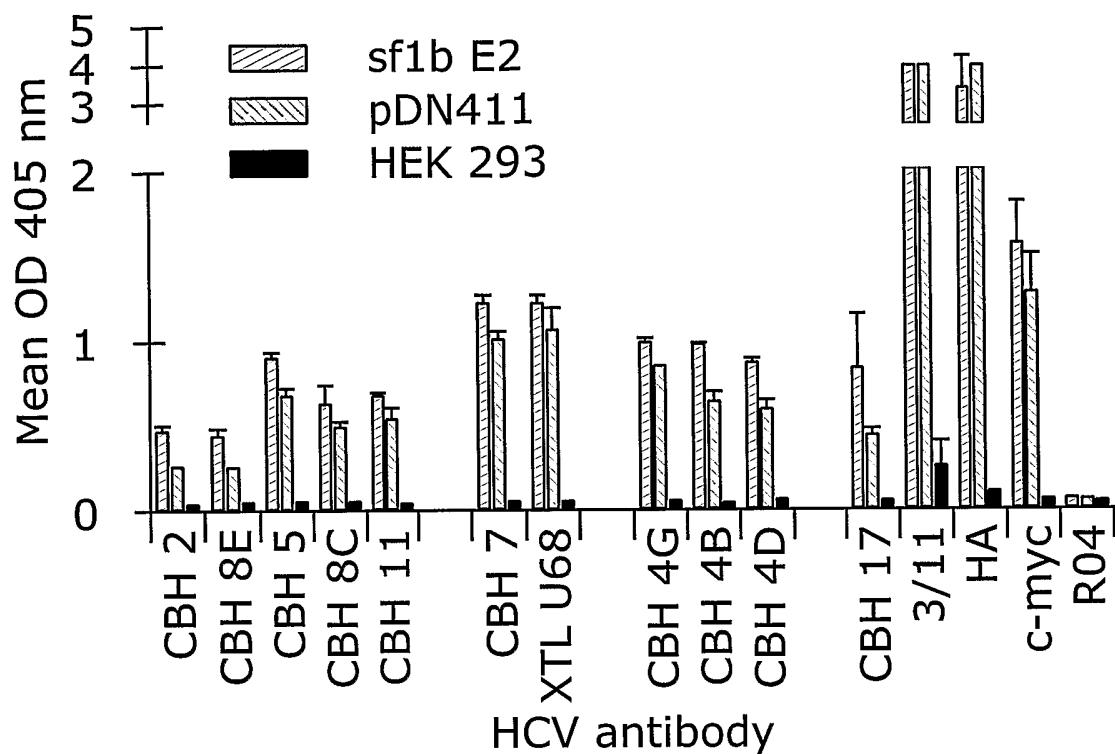


FIG. 24

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HCV E2 Deletion Constructs

HCV 1b E2 w or w/o HVR-1



HCV H1a E2 w or w/o HVR-1

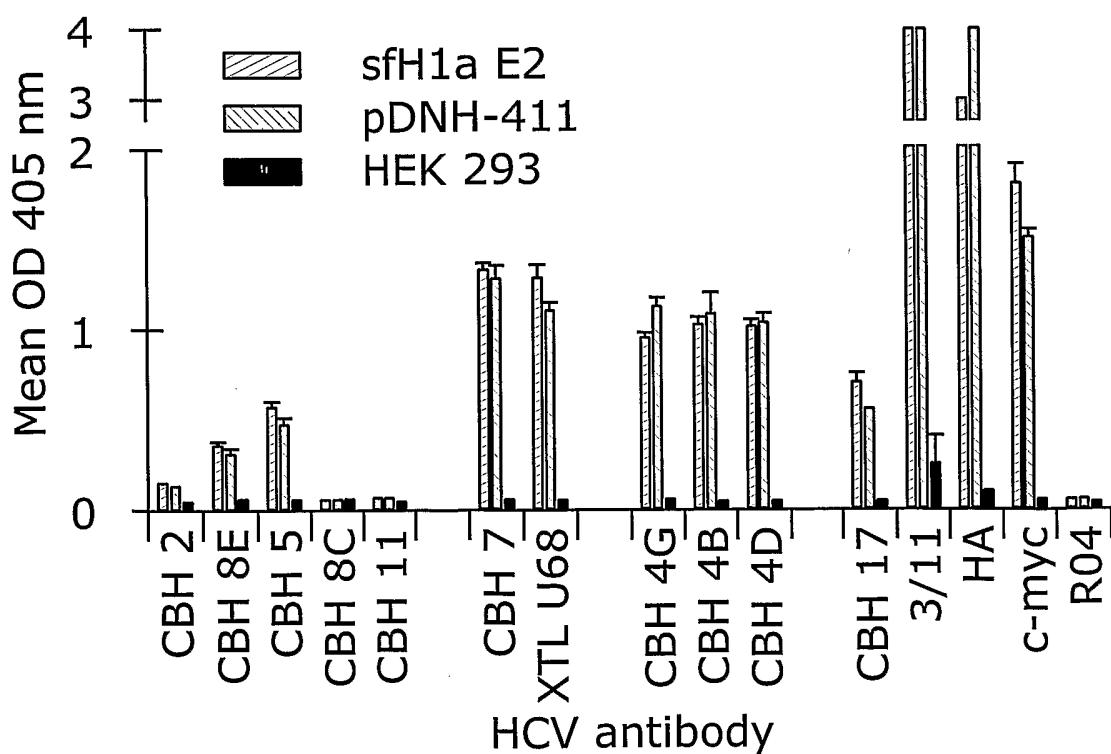
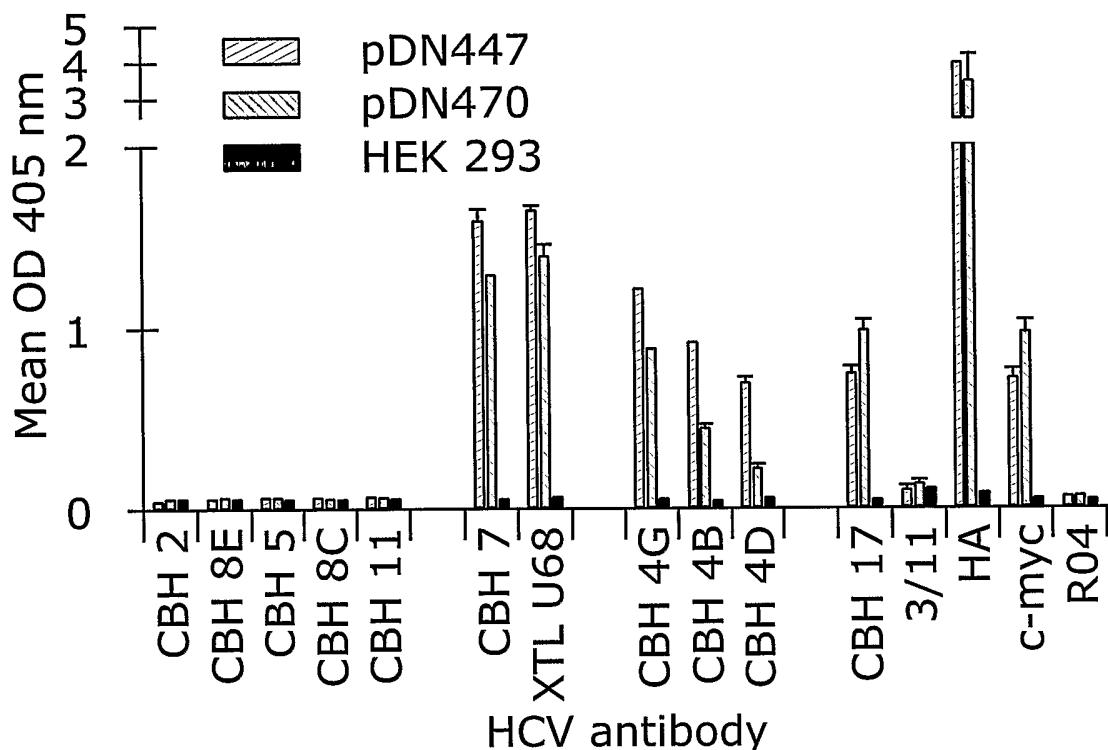


FIG. 25A

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HCV E2 Deletion Constructs

HCV 1b E2 N-terminal deletions



HCV 1b E2 C-terminal deletions

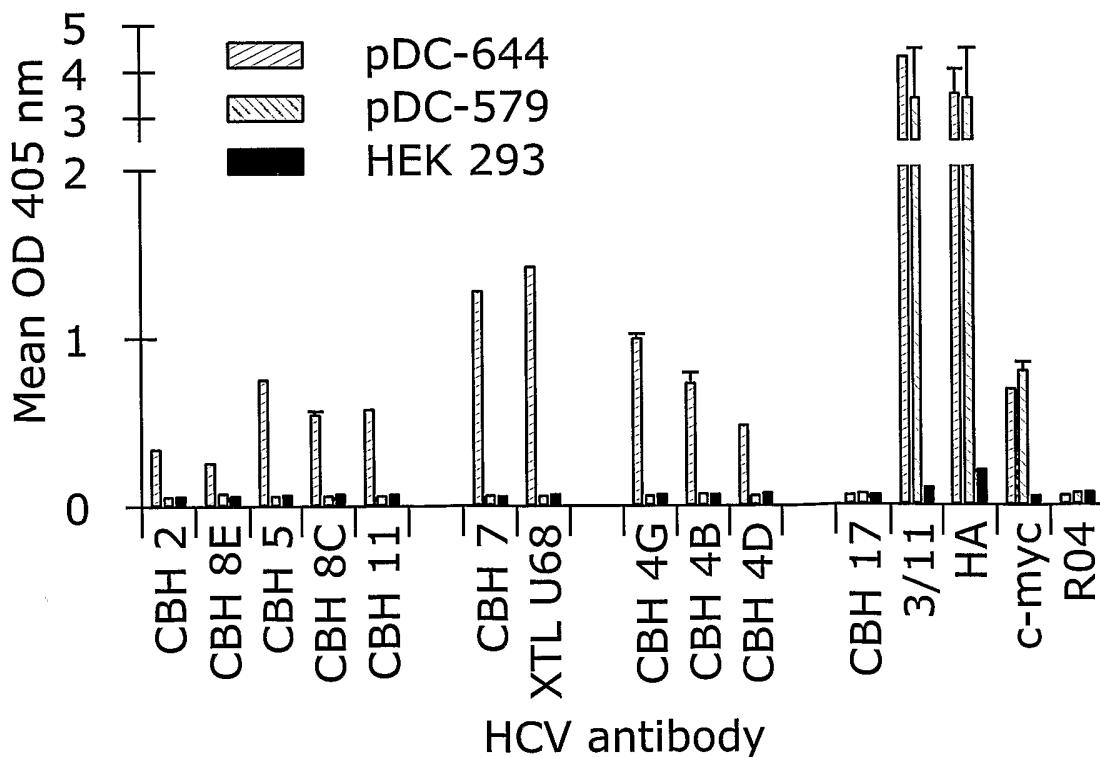


FIG. 25B

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HCV sera have variable levels of antibodies that inhibit CBH-2 & CBH-7

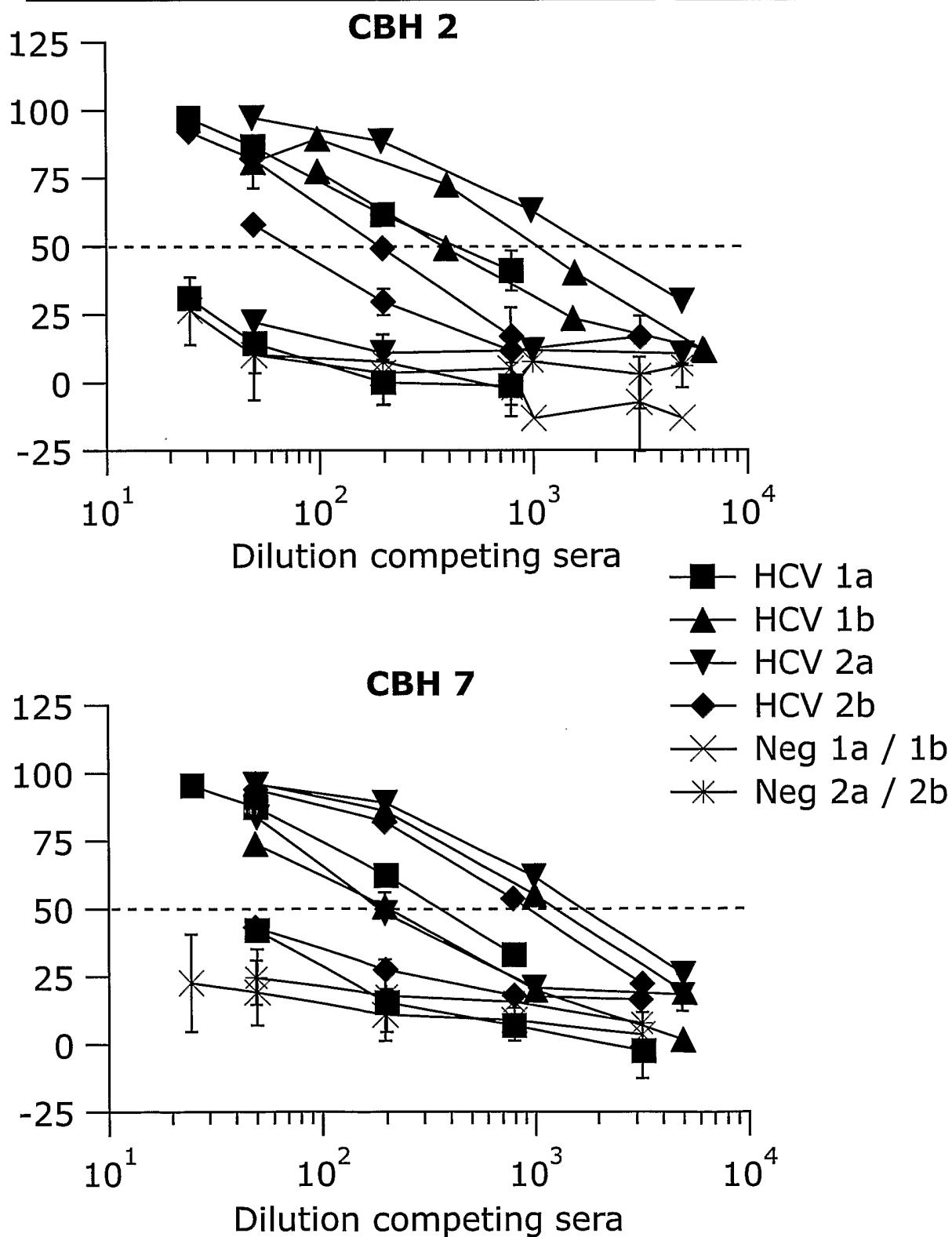


FIG. 26

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HCV sera have variable levels of antibodies that inhibit CBH-2 & CBH-7

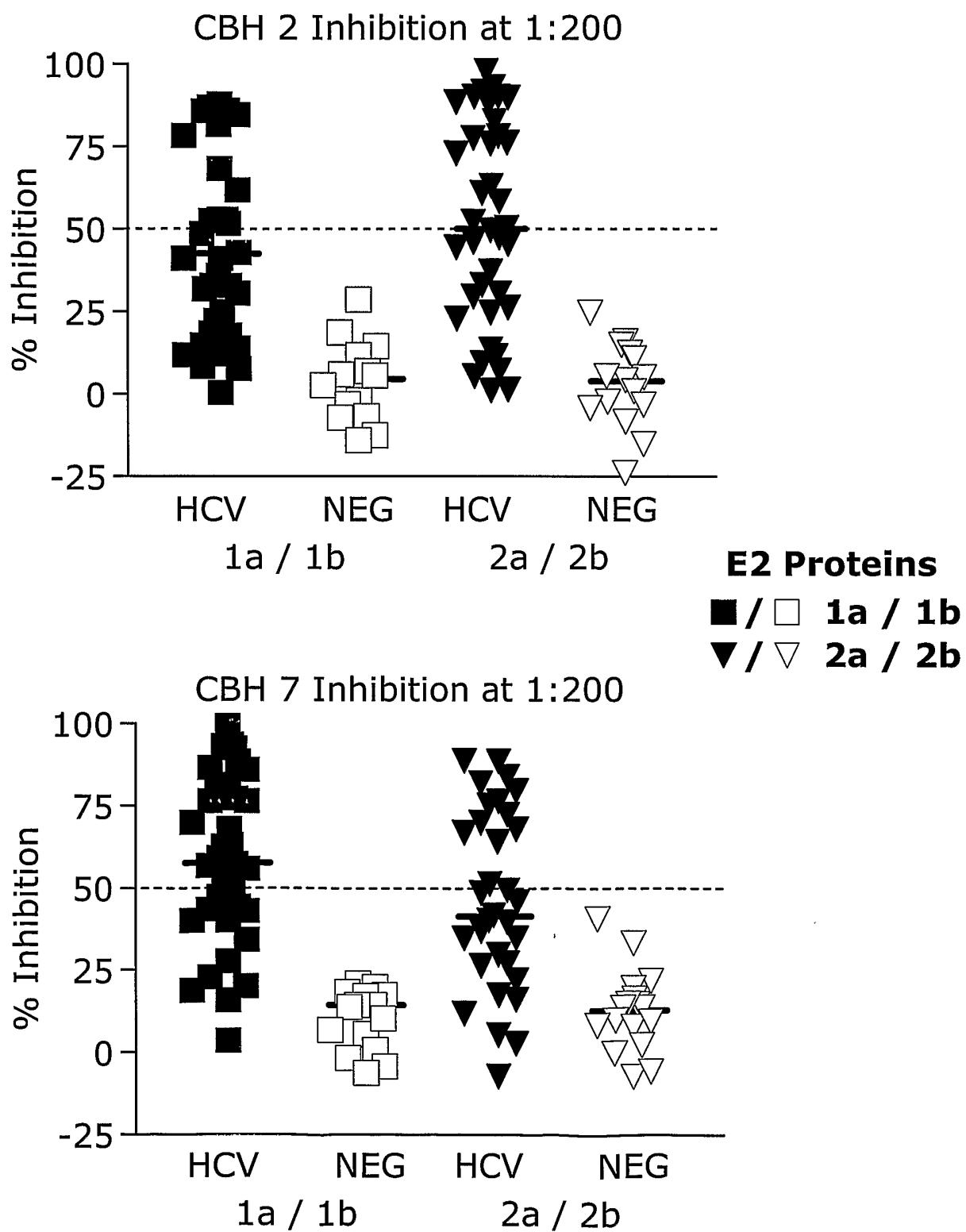


FIG. 27

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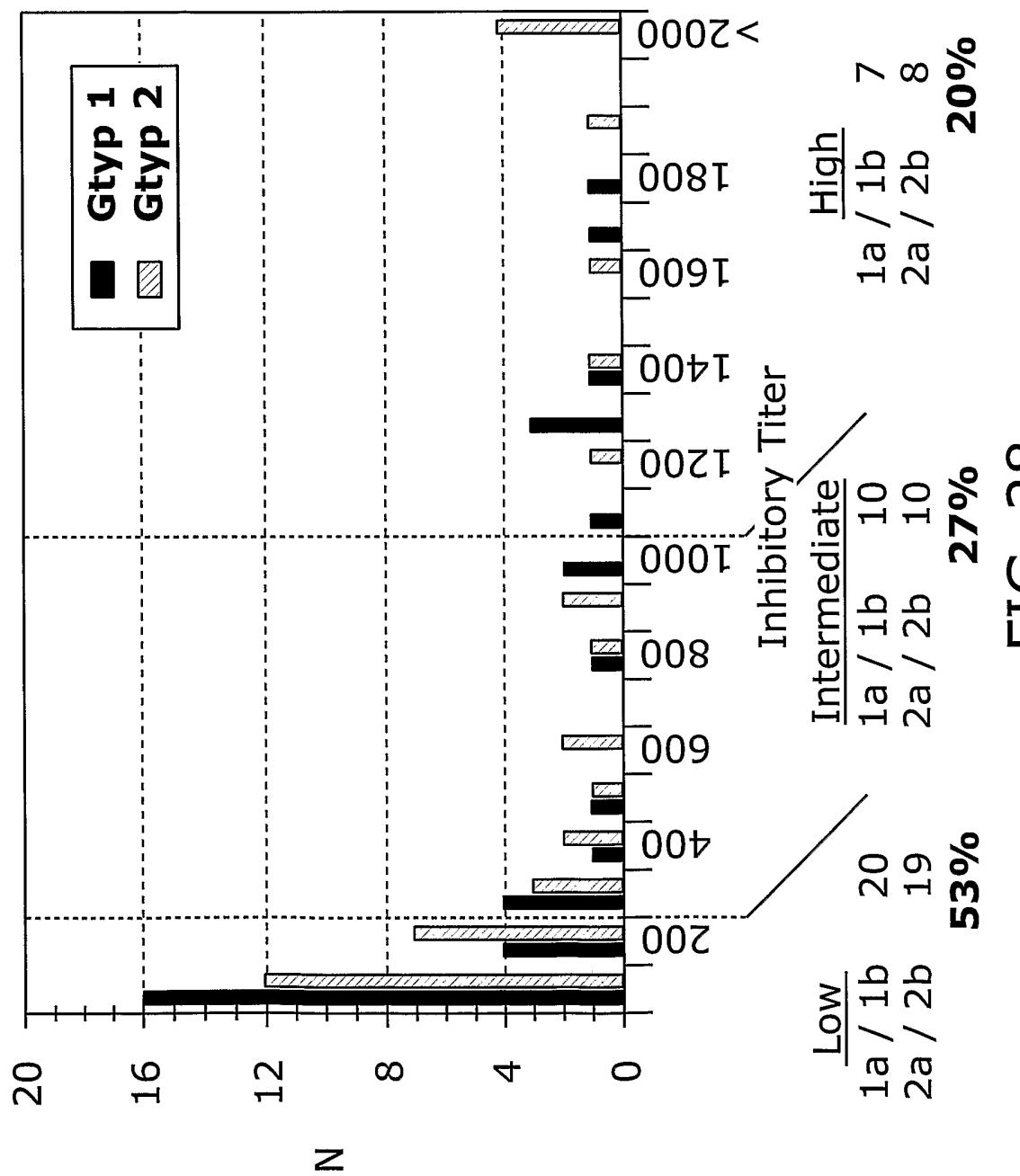
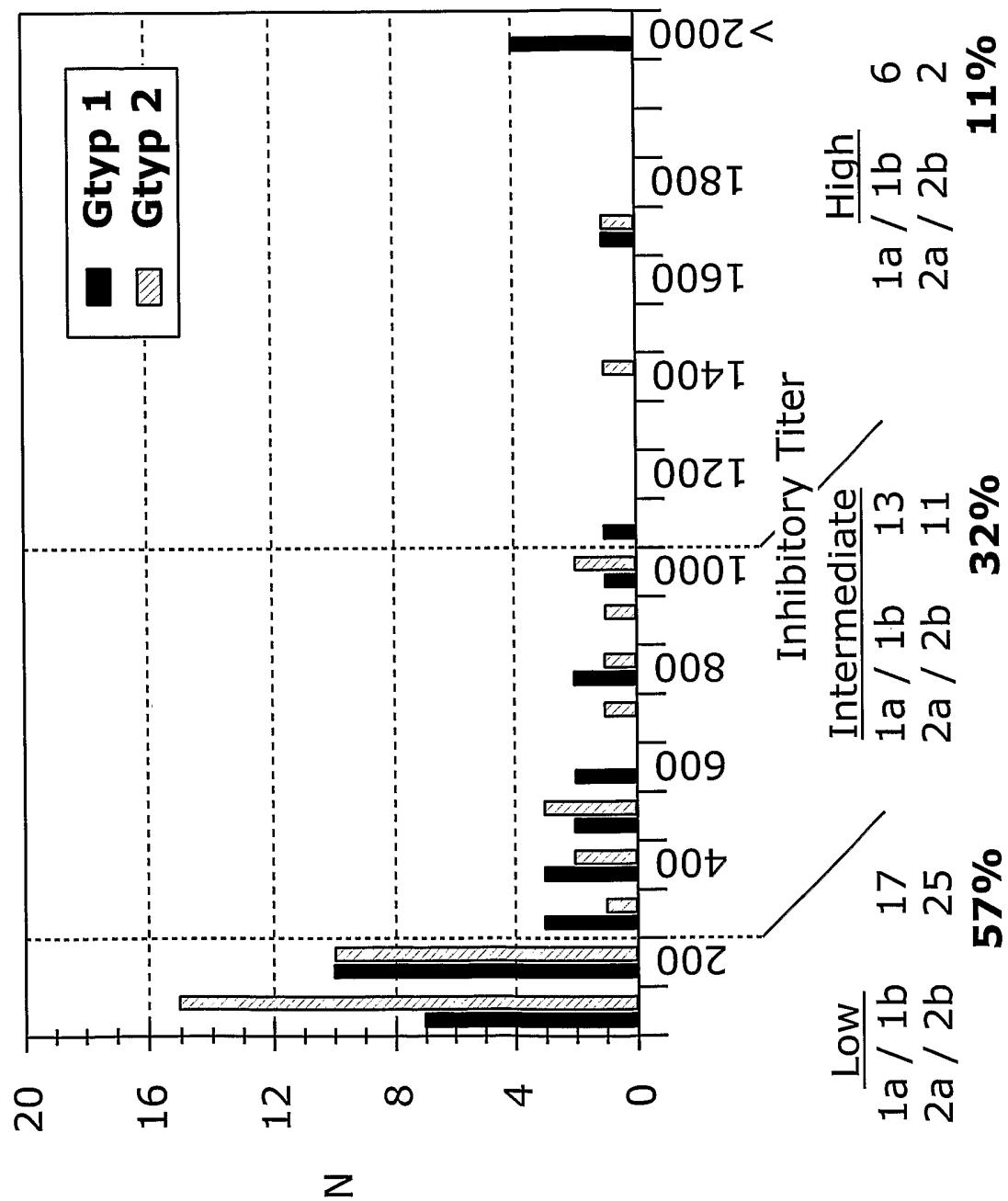
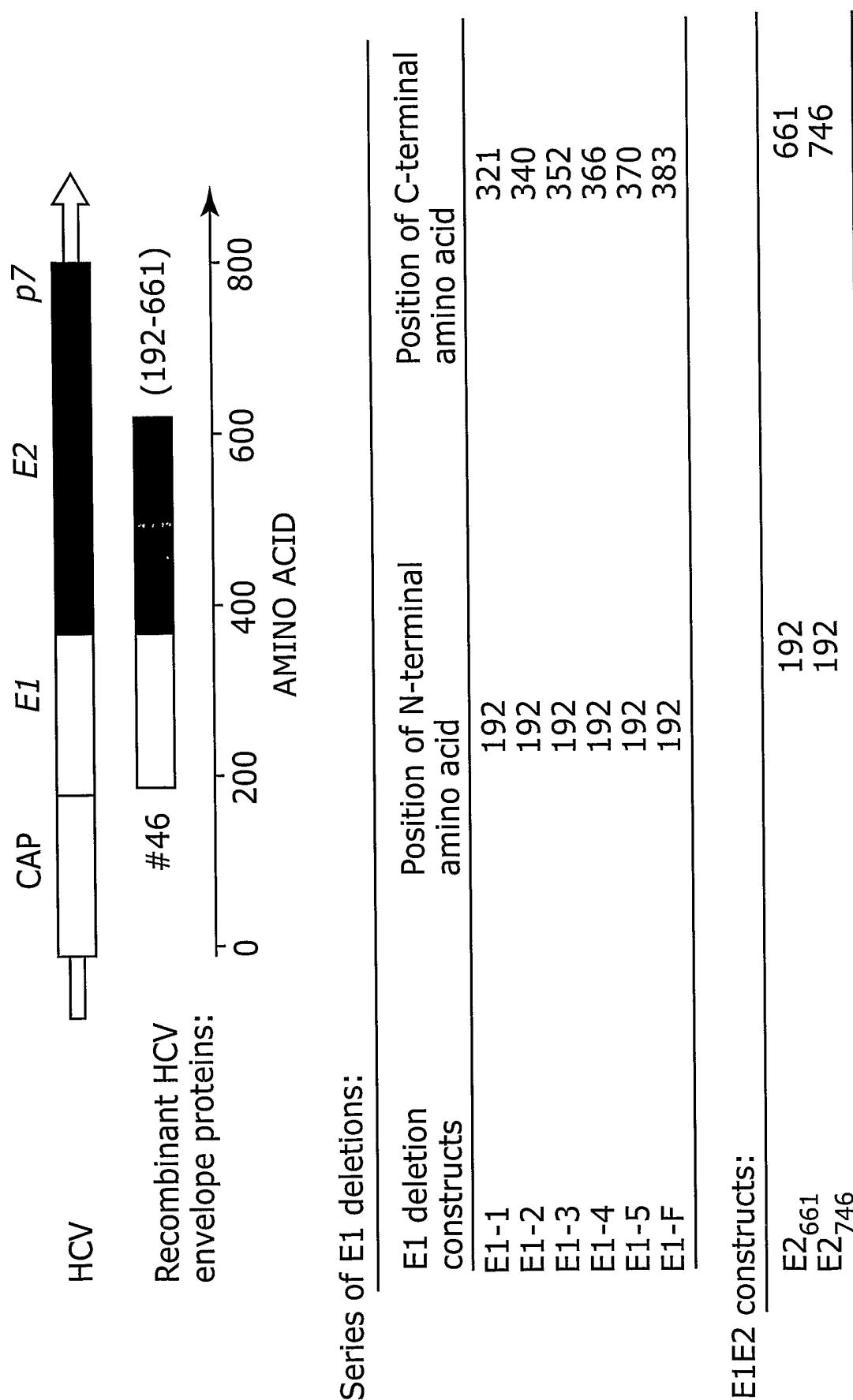


FIG. 28

35/50**FIG. 29**

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Name	Sequences									
ZYK-E1	200	210	220	230	240	250				
HPCJ491	YEVRNVSGV	YHVTNDCSNS	SIVYEADMI	MHTPGCVPCV	REGNTSRCWV	ALTPTLAARN				
HPCST90	...I	...P...	...V.	...S...	...S...	...D				
	...Q...	...S...	...A.	...L...	...S...	...V...				
ZYK-E1	260	270	280	290	300	310				
HPCJ491	ASVPTAAIRR	HIDLLVGTAT	FCSAMYVGDL	CGSVFLVSQL	FTFSPPRRHHT	VQDCNCSTIYP				
HPCST90	...TT...	...V...	...A	...I...	...E	...				
	GKL..TQL...	...S...	...L...	...G...	...W.	...T...				
ZYK-E1	320	330	340	350	360	370				
HPCJ491	GHVTGHRMAW	DMMMNWSPTA	ALVVSQQLRI	PQAVMDMVAG	AHWGVLAGLA	YYSMAGNMAK				
HPCST90	...S...	...T	...V	...I...	...I...	...V...				
ZYK-E1	380									
HPCJ491	VLIVMLLFAAG	VDG								
HPCST90	...A...	...A								
	...V...	...L...								

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FIG. 31

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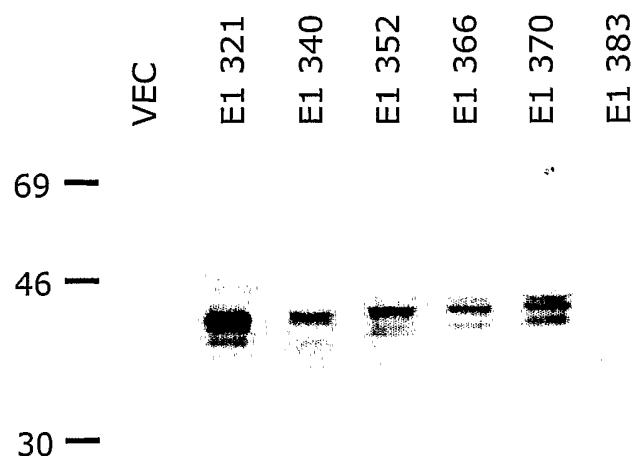


FIG. 32A

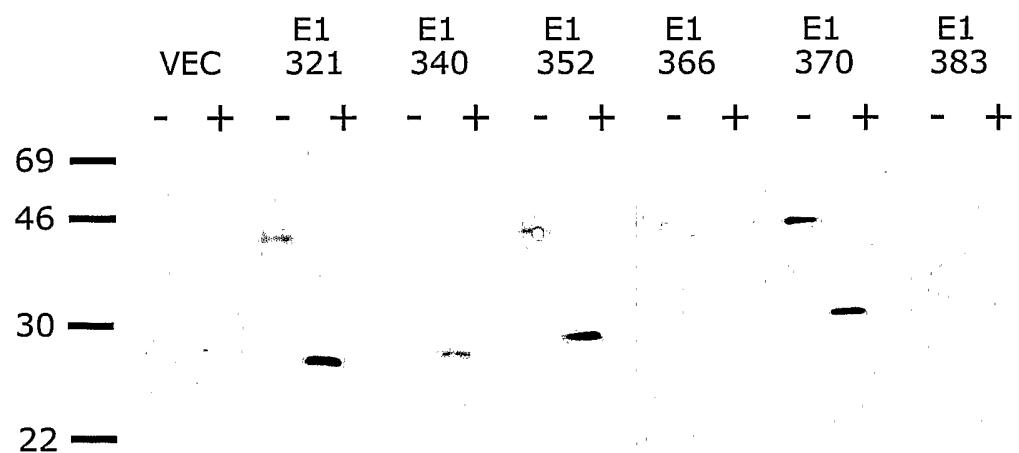


FIG. 32B

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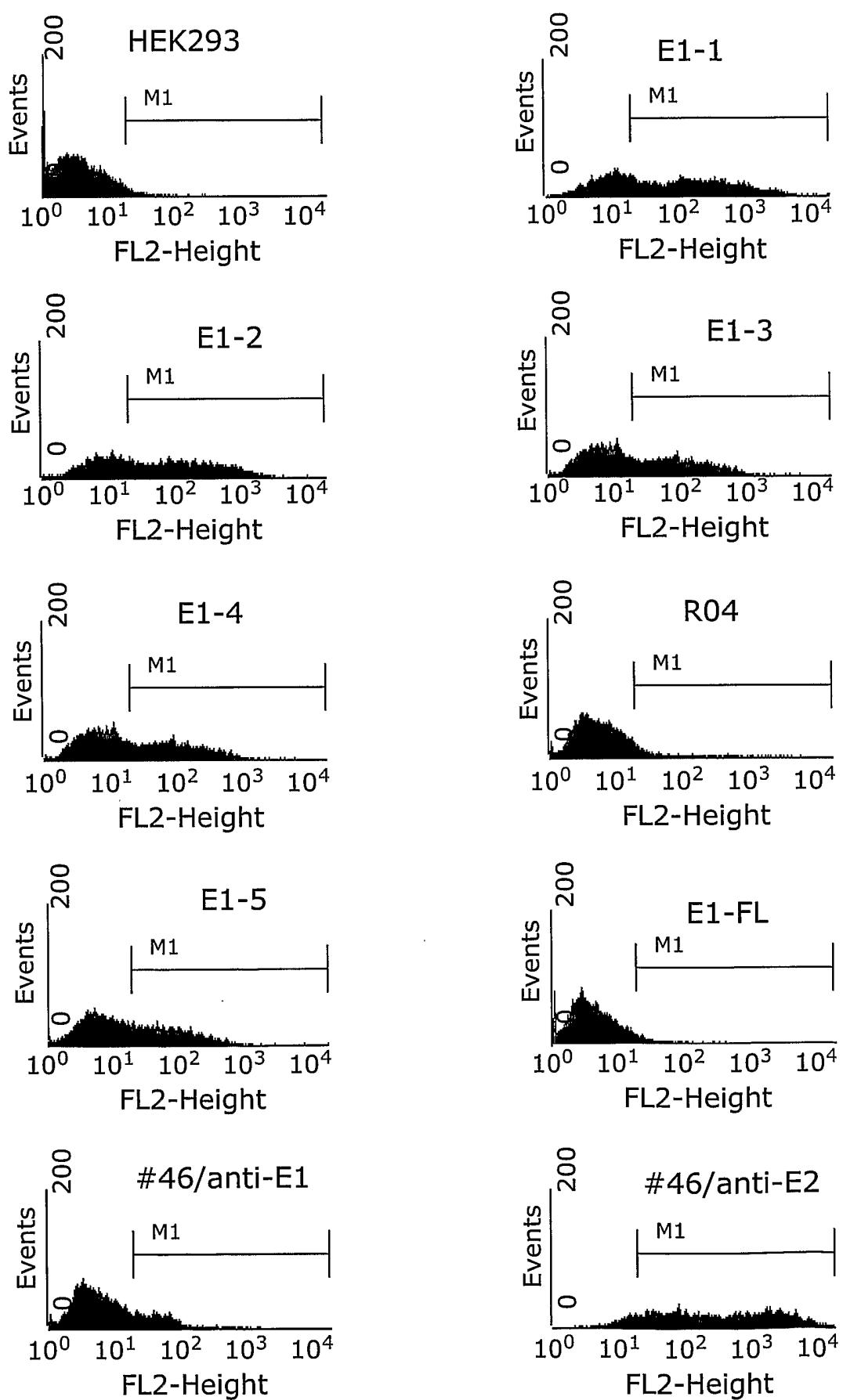


FIG. 33

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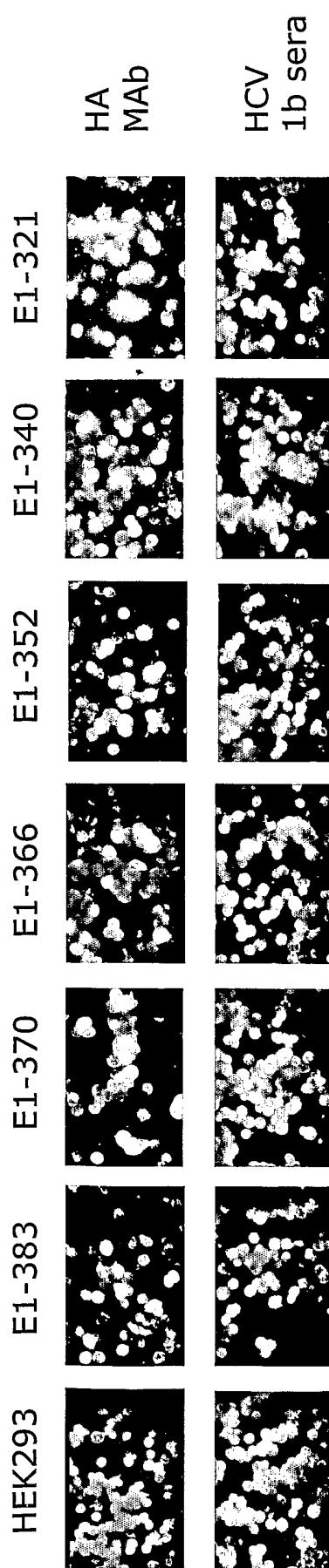


FIG. 34

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Immunoreactivity of E1 and E1E2 constructs to human antibodies in HCV positive serum

Sample	HCV E1 CONSTRUCTS						293 Cells
	E1-321 (1)	E1-340 (2)	E1-352 (3)	E1-366 (4)	E1-370 (5)	E1-383 (FL)	
TYPE 1b SAMPLES							
J46312(JB)	+	0	+	0	+	0	0
2746	+	+	+	+	+	+	0
2680	+	+	+	+	+	+	0
2527	0	+	+	+	0	+	0
2221	0	0	0	0	0	0	0
884	0	0	0	0	0	0	0
2572	+	+	+	+	+	+	0
2260	+	+	+	+	0	+	0
2580	+	+	+	+	+	+	0
2992	+	+	+	+	+	+	0
2757	0	+	+	+	0	+	0
HC04	+	+	+	+	+	+	+
HC07	+	+	+	+	+	+	0
HC10	0	0	0	0	0	0	0
HC15	+	0	+	0	0	+	0
HC26	+	+	+	+	+	+	0
HC29	+	+	+	+	+	+	0
	12/17 (70%)	12/17 (70%)	14/17 (82%)	12/17 (70%)	13/17 (76%)	9/17 (53%)	17/17 (100%)
							1/17 (6%)
TYPE 1a SAMPLES							
1847	0	0	0	0	0	0	0
2234	0	+	0	+	0	0	0
2290	+	0	+	0	0	0	0
2295	0	0	0	0	0	0	0
2166	+	+	+	+	0	0	0
2021	0	0	0	0	0	0	0
HC03	0	0	0	0	0	0	0
Notes:	2/7 (29%)	2/7 (29%)	3/7 (43%)	1/7 (14%)	2/7 (29%)	0/7 (0%)	7/7 (100%)
							0/7 (0%)

*All serum samples tested at 1:40 dilution.

*Sample HC04 appears to have anti-cellular antibodies.

FIG. 35

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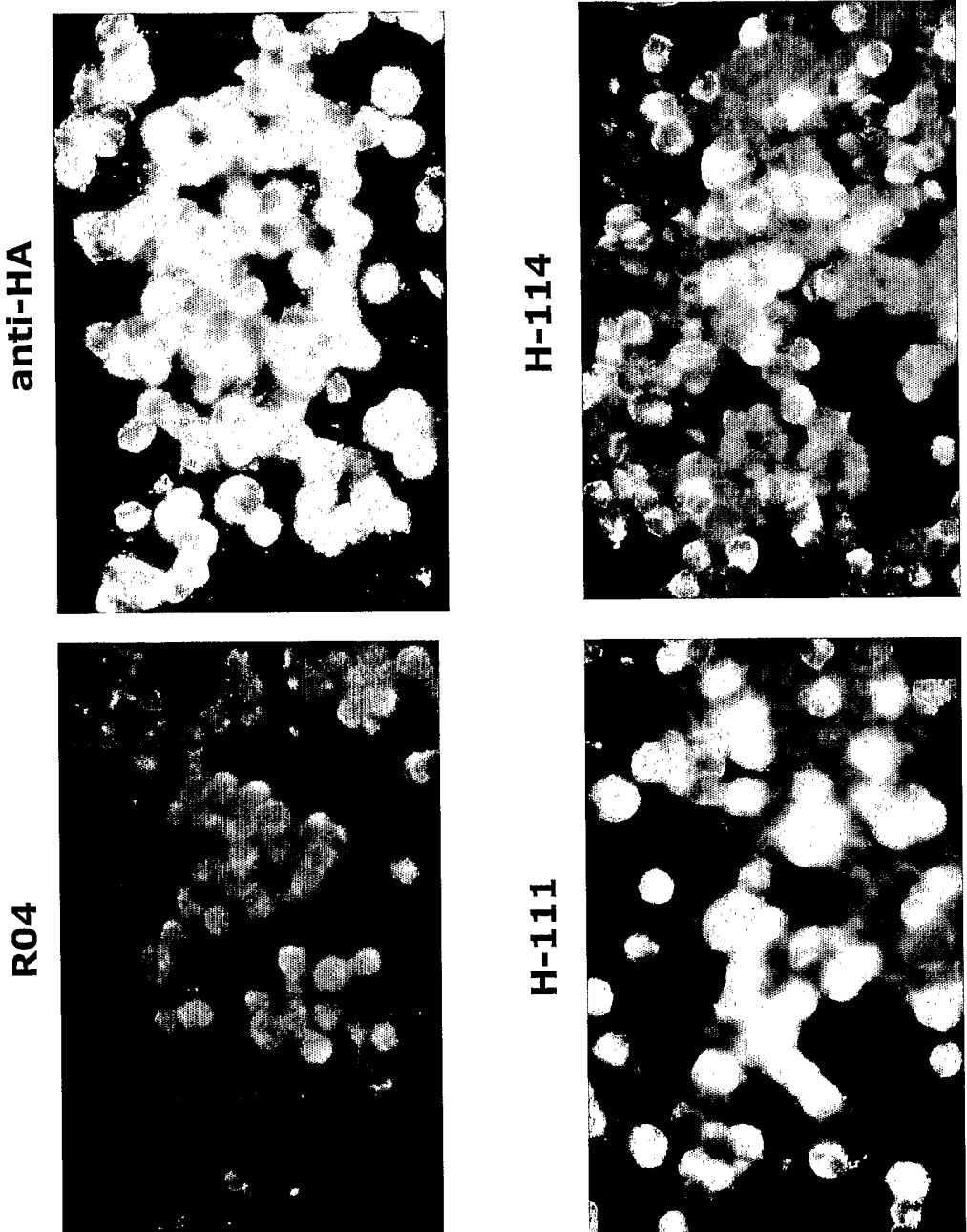


FIG. 36

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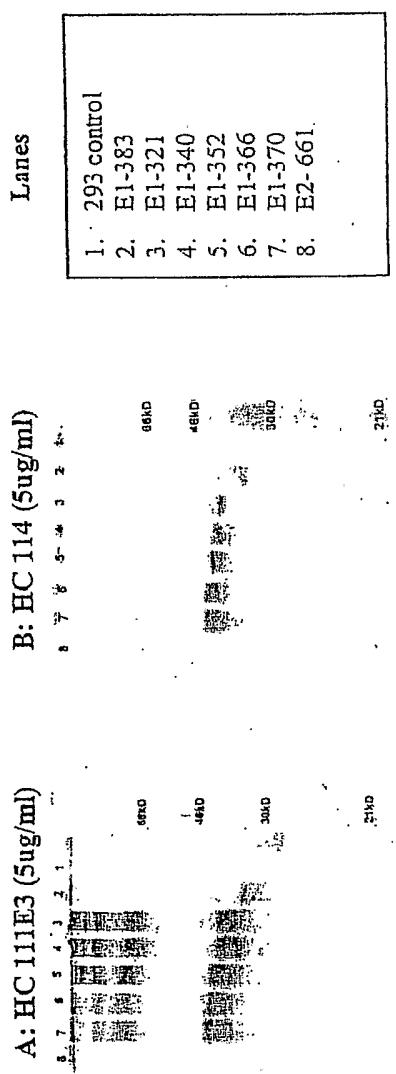


FIG. 37

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E1-352

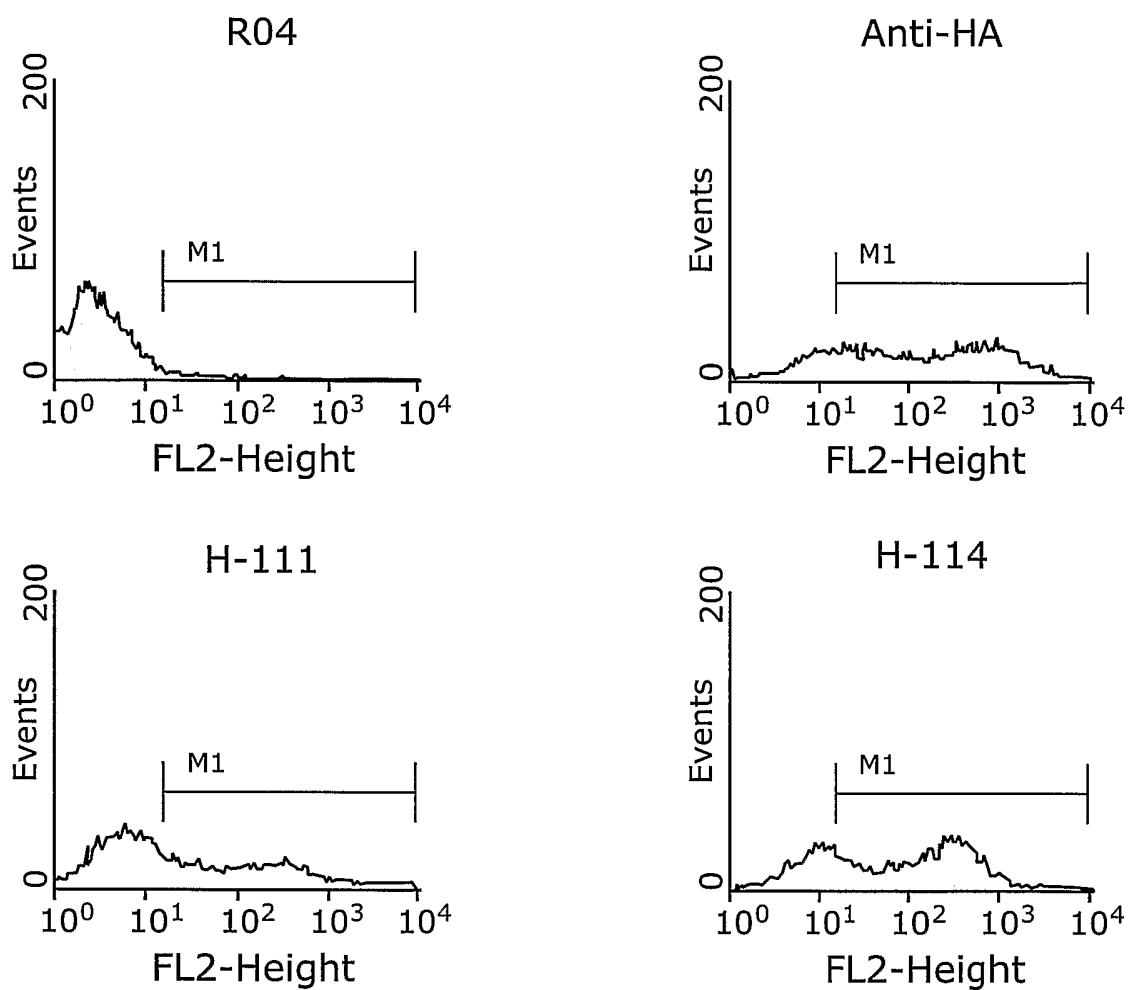
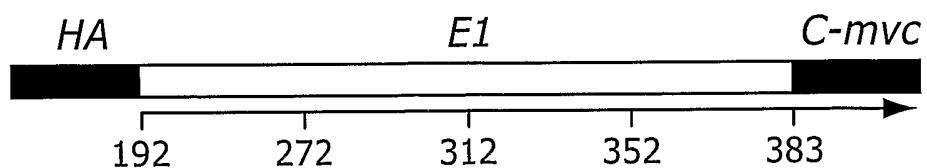


FIG. 38

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E1 deletions	IFA		
	HA	111	114
E1 (192-370)	+	+	+
E1 (192-366)	+	+	+
E1 (192-352)	+	+	+
E1 (192-340)	+	+	+
E1 (192-321)	+	+	+
E1 (192-296)	+	+	-
E1 (192-269)	+	+	-
E1 (192-250)	+	+	-
E1 (192-231)	+	+	-
E1 (192-211)	+	+	-
E1 (296-321)	+	-	-
E1 (192-313)	+	+	+
E1 (192-305)	+	+	-
E1 (199-321)	+	-	+
E1 (206-321)	+	-	+
E1 (212-313)	+	-	-
E1 (244-313)	+	-	-
E1 (262-313)	+	-	-

FIG. 39

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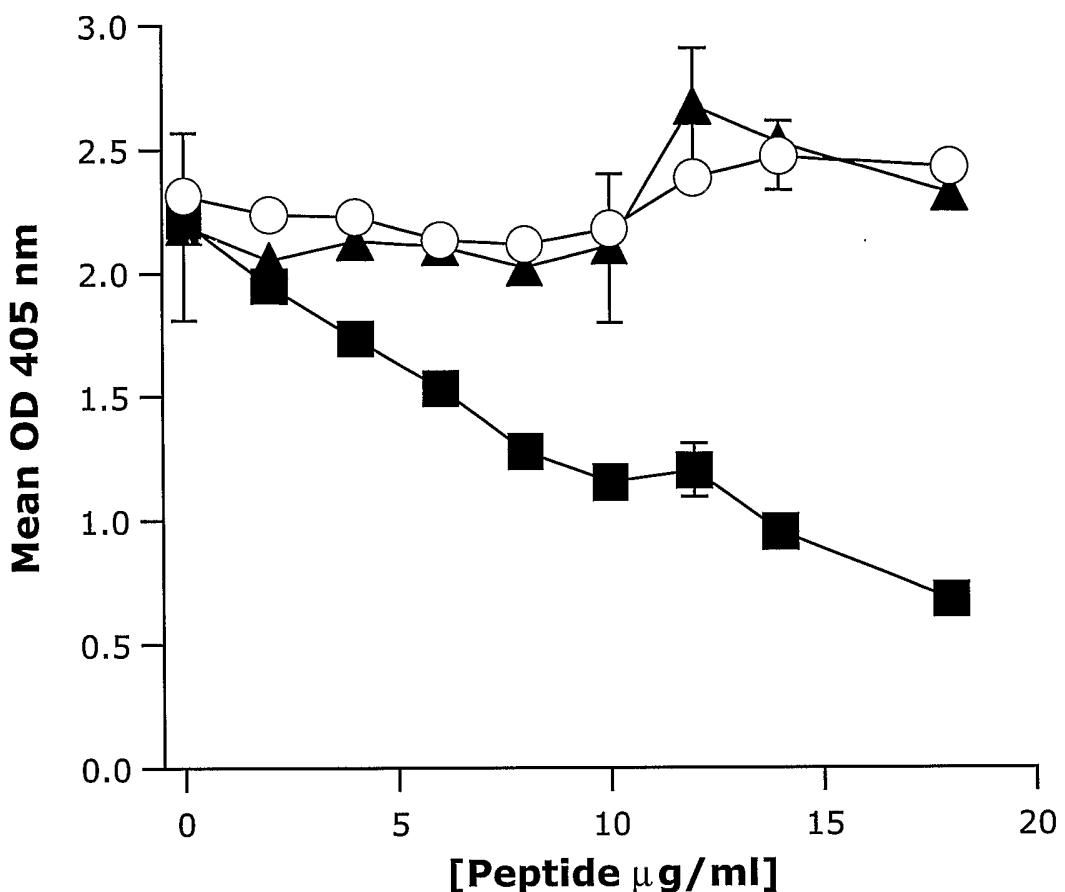


FIG. 40

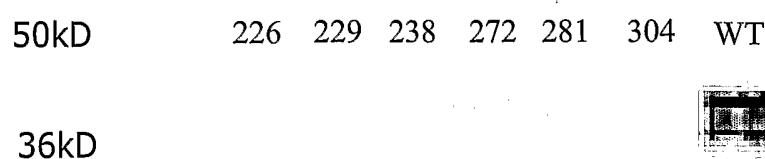


FIG. 41

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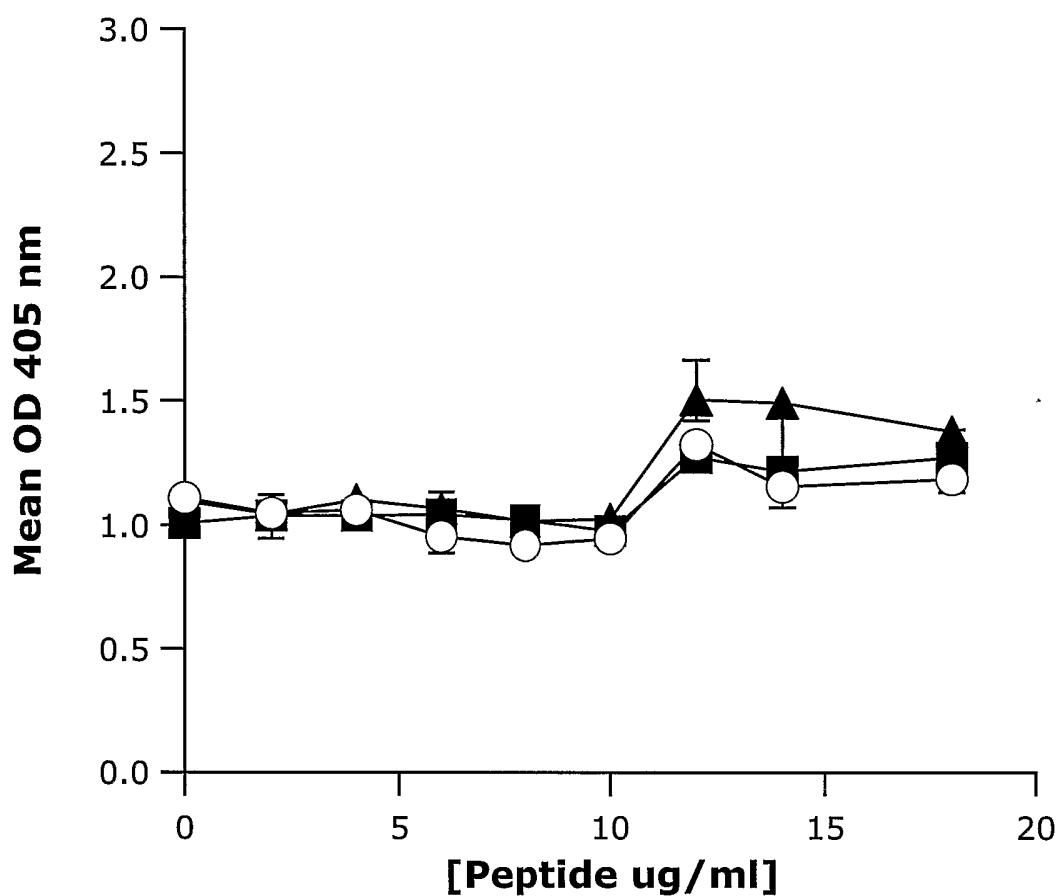


FIG. 42

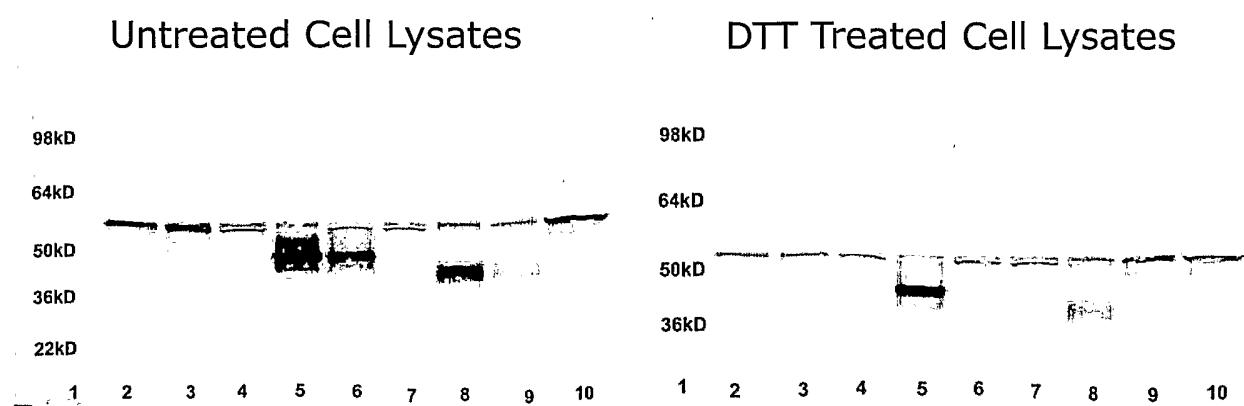
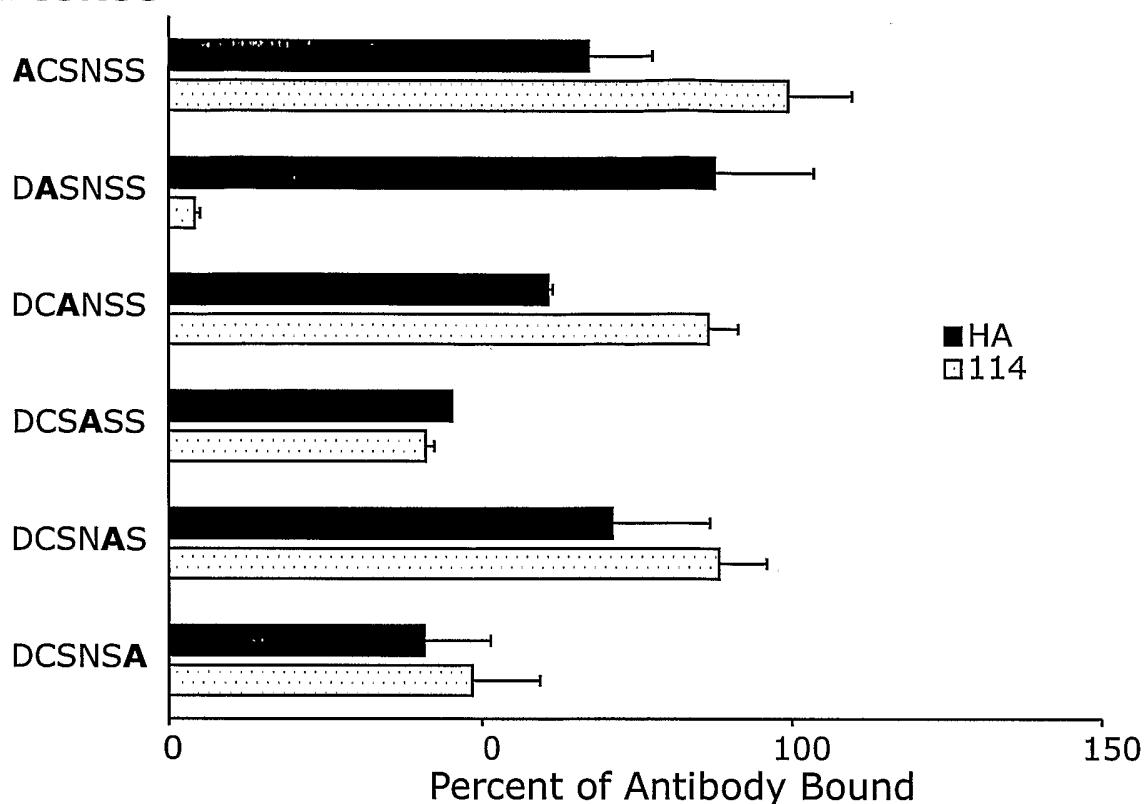
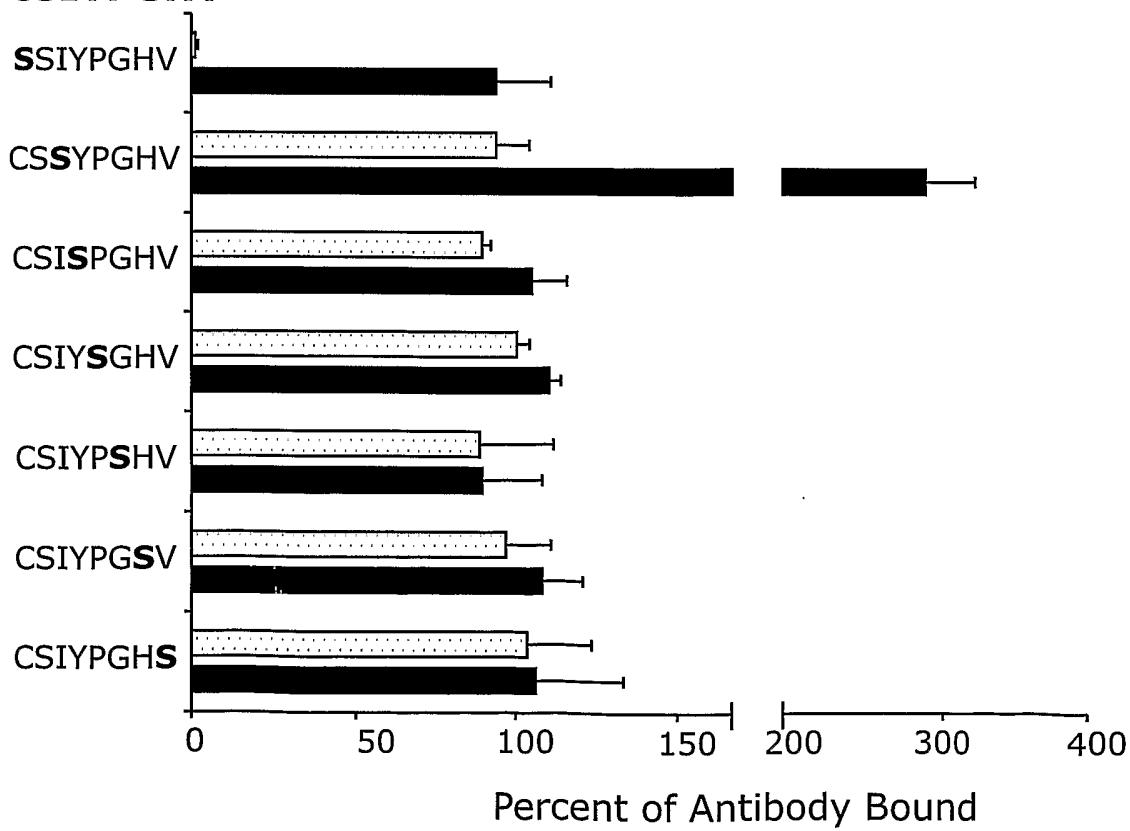


FIG. 44

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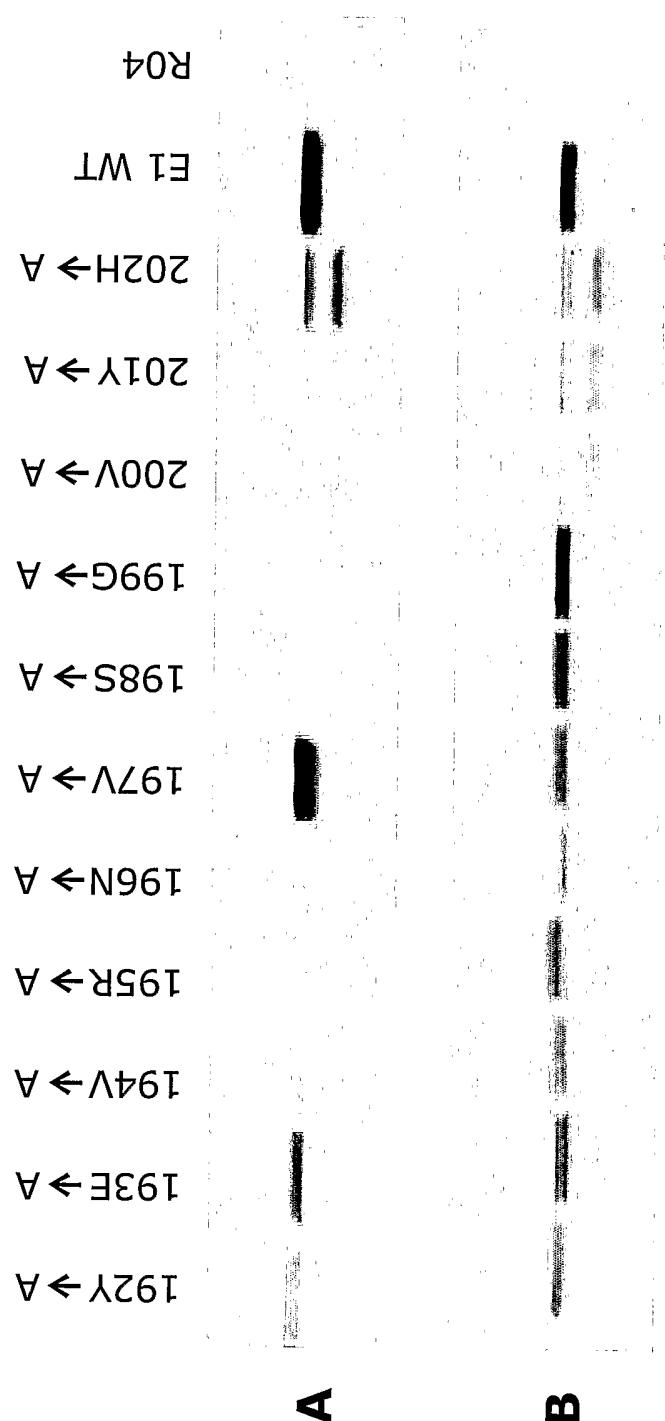
DCSNSS**FIG. 43A****CSIYPGHV****FIG. 43B**

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C₂₀₇.....C₂₂₆ C₂₂₉.....C₂₃₈.....C₂₇₂ C₂₈₁.....C₃₀₄ C₃₀₆

Plasmid	Mutants	IFA & comments			
		HA	H-114	H-111	R04
107	E1 WT	+	--	+	--
817	E1-Cys-226 /A	+	--	+	--
818	E1-Cys-226 /A	+	--	+	--
821	E1-Cys-229 /A	+	--	+	--
822	E1-Cys-229 /A	+	--	+	--
825	E1-Cys-238 /A	+	--	+	--
826	E1-Cys-238 /A	+	--	+	--
829	E1-Cys-272 /A	+	+	+	--
830	E1-Cys-272 /A	+	+	+	--
833	E1-Cys-281 /A	+	+	+	--
834	E1-Cys-281 /A	+	+	+	--
837	E1-Cys-304 /A	+	--	+	--
838	E1-Cys-304 /A	+	--	+	--

FIG. 45

50/50**FIG. 46**

SEQUENCE LISTING

<110> Foung, et al.

<120> Prevention and Treatment of HCV Infection Employing Antibodies Directed Against Conformational and Linear Epitopes

<130> 2002850-0039

<140> TBA

<141> 2003-06-27

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 160

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Is a comparison of sequences of HCV

<400> 1

ctcaactgga ttcaccaaag tgtgcggagc gcctccttgt gtcatcgag gggcgggcaa 60
caacacccctg cactgccccca ctgattgctt ccgcaagcat ccggacgcca catactctcg 120
gtgcggctcc ggtccctgga tcacacccag gtgcctggtc 160

<210> 2

<211> 159

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Is a comparison of sequences of HCV

<400> 2

ctcaactgga ttcaccaaagt gtgcggagcg ccccccgttg tcatcgagg ggcgggcaac 60
aacacccctgc gctgccccac tgattgttc cgcaagcatc cggaagccac gtactctcg 120
tgcggctccg gtccctggat tacgccccagg tgcctggtc 159

<210> 3

<211> 159
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Is a comparison
of sequences of HCV

<400> 3
tagtactggg ttcactaaga cgtgcggagc ccccccgtgta acatcgaaaa ggtcggttaac 60
cgcaccccttga tctgccccac ggactgtttc cggaagcacc ccggaggctac ttacacaaaa 120
tgtggctcgg ggccctggtt gacgcctagg tgcctagta 159

<210> 4
<211> 161
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Is a comparison
of sequences of HCV

<400> 4
tggcacaggg ttcactaaga ctgtgtggg gccccccatg taacatcgaaaa ggggtcggttaac 60
atcgacacccctt gacttggccc acggactgtt tccggaaagca ccccgaggct acttacacca 120
aatgtggttc ggggccttgg ctgacgccta ggtgcatagt t 161

<210> 5
<211> 166
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Is a comparison
of sequences of HCV

<400> 5
tggcacaggg tacactaaga ctgtgtggcag accaccctgc cgcattaggg ctgactttaa 60
tgccagcatg gacttggttgt gccccacggc ctgttttagg aagcaccctg atactaccta 120
catcaaatgt gggtctgggc ctggctgac gccaagggtgc ataatt 166

<210> 6
<211> 167
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Is a comparison
of sequences of HCV

<400> 6

tggcacaggt tacactaaga cttgtggcag accaccctgc cgcat taggg ctgactttaa 60
tgccagcacg gacttggttg tgccccacgg actgttttag gaagcaccct gaaactactt 120
acatcaaatg tggttctggg cctctgctga cgccaaagtg cataata 167

<210> 7

<211> 166

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Is a comparison
of sequences of HCV

<400> 7

tgggacaggg tacactaaga catgtggtag accaccctgc cgcat tagga aagactataa 60
tggcagtatc gatattttgt gcccccacaga ctgttttagg aagcacccag atactaccta 120
tctcaaatgt ggagcagggc ctctgttaac tccaaagtgc ataata 166

<210> 8

<211> 166

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Is a comparison
of sequences of HCV

<400> 8

tgggacaggg tacactaaga catgtggtag accaccctgc cgcat tagga aagactataa 60
tggacagctc gacttattgt gcccccacaga ctgttttaga aagcacccag atactaccta 120
tctcaaatgt ggagcggggc ctctgttgac cccaaaatgc ataata 166

<210> 9

<211> 160

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Describes

sequences amplified from the central region of the HCV E2 vaccinia virus clones.

<400> 9
ctcaactgga ttcaccaaag tgtgcggagc gccccctgt gtcatcgag gggcgggcaa 60
caacacccctg cgctgccccca ctgattgttt ccgcaagcat ccggaagcca cgtactctcg 120
gtgcggctcc ggtccctgga ttacgcccag gtgcctggtc 160

<210> 10
<211> 160
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Describes sequences amplified from the central region of the HCV E2 vaccinia virus clones.

<400> 10
tggcacaggg ttcaccaaaga cgtgtgggc ccccccattgt aacatcgaaa gggtcggcaa 60
taacacccctg acttgccccca cggactgttt ccggaagcac cccgaggcca cttacaccaa 120
atgtggttcg gggccttggc tgacacccatgtt gtgcata 160

<210> 11
<211> 164
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Describes sequences amplified from the central region of the HCV E2 vaccinia virus clones.

<400> 11
ctccactgtt tcacccaaac ttgcggcgca ccaccctgcc gcatcagagc tgactttaat 60
gccagcacgg acctgctgtg ccccacggac tgtttcagga agcatcctga agccacttac 120
atcaaatagtg gctctgggcc cctgtgacgc caaagtgcct gata 164

<210> 12
<211> 166
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Describes

sequences amplified from the central region of the HCV E2 vaccinia virus clones.

<400> 12

tgggactggg ttcactaaga catgcgggtgc accaccctgc cgcatttagga gggactgcaa 60
cggaaccctc gacctattgt gccccacaga ctgtttcaga aagcacccag atactaccta 120
ccttaagtgt ggagcggggc ctgggttgc ccccaaatgc atggta 166

<210> 13

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Flag epitope

<400> 13

Asp Tyr Lys Asp Asp Asp Asp Lys
1 . 5

<210> 14

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:The T7 tag sequence

<400> 14

Met Ala Ser Met Thr Gly Gly Gln Met Gly
1 . 5 . 10

<210> 15

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:The S-tag sequence

<400> 15

Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
1 . 5 . 10 . 15

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Reverse transcription reactions were performed using MMLV reverse transcriptase employing the reverse HCV specific primer

<400> 16
cgcgcacraa gtasgggact 20

<210> 17
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3 units of ampliTaq polymerase, and the forward primer HCV

<400> 17
Cys Gly Cys Ala Thr Gly Gly Cys Ile Thr Gly Gly Ala Tyr Ala
1 5 10 15
Thr Gly Ala Thr Gly
20

<210> 18
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide primers were designed to amplify fragments that expressed the final 39 amino acids of E1

<400> 18
Cys Gly Ala Gly Gly Cys Ile Thr Cys Ala Thr Ala Thr Gly Ala Thr
1 5 10 15

Cys Gly Cys Thr Gly Gly Thr Gly Cys Thr Thr Gly Gly
20 25

<210> 19
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide
primers were designed to amplify fragments that
expressed the final 39 amino acids of E1

<400> 19
cggaatccct gcagctacaa actggcttga agaatcca 38

<210> 20
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide
primers were designed to amplify fragments that
expressed the final 39 amino acids of E1

<400> 20
cgcatatgga gctcgcgggg gcccactggg gagt 34

<210> 21
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide
primers were designed to amplify fragments that
expressed the final 39 amino acids of E1

<400> 21
gctctagact gcagctatat gccagcctgg agcaccat 38

<210> 22
<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide primers were designed to amplify fragments that expressed the final 39 amino acids of E1

<400> 22

cgctcgagcc atggttggcg gggctcattg gggc

34

<210> 23

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide primers were designed to amplify fragments that expressed the final 39 amino acids of E1

<400> 23

tcgaattcgg atcctacaaa gcacctttta ggagataa

40

<210> 24

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide primers were designed to amplify fragments that expressed the final 39 amino acids of E1

<400> 24

cgctcgagcc atggtttcg gcggccattg ggtg

34

<210> 25

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide primers were designed to amplify fragments that

expressed the final 39 amino acids of E1

<400> 25

tcgaattcgg atcctacaga gacgctttaa ggaggttaggc

40

<210> 26

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide primers were designed to amplify fragments that expressed the final 39 amino acids of E1

<400> 26

Thr Gly Gly Thr Thr Cys Gly Gly Asx Thr Gly Tyr Trp Cys Ile Thr
1 5 10 15

Gly Gly Ala Thr Gly Ala Ala

20

<210> 27

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide primers were designed to amplify fragments that expressed the final 39 amino acids of E1

<400> 27

Thr Ala Ala Thr Gly Cys Cys Ala Ile Ala Arg Cys Cys Lys Arg Thr
1 5 10 15

Ala Ile Gly Gly Thr Ala Gly Thr Cys

20 25

<210> 28

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Shows an alignment of amino acid sequences of E1 constructs from HCV E1 1b (ZYK-E1); full-length HCV 1b (HPCJ491); and H isolate of HDV

<400> 28
Tyr Glu Val Arg Asn Val Ser
1 5

<210> 29
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Shows an alignment of amino acid sequences of E1 constructs from HCV E1 1b (ZYK-E1); full-length HCV 1b (HPCJ491); and H isolate of HDV

<400> 29
Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn
1 5 10

<210> 30
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Shows an alignment of amino acid sequences of E1 constructs from HCV E1 1b (ZYK-E1); full-length HCV 1b (HPCJ491); and H isolate of HDV

<400> 30
Cys Asn Cys Ser Ile Tyr Pro Gly His Val Tyr Gly
1 5 10

<210> 31
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Shows an alignment of amino acid sequences of E1 constructs from HCV E1 1b (ZYK-E1); full-length HCV 1b (HPCJ491); and H isolate of HDV

<400> 31
Asp Cys Ser Asn Ser Ser
1 5

<210> 32
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Shows an alignment of amino acid sequences of E1 constructs from HCV E1 1b (ZYK-E1); full-length HCV 1b (HPCJ491); and H isolate of HDV

<400> 32
Asp Cys Ser Asn Ser Ser
1 5

<210> 33
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Shows an alignment of amino acid sequences of E1 constructs from HCV E1 1b (ZYK-E1); full-length HCV 1b (HPCJ491); and H isolate of HDV

<400> 33
Cys Ser Ile Ser Pro Gly His Val
1 5

<210> 34
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Shows an alignment of amino acid sequences of E1 constructs from HCV E1 1b (ZYK-E1); full-length HCV 1b (HPCJ491); and H isolate of HDV

<400> 34
Cys Ser Ile Tyr Pro Gly His Val
1 5

<210> 35
<211> 192
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Shows an alignment of amino acid sequences of E1 constructs from HCV E1 1b (ZYK-E1); full-length HCV 1b (HPCJ491); and H isolate of HDV

<400> 35
Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp Cys
1 5 10 15

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr
20 25 30

Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Thr Ser Arg Cys Trp
35 40 45

Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr
50 55 60

Ala Ala Ile Arg Arg His Ile Asp Leu Leu Val Gly Thr Ala Thr Phe
65 70 75 80

Cys Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val
85 90 95

Ser Gln Leu Phe Thr Phe Ser Pro Arg Arg His His Thr Val Gln Asp
100 105 110

Cys Asn Cys Ser Ile Tyr Pro Gly His Val Thr Gly His Arg Met Ala
115 120 125

Trp Asp Met Met Met Asn Trp Ser Pro Thr Ala Ala Leu Val Val Ser
130 135 140

Gln Leu Leu Arg Ile Pro Gln Ala Val Met Asp Met Val Ala Gly Ala
145 150 155 160

His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Ala Gly Asn
165 170 175

Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
180 185 190

<210> 36

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Shows an alignment of amino acid sequences of E1 constructs from HCV E1 1b (ZYK-E1); full-length HCV 1b (HPCJ491); and H isolate of HDV

<400> 36

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
1 5 10 15

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Val Ile Met His Thr
20 25 30

Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ser Ser Arg Cys Trp
35 40 45

Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asp Ala Ser Val Pro Thr
50 55 60

Thr Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Thr Ala Ala Phe
65 70 75 80

Cys Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Ile Phe Leu Val
85 90 95

Ser Gln Leu Phe Thr Phe Ser Pro Arg Arg His Glu Thr Val Gln Asp
100 105 110

Cys Asn Cys Ser Ile Tyr Pro Gly His Val Ser Gly His Arg Met Ala

115	120	125
Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser		
130	135	140
Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala		
145	150	155
His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn		
165	170	175
Trp Ala Lys Val Leu Ile Val Ala Leu Leu Phe Ala Gly Val Asp Gly		
180	185	190

<210> 37
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Shows an alignment of amino acid sequences of E1 constructs from HCV E1 1b (ZYK-E1); full-length HCV 1b (HPCJ491); and H isolate of HDV

<400> 37
Tyr Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val Thr Asn Asp Cys
1 5 10 15

Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu His Thr
20 25 30

Pro Gly Cys Val Pro Cys Val Arg Glu Ser Asn Ser Ser Arg Cys Trp
35 40 45

Val Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Thr
50 55 60

Thr Gln Leu Arg Arg His Val Asp Leu Leu Val Gly Ser Ala Ala Leu
65 70 75 80

Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser Ile Phe Leu Val
85 90 95

Gly Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Asp
100 105 110

Cys Asn Cys Thr Ile Tyr Pro Gly His Ile Ser Gly His Arg Met Ala
115 120 125

Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ala
130 135 140

Gln Leu Leu Arg Ile Pro Gln Ala Pro Ile Val Asp Met Ile Ala Gly
145 150 155 160

Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met Val Gly
165 170 175

Asn Trp Ala Lys Val Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp
180 185 190

Ala

<210> 38

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Indicates
presence and size (in amino acids) of IgK signal
peptide, hemagglutinin epitope and linker amino
acids

<400> 38

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp
20

<210> 39

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Indicates

presence and size (in amino acids) of IgK signal peptide, hemagglutinin epitope and linker amino acids

<400> 39
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 40
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Indicates presence and size (in amino acids) of linker sequence, c-myc epitope and PDGFR transmembrane domain

<400> 40
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 41
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Indicates presence and size (in amino acids) of linker sequence, c-myc epitope and PDGFR transmembrane domain

<400> 41
Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu
1 5 10 15

Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
20 25 30

Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro
35 40 45

Arg