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(54) **Title**: MULTI-VALENT HEPATITIS B VIRUS ANTIGEN BINDING MOLECULES AND USES THEREOF

(57) **Abstract**: This disclosure provides a multimeric hepatitis B virus (HBV) protein binding molecule, e.g., a dimeric IgA or a pentameric or hexameric IgM binding molecule, comprising at least two bivalent binding units, or variants or fragments thereof, each comprising at least two antibody heavy chain constant regions or fragments thereof, wherein each heavy chain constant region or fragment thereof is associated with an HBV antigen binding domain. The disclosure also provides compositions comprising the multimeric binding molecules, polynucleotides encoding the multimeric binding molecules, and methods to make and use the multimeric binding molecules.

# MULTI-VALENT HEPATITIS B VIRUS ANTIGEN BINDING MOLECULES AND USES THEREOF

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## CROSS REFERENCE TO RELATED APPLICATION

**[0001]** This application claims the benefit of U.S. Provisional Application Serial No. 62/137,881, filed on March 25, 2015, which is incorporated herein by reference in its entirety.

## BACKGROUND

**[0002]** Hepatitis B virus (HBV) belongs to the class of double stranded DNA viruses and is presently known to include four major serotypes (adr, adw, ayr, and ayw) and eight major genotypes (A though H). The serotypes are based on variations in envelope protein sequences while the eight genotypes are distinctly distributed across the world in specific geographical areas. Genotypic differences have been linked to disease severity and effectiveness of response to treatment (see Kramvis *et al.*, *Vaccine*, 23(19):2409–23, 2005, and Magnius *et al.*, *Intervirology*, 38(1–2):24–34, 1995).

**[0003]** The HBV genome is comprised of circular DNA that is partially double stranded. That is, there are portions of the genome that are single stranded. The longer portion of the HBV genome is 3020 to 3320 nucleotides in length, while the shorter portion is 1700 to 2800 nucleotides in length. The longer portion of the HBV genome is linked to the viral DNA polymerase.

**[0004]** HBV-infected cells can produce, in addition to infectious virus particles, spherical and filamentous non-infectious particles lacking a core. These non-infectious particles can outnumber infectious particles in an HBV-infected individual by as much as 1,000 to 100,000 fold (see Chai *et al. J. Virol.* 82:7812-7817, 2005).

**[0005]** There are five viral proteins produced by HBV, including the following:

1. Envelope protein (also known as surface antigen, HBsAg, encoded by the S gene);
2. Polymerase (pol, encoded by the P gene);
3. Hepatitis B X-protein (HBxAg, X-antigen, encoded by the X gene);
4. Nucleocapsid or core antigen (HBcAg, encoded by the C gene); and
5. Precore (HBeAg, encoded by the core and Pre-C genes).

**[0006]** The HBsAg is produced in three sizes from the three independent start codons in the HBV genome. The Small, Medium and Large versions of this gene product are a combination of one or more of the three designated domains: (i) S alone (S), (ii) pre-S2 and S (M), or (iii) pre-S1 and pre-S2 and S (L) (FIG. 1A). Infectious particles most often possess all three versions of this antigen, and can enter hepatocytes via the interaction between pre-S1 protein (**FIG. 1B**) and the NTCP receptor (sodium taurocholate co-transporting polypeptide, or liver bile acid transporter, encoded by the *SLC10A1* gene). Thus, the pre-S1 antigen is associated with infection and is preferentially expressed in infectious viral particles. (Hong *et al.*, *Virology*, 318:134-141, 2004; Park *et al.*, *Antiviral Res.*, 68:109-115, 2005).

**[0007]** HBeAg is the precore protein and is secreted. The precore protein has been shown to play an immune regulatory role. HBeAg has been found to regulate the immune response to the core antigen. (Chen *et al.*, *Proc. Natl. Acad. Sci. USA*, 101:14913–14918, 2004).

**[0008]** While the functions of the capsid, polymerase and surface antigen proteins seem clear, the function of the "X" gene has yet to be fully elucidated, though it is known to play a role in the development of hepatocellular carcinoma (HCC). (Tang *et al.*, *Cancer Sci.*, 97:977-983, 2006, Ng *et al.*, *J. Gastroent.*, 46:974-990, 2011, and Kew, Michael C., *J. Gastro. Hepat.*, 26 Suppl. 1:144-152, 2011).

**[0009]** The hepatitis B virus is believed to have infected more than 2 billion people around the world. There are believed to be 350 to 400 million chronically or persistently infected individuals worldwide and HBV or complications from HBV infection results in 780,000 deaths per year worldwide. HBV is fifty to one hundred times more infectious than the human immunodeficiency virus (HIV). HBV is transmitted by exposure to infectious blood or body fluids. Symptoms of infection commonly include loss of appetite, fatigue, a low fever, jaundice, aches in muscles and joints, nausea and vomiting, yellow skin and dark urine. Some individuals are not able to completely clear the virus from their system, resulting in a chronic infection that can result in liver damage and cirrhosis. About 15 to 40% of chronic HBV patients develop liver

cirrhosis and/or HCC. (Xu *et al.*, *Canc. Lett.*, 345:216-222, 2014). The HBV viral genome persists in the genome of the host and can be reactivated after being cleared, leading to new HBV symptoms. The rate of liver cancer is much higher in those who have an HBV infection.

**[0010]** Both clearance and pathogenesis of the virus are mediated by the adaptive, or acquired, immune response. This includes both a humoral (antibody-mediated) immunity component and cell-mediated immune component. In particular, infection triggers response of virus-specific cytotoxic T lymphocytes (CTL), which produce most of the observed injury to liver tissue in chronic infections.

**[0011]** Many preventive strategies have been developed to combat HBV infection. Vaccines have been developed based on recombinant surface antigen of the virus. (*See*, WO 2014/0489101 and Shouval, D., *J. Hepatol.* 39 (Suppl. l):70-76, 2003). In addition, an HBV immunoglobulin (HBIG) has been developed from human sera from high titer individuals. HBIG is typically provided to infants of HBV infected mothers to prevent transmission to the child. If HBIG is administered within 24 hours of known exposure, HBV infection can be prevented. HBIG is also commonly administered to HBV infected liver transplant patients to prevent re-infection of the new tissue.

**[0012]** Chronically infected individuals are candidates for therapy. However, there is presently no approved treatment known to clear chronic HBV infection. Available therapies can block further infection by precluding the virus from replicating. Various monoclonal antibodies and combination therapies have been investigated for the purpose of treating and/or curing HBV infection, including chronic HBV infection, but none have been commercialized.

**[0013]** The treatment options for chronic infection, *e.g.*, interferon and lamivudine, are only modestly effective and are known to cause severe side effects. Despite efforts directed toward the development of therapies for treatment or prevention of HBV infection, there remains a continuing need to develop new therapies targeting HBV infection, *e.g.*, chronic HBV infection. It is an object of the present invention to go someway towards meeting this need and/or to at least provide the public with a useful choice.

# SUMMARY

[0013A] In a first aspect, the invention provides a multimeric antibody comprising at least two bivalent binding units, or functional variants or functional fragments thereof;

wherein each binding unit comprises two IgM or IgA antibody heavy chain constant regions or functional fragments thereof, each associated with an antigen binding domain;

wherein the antigen binding domains specifically bind to a hepatitis B virus (HBV) antigen expressed on the surface of infectious viral particles, on the surface of HBV infected cells, or a combination thereof, and

wherein the multimeric antibody is more potent in inhibiting HBV proliferation, enhancing HBV clearance, controlling HBV infectivity and/or controlling HBV growth than a reference IgG antibody comprising the antigen binding domain that specifically binds to the HBV antigen.[0013B] In a second aspect, the invention provides an isolated IgM antibody or functional fragment thereof comprising a J-chain or functional fragment thereof or functional variant thereof and five binding units, each comprising two heavy chains and two light chains, wherein each heavy chain comprises a human Mu constant region or functional fragment thereof, and the heavy chain variable region amino acid sequence SEQ ID NO: 62, and wherein each light chain comprises a human kappa constant region and the light chain variable region amino acid sequence SEQ ID NO: 6; wherein the antibody or functional fragment thereof can assemble into a pentameric IgM antibody that can specifically bind to the pre-S1 region of HBV surface antigen.

[0013C] In a third aspect, the invention provides a polynucleotide comprising a nucleic acid sequence that encodes at least one polypeptide subunit of the multimeric antibody according to the first aspect, or the isolated IgM antibody or functional fragment thereof according to the second aspect, wherein the polypeptide subunit comprises the IgM heavy chain constant region and at least the antibody VH portion of an antibody binding domain that specifically binds to a hepatitis B virus (HBV) antigen expressed on the surface of infectious viral particles, on the surface of HBV-infected cells, or a combination thereof, and/or the polypeptide subunit comprises the antibody VL portion of an antibody binding domain that specifically binds to a hepatitis B virus (HBV) antigen expressed on the surface of infectious viral particles, on the surface of HBV-infected cells, or a combination thereof.

[0013D] In a fourth aspect, the invention provides a composition comprising:

(a) a first polynucleotide comprising a nucleic acid sequence that encodes the IgM heavy chain constant region and at least the antibody VH portion of the antibody binding domain of the multimeric antibody according to the first aspect, or the isolated IgM antibody or functional fragment thereof according to the second aspect; and

(b) a second polynucleotide comprising a nucleic acid sequence that encodes the VL portion of the antibody binding domain of the multimeric antibody according to the first aspect, or the isolated IgM antibody or functional fragment thereof according to the second aspect.

[0013E] In a fifth aspect, the invention relates to host cell comprising the composition according to the fourth aspect, wherein the host cell can express the multimeric antibody according to the first aspect, or the isolated IgM antibody or functional fragment thereof according to the second aspect.

[0013F] In a sixth aspect, the invention provides a method of producing the multimeric antibody according to the first aspect, or the isolated IgM antibody or functional fragment thereof according to the second aspect, comprising culturing the host cell according to the fifth aspect, and recovering the multimeric antibody or the isolated IgM antibody or functional fragment thereof.

[0013G] In a seventh aspect, the invention provides a method of controlling hepatitis B virus (HBV) proliferation, latency, or maintenance in chronically-infected cells, comprising contacting a mixture of HBV and HBV-susceptible cells with the multimeric antibody according to the first aspect, or the isolated IgM antibody or functional fragment thereof according to the second aspect, wherein the multimeric antibody or isolated IgM antibody or functional fragment thereof is more potent than a reference IgG antibody comprising the antigen binding domain that specifically binds to the HBV antigen.

[0013H] In an eighth aspect, the invention provides a method of treating a disease or condition caused by or exacerbated by hepatitis B virus (HBV) infection in a patient, comprising administering to a patient infected with HBV or susceptible to HBV infection the multimeric antibody according to the first aspect, or the isolated IgM antibody or functional fragment thereof according to the second aspect, wherein multimeric antibody or isolated IgM antibody or functional fragment thereof is more potent than a reference IgG antibody comprising the antigen binding domain that specifically binds to the HBV antigen.

## BRIEF DESCRIPTION

**[0014]** Disclosed are various embodiments of multimeric binding molecules that possess specificity for binding one or more hepatitis B antigens. This disclosure includes a multimeric binding molecule that includes at least two bivalent binding units, or variants or fragments thereof; where each binding unit includes at least two antibody heavy chain constant regions or fragments thereof, each associated with an antigen binding domain; where at least one antigen binding domain specifically binds to a hepatitis B virus (HBV) antigen expressed on the surface of infectious viral particles, on the surface if HBV infected cells, or a combination thereof, and where the binding molecule is more potent than a reference single bivalent binding unit that includes the same antigen binding domain that specifically binds to the HBV antigen. In certain embodiments, the reference single bivalent binding unit is an IgG antibody.

**[0015]** In certain embodiments, the binding molecule can be a dimeric binding molecule including two bivalent IgA binding units or fragments thereof and a J-chain or fragment or variant thereof, where each binding unit includes two IgA heavy chain constant regions or fragments thereof each associated with an antigen-binding domain. In certain embodiments, the dimeric binding molecule can further include a secretory component, or fragment or variant thereof. In certain embodiments, the IgA heavy chain constant regions or fragments thereof each include a Cα2 domain or a Cα3-tp domain, and can further include a Cα1 domain. In certain embodiments, the IgA heavy chain constant region is a human IgA constant region. In certain embodiments, each binding unit of a dimeric binding molecule described herein can include two IgA heavy chains each including a VH situated amino terminal to the IgA constant region or fragment thereof, and two immunoglobulin light chains each including a VL situated amino terminal to an immunoglobulin light chain constant region.

**[0016]** In certain embodiments the binding molecule can be a pentameric or a hexameric binding molecule including five or six bivalent IgM binding units, respectively, where each binding unit includes two IgM heavy chain constant regions or fragments thereof each associated with an antigen binding domain. In certain embodiments the IgM heavy chain constant regions or fragments thereof each include a Cμ3 domain and a Cμ4-tp domain, and can further include a Cμ2 domain, a Cμ1 domain, or any combination thereof. In certain embodiments a pentameric binding molecule is described that further includes a J-chain, or fragment thereof, or variant

thereof. In certain embodiments at least one heavy chain constant region of a hexameric or pentameric binding molecule as described herein is a human IgM constant region. In certain embodiments each binding unit of a hexameric or pentameric binding molecule as described herein includes two heavy chains each including a VH situated amino terminal to the constant region or fragment thereof, and two immunoglobulin light chains each including a VL situated amino terminal to an immunoglobulin light chain constant region.

**[0017]** In certain embodiments, at least one binding unit of a dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody described herein includes two antigen binding domains that specifically bind to a hepatitis B virus (HBV) antigen expressed on the surface of infectious viral particles, on the surface of HBV-infected cells, or a combination thereof, and the two heavy chains within the binding unit are identical. In certain embodiments, the two light chains within the binding unit are identical. In certain embodiments, the light chain constant regions of the binding unit are human lambda constant regions or human kappa constant regions. In certain embodiments the binding molecule includes at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, or at least twelve antigen binding domains that specifically bind to a hepatitis B virus (HBV) antigen expressed on the surface of infectious viral particles, on the surface of HBV-infected cells, or a combination thereof. In certain embodiments at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven or at least twelve of the binding domains are identical.

**[0018]** Where the binding molecule is pentameric, the binding molecule can further include a J-chain, or fragment thereof, or functional fragment thereof, or a functional variant thereof. In certain embodiments, the J-chain or fragment thereof includes the amino acid sequence SEQ ID NO: 54 or a functional fragment thereof. In certain embodiments, the J-chain or fragment thereof can further include a heterologous polypeptide. The heterologous polypeptide can be directly or indirectly fused to the J-chain or fragment thereof. In certain embodiments the heterologous polypeptide can be indirectly fused to the J-chain or fragment thereof via a peptide linker. In certain embodiments the peptide linker can include, *e.g.*, at least 5 amino acids, but no more than 25 amino acids. In certain embodiments the peptide linker consists of GGGGSGGGGSGGGGS (SEQ ID NO: 72). The heterologous polypeptide can be fused to or near the N-terminus of the J-chain or fragment thereof, the C-terminus of the J-chain or

fragment thereof, or to both the N-terminus and C-terminus of the J-chain or fragment thereof. In certain embodiments the heterologous polypeptide can include a binding domain, *e.g.*, an antibody or antigen-binding fragment thereof. The antigen-binding fragment can be, for example, an Fab fragment, an Fab' fragment, an $F(ab')_2$ fragment, an Fd fragment, an Fv fragment, a single-chain Fv (scFv) fragment, a disulfide-linked Fv (sdFv) fragment, or any combination thereof. In certain embodiments the heterologous polypeptide can specifically bind to CD3ε. For example in certain embodiments the modified J-chain can include the amino acid sequence SEQ ID NO: 68 (V15J) or SEQ ID NO: 71 (J15V). Moreover in certain embodiments, these particular modified J-chains can further include a signal peptide, where the modified J-chain then includes the amino acid sequence SEQ ID NO: 67 (V15J) or SEQ ID NO: 70 (J15V).

**[0019]** In certain embodiments, the HBV antigen bound by a dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody as described herein is expressed on the surface of infectious viral particles, on the surface of HBV infected cells, or a combination thereof in higher density than the HBV antigen is expressed on non-infectious sub-viral particles. In certain embodiments, the HBV antigen is a hepatitis B surface antigen (HBsAg), a precore antigen, a core antigen, an X-antigen, or any combination thereof. In certain embodiments where the binding molecule binds to an HBsAg, it can include an S region (S), a pre-S2 and S region, or pre-S1, Pre-S2 and S regions, or fragments thereof.

**[0020]** In certain embodiments, at least one antigen binding domain of a dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody as described herein includes the HCDR1, HCDR2, and HCDR3 regions, or the HCDR1, HCDR2, and HCDR3 regions containing one or two single amino acid substitutions, and the LCDR1, LCDR2, and LCDR3 regions, or the LCDR1, LCDR2, and LCDR3 regions containing one or two single amino acid substitutions, as contained in the VH and VL amino acid sequences SEQ ID NO: 1 and SEQ ID NO: 3, SEQ ID NO: 2 and SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8, SEQ ID NO: 7 and SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 11, SEQ ID NO: 14 and SEQ ID NO: 15, SEQ ID NO: 16 and SEQ ID NO: 21, SEQ ID NO: 17 and SEQ ID NO: 22, SEQ ID NO: 18 and SEQ ID NO: 23, SEQ ID NO: 19 and SEQ ID NO: 24, SEQ ID NO: 20 and SEQ ID NO: 25, SEQ ID NO: 26 and SEQ ID NO: 27, SEQ ID NO: 26 and SEQ ID NO: 28, SEQ ID NO: 26 and SEQ ID NO: 29, SEQ ID NO: 30 and SEQ ID NO: 31, SEQ ID NO: 32 and SEQ ID NO: 33, SEQ ID NO: 34 and SEQ ID NO: 35,

SEQ ID NO: 34 and SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38, SEQ ID NO: 39 and SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44, SEQ ID NO: 45 and SEQ ID NO: 46, SEQ ID NO: 47 and SEQ ID NO: 48, SEQ ID NO: 49 and SEQ ID NO: 50, SEQ ID NO: 51 and SEQ ID NO: 52, SEQ ID NO: 62 and SEQ ID NO: 6, SEQ ID NO: 73 and SEQ ID NO: 74, or SEQ ID NO: 75 and SEQ ID NO: 76, respectively.

**[0021]** In certain embodiments, at least one antigen binding domain of a dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody as described herein includes the HCDR1, HCDR2, and HCDR3 regions, or the HCDR1, HCDR2, and HCDR3 regions containing one or two single amino acid substitutions, of the VH amino acid sequence SEQ ID NO: 12 or SEQ ID NO: 13.

**[0022]** In certain embodiments, at least one antigen binding domain of a dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody as described herein includes an antibody heavy chain variable region (VH) and an antibody light chain variable region (VL), where the VH and VL include, respectively, amino acid sequences that are at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 1 and SEQ ID NO: 3, SEQ ID NO: 2 and SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8, SEQ ID NO: 7 and SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 11, SEQ ID NO: 14 and SEQ ID NO: 15, SEQ ID NO: 16 and SEQ ID NO: 21, SEQ ID NO: 17 and SEQ ID NO: 22, SEQ ID NO: 18 and SEQ ID NO: 23, SEQ ID NO: 19 and SEQ ID NO: 24, SEQ ID NO: 20 and SEQ ID NO: 25, SEQ ID NO: 26 and SEQ ID NO: 27, SEQ ID NO: 26 and SEQ ID NO: 28, SEQ ID NO: 26 and SEQ ID NO: 29, SEQ ID NO: 30 and SEQ ID NO: 31, SEQ ID NO: 32 and SEQ ID NO: 33, SEQ ID NO: 34 and SEQ ID NO: 35, SEQ ID NO: 34 and SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38, SEQ ID NO: 39 and SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44, SEQ ID NO: 45 and SEQ ID NO: 46, SEQ ID NO: 47 and SEQ ID NO: 48, SEQ ID NO: 49 and SEQ ID NO: 50, SEQ ID NO: 51 and SEQ ID NO: 52, SEQ ID NO: 62 and SEQ ID NO: 6, SEQ ID NO: 73 and SEQ ID NO: 74, or SEQ ID NO: 75 and SEQ ID NO: 76.

**[0023]** In certain embodiments, at least one antigen binding domain of a dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody as described herein includes an antibody VH, where the VH includes an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 12 or SEQ ID NO: 13.

**[0024]** In certain embodiments the binding molecule as described herein is a hexameric or pentameric IgM antibody or fragment thereof that includes an IgM heavy chain including the amino acid sequence SEQ ID NO: 58 and a light chain including the amino acid sequence SEQ ID NO: 59. In certain embodiments the binding molecule as described herein is a hexameric or pentameric IgM antibody or fragment thereof that includes an IgM heavy chain including the amino acid sequence SEQ ID NO: 63 and a light chain including the amino acid sequence SEQ ID NO: 59.

**[0025]** In certain embodiments, a dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody as described herein can be more potent in virus neutralization, killing of infected cells, enhancing viral clearance, controlling HBV proliferation, latency, or maintenance in chronically-infected cells, than a reference single binding unit that includes the same HBV-binding antigen binding domains.

**[0026]** The disclosure further describes an isolated IgM antibody or fragment thereof that includes a J-chain, or functional fragment or variant thereof, and five binding units, each including two heavy chains and two light chains, where each heavy chain or fragment thereof that includes a human Mu constant region or fragment thereof, and the heavy chain variable region amino acid sequence SEQ ID NO: 62, and wherein each light chain can include a human kappa constant region and the light chain variable region amino acid sequence SEQ ID NO: 6; wherein the antibody or fragment thereof can assemble into a pentameric IgM antibody that can specifically bind to the pre-S1 region of HBV surface antigen. In certain embodiments, the heavy chain of the IgM antibody or fragment thereof includes the amino acid sequence SEQ ID NO: 63, and the light chain of the IgM antibody or fragment thereof includes the amino acid sequence SEQ ID NO: 59. In certain embodiments, the J-chain or fragment thereof includes the amino acid sequence SEQ ID NO: 54 or a functional fragment thereof. In certain embodiments, the J-chain or fragment thereof can further include a heterologous polypeptide. The heterologous polypeptide can be directly or indirectly fused to the J-chain or fragment thereof. In certain embodiments the heterologous polypeptide can be indirectly fused to the J-chain or fragment thereof via a peptide linker. In certain embodiments the peptide linker can include, *e.g.*, at least 5 amino acids, but no more than 25 amino acids. In certain embodiments the peptide linker consists of GGGGSGGGGSGGGGS (SEQ ID NO: 72). The heterologous polypeptide can be fused to or near the N-terminus of the J-chain or fragment thereof, the C-terminus of the J-chain or fragment thereof, or to both the N-terminus and C-terminus of the J-chain or fragment

thereof. In certain embodiments the heterologous polypeptide can include a binding domain, *e.g.*, an antibody or antigen-binding fragment thereof. The antigen-binding fragment can be, for example, an Fab fragment, an Fab' fragment, an $F(ab')_2$ fragment, an Fd fragment, an Fv fragment, a single-chain Fv (scFv) fragment, a disulfide-linked Fv (sdFv) fragment, or any combination thereof. In certain embodiments the heterologous polypeptide can specifically bind to CD3ε. For example in certain embodiments the modified J-chain can include the amino acid sequence SEQ ID NO: 68 (V15J) or SEQ ID NO: 71 (J15V). Moreover in certain embodiments, these particular modified J-chains can further include a signal peptide, where the modified J-chain then includes the amino acid sequence SEQ ID NO: 67 (V15J) or SEQ ID NO: 70 (J15V).

**[0027]** The disclosure further describes a composition that includes the dimeric, pentameric or hexameric binding molecule as described herein or the isolated IgM antibody as described herein.

**[0028]** This disclosure also describes a polynucleotide that includes a nucleic acid sequence that encodes a polypeptide subunit of the dimeric, pentameric, or hexameric binding molecule, *e.g.*, the IgM antibody as described herein, where the polypeptide subunit includes the IgM heavy chain constant region and at least the antibody VH portion of an antibody binding domain that specifically binds to a hepatitis B virus (HBV) antigen expressed on the surface of infectious viral particles, on the surface if HBV infected cells, or a combination thereof. In certain embodiments, the polypeptide subunit includes a human IgA or IgM constant region or fragment thereof fused to the C-terminal end of a VH that includes: the HCDR1, HCDR2, and HCDR3 domains, or the HCDR1, HCDR2, and HCDR3 domains containing one or two single amino acid substitutions in one or more HCDRs, of the VH amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 26, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 62, SEQ ID NO: 73, or SEQ ID NO: 75; or an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 26, SEQ ID NO:

30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 62, SEQ ID NO: 73, or SEQ ID NO: 75.

**[0029]** This disclosure also describes a polynucleotide that includes a nucleic acid sequence that encodes a polypeptide subunit of the dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody as described herein, where the polypeptide subunit includes the antibody VL portion of an antibody binding domain that specifically binds to a hepatitis B virus (HBV) antigen expressed on the surface of infectious viral particles, on the surface of HBV-infected cells, or a combination thereof. In certain embodiments the polypeptide subunit can include a human antibody light chain constant region or fragment thereof fused to the C-terminal end of a VL that includes the LCDR1, LCDR2, and LCDR3 domains, or the LCDR1, LCDR2, and LCDR3 domains containing one or two single amino acid substitutions in one or more LCDRs, of the VL amino acid sequence SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 74, or SEQ ID NO: 76; or an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 74, or SEQ ID NO: 76.

**[0030]** The disclosure further describes a composition that includes a polynucleotide that encodes a heavy chain and a polynucleotide that encodes a light chain. The polynucleotides that are included in the composition can be contained on a single vector, or can be situated on separate vectors. In certain embodiments the composition can further include a polynucleotide that includes a nucleic acid sequence encoding a J-chain, or fragment thereof, or variant thereof, which can be on an entirely separate vector or on the same vector or vectors as either the heavy chain encoding polynucleotide and/or the light chain encoding polynucleotide.

**[0031]** The one, two, or more vectors described above are also described by the disclosure.

**[0032]** In an additional embodiment, the disclosure describes a host cell that includes the described polynucleotide, the described composition, or the described vector or vectors, where the host cell can express a dimeric, pentameric, or hexameric binding molecule as described herein, *e.g.*, the isolated IgM antibody described herein, or a subunit thereof. The disclosure also describes a method of producing a dimeric, pentameric, or hexameric binding molecule as described herein, *e.g.*, the isolated IgM antibody as described herein, where the method includes culturing the described host cell, and recovering the binding molecule.

**[0033]** The disclosure further describes a method of controlling hepatitis B virus (HBV) proliferation, latency, or maintenance in chronically-infected cells, *e.g.*, controlling viral attachment, infectivity, replication, latency, egress, etc., where the method includes contacting a mixture of HBV and HBV-susceptible cells with the dimeric, pentameric, or hexameric binding molecule as described herein, *e.g.*, the isolated IgM antibody described herein, where HBV replication is controlled at a greater potency than an IgG antibody including at least one antigen binding domain in common with the binding molecule.

**[0034]** The disclosure further includes a method of treating a disease or condition caused by or exacerbated by hepatitis B virus (HBV) infection in a patient, where the method includes administering to a patient infected with HBV or susceptible to HBV infection the dimeric, pentameric, or hexameric binding molecule as described herein, *e.g.*, the isolated IgM antibody described herein. In certain embodiments, the binding molecule can be more potent than a reference single binding unit antibody, *e.g.*, an IgG antibody that includes at least one antigen binding domain that specifically binds to the same HBV antigen as the binding molecule or IgM antibody. In certain embodiments the disease or condition can be, *e.g.*, acute hepatitis, chronic hepatitis, liver inflammation, cirrhosis of the liver, liver failure, hepatocellular carcinoma (HCC), or any combination thereof. In certain embodiments, the patient can exhibit one or more HBV disease symptoms such as, but not limited to increased viral load, virus shedding, abdominal pain, dark urine, fever, joint pain, loss of appetite, nausea and vomiting, weakness and fatigue, jaundice, or a combination thereof.

**[0035]** The disclosure further includes a method for identifying a binding molecule that binds to the surface of infectious virus particles, the surface of virus-infected cells, or a combination thereof with greater affinity, greater avidity, or a combination thereof, than to non-infectious virus

particles, where the method includes: (a) contacting a test binding molecule with an infectious viral particle and measuring the affinity or avidity of the test binding molecule for binding to the infectious viral particle; (b) contacting the test binding molecule with a non-infectious version of the virus particle and measuring the affinity or avidity of the test binding molecule for binding to the non-infectious particle; (c) comparing the results of steps (a) and (b); and (d) identifying test compounds in which the affinity or avidity measured in step (a) is higher than the affinity or avidity measured in step (b).

**[0036]** In another embodiment, the disclosure includes a method for identifying a binding molecule that binds to the surface of a cell infected with a virus of interest with greater affinity, greater avidity, or a combination thereof, than to a cell not infected with virus, where the method includes: (a) contacting a test binding molecule with a virus-infected cell and measuring the affinity or avidity of the test binding molecule for binding to the virus-infected cell; (b) contacting the test binding molecule with a cell not infected with virus and measuring the affinity or avidity of the test binding molecule for binding to the non-infected cell, where the non-infected cell is identical to the virus-infected cell except that it is not infected; (c) comparing the results of steps (a) and (b); and (d) identifying test compounds in which the affinity or avidity measured in step (a) is higher than the affinity or avidity measured in step (b).

**[0037]** In another embodiment the disclosure includes a method for identifying a binding molecule that binds to the surface of infectious hepatitis B virus (HBV) viral particles, the surface of HBV-infected cells, or a combination thereof with greater affinity, greater avidity, or a combination thereof, than to HBV subviral particles, where the method includes: (a) contacting a test binding molecule with an HBV viral particle and measuring the affinity or avidity of the test binding molecule for binding to an HBV viral particle; (b) contacting the test binding molecule with an HBV subviral particle and measuring the affinity or avidity of the test binding molecule for binding to an HBV subviral particle; (c) comparing the results of steps (a) and (b); and (d) identifying test compounds in which the affinity or avidity measured in step (a) is higher than the affinity or avidity measured in step (b).

**[0038]** In another embodiment the disclosure includes a method for identifying a binding molecule that binds to the surface of a cell infected with hepatitis B virus (HBV) with greater affinity, greater avidity, or a combination thereof, than to a cell not infected with HBV, where the method includes: (a) contacting a test binding molecule with an HBV-infected cell and measuring the

affinity or avidity of the test binding molecule for binding to the HBV-infected cell; (b) contacting the test binding molecule with a cell not infected with HBV and measuring the affinity or avidity of the test binding molecule for binding to a cell not infected with HBV, where the non-infected cell is identical to the HBV-infected cell except that it is not infected; (c) comparing the results of steps (a) and (b); and (d) identifying test compounds in which the affinity or avidity measured in step (a) is higher than the affinity or avidity measured in step (b). In certain embodiments the HBV-infected cell is a human cell. In certain embodiments the test binding molecule is the dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody described herein.

## BRIEF DESCRIPTION OF THE FIGURES

**[0039]** **Figure 1A**: linear structure of the HBV surface protein.

**[0040]** **Figure 1B:** conformation of the HBV surface protein in a membrane

**[0041]** **Figure 2A**: SDS polyacrylamide gel showing expression products from various HBV24 IgM constructs.

**[0042]** **Figure 2B**: SDS polyacrylamide gel showing expression products from HBV23 IgG and IgM constructs.

**[0043]** **Figure 2C**: SDS polyacrylamide gel showing expression products from HBV19 IgG and IgM constructs.

**[0044]** **Figure 3A**: ELISA results showing binding of purified HBV24M2V15J (triangles), purified HBV24G (squares), and HBV24G supernatant (circles) to HBsAg-L.

**[0045]** **Figure 3B**: ELISA results showing binding of purified HBV23MJ (triangles), purified HBV24G (squares) to HBsAg-L.

**[0046]** **Figure 4:** FACS analysis of HBV antibody binding to PLC hepatocarcinoma cells. Top Row: Anti-S antibody (HBV23 anti-HBsAg), IgG and IgM + human J-chain; bottom row: Anti preS1 antibody (HBV24G and HBV24M2V15J), IgG and IgM+V15J. The unlabeled histograms in each panel represent unstained PLC cells and PLC cells stained with the appropriate human antibody isotype controls (IgG or IgM).

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# DETAILED DESCRIPTION

Definitions

**[0047]** The term "a" or "an" entity refers to one or more of that entity; for example, "a binding molecule," is understood to represent one or more binding molecules. As such, the terms "a" (or "an"), "one or more," and "at least one" can be used interchangeably herein.

**[0048]** Furthermore, "and/or" where used herein is to be taken as specific disclosure of each of the two specified features or components with or without the other. Thus, the term and/or" as used in a phrase such as "A and/or B" herein is intended to include "A and B," "A or B," "A" (alone), and "B" (alone). Likewise, the term "and/or" as used in a phrase such as "A, B, and/or C" is intended to encompass each of the following embodiments: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

[0048A] The term “comprising” as used in this specification and claims means “consisting at least in part of”. When interpreting statements in this specification, and claims which include the term “comprising”, it is to be understood that other features that are additional to the features prefaced by this term in each statement or claim may also be present. Related terms such as “comprise” and “comprised” are to be interpreted in similar manner.

**[0049]** Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure is related. For example, the Concise Dictionary of Biomedicine and Molecular Biology, Juo, Pei-Show, 2nd ed., 2002, CRC Press; The Dictionary of Cell and Molecular Biology, 3rd ed., 1999, Academic Press; and the Oxford Dictionary Of Biochemistry And Molecular Biology, Revised, 2000, Oxford University Press, provide one of skill with a general dictionary of many of the terms used in this disclosure.

**[0050]** Units, prefixes, and symbols are denoted in their Système International de Unites (SI) accepted form. Numeric ranges are inclusive of the numbers defining the range. Unless otherwise indicated, amino acid sequences are written left to right in amino to carboxy orientation. The headings provided herein are not limitations of the various embodiments or aspects of the disclosure, which can be had by reference to the specification as a whole. Accordingly, the

terms defined immediately below are more fully defined by reference to the specification in its entirety.

**[0051]** As used herein, the term “non-naturally occurring” substance, composition, entity, and/or any combination of substances, compositions, or entities, or any grammatical variants thereof, is a conditional term that explicitly excludes, but only excludes, those forms of the substance, composition, entity, and/or any combination of substances, compositions, or entities that are well-understood by persons of ordinary skill in the art as being “naturally-occurring,” or that are, or might be at any time, determined or interpreted by a judge or an administrative or judicial body to be, “naturally-occurring.”

**[0052]** As used herein, the term “polypeptide” is intended to encompass a singular “polypeptide” as well as plural “polypeptides,” and refers to a molecule composed of monomers (amino acids) linearly linked by amide bonds (also known as peptide bonds). The term "polypeptide" refers to any chain or chains of two or more amino acids, and does not refer to a specific length of the product. Thus, peptides, dipeptides, tripeptides, oligopeptides, “protein,” “amino acid chain,” or any other term used to refer to a chain or chains of two or more amino acids are included within the definition of "polypeptide,” and the term “polypeptide” can be used instead of, or interchangeably with any of these terms. The term "polypeptide" is also intended to refer to the products of post-expression modifications of the polypeptide, including without limitation glycosylation, acetylation, phosphorylation, amidation, and derivatization by known protecting/blocking groups, proteolytic cleavage, or modification by non-naturally occurring amino acids. A polypeptide can be derived from a biological source or produced by recombinant technology, but is not necessarily translated from a designated nucleic acid sequence. It can be generated in any manner, including by chemical synthesis.

**[0053]** A polypeptide as disclosed herein can be of a size of about 3 or more, 5 or more, 10 or more, 20 or more, 25 or more, 50 or more, 75 or more, 100 or more, 200 or more, 500 or more, 1,000 or more, or 2,000 or more amino acids. Polypeptides can have a defined three-dimensional structure, although they do not necessarily have such structure. Polypeptides with a defined three-dimensional structure are referred to as folded, and polypeptides that do not possess a defined three-dimensional structure, but rather can adopt a large number of different conformations, and are referred to as unfolded. As used herein, the term glycoprotein refers to a

*protein* coupled to at least one carbohydrate moiety that is attached to the protein via an oxygen-containing or a nitrogen-containing side chain of an amino acid, *e.g.*, a serine or an asparagine.

**[0054]** By an "isolated" polypeptide or a fragment, variant, or derivative thereof is intended a polypeptide that is not in its natural milieu. No particular level of purification is required. For example, an isolated polypeptide can be removed from its native or natural environment. Recombinantly produced polypeptides and proteins expressed in host cells are considered isolated as disclosed herein, as are native or recombinant polypeptides that have been separated, fractionated, or partially or substantially purified by any suitable technique.

**[0055]** As used herein, the term “non-naturally occurring” polypeptide, or any grammatical variants thereof, is a conditional term that explicitly excludes, but only excludes, those forms of the polypeptide that are well-understood by persons of ordinary skill in the art as being “naturally-occurring,” or that are, or might be at any time, determined or interpreted by a judge or an administrative or judicial body to be, “naturally-occurring.”

**[0056]** Other polypeptides disclosed herein are fragments, derivatives, analogs, or variants of the foregoing polypeptides, and any combination thereof. The terms "fragment," "variant," "derivative" and "analog" as disclosed herein include any polypeptides that retain at least some of the properties of the corresponding native antibody or polypeptide, for example, specifically binding to an antigen. Fragments of polypeptides include, for example, proteolytic fragments, as well as deletion fragments, in addition to specific antibody fragments discussed elsewhere herein. Variants of, *e.g.*, a polypeptide include fragments as described above, and also polypeptides with altered amino acid sequences due to amino acid substitutions, deletions, or insertions. In certain embodiments, variants can be non-naturally occurring. Non-naturally occurring variants can be produced using art-known mutagenesis techniques. Variant polypeptides can comprise conservative or non-conservative amino acid substitutions, deletions or additions. Derivatives are polypeptides that have been altered so as to exhibit additional features not found on the original polypeptide. Examples include fusion proteins. Variant polypeptides can also be referred to herein as "polypeptide analogs." As used herein a "derivative" of a polypeptide can also refer to a subject polypeptide having one or more amino acids chemically derivatized by reaction of a functional side group. Also included as "derivatives" are those peptides that contain one or more derivatives of the twenty standard amino acids. For example, 4-hydroxyproline can be substituted for proline; 5-hydroxylysine can

be substituted for lysine; 3-methylhistidine can be substituted for histidine; homoserine can be substituted for serine; and ornithine can be substituted for lysine.

**[0057]** A "conservative amino acid substitution" is one in which one amino acid is replaced with another amino acid having a similar side chain. Families of amino acids having similar side chains have been defined in the art, including basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). For example, substitution of a phenylalanine for a tyrosine is a conservative substitution. In certain embodiments, conservative substitutions in the sequences of the polypeptides and antibodies described herein do not abrogate the binding of the polypeptide or antibody containing the amino acid sequence, to the antigen to which the binding molecule binds. Methods of identifying nucleotide and amino acid conservative substitutions that do not eliminate antigen-binding are well-known in the art (see, *e.g.*, Brummell *et al.*, *Biochem.* 32:1180-1 187 (1993); Kobayashi *et al.*, *Protein Eng.* 12(10):879-884 (1999); and Burks *et al.*, *Proc. Natl. Acad. Sci. USA* 94:.412-417 (1997)).

**[0058]** The term "polynucleotide" is intended to encompass a singular nucleic acid as well as plural nucleic acids, and refers to an isolated nucleic acid molecule or construct, *e.g.*, messenger RNA (mRNA), cDNA, or plasmid DNA (pDNA). A polynucleotide can comprise a conventional phosphodiester bond or a non-conventional bond (*e.g.*, an amide bond, such as found in peptide nucleic acids (PNA)). The terms "nucleic acid" or “nucleic acid sequence” refer to any one or more nucleic acid segments, *e.g.*, DNA or RNA fragments, present in a polynucleotide.

**[0059]** By an "isolated" nucleic acid or polynucleotide is intended any form of the nucleic acid or polynucleotide that is separated from its native environment. For example, gel-purified polynucleotide, or a recombinant polynucleotide encoding a polypeptide contained in a vector would be considered to be “isolated.” Also, a polynucleotide segment, *e.g.*, a PCR product, that has been engineered to have restriction sites for cloning is considered to be “isolated.” Further examples of an isolated polynucleotide include recombinant polynucleotides maintained in heterologous host cells or purified (partially or substantially) polynucleotides in a non-native solution such as a buffer or saline. Isolated RNA molecules include *in vivo* or *in vitro* RNA

transcripts of polynucleotides, where the transcript is not one that would be found in nature. Isolated polynucleotides or nucleic acids further include such molecules produced synthetically. In addition, polynucleotide or a nucleic acid can be or can include a regulatory element such as a promoter, ribosome binding site, or a transcription terminator.

**[0060]** As used herein, a “non-naturally occurring” polynucleotide, or any grammatical variants thereof, is a conditional definition that explicitly excludes, but only excludes, those forms of the polynucleotide that are well-understood by persons of ordinary skill in the art as being “naturally-occurring,” or that are, or that might be at any time, determined or interpreted by a judge or an administrative or judicial body to be, “naturally-occurring.”

**[0061]** As used herein, a "coding region" is a portion of nucleic acid that consists of codons translated into amino acids. Although a "stop codon" (TAG, TGA, or TAA) is not translated into an amino acid, it can be considered to be part of a coding region, but any flanking sequences, for example promoters, ribosome binding sites, transcriptional terminators, introns, and the like, are not part of a coding region. Two or more coding regions can be present in a single polynucleotide construct, *e.g.*, on a single vector, or in separate polynucleotide constructs, *e.g.*, on separate (different) vectors. Furthermore, any vector can contain a single coding region, or can comprise two or more coding regions, *e.g.*, a single vector can separately encode an immunoglobulin heavy chain variable region and an immunoglobulin light chain variable region. In addition, a vector, polynucleotide, or nucleic acid can include heterologous coding regions, either fused or unfused to another coding region. Heterologous coding regions include without limitation, those encoding specialized elements or motifs, such as a secretory signal peptide or a heterologous functional domain.

**[0062]** In certain embodiments, the polynucleotide or nucleic acid is DNA. In the case of DNA, a polynucleotide comprising a nucleic acid that encodes a polypeptide normally can include a promoter and/or other transcription or translation control elements operably associated with one or more coding regions. An operable association is when a coding region for a gene product, *e.g.*, a polypeptide, is associated with one or more regulatory sequences in such a way as to place expression of the gene product under the influence or control of the regulatory sequence(s). Two DNA fragments (such as a polypeptide coding region and a promoter associated therewith) are "operably associated" if induction of promoter function results in the transcription of mRNA encoding the desired gene product and if the nature of the linkage

between the two DNA fragments does not interfere with the ability of the expression regulatory sequences to direct the expression of the gene product or interfere with the ability of the DNA template to be transcribed. Thus, a promoter region would be operably associated with a nucleic acid encoding a polypeptide if the promoter was capable of effecting transcription of that nucleic acid. The promoter can be a cell-specific promoter that directs substantial transcription of the DNA in predetermined cells. Other transcription control elements, besides a promoter, for example enhancers, operators, repressors, and transcription termination signals, can be operably associated with the polynucleotide to direct cell-specific transcription.

**[0063]** A variety of transcription control regions are known to those skilled in the art. These include, without limitation, transcription control regions that function in vertebrate cells, such as, but not limited to, promoter and enhancer segments from cytomegaloviruses (the immediate early promoter, in conjunction with intron-A), simian virus 40 (the early promoter), and retroviruses (such as Rous sarcoma virus). Other transcription control regions include those derived from vertebrate genes such as actin, heat shock protein, bovine growth hormone and rabbit ß-globin, as well as other sequences capable of controlling gene expression in eukaryotic cells. Additional suitable transcription control regions include tissue-specific promoters and enhancers as well as lymphokine-inducible promoters (*e.g.*, promoters inducible by interferons or interleukins).

**[0064]** Similarly, a variety of translation control elements are known to those of ordinary skill in the art. These include, but are not limited to ribosome binding sites, translation initiation and termination codons, and elements derived from picornaviruses (particularly an internal ribosome entry site, or IRES, also referred to as a CITE sequence).

**[0065]** In other embodiments, a polynucleotide can be RNA, for example, in the form of messenger RNA (mRNA), transfer RNA, or ribosomal RNA.

**[0066]** Polynucleotide and nucleic acid coding regions can be associated with additional coding regions that encode secretory or signal peptides, which direct the secretion of a polypeptide encoded by a polynucleotide as disclosed herein. According to the signal hypothesis, proteins secreted by mammalian cells have a signal peptide or secretory leader sequence that is cleaved from the mature protein once export of the growing protein chain across the rough endoplasmic reticulum has been initiated. Those of ordinary skill in the art are aware that polypeptides secreted by vertebrate cells can have a signal peptide fused to the N-terminus of the polypeptide, which is cleaved from the complete or "full length" polypeptide to produce a secreted or "mature" form

of the polypeptide. In certain embodiments, the native signal peptide, *e.g.*, an immunoglobulin heavy chain or light chain signal peptide is used, or a functional derivative of that sequence that retains the ability to direct the secretion of the polypeptide that is operably associated with it. Alternatively, a heterologous mammalian signal peptide, or a functional derivative thereof, can be used. For example, the wild-type leader sequence can be substituted with the leader sequence of human tissue plasminogen activator (TPA) or mouse ß-glucuronidase.

**[0067]** Disclosed herein are certain binding molecules, or antigen-binding fragments, variants, or derivatives thereof. Unless specifically referring to full-sized antibodies, the term "binding molecule" encompasses full-sized antibodies as well as antigen-binding subunits, fragments, variants, analogs, or derivatives of such antibodies, *e.g.*, engineered antibody molecules or fragments that bind antigen in a manner similar to antibody molecules, but which use a different scaffold.

**[0068]** As used herein, the term “binding molecule” refers in its broadest sense to a molecule that specifically binds to a receptor, *e.g.*, an epitope or an antigenic determinant. As described further herein, a binding molecule can comprise one or more “antigen binding domains” described herein. A non-limiting example of a binding molecule is an antibody or fragment thereof that retains antigen-specific binding.

**[0069]** The terms “binding domain” and “antigen binding domain” are used interchangeably herein and refer to a region of a binding molecule that is necessary and sufficient to specifically bind to an epitope. For example, an “Fv,” *e.g.*, a variable heavy chain and variable light chain of an antibody, either as two separate polypeptide subunits or as a single chain, is considered to be a “binding domain.”

**[0070]** Other antigen binding domains include, without limitation, the variable heavy chain (VHH) of an antibody derived from a camelid species, or six immunoglobulin complementarity determining regions (CDRs) expressed in a fibronectin scaffold. A “binding molecule” as described herein can include one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve or more “antigen binding domains.”

**[0071]** The terms "antibody" and "immunoglobulin" can be used interchangeably herein. An antibody (or a fragment, variant, or derivative thereof as disclosed herein) includes at least the variable region of a heavy chain (for camelid species) or at least the variable region of a heavy chain and a light chain. Basic immunoglobulin structures in vertebrate systems are relatively well

understood. *See*, *e.g.*, Harlow *et al.*, Antibodies: A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988). Unless otherwise stated, the term "antibody" encompasses anything ranging from a small antigen-binding fragment of an antibody to a full sized antibody, *e.g.*, an IgG antibody that includes two complete heavy chains and two complete light chains, an IgA antibody that includes four complete heavy chains and four complete light chains and can include a J-chain and/or a secretory component, or an IgM antibody that includes ten or twelve complete heavy chains and ten or twelve complete light chains and can include a J-chain.

**[0072]** As will be discussed in more detail below, the term "immunoglobulin" comprises various broad classes of polypeptides that can be distinguished biochemically. Those skilled in the art will appreciate that heavy chains are classified as gamma, mu, alpha, delta, or epsilon, ($\gamma$, $\mu$, $\alpha$, $\delta$, $\varepsilon$) with some subclasses among them (*e.g.*, $\gamma$1-$\gamma$4 or $\alpha$1-$\alpha$2)). It is the nature of this chain that determines the "class" of the antibody as IgG, IgM, IgA IgG, or IgE, respectively. The immunoglobulin subclasses (isotypes) *e.g.*, $IgG_1$, $IgG_2$, $IgG_3$, $IgG_4$, $IgA_1$, $IgA_2$, etc. are well characterized and are known to confer functional specialization. Modified versions of each of these classes and isotypes are readily discernible to the skilled artisan in view of the instant disclosure and, accordingly, are within the scope of this disclosure.

**[0073]** Light chains are classified as either kappa or lambda ($\kappa$, $\lambda$). Each heavy chain class can be bound with either a kappa or lambda light chain. In general, the light and heavy chains are covalently bonded to each other, and the "tail" portions of the two heavy chains are bonded to each other by covalent disulfide linkages or non-covalent linkages when the immunoglobulins are generated either by hybridomas, B cells or genetically engineered host cells. In the heavy chain, the amino acid sequences run from an N-terminus at the forked ends of the Y configuration to the C-terminus at the bottom of each chain. The basic structure of certain antibodies, *e.g.*, IgG antibodies, includes two heavy chain subunits and two light chain subunits covalently connected via disulfide bonds to form a "Y" structure, also referred to herein as an "H2L2" structure, or a "binding unit."

**[0074]** The term "binding unit" is used herein to refer to the portion of a binding molecule, *e.g.*, an antibody or antigen-binding fragment thereof that corresponds to a standard immunoglobulin structure, *i.e.*, two heavy chains or fragments thereof and two light chains or fragments thereof, or two heavy chains or fragments thereof derived, *e.g.*, from a camelid or condricthoid antibody. In certain embodiments, *e.g.*, where the binding molecule is a single binding unit IgG antibody

or antigen-binding fragment thereof, the terms "binding molecule" and "binding unit" are equivalent. In other embodiments, *e.g.*, where the binding molecule is an IgA dimer, an IgM pentamer, or an IgM hexamer, the binding molecule is "multimeric" and comprises two or more "binding units." Two in the case of an IgA dimer, or five or six in the case of an IgM pentamer or hexamer, respectively. A binding unit need not include full-length antibody heavy and light chains, but will typically be bivalent, *i.e.*, will include two "antigen binding domains," as defined below. Certain binding molecules described in this disclosure are pentameric or hexameric, and include five or six bivalent binding units that include IgM constant regions or fragments thereof.

**[0075]** As used herein, a binding molecule comprising two or more binding units, *e.g.*, two, five, or six binding units, can be referred to as "multimeric." The term "multimeric" means possessing more than one unit. Thus, for example, a "multimeric binding molecule" will possess more than one binding unit. A multimeric binding molecule could possess as many as two, three four, five or even six or more binding units.

**[0076]** The term "native sequence J-chain" or "native J-chain" as used herein refers to J-chain of native sequence IgM or IgA antibodies of any animal species, including mature human J-chain, the amino acid sequence of which is presented as SEQ ID NO: 54.

**[0077]** The term "modified J-chain" is used herein to refer to variants of native sequence J- chain polypeptides comprising a heterologous moiety, *e.g.*, a heterologous polypeptide, *e.g.*, an extraneous binding domain introduced into the native sequence. The introduction can be achieved by any means, including direct or indirect fusion of the heterologous polypeptide or other moiety or by attachment through a peptide or chemical linker. The term "modified human J-chain" encompasses, without limitation, a native sequence human J-chain of the amino acid sequence of SEQ ID NO: 54 or functional fragment thereof modified by the introduction of a heterologous moiety, *e.g.*, a heterologous polypeptide, *e.g.*, an extraneous binding domain. In certain embodiments the heterologous moiety does not interfere with efficient polymerization of IgM into a pentamer or IgA into a dimer and binding of such polymers to a target. Exemplary modified J-chains can be found, *e.g.*, in PCT Publication No. WO 2015/153912, which is incorporated herein by reference in its entirety.

**[0078]** The terms "valency," "bivalent," "multivalent" and grammatical equivalents, refer to the number of antigen binding domains in given binding molecule or binding unit. As such, the

terms “bivalent”, “tetravalent”, and “hexavalent” in reference to a given binding molecule denote the presence of two antigen binding domains, four antigen binding domains, and six antigen binding domains, respectively. In a typical IgM-derived binding molecule, each binding unit is bivalent, whereas the binding molecule itself can have 10 or 12 valencies. A bivalent or multivalent binding molecule can be monospecific, *i.e.*, all of the antigen binding domains are the same, or can be bispecific or multispecific, *e.g.*, where two or more antigen binding domains are different, *e.g.*, bind to different epitopes on the same antigen, or bind to entirely different antigens.

**[0079]** The term “epitope” includes any molecular determinant capable of specific binding to an antibody. In certain embodiments, an epitope can include chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl, or sulfonyl, and, in certain embodiments, can have three dimensional structural characteristics, and or specific charge characteristics. An epitope is a region of a target that is bound by an antibody.

**[0080]** “Multispecific binding molecules or antibodies” or “bispecific binding molecules or antibodies” refer to binding molecules, antibodies, or antigen-binding fragments thereof that have the ability to specifically bind to two or more different epitopes on the same or different target(s). "Monospecific" refers to the ability to bind only one epitope.

**[0081]** The term “target” is used in the broadest sense to include substances that can be bound by a binding molecule. A target can be, *e.g.*, a polypeptide, a nucleic acid, a carbohydrate, a lipid, or other molecule. Moreover, a “target” can, for example, be a cell, an organ, or an organism that comprises an epitope bound that can be bound by a binding molecule.

**[0082]** Antibody light and heavy chains are divided into regions of structural and functional homology. The terms "constant" and "variable" are used functionally. In this regard, it will be appreciated that the variable regions (which can be called “variable domains” interchangeably herein) of both the variable light (VL) and variable heavy (VH) chain portions determine antigen recognition and specificity. Conversely, the constant domains of the light chain (CL) and the heavy chain (*e.g.*, CH1, CH2 or CH3) confer biological properties such as secretion, transplacental mobility, Fc receptor binding, complement binding, and the like. By convention the numbering of the constant region domains increases as they become more distal from the antigen binding site or amino-terminus of the antibody. The N-terminal portion is a variable

region and at the C-terminal portion is a constant region; the CH3 (or CH4 in the case of IgM) and CL domains are at the carboxy-terminus of the heavy and light chain, respectively.

**[0083]** A "full length IgM antibody heavy chain" is a polypeptide that includes, in N-terminal to C-terminal direction, an antibody heavy chain variable region (VH), an antibody constant heavy chain constant domain 1 (CM1 or Cμ1), an antibody heavy chain constant domain 2 (CM2 or Cμ2), an antibody heavy chain constant domain 3 (CM3 or Cμ3), and an antibody heavy chain constant domain 4 (CM4 or Cμ4), which can also include a tailpiece.

**[0084]** A "full length IgA antibody heavy chain" is a polypeptide that includes, in N-terminal to C-terminal direction, an antibody heavy chain variable region (VH), an antibody constant heavy chain constant domain 1 (CA1 or Cα1), an antibody heavy chain constant domain 2 (CA2 or Cα2), an antibody heavy chain constant domain 3 (CA3 or Cα3), and a tailpiece. The structure of monomeric and secretory IgA is described, *e.g.*, in Woof, JM and Russell, MW, *Mucosal Immunology 4*:590-597 (2011).

**[0085]** As indicated above, a variable region, *i.e.*, the "antigen binding domain," allows the binding molecule to selectively recognize and specifically bind epitopes on antigens. That is, the VL domain and VH domain, or subset of the complementarity determining regions (CDRs), of a binding molecule, *e.g.*, an antibody combine to form the variable region that defines a three dimensional antigen binding site. More specifically, the antigen binding site is defined by three CDRs on each of the VH and VL chains. Certain antibodies form larger structures. For example, IgA can form a molecule that includes two H2L2 units and a J-chain, all covalently connected via disulfide bonds, and IgM can form a pentameric or hexameric molecule that includes five or six H2L2 units and, in some embodiments, a J-chain covalently connected via disulfide bonds. In certain embodiments, polymeric IgA and IgM molecules can also contain a secretory component that can also be covalently connected via disulfide bonds.

**[0086]** The six "complementarity determining regions" or "CDRs" present in an antibody antigen binding domain are short, non-contiguous sequences of amino acids that are specifically positioned to form the antigen binding domain as the antibody assumes its three dimensional configuration in an aqueous environment. The remainder of the amino acids in the antigen binding domain, referred to as "framework" regions, show less inter-molecular variability. The framework regions largely adopt a β-sheet conformation and the CDRs form loops that connect, and in some cases form part of, the β-sheet structure. Thus, framework regions act to form a

scaffold that provides for positioning the CDRs in correct orientation by inter-chain, non-covalent interactions. The antigen binding domain formed by the positioned CDRs defines a surface complementary to the epitope on the immunoreactive antigen. This complementary surface promotes the non-covalent binding of the antibody to its cognate epitope. The amino acids that make up the CDRs and the framework regions, respectively, can be readily identified for any given heavy or light chain variable region by one of ordinary skill in the art, since they have been defined in various different ways (*see*, "Sequences of Proteins of Immunological Interest," Kabat, E., *et al.*, U.S. Department of Health and Human Services, (1983); and Chothia and Lesk, *J. Mol. Biol.*, *196*:901-917 (1987), which are incorporated herein by reference in their entireties).

**[0087]** In the case where there are two or more definitions of a term that is used and/or accepted within the art, the definition of the term as used herein is intended to include all such meanings unless explicitly stated to the contrary. A specific example is the use of the term "complementarity determining region" ("CDR") to describe the non-contiguous antigen combining sites found within the variable region of both heavy and light chain polypeptides. These particular regions have been described, for example, by Kabat *et al.*, U.S. Dept. of Health and Human Services, "Sequences of Proteins of Immunological Interest" (1983) and by Chothia *et al.*, *J. Mol. Biol.* 196:901-917 (1987), which are incorporated herein by reference. The Kabat and Chothia definitions include overlapping or subsets of amino acids when compared against each other. Nevertheless, application of either definition (or other definitions known to those of ordinary skill in the art) to refer to a CDR of an antibody or variant thereof is intended to be within the scope of the term as defined and used herein, unless otherwise indicated. The appropriate amino acids that encompass the CDRs as defined by each of the above cited references are set forth below in Table 1 as a comparison. The exact amino acid numbers that encompass a particular CDR will vary depending on the sequence and size of the CDR. Those skilled in the art can routinely determine that amino acids comprise a particular CDR given the variable region amino acid sequence of the antibody.

Table 1 CDR Definitions*

| | **Kabat** | **Chothia** |
|---|---|---|
| VH CDR1 | 31-35 | 26-32 |

| | | |
|---|---|---|
| VH CDR2 | 50-65 | 52-58 |
| VH CDR3 | 95-102 | 95-102 |
| VL CDR1 | 24-34 | 26-32 |
| VL CDR2 | 50-56 | 50-52 |
| VL CDR3 | 89-97 | 91-96 |

*Numbering of all CDR definitions in Table 1 is according to the numbering conventions set forth by Kabat *et al.* (see below).

**[0088]** Immunoglobulin variable domains can also be analyzed, *e.g.*, using the IMGT information system (www://imgt.cines.fr/) (IMGT®/V-Quest) to identify variable region segments, including CDRs. (*See, e.g.*, Brochet *et al.*, *Nucl. Acids Res.*, 36:W503-508, 2008).

**[0089]** Kabat *et al.* also defined a numbering system for variable domain sequences that is applicable to any antibody. One of ordinary skill in the art can unambiguously assign this system of "Kabat numbering" to any variable domain sequence, without reliance on any experimental data beyond the sequence itself. As used herein, "Kabat numbering" refers to the numbering system set forth by Kabat *et al.*, U.S. Dept. of Health and Human Services, "Sequence of Proteins of Immunological Interest" (1983). Unless use of the Kabat numbering system is explicitly noted, however, consecutive numbering is used for all amino acid sequences in this disclosure.

**[0090]** Binding molecules, *e.g.*, antibodies or antigen-binding fragments, variants, or derivatives thereof include, but are not limited to, polyclonal, monoclonal, human, humanized, or chimeric antibodies, single chain antibodies, epitope-binding fragments, *e.g.*, Fab, Fab' and $F(ab')_2$, Fd, Fvs, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv), fragments comprising either a VL or VH domain, fragments produced by a Fab expression library. ScFv molecules are known in the art and are described, *e.g.*, in US patent 5,892,019. Immunoglobulin or antibody molecules encompassed by this disclosure can be of any type (*e.g.*, IgG, IgE, IgM, IgD, IgA, and IgY), class (*e.g.*, IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule. Also contemplated are immunoglobulin new antigen receptor (IgNAR) isotypes that are bivalent and comprise a single chain that includes an IgNAR variable domain (VNAR). (*See*, Walsh *et al.*, *Virol.*, 411:132-141, 2011).

**[0091]** By "specifically binds," it is generally meant that a binding molecule, *e.g.*, an antibody or fragment, variant, or derivative thereof binds to an epitope via its antigen binding domain, and that the binding entails some complementarity between the antigen binding domain and the

epitope. According to this definition, a binding molecule is said to "specifically bind" to an epitope when it binds to that epitope, via its antigen binding domain more readily than it would bind to a random, unrelated epitope. The term "specificity" is used herein to qualify the relative affinity by which a certain binding molecule binds to a certain epitope. For example, binding molecule "A" can be deemed to have a higher specificity for a given epitope than binding molecule "B," or binding molecule "A" can be said to bind to epitope "C" with a higher specificity than it has for related epitope "D."

**[0092]** A binding molecule, *e.g.*, an antibody or fragment, variant, or derivative thereof disclosed herein can be said to bind a target antigen with an off rate (k(off)) of less than or equal to $5 \times 10^{-2}$ $sec^{-1}$, $10^{-2}$ $sec^{-1}$, $5 \times 10^{-3}$ $sec^{-1}$, $10^{-3}$ $sec^{-1}$, $5 \times 10^{-4}$ $sec^{-1}$, $10^{-4}$ $sec^{-1}$, $5 \times 10^{-5}$ $sec^{-1}$, or $10^{-5}$ $sec^{-1}$ $5 \times 10^{-6}$ $sec^{-1}$, $10^{-6}$ $sec^{-1}$, $5 \times 10^{-7}$ $sec^{-1}$ or $10^{-7}$ $sec^{-1}$.

**[0093]** A binding molecule, *e.g.*, an antibody or antigen-binding fragment, variant, or derivative disclosed herein can be said to bind a target antigen with an on rate (k(on)) of greater than or equal to $10^3$ $M^{-1}$ $sec^{-1}$, $5 \times 10^3$ $M^{-1}$ $sec^{-1}$, $10^4$ $M^{-1}$ $sec^{-1}$, $5 \times 10^4$ $M^{-1}$ $sec^{-1}$, $10^5$ $M^{-1}$ $sec^{-1}$, $5 \times 10^5$ $M^{-1}$ $sec^{-1}$, $10^6$ $M^{-1}$ $sec^{-1}$, or $5 \times 10^6$ $M^{-1}$ $sec^{-1}$ or $10^7$ $M^{-1}$ $sec^{-1}$.

**[0094]** A binding molecule, *e.g.*, an antibody or fragment, variant, or derivative thereof is said to competitively inhibit binding of a reference antibody or antigen binding fragment to a given epitope if it preferentially binds to that epitope to the extent that it blocks, to some degree, binding of the reference antibody or antigen binding fragment to the epitope. Competitive inhibition can be determined by any method known in the art, for example, competition ELISA assays. A binding molecule can be said to competitively inhibit binding of the reference antibody or antigen binding fragment to a given epitope by at least 90%, at least 80%, at least 70%, at least 60%, or at least 50%.

**[0095]** As used herein, the term "affinity" refers to a measure of the strength of the binding of an individual epitope with one or more antigen binding domains, *e.g.*, of an immunoglobulin molecule. *See*, *e.g.*, Harlow *et al.*, Antibodies: A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988) at pages 27-28. As used herein, the term "avidity" refers to the overall stability of the complex between a population of antigen binding domains and an antigen. *See*, *e.g.*, Harlow at pages 29-34. Avidity is related to both the affinity of individual antigen binding domains in the population with specific epitopes, and also the valencies of the immunoglobulins and the antigen. For example, the interaction between a bivalent monoclonal

antibody and an antigen with a highly repeating epitope structure, such as a polymer, would be one of high avidity. An interaction between a between a bivalent monoclonal antibody with a receptor present at a high density on a cell surface would also be of high avidity.

**[0096]** Binding molecules or antigen binding fragments, variants or derivatives thereof as disclosed herein can also be described or specified in terms of their cross-reactivity. As used herein, the term "cross-reactivity" refers to the ability of `a binding molecule, *e.g.*, an antibody or fragment, variant, or derivative thereof, specific for one antigen, to react with a second antigen; a measure of relatedness between two different antigenic substances. Thus, a binding molecule is cross reactive if it binds to an epitope other than the one that induced its formation. The cross reactive epitope generally contains many of the same complementary structural features as the inducing epitope, and in some cases, can actually fit better than the original.

**[0097]** A binding molecule, *e.g.*, an antibody or fragment, variant, or derivative thereof can also be described or specified in terms of its binding affinity to an antigen. For example, a binding molecule can bind to an antigen with a dissociation constant or $K_D$ no greater than $5 \times 10^{-2}$ M, $10^{-2}$ M, $5 \times 10^{-3}$ M, $10^{-3}$ M, $5 \times 10^{-4}$ M, $10^{-4}$ M, $5 \times 10^{-5}$ M, $10^{-5}$ M, $5 \times 10^{-6}$ M, $10^{-6}$ M, $5 \times 10^{-7}$ M, $10^{-7}$ M, $5 \times 10^{-8}$ M, $10^{-8}$ M, $5 \times 10^{-9}$ M, $10^{-9}$ M, $5 \times 10^{-10}$ M, $10^{-10}$ M, $5 \times 10^{-11}$ M, $10^{-11}$ M, $5 \times 10^{-12}$ M, $10^{-12}$ M, $5 \times 10^{-13}$ M, $10^{-13}$ M, $5 \times 10^{-14}$ M, $10^{-14}$ M, $5 \times 10^{-15}$ M, or $10^{-15}$ M.

**[0098]** Antibody fragments including single-chain antibodies or other antigen binding domains can exist alone or in combination with one or more of the following: hinge region, CH1, CH2, CH3, or CH4 domains, J-chain, or secretory component. Also included are antigen-binding fragments that can include any combination of variable region(s) with one or more of a hinge region, CH1, CH2, CH3, or CH4 domains, a J-chain, or a secretory component. Binding molecules, *e.g.*, antibodies, or antigen-binding fragments thereof can be from any animal origin including birds and mammals. The antibodies can be human, murine, donkey, rabbit, goat, guinea pig, camel, llama, horse, or chicken antibodies. In another embodiment, the variable region can be condricthoid in origin (*e.g.*, from sharks). As used herein, "human" antibodies include antibodies having the amino acid sequence of a human immunoglobulin and include antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulins and can in some instances express endogenous immunoglobulins and some not, as described *infra* and, for example in, U.S. Pat. No. 5,939,598 by Kucherlapati *et al*.

**[0099]** As used herein, the term "heavy chain subunit" or "heavy chain domain" includes amino acid sequences derived from an immunoglobulin heavy chain, a binding molecule, *e.g.*, an antibody comprising a heavy chain subunit can include at least one of: a VH domain, a CH1 domain, a hinge (*e.g.*, upper, middle, and/or lower hinge region) domain, a CH2 domain, a CH3 domain, a CH4 domain, or a variant or fragment thereof. For example, a binding molecule, *e.g.*, an antibody or fragment, variant, or derivative thereof can include, in addition to a VH domain, a CH1 domain; CH1 domain, a hinge, and a CH2 domain; a CH1 domain and a CH3 domain; a CH1 domain, a hinge, and a CH3 domain; or a CH1 domain, a hinge domain, a CH2 domain, and a CH3 domain. In certain embodiments a binding molecule, *e.g.*, an antibody or fragment, variant, or derivative thereof can include, in addition to a VH domain, a CH3 domain and a CH4 domain; or a CH3 domain, a CH4 domain, and a J-chain. Further, a binding molecule for use in the disclosure can lack certain constant region portions, *e.g.*, all or part of a CH2 domain. It will be understood by one of ordinary skill in the art that these domains (*e.g.*, the heavy chain subunit) can be modified such that they vary in amino acid sequence from the original immunoglobulin molecule.

**[0100]** The heavy chain subunits of a binding molecule, *e.g.*, an antibody or fragment thereof, can include domains derived from different immunoglobulin molecules. For example, a heavy chain subunit of a polypeptide can include a CH1 domain derived from an IgG1 molecule and a hinge region derived from an IgG3 molecule. In another example, a heavy chain subunit can include a hinge region derived, in part, from an IgG1 molecule and, in part, from an IgG3 molecule. In another example, a heavy chain subunit can comprise a chimeric hinge derived, in part, from an IgG1 molecule and, in part, from an IgG4 molecule.

**[0101]** As used herein, the term "light chain subunit" or "light chain domain" includes amino acid sequences derived from an immunoglobulin light chain. The light chain subunit includes at least one of a VL or CL (*e.g.*, Cκ or Cλ) domain.

**[0102]** Binding molecules, *e.g.*, antibodies or antigen binding fragments, variants, or derivatives thereof can be described or specified in terms of the epitope(s) or portion(s) of an antigen that they recognize or specifically bind. The portion of a target antigen that specifically interacts with the antigen binding domain of an antibody is an "epitope," or an "antigenic determinant." A target antigen can comprise a single epitope or at least two epitopes, and can include any number of epitopes, depending on the size, conformation, and type of antigen.

**[0103]** As previously indicated, the subunit structures and three dimensional configuration of the constant regions of the various immunoglobulin classes are well known. As used herein, the term "VH region" or "VH domain" includes the amino terminal variable domain of an immunoglobulin heavy chain and the term "CH1 domain" includes the first (most amino terminal) constant region domain of an immunoglobulin heavy chain. The CH1 domain is adjacent to the VH domain and is amino terminal to the hinge region of a typical IgG heavy chain molecule.

**[0104]** As used herein the term "CH2 domain" includes the portion of a heavy chain molecule that extends, *e.g.*, from about amino acid 244 to amino acid 360 of an IgG antibody using conventional numbering schemes (amino acids 244 to 360, Kabat numbering system; and amino acids 231-340, EU numbering system; see Kabat EA *et al.*, *op. cit.* The CH3 domain extends from the CH2 domain to the C-terminal of the IgG molecule and comprises approximately 108 amino acids. Certain immunoglobulin classes, *e.g.*, IgM, further include a CH4 region.

**[0105]** As used herein, the term "hinge region" includes the portion of a heavy chain molecule that joins the CH1 domain to the CH2 domain in IgG, IgA, and IgD heavy chains. This hinge region comprises approximately 25 amino acids and is flexible, thus allowing the two N-terminal antigen binding regions to move independently.

**[0106]** As used herein the term "disulfide bond" includes the covalent bond formed between two sulfur atoms. The amino acid cysteine comprises a thiol group that can form a disulfide bond or bridge with a second thiol group. In certain IgG molecules, the CH1 and CL regions are linked by a disulfide bond and the two heavy chains are linked by two disulfide bonds at positions corresponding to 239 and 242 using the Kabat numbering system (position 226 or 229, EU numbering system).

**[0107]** As used herein, the term "chimeric antibody" refers to an antibody in which the immunoreactive region or site is obtained or derived from a first species and the constant region (which can be intact, partial or modified) is obtained from a second species. In some embodiments the target binding region or site will be from a non-human source (*e.g.* mouse or primate) and the constant region is human.

**[0108]** The terms "multispecific antibody, or "bispecific antibody" refer to an antibody that has antigen binding domains that are specific for two or more different epitopes within a single antibody molecule (or "binding unit"). Other binding molecules in addition to the canonical antibody structure can be constructed with two different binding specificities. Epitope binding by

bispecific or multispecific antibodies can be simultaneous or sequential. Triomas and hybrid hybridomas are two examples of cell lines that can secrete bispecific antibodies. Bispecific antibodies can also be constructed by recombinant means. (Ströhlein and Heiss, *Future Oncol.* *6*:1387-94 (2010); Mabry and Snavely, *IDrugs*. *13*:543-9 (2010)). A bispecific antibody can also be a diabody. Thus, a bispecific binding molecule that is multimeric could potentially possess several different antigen binding domains, each with a different specificity. For instance, an IgM binding molecule would be considered multimeric, containing five or six binding units, and each binding unit possessing possibly two antigen binding domains. In such an IgM binding molecule, there could be as many as two, three, four, five, six, seven, eight, nine, ten, eleven, or even twelve different specificities, since each antigen binding domain can bind a different, distinguishable epitope.

**[0109]** As used herein, the term "engineered antibody" refers to an antibody in which the variable domain in either the heavy and light chain or both is altered by at least partial replacement of one or more amino acids in either the CDR or framework regions. In certain embodiments entire CDRs from an antibody of known specificity can be grafted into the framework regions of a heterologous antibody. Although alternate CDRs can be derived from an antibody of the same class or even subclass as the antibody from which the framework regions are derived, CDRs can also be derived from an antibody of different class, *e.g.*, from an antibody from a different species. An engineered antibody in which one or more "donor" CDRs from a non-human antibody of known specificity are grafted into a human heavy or light chain framework region is referred to herein as a "humanized antibody." In certain embodiments not all of the CDRs are replaced with the complete CDRs from the donor variable region and yet the antigen binding capacity of the donor can still be transferred to the recipient variable domains. Given the explanations set forth in, *e.g.*, U. S. Pat. Nos. 5,585,089, 5,693,761, 5,693,762, and 6,180,370, it will be well within the competence of those skilled in the art, either by carrying out routine experimentation or by trial and error testing to obtain a functional engineered or humanized antibody.

**[0110]** As used herein the term “engineered” includes manipulation of nucleic acid or polypeptide molecules by synthetic means (*e.g.* by recombinant techniques, *in vitro* peptide synthesis, by enzymatic or chemical coupling of peptides or some combination of these techniques).

**[0111]** As used herein, the terms "linked," "fused" or "fusion" or other grammatical equivalents can be used interchangeably. These terms refer to the joining together of two more elements or

components, by whatever means including chemical conjugation or recombinant means. An "in-frame fusion" refers to the joining of two or more polynucleotide open reading frames (ORFs) to form a continuous longer ORF, in a manner that maintains the translational reading frame of the original ORFs. Thus, a recombinant fusion protein is a single protein containing two or more segments that correspond to polypeptides encoded by the original ORFs (which segments are not normally so joined in nature.) Although the reading frame is thus made continuous throughout the fused segments, the segments can be physically or spatially separated by, for example, in-frame linker sequence. For example, polynucleotides encoding the CDRs of an immunoglobulin variable region can be fused, in-frame, but be separated by a polynucleotide encoding at least one immunoglobulin framework region or additional CDR regions, as long as the "fused" CDRs are co-translated as part of a continuous polypeptide.

**[0112]** In the context of polypeptides, a "linear sequence" or a "sequence" is an order of amino acids in a polypeptide in an amino to carboxyl terminal direction in which amino acids that neighbor each other in the sequence are contiguous in the primary structure of the polypeptide.

**[0113]** A portion of a polypeptide that is “amino-terminal” or “N-terminal” to another portion of a polypeptide is that portion that comes earlier in the sequential polypeptide chain. Similarly a portion of a polypeptide that is “carboxy-terminal” or “C-terminal” to another portion of a polypeptide is that portion that comes later in the sequential polypeptide chain. For example in a typical antibody, the variable domain is “N-terminal” to the constant region, and the constant region is “C-terminal” to the variable domain.

**[0114]** The term “expression” as used herein refers to a process by which a gene produces a biochemical, for example, a polypeptide. The process includes any manifestation of the functional presence of the gene within the cell including, without limitation, gene knockdown as well as both transient expression and stable expression. It includes without limitation transcription of the gene into messenger RNA (mRNA), and the translation of such mRNA into polypeptide(s). If the final desired product is a biochemical, expression includes the creation of that biochemical and any precursors. Expression of a gene produces a "gene product." As used herein, a gene product can be either a nucleic acid, *e.g.*, a messenger RNA produced by transcription of a gene, or a polypeptide that is translated from a transcript. Gene products described herein further include nucleic acids with post transcriptional modifications, *e.g.*, polyadenylation, or polypeptides with post

translational modifications, *e.g.*, methylation, glycosylation, the addition of lipids, association with other protein subunits, proteolytic cleavage, and the like.

**[0115]** Terms such as "treating" or "treatment" or "to treat" or "alleviating" or "to alleviate" refer to therapeutic measures that cure, slow down, lessen symptoms of, and/or halt or slow the progression of an existing diagnosed pathologic condition or disorder. Terms such as “prevent,” “prevention,” “avoid,” “deterrence” and the like refer to prophylactic or preventative measures that prevent the development of an undiagnosed targeted pathologic condition or disorder. Thus, “those in need of treatment” can include those already with the disorder; those prone to have the disorder; and those in whom the disorder is to be prevented.

**[0116]** By "subject" or "individual" or "animal" or "patient" or “mammal,” is meant any subject, particularly a mammalian subject, for whom diagnosis, prognosis, or therapy is desired. Mammalian subjects include humans, domestic animals, farm animals, and zoo, sports, or pet animals such as dogs, cats, guinea pigs, rabbits, rats, mice, horses, swine, cows, bears, and so on.

**[0117]** As used herein, phrases such as “a subject that would benefit from therapy” and “an animal in need of treatment” includes subjects, such as mammalian subjects, that would benefit from administration of a binding molecule such as an antibody, comprising one or more antigen binding domains. Such binding molecules, *e.g.*, antibodies, can be used, *e.g.*, for a diagnostic procedures and/or for treatment or prevention of a disease.

**[0118]** As used herein, hepatitis B surface antigen, or “HBsAg” refers to the surface glycoprotein of HBV. HBsAg produced in three sizes from the three independent start codons in the HBV genome. The Small, Medium and Large versions of this gene product are a combination of one or more of the three designated domains: (i) S alone (S), (ii) pre-S2 and S (M), or (iii) pre-S1 and pre-S2 and S (L) (FIG. 1A). HBsAg varies amongst serotypes and strains, but an exemplary “L” version of HBsAg comprises the following amino acid sequence:

MGGWSSKPRKGMGTNLSVPNPLGFFPDHQLDPAFGANSNNPDW
DFNPIKDHWPAANQVGVGAFGPGLTPPHGGILGWSPQAQGILTTV
STIPPPASTNRQSGRQPTPISPPLRDSHPQAMQWNSTAFHQALQDP
RVRGLYFPAGGSSSGTVNPAPNIASHISSISARTGDPVTNMENITSG
FLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGSPVCLGQNS
QSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQ
GMLPVCPLIPGSTTTSTGPCKTCTTPAQGNSMFPSCCCTKPTDGNC
TCIPIPSSWAFAKYLWEWASVRFSWLSLLVPFVQWFVGLSPTVWL
SAIWMMWYWGPSLYSIVSPFIPLLPIFFCLWVYI (SEQ ID NO: 79).

**[0119]** The preS1 region is underlined, and the preS2 region is double-underlined. The precursor HBsAg, including the signal peptide, is presented below:

MEWSWVFLFFLSVTTGVHSMGGWSSKPRKGMGTNLSVPNPLGFF
PDHQLDPAFGANSNNPDWDFNPIKDHWPAANQVGVGAFGPGLTP
PHGGILGWSPQAQGILTTVSTIPPPASTNRQSGRQPTPISPPLRDSHP
QAMQWNSTAFHQALQDPRVRGLYFPAGGSSSGTVNPAPNIASHIS
SISARTGDPVTNMENITSGFLGPLLVLQAGFFLLTRILTIPQSLDSW
WTSLNFLGGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFI
IFLFILLLCLIFLLVLLDYQGMLPVCPLIPGSTTTSTGPCKTCTTPAQ
GNSMFPSCCCTKPTDGNCTCIPIPSSWAFAKYLWEWASVRFSWLS
LLVPFVQWFVGLSPTVWLSAIWMMWYWGPSLYSIVSPFIPLLPIFF
CLWVYI )SEQ ID NO: 78).

**[0120]** As used herein the "PreS1 region" of the HBsAg refers to the 108-amino acid N-terminus of the HBsAg, comprising an amino acid sequence at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% identical to the amino acid sequence:

MGGWSSKPRQGMGTNLSVPNPLGFFPDHQLDPAFGANSNNPDWDFNPNK
DQWPEANQVGAGAFGPGFTPPHGGLLGWSPQAQGILTTVPAAPPPASTN
RQSGRQPTPISPPLRDSHPQA (SEQ ID NO: 60).

**[0121]** SEQ ID NO: 60 is derived from the *ad* serotype of HBV, but this region of HBsAg is conserved across HBV serotypes. Neutralizing monoclonal antibodies have been shown to bind to the region spanning amino acids 20-47 (underlined). For example, antibodies related to the murine antibody KR127 (see, *e.g.*, U.S. Patent No. 7,115,723, U.S. Patent No. 8,420,353, Hong *et al.*, Virol., 318:131-141, 2004, and Kim, J.H., *et al.* FEBS Letters 589:193-200 (2015)) bind to an epitope within amino acids 37-47 of SEQ ID NO: 60. Monoclonal antibody 2D028 (WO 2011/045079A1) binds to an epitope within amino acids 38 to 47 of SEQ ID NO: 60. Another Pre-S1 antibody, F35.25 (Petit, *et al.*, Mol Immunol. 1989 Jun;26(6):531-7) binds to an epitope within amino acids 32-53 of SEQ ID NO: 60). Another Pre-S1 antibody, 5a19 (Pizarro, *et al.*, FEBS Letters 509:463-468 (2001)) binds to an epitope within amino acids 37-43 of the *ay* serotype of pre-S1 (NTANPDW, SEQ ID NO: 77). The pre-S1 region is involved in hepatocyte receptor binding (**FIG. 1A. and FIG. 1B**).

**[0122]** As used herein, the hepatitis B X protein or X antigen (HBxAg) refers the 154 amino acid X protein produced by hepatitis B virus. HBxAg comprises an amino acid sequence at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% identical to the amino acid sequence:

MAARVCCQLDPARDVLCLRPVGAESRGRPVSGPFGTLPSPSSSAVPADH
GAHLSLRGLPVCAFSSAGPCALRFTSARRMETTVNAHQVLPKVLHKRTL
GLSAMSTTDLEAYFKDCLFKDWEELGEEIRLKVFVLGGCRHKLVCSPAP
CNFFTSA (SEQ ID NO: 61).

**[0123]** The protein can be involved in the development of hepatocellular carcinoma (HCC) (Seifer, M., *et al*., J Hepatology; 13 (suppl. 4): S61-S65). Antibodies to HBxAg have been shown to reduce tumor size and improve survival in mice with HCC tumors (Li *et al*. Zhonghua Yi Xue Za Zhi. 1996 Apr;76(4):271-4).

IgM Binding Molecules

**[0124]** IgM is the first immunoglobulin produced by B cells in response to stimulation by antigen, and is present at around 1.5 mg/ml in serum with a half-life of 5 days. IgM is typically multimeric, *e.g*., a pentameric or hexameric molecule. Thus, IgM molecules are "multimeric" binding molecules. Each of the five, or six, IgM binding units includes two light and two heavy chains. While IgG contains three heavy chain constant domains (CH1, CH2 and CH3), as explained above, the heavy (μ) chain of IgM additionally contains a fourth constant domain (CH4), that includes a C-terminal "tailpiece." The human IgM constant region typically comprises the amino acid sequence SEQ ID NO: 53. The human Cμ1 region ranges from about amino acid 5 to about amino acid 102 of SEQ ID NO: 53; the human Cμ2 region ranges from about amino acid 114 to about amino acid 205 of SEQ ID NO: 53, the human Cμ3 region ranges from about amino acid 224 to about amino acid 319 of SEQ ID NO: 53, the Cμ 4 region ranges from about amino acid 329 to about amino acid 430 of SEQ ID NO: 53, and the tailpiece ranges from about amino acid 431 to about amino acid 453 of SEQ ID NO: 53. The amino acid sequence of the human IgM constant region (SEQ ID NO: 53) is provided below:

GSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITLSWKYKNNSD
ISSTRGFPSVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKE
KNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVS
WLREGKQVGSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLGQSMFT
CRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPPSFASIFLTKSTKLTCL
VTDLTTYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEASICEDD
WNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNL
RESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRY
FAHSILTVSEEEWNTGETYTCVAHEALPNRVTERTVDKSTGKPTLYNVS
LVMSDTAGTCY

**[0125]** An IgM binding molecule can comprise five binding units (each an "IgM binding unit") that can form a complex with an additional small polypeptide chain (the J-chain) to form a pentameric IgM binding molecule. The human J-chain comprises the amino acid sequence SEQ ID NO: 54. Without the J-chain, IgM binding units typically assemble into a hexameric IgM binding molecule. While not wishing to be bound by theory, the assembly of IgM binding units into a hexameric or pentameric binding molecule is thought to involve the Cμ3 and Cμ4 domains. Accordingly, a hexameric or pentameric IgM binding molecule included in this disclosure typically includes IgM constant regions that include at least the Cμ3 and Cμ4 domains. The amino acid sequence of the human J-chain (SEQ ID NO: 54) is provided below:

MKNHLLFWGVLAVFIKAVHVKAQEDERIVLVDNKCKCARITSRIIRSSE
DPNEDIVERNIRIIVPLNNRENISDPTSPLRTRFVYHLSDLCKKCDPTE
VELDNQIVTATQSNICDEDSATETCYTYDRNKCYTAVVPLVYGGETKMV
ETALTPDACYPD

**[0126]** An IgM heavy chain constant region can additionally include a Cμ2 domain or a fragment thereof, a Cμ1 domain or a fragment thereof, and/or other IgM heavy chain domains. In certain embodiments, a binding molecule as described herein can include a complete IgM heavy (μ) chain constant domain, *e.g.*, SEQ ID NO: 53, or a variant, derivative, or analog thereof.

Pentameric or Hexameric IgM HBV Binding Molecules

**[0127]** This disclosure includes a pentameric or hexameric HBV binding molecule, *i.e.*, a binding molecule possessing five or six "binding units" as defined herein, which can specifically bind to an HBV antigen, *e.g.*, HBsAg, *e.g.*, the pre-S1 region of HBsAg. A binding molecule as described herein can possess improved binding characteristics or biological activity as compared to a binding molecule composed of a single binding unit, *e.g.*, an IgG antibody. In other words, the pentameric or hexameric IgM binding molecule described herein can in some embodiments enhance viral clearance, and be more potent, *e.g.*, as compared with a reference single binding unit comprising just two HBV-specific antigen binding domains. The term "improved binding characteristics" is further clarified as follows. The pentameric or hexameric IgM binding molecule described herein, when administered to an individual in need thereof, can exhibit an activity that is empirically determined to be stronger, more potent, or require less binding molecule by mass or molar equivalents, to (i) neutralize, *e.g.*, reduce the infectivity of an infectious HBV virion, (ii) reduce the number of HBV-infected cells (including HCC cells, latently infected cells, and chronically

infected cells), (iii) prevent HBV infection, (iv) enhance viral clearance, *e.g.*, through enhanced killing of infected cells, and/or (v) improve the signs and symptoms of HBV infection, as compared with an single, *i.e.* non-multimeric, binding molecule comprising just one binding unit that possesses antigen binding domains identical in sequence to those of the pentameric or hexameric IgM binding molecule described herein.

**[0128]** A binding molecule as described herein can likewise possess distinctive characteristics compared to multivalent binding molecules composed of synthetic or chimeric structures. For example, use of human IgM constant regions can afford reduced immunogenicity and thus increased safety relative to a binding molecule containing chimeric constant regions or synthetic structures. Moreover, an IgM-based binding molecule can consistently form hexameric or pentameric oligomers resulting in a more homogeneous expression product. Superior complement fixation can also be an advantageous effector function of IgM-based binding molecules.

**[0129]** The reference single binding unit referred to above can be an IgG binding unit. The reference IgG binding unit can be of any isotype, such as IgG1, IgG2, IgG3, or IgG4, etc. The reference binding unit is typically from the same animal. Thus if the multimeric binding molecule is human, the reference single binding unit would also be human, but not necessarily human. That is, the reference single binding unit can be a humanized antibody of the IgG type. Conversely, if the multimeric binding molecule is a rabbit binding molecule, the reference single binding unit would also be a rabbit binding unit. Further, if the multimeric binding molecule is comprised of one or more binding unit fragments, then the reference single binding unit would also be an equivalent single binding unit fragment. In other words, the reference single binding unit is otherwise identical in sequence and structure to the binding units contained in the multimeric binding molecule except that the reference single binding unit is an equivalent single binding unit.

**[0130]** In certain embodiments, the disclosure includes a pentameric or hexameric binding molecule comprising five or six binding units, respectively, where each binding unit includes two IgM heavy chain constant regions or fragments thereof. In certain embodiments, the two IgM heavy chain constant regions are human heavy chain constant regions. In some embodiments, the antigen binding domains in the IgM binding molecule are human in origin, or humanized, or a combination thereof.

**[0131]** Where the multimeric binding molecule described herein is pentameric, the binding molecule can further comprise a J-chain, or functional fragment thereof, or variant thereof. Where

the pentameric IgM binding molecule contains a J-chain, the J-chain can be of the same species as the IgM binding molecule. That is, if the pentameric IgM binding molecule is human, the J-chain can also be human. In certain embodiments, the J-chain is a modified J-chain comprising a heterologous moiety or one or more heterologous moieties, *e.g.*, a heterologous polypeptide sequence, *e.g.*, an extraneous binding domain introduced into the native sequence. In certain embodiments the extraneous binding domain specifically binds to CD3, *e.g.*, CD3ε. In certain embodiments the mature modified J-chain comprises V15J (SEQ ID NO: 68) or J15V (SEQ ID NO: 71).

**[0132]** An IgM heavy chain constant region can include one or more of a Cμ1 domain, a Cμ2 domain, a Cμ3 domain, and/or a Cμ4 domain, provided that the constant region can serve a desired function in the binding molecule, *e.g.*, associate with second IgM constant region to form an antigen binding domain, or associate with other binding units to form a hexamer or a pentamer. In certain embodiments the two IgM heavy chain constant regions or fragments thereof within an individual binding unit each comprise a Cμ3 domain or fragment thereof, a Cμ4 domain or fragment thereof, a tailpiece (TP) or fragment thereof, or any combination of a Cμ3 domain a Cμ domain, and a TP or fragment thereof. In certain embodiments the two IgM heavy chain constant regions or fragments thereof within an individual binding unit each further comprise a Cμ2 domain or fragment thereof, a Cμ1 domain or fragment thereof, or a Cμ1 domain or fragment thereof and a Cμ2 domain or fragment thereof.

**[0133]** In certain embodiments each of the two IgM heavy chain constant regions in a binding unit is associated with an antigen binding domain, for example an Fv portion of an antibody, *e.g.*, a VH and a VL of a human or murine antibody. In certain embodiments, at least one antigen binding domain of a binding molecule as described herein is a cross-reactive HBV antigen binding domain, *e.g.*, an antigen binding domain that can specifically bind to two, three, four, or more HBV subtypes. In other embodiments, an IgM binding molecule as described herein can comprise binding units wherein each binding unit possesses a different and distinguishable specificity. Thus, a pentameric IgM binding molecule could possess as many as five different specificities and thereby bind to every different HBV subtype presently known. Further, because each binding unit of a pentameric IgM binding molecule possesses two antigen binding domains, and because each of these two antigen binding domains can independently bind a different antigen or different epitope on the same antigen, a pentameric IgM binding molecule can bind as many as two, three,

four, five, six, seven, eight, nine or even ten different antigens or epitopes, across different HBV subtypes. Likewise, a hexameric IgM binding molecule can comprise binding units wherein each binding unit possesses a different and distinguishable specificity. Thus, a hexameric IgM binding molecule could possess as many as twelve different specificities and thereby bind to every different HBV subtype presently known. Further, because each binding unit of a hexameric IgM binding molecule possess two antigen binding domains, and because each of these two antigen binding domains can independently bind a different antigen or different epitope on the same antigen, a hexameric IgM binding molecule as disclosed herein can bind as many as two, three, four, five, six, seven, eight, nine, ten, eleven or even twelve different antigens or epitopes, across different HBV subtypes.

**[0134]** In certain embodiments, at least one antigen binding domain binds to the S region, the pre-S2 region, and/or the pre-S1 region of the HBV virion surface envelope protein (HBsAg), or the HBV X protein. In certain embodiments, at least one antigen binding domain specifically binds to the pre-S1 region. In some embodiments the multimeric binding molecule binds to an HBV antigen that comprises pre-S1, pre-S2 and S. In some embodiments the HBV antigen is pre-S1 and pre-S2, or pre-S1 and S, or pre-S2 and S. The binding unit that binds to the pre-S1 antigen can possess one or more different specificities for the pre-S1 antigen. That is, at least one binding unit of a multimeric binding molecule described herein is specific for pre-S1 protein of the HBV envelope protein and because each binding unit can possess as many as two antigen binding domains, each antigen binding domain can bind to different and distinguishable epitopes on the pre-S1 protein. In other embodiments, when the multimeric binding molecule comprises more than one binding unit, each binding unit can independently be specific for a different HBV antigen. Thus, in a multimeric binding molecule comprising at least two binding units, one binding unit can possess specificity for pre-S1 antigen, another binding unit can possess specificity for S antigen, etc. Alternatively, all of the binding units can possess identical specificity for pre-S1, for example. Thus, just as each binding unit can be comprised of different antigen binding domains, a multimeric binding molecule can possess one or more specificities for different HBV antigens. In some embodiments, all binding units of a multimeric binding molecule possess specificity for pre-S1 antigen.

**[0135]** HBV antigen targets for the binding units of multimeric binding molecule described herein can be expressed on the surface of an infectious HBV virion, on the surface of HBV-infected cells, or a combination thereof in higher density than the HBV antigen is expressed on non-infectious

sub-viral particles. For instance, it is known that pre-S1 is expressed in higher density, *i.e.* in greater number, on infectious HBV virion particles than on non-infectious, spherical and filamentous, HBV virion particles. (Hong *et al.*, *Virology*, 318:134-141, 2004; Heerman *et al.*, *J. Virol.*, 52(2):396-402, 1984; and Park *et al.*, *Antiviral Res.*, 68:109-115, 2005). In certain embodiments, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, or at least twelve antigen binding domains of the binding units of a multimeric binding molecule as described herein can specifically bind to a hepatitis B virus (HBV) antigen expressed on the surface of infectious viral particles, on the surface of HBV infected cells, or a combination thereof. While not wishing to be bound by theory, multimeric binding molecules possessing specificity for an HBV antigen that is more highly expressed in infectious HBV virions can be more effective, possess higher activity, be more potent or require fewer molecules to achieve the desired activity of enhancing viral clearance, *e.g.*, through killing of infected cells, suppressing infectivity, *e.g.*, through virus neutralization, and/or suppressing growth or maintenance of the HBV virus in an infected individual, *e.g.*, an acutely, chronically, or latently infected individual, than a reference single binding unit, as discussed above.

**[0136]** Alternatively, the HBV antigen can be any one or more of the HBV proteins including envelope proteins (S, M and/or L), precore antigen (*e.g.*, HBeAg), core antigen (*e.g.*, HBcAg), and X-antigen (*e.g.*, HBx). Further, a multimeric binding molecule as described herein can possess binding units, each of which independently possess specificity for any one or more of these HBV antigens. Thus, a single multimeric binding molecule can, for example, possess specificity for one or more of the HBV antigens including envelope proteins (S, M and/or L), precore antigen, core antigen and X-antigen.

IgA Binding Molecules

**[0137]** IgA plays a critical role in mucosal immunity, and comprises about 15% of total immunoglobulin produced. IgA is a monomeric or dimeric molecule. A dimeric binding molecule as described herein can possess binding characteristics or biological activity that can be distinguished from a binding molecule comprising five or six binding units, *e.g.*, a hexameric or pentameric IgM antibody. For example, a dimeric binding molecule would be smaller, and could achieve better tissue penetration. IgA binding molecules can be manufactured by expression *in vitro* to include two IgA monomers and a J-chain. IgA molecules can then be administered to an

individual, *e.g.*, through intravenous infusion, and IgA molecules that migrate to mucous membranes or mucosal tissue can bind to and form a complex with a secretory component produced by epithelial cells, forming sIgA. Oligomeric sIgA is translocated across epithelial cells where ultimately sIgA is delivered to the mucosal surface. (Kaetzel *et al.*, *Proc. Natl. Acad. Sci. USA* 88(19):8796–8800). Therefore, delivery of IgA to the blood stream can provide targeting of mucosal tissues.

**[0138]** An IgA binding unit includes two light and two heavy chains. IgA contains three heavy chain constant domains (Cα1, Cα2 and Cα3), and includes a C-terminal "tailpiece." Human IgA has two subtypes, IgA1 and IgA2. The human IgA1 constant region typically comprises the amino acid sequence SEQ ID NO: 55:

ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVT
ARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVT
VPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTC
TLTGLRDASGVTFTWTPSSGKSAVQGPPERDLCGCYSVSSVLPGCAEPW
NHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEELALNEL
VTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAV
TSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSV
VMAEVDGTCY

**[0139]** The human Cα1 region ranges from about amino acid 6 to about amino acid 98 of SEQ ID NO: 55; the human Cα2 region ranges from about amino acid 125 to about amino acid 220 of SEQ ID NO: 55, the human Cα3 region ranges from about amino acid 228 to about amino acid 330 of SEQ ID NO: 55, and the tailpiece ranges from about amino acid 331 to about amino acid 352 of SEQ ID NO: 55. The human IgA2 constant region typically comprises the amino acid sequence SEQ ID NO: 56:

ASPTSPKVFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWSESGQNVT
ARNFPPSQDASGDLYTTSSQLTLPATQCPDGKSVTCHVKHYTNPSQDVT
VPCPVPPPPPCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGATF
TWTPSSGKSAVQGPPERDLCGCYSVSSVLPGCAQPWNHGETFTCTAAHP
ELKTPLTANITKSGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPK
DVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKK
GDTFSCMVGHEALPLAFTQKTIDRMAGKPTHVNVSVVMAEVDGTCY

**[0140]** The human Cα1 region ranges from about amino acid 6 to about amino acid 98 of SEQ ID NO: 56; the human Cα2 region ranges from about amino acid 112 to about amino acid 207 of SEQ ID NO: 56, the human Cα3 region ranges from about amino acid 215 to about amino acid 317 of

SEQ ID NO: 56, and the tailpiece ranges from about amino acid 318 to about amino acid 340 of SEQ ID NO: 56.

**[0141]** Two IgA binding units can form a complex with two additional polypeptide chains, the J-chain (SEQ ID NO: 54) and the secretory component (SEQ ID NO: 57) to form a secretory IgA (sIgA) antibody. While not wishing to be bound by theory, the assembly of IgA binding units into a dimeric sIgA binding molecule is thought to involve the Cα3 and tailpiece domains. Accordingly, a dimeric IgA binding molecule described in this disclosure typically includes IgA constant regions that include at least the Cα3 and tailpiece domains. The amino acid sequence of the secretory component (SEQ ID NO: 57) is provided below:

KSPIFGPEEVNSVEGNSVSITCYYPPTSVNRHTRKYWCRQGARGGCITL
ISSEGYVSSKYAGRANLTNFPENGTFVVNIAQLSQDDSGRYKCGLGINS
RGLSFDVSLEVSQGPGLLNDTKVYTVDLGRTVTINCPFKTENAQKRKSL
YKQIGLYPVLVIDSSGYVNPNYTGRIRLDIQGTGQLLFSVVINQLRLSD
AGQYLCQAGDDSNSNKKNADLQVLKPEPELVYEDLRGSVTFHCALGPEV
ANVAKFLCRQSSGENCDVVVNTLGKRAPAFEGRILLNPQDKDGSFSVVI
TGLRKEDAGRYLCGAHSDGQLQEGSPIQAWQLFVNEESTIPRSPTVVKG
VAGGSVAVLCPYNRKESKSIKYWCLWEGAQNGRCPLLVDSEGWVKAQYE
GRLSLLEEPGNGTFTVILNQLTSRDAGFYWCLTNGDTLWRTTVEIKIIE
GEPNLKVPGNVTAVLGETLKVPCHFPCKFSSYEKYWCKWNNTGCQALPS
QDEGPSKAFVNCDENSRLVSLTLNLVTRADEGWYWCGVKQGHFYGETAA
VYVAVEERKAAGSRDVSLAKADAAPDEKVLDSGFREIENKAIQDPR

**[0142]** An IgA heavy chain constant region can additionally include a Cα2 domain or a fragment thereof, a Cα1 domain or a fragment thereof, and/or other IgA heavy chain domains. In certain embodiments, a binding molecule as described herein can include a complete IgA heavy (α) chain constant domain, *e.g.*, SEQ ID NO: 55 or SEQ ID NO: 56, or a fragment thereof.

Dimeric HBV Binding Molecules

**[0143]** This disclosure includes a multimeric binding molecule, *e.g.*, a multimeric binding molecule comprising two or more IgA molecules, where each IgA molecule can comprise one or two "binding units" as defined herein, that can specifically bind to an HBV antigen, *e.g.*, HBsAg, *e.g.*, the pre-S1 region of HBsAg. As explained above in the context of IgM multimeric binding molecules, an IgA multimeric binding molecule as described herein can possess improved binding characteristics or biological activity as compared to a binding molecule composed of a reference single binding unit, *e.g.*, a single binding unit IgG antibody. In other words, the IgA binding

molecule described herein can in some embodiments enhance viral clearance, and/or be more potent in, *e.g.*, enhancing viral clearance, *e.g.*, through killing of infected cells, suppressing infectivity, *e.g.*, through virus neutralization, and/or suppressing growth or maintenance of the HBV virus in an infected individual, *e.g.*, an acutely, chronically, or latently infected individual, as compared with a reference single binding unit comprising just two HBV-specific antigen binding domains. The term "improved binding characteristics" can be further clarified as follows. The IgA binding molecule described herein, when administered to an individual in need thereof, can exhibit an activity that is empirically determined to be stronger, more potent, or require less binding molecule by mass or molar equivalents, to enhance viral clearance, reduce the infectivity of an infectious HBV virion, and/or reduce the growth of an infectious HBV virion in an infected individual, as compared with an single, *i.e.* non-multimeric, binding molecule comprising just one binding unit that possesses antigen binding domains identical in sequence to those of the IgA binding molecule described herein.

**[0144]** The reference single binding unit referred to above can be an IgG binding unit. The reference IgG binding unit can be of any isotype, such as IgG1, IgG2, IgG3, or IgG4, etc. The reference binding unit is typically from the same animal. Thus if the multimeric binding molecule is human, the reference single binding unit would also be human, but not necessarily human. That is, the reference single binding unit can be a humanized antibody of the IgG type. Conversely, if the multimeric binding molecule is a rabbit binding molecule, the reference single binding unit would also be a rabbit binding unit. Further, if the multimeric binding molecule is comprised of one or more binding unit fragments, then the reference single binding unit would also be an equivalent single binding unit fragment. In other words, the reference single binding unit is otherwise identical in sequence and structure to the binding units contained in the multimeric binding molecule except that the reference single binding unit is an equivalent single binding unit.

**[0145]** In certain embodiments, the disclosure includes a multimeric binding molecule comprising two bivalent binding units, where each binding unit includes two IgA heavy chain constant regions or fragments thereof. In certain embodiments, the two IgA heavy chain constant regions are human heavy chain constant regions. The IgA binding units can be human, or humanized, binding units, or a combination thereof. Alternatively, the IgM binding units can be of mixed species in a single IgM binding molecule.

**[0146]** A multimeric, *e.g.*, dimeric IgA binding molecule as described herein can further comprise a J-chain, or functional fragment thereof, or variant thereof. In certain embodiments, the J-chain is a modified J-chain comprising a heterologous moiety or one or more heterologous moieties, *e.g.*, a heterologous polypeptide sequence, *e.g.*, an extraneous binding domain introduced into the native sequence. In certain embodiments the extraneous binding domain specifically binds to CD3, *e.g.*, CD3ε. In certain embodiments the mature modified J-chain comprises V15J (SEQ ID NO: 68) or J15V (SEQ ID NO: 71). A multimeric IgA binding molecule as described herein can further comprise a secretory component, or fragment thereof, or variant thereof.

**[0147]** An IgA heavy chain constant region can include one or more of a Cα1 domain, a Cα2 domain, and/or a Cα3 domain, provided that the constant region can serve a desired function in the binding molecule, *e.g.*, associate with second IgA constant region to form an antigen binding domain, or associate with another IgA binding unit to form a dimeric binding molecule. In certain embodiments the two IgA heavy chain constant regions or fragments thereof within an individual binding unit each comprise a Cα3 domain or fragment thereof, a tailpiece (TP) or fragment thereof, or any combination of a Cα3 domain, a TP, or fragment thereof. In certain embodiments the two IgA heavy chain constant regions or fragments thereof within an individual binding unit each further comprise a Cα2 domain or fragment thereof, a Cα1 domain or fragment thereof, or a Cα1 domain or fragment thereof and a Cα2 domain or fragment thereof.

**[0148]** In certain embodiments each of the two IgA heavy chain constant regions in a given antigen binding domain is associated with an antigen binding domain, for example an Fv portion of an antibody, *e.g.*, a VH and a VL of a human or murine antibody. In certain embodiments, at least one antigen binding domain of a binding molecule as described herein is a cross-reactive HBV antigen binding domain, *e.g.*, an antigen binding domain that can specifically bind to two, three, four, or more HBV subtypes. In certain embodiments at least one antigen binding domain binds to the pre-S1 or X antigen of the HBV virion.

**[0149]** In other embodiments, an IgA binding molecule as described herein can comprise binding units wherein each binding unit can possess two antigen binding domains, each with a different and distinguishable specificity. Thus, a dimeric IgA binding molecule could possess as many as four different specificities.

**[0150]** In certain embodiments at least one antigen binding domain binds to the S region, the pre-S2 region, and/or the pre-S1 region of the HBV virion envelope protein (HBsAg). In certain

embodiments, at least one antigen binding domain specifically binds to the pre-S1 protein. In some embodiments the multimeric binding molecule binds to an HBV antigen that comprises pre-S1, pre-S2 and S. In some embodiments the HBV antigen is pre-S1 and pre-S2, or pre-S1 and S, or pre-S2 and S. The binding unit that binds to the pre-S1 antigen can possess one or more different specificities for the pre-S1 antigen. That is, at least one binding unit of a multimeric binding molecule as described herein is specific for pre-S1 protein of the HBV envelope protein and because each binding unit can possess as many as two antigen binding domains, each antigen binding domain can bind to different and distinguishable epitopes on the pre-S1 protein. In other embodiments, when the multimeric binding molecule comprises more than one binding unit, each binding unit can independent be specific for a different HBV antigen. Thus, in a multimeric binding molecule comprising at least two bivalent binding units, one binding unit can possess specificity for pre-S1 antigen; another binding unit can possess specificity for S antigen, etc. Alternatively, all of the binding units can possess identical specificity for pre-S1, for example. Thus, just as each binding unit can be comprised of different antigen binding domains, a multimeric binding molecule can possess one or more specificities for different HBV antigens. In an embodiment of the disclosure, all binding units of the multimeric binding molecule possess specificity for pre-S1 antigen. In certain embodiments at least one antigen binding domain binds to the HBV X antigen (HBxAg).

**[0151]** The HBV antigen for which a binding unit of a described multimeric binding molecule possesses specificity can be expressed on the surface of an infectious HBV virion, on the surface of HBV-infected cells, or a combination thereof in higher density than the HBV antigen is expressed on non-infectious sub-viral particles. For instance, it is known that pre-S1 is expressed in higher density, *i.e.* in greater number, on infectious HBV virion particles than on non-infectious, spherical and filamentous, HBV virion particles. (Hong *et al.*, *Virology*, 318:134-141, 2004; Park *et al.*, *Antiviral Res.*, 68:109-115, 2005). In certain embodiments, at least two, at least three, or at least four antigen binding domains of a multimeric binding molecule described herein specifically bind to a hepatitis B virus (HBV) antigen expressed on the surface of infectious viral particles, on the surface if HBV infected cells, or a combination thereof. When expressed on the surface of infected cells, the higher-density HBV antigen can be found in the context of MHC molecules expressed on the surface of infected cells. While not wishing to be bound by theory, multimeric binding molecules possessing specificity for an HBV antigen that is more highly expressed in infectious

HBV virions can be more effective, possess higher activity, be more potent or require less molecules to achieve the desired activity of enhancing viral clearance, suppressing infectivity, and/or suppressing growth of the HBV virus in an infected individual, than a reference single binding unit, as discussed above.

**[0152]** Alternatively, the HBV antigen can be any one or more of the HBV proteins including HBsAg envelope proteins (S, M and/or L), precore antigen (*e.g.*, HBeAg), core antigen (*e.g.*, HBcAg) and X-antigen (*e.g.*, HBx). Further, a multimeric binding molecule as described herein can possess binding units that each independently possesses specificity for any one or more of these HBV antigens. Thus, a single multimeric binding molecule can, for example, possess specificity for one or more of the HBV antigens including envelope proteins (S, M and/or L), precore antigen, core antigen and X-antigen.

Modified J-Chains

**[0153]** In certain embodiments HBV binding molecules described herein can be bispecific, incorporating a modified J-chain. As described herein and in PCT Publication No. WO 2015/153912 , a modified J-chain can comprise a heterologous moiety, *e.g.*, a heterologous polypeptide, *e.g.*, an extraneous binding domain, which can include, for example, a polypeptide binding domain capable of specifically binding to a target. The binding domain can be, for example, an antibody or antigen-binding fragment thereof, an antibody-drug conjugate or antigen-binding fragment thereof, or an antibody-like molecule. A polypeptide binding domain can be introduced into a J-chain by appropriately selecting the location and type of addition (*e.g.* direct or indirect fusion, chemical tethering, etc.).

**[0154]** In certain embodiments, the binding domain can be an antibody or an antigen-binding fragment of an antibody, including monospecific, bispecific, and multi-specific antibodies and antibody fragments. The antibody fragment can be, without limitation, a Fab fragment, a Fab' fragment, a $F(ab')_2$ fragment, an scFv, $(scFv)_2$ fragment, single-chain antibody molecules, minibodies, or multispecific antibodies formed from antibody fragments. In certain embodiments, the antibody fragment is a scFv.

**[0155]** In other embodiments, the binding domain can be an antibody-like molecule, for example, a human domain antibody (dAb), Dual-Affinity Re-Targeting (DART) molecule, a diabody, a di-diabody, dual-variable domain antibody, a Stacked Variable Domain antibody, a Small Modular

Immuno Pharmaceutical (SMIP), a Surrobody, a strand-exchange engineered domain (SEED)-body, or TandAb.

**[0156]** The binding domain can be introduced into the native J-chain sequence at any location that allows the binding of the binding domain to its binding target without interfering with the binding of the recipient IgM or IgA molecule to its binding target or binding targets or the ability of the J-chain to effectively incorporate into an IgA dimer or an IgM pentamer. In certain embodiments the binding domain can be inserted at or near the C-terminus, at or near the mature N-terminus (*i.e.*, amino acid number 23 of SEQ ID NO: 54 following cleavage of the signal peptide) or at an internal location that, based on the three-dimensional structure of the J-chain is accessible. In certain embodiments, the binding domain can be introduced into the native sequence J-chain without about 10 residues from the C-terminus or without about 10 amino acid residues from the mature N-terminus, of the human J-chain of SEQ ID NO: 54. In another embodiment, the binding domain can be introduced into the native sequence human J-chain of SEQ ID NO: 54 in between cysteine residues 114 and 123 of SEQ ID NO: 54, or at an equivalent location of another native sequence J-chain. In a further embodiment, the binding domain can be introduced into a native sequence J-chain, such as a J-chain of SEQ ID NO: 54, at or near a glycosylation site. In certain embodiments, the binding domain can be introduced into the native sequence human J-chain of SEQ ID NO: 54 within about 10 amino acid residues from the C-terminus.

**[0157]** Introduction can be accomplished by direct or indirect fusion, *i.e.* by the combination of the J-chain and binding domain in one polypeptide chain by in-frame combination of their coding nucleotide sequences, with or without a peptide linker. The peptide linker (indirect fusion), if used, can be about 1 to 50, or about 1 to 40, or about 1 to 30, or about 1 to 20, or about 1 to 10, or about 1 to 5, or about 10 to 20 amino acids in length, and can be present at one or both ends of the binding domain to be introduced into the J-chain sequence. In certain embodiments, the peptide linker is about 1 to 5, about 10 to 20, or about 10 to 15 amino acids long. In certain embodiments the peptide linker is 15 amino acids long. In certain embodiments the peptide linker is $(GGGGS)_3$ (SEQ ID NO: 72).

**[0158]** It is also possible to introduce more than one heterologous polypeptide, *e.g.*, more than one binding domain, into a J-chain.

**[0159]** The modified J-chain can be produced by well-known techniques of recombinant DNA technology, by expressing a nucleic acid encoding the modified J-chain in a suitable prokaryotic or eukaryotic host organism.

**[0160]** The modified J-chain can also be co-expressed with the heavy and light chains of the recipient IgM or IgA binding molecules as described elsewhere herein. The recipient binding molecule, prior to the modified J-chain incorporation, can be monospecific, bispecific or multi-specific, *e.g.*, a monospecific, bispecific, or multispecific IgA or IgM antibody. Bispecific and multi-specific IgM and IgA binding molecules, including antibodies, are described, for example, in U.S. Application Serial Nos. 61/874,277 and 61/937,984, the entire contents of which are hereby expressly incorporated by reference.

**[0161]** In certain embodiments, an anti-HBV IgM or IgA binding molecule as described herein can include a modified J-chain with binding specificity for an immune effector cell, such as a T-cell, NK-cell, a macrophage, or a neutrophil. In certain embodiments the effector cell is a T-cell and the binding target is CD3 (discussed below). By activating and redirecting effector cells, *e.g.* effector T-cells (T-cell dependent killing or TDCC), to infected cells expressing HBV antigens, *e.g.*, HBsAg, on their surface, a bispecific anti-HBV x anti-CD3 IgM or IgA binding molecule as described herein can produce an enhanced immune response against the target, the response comprising, *e.g.*, complement-mediated cytotoxicity, antibody dependent cellular cytotoxicity (ADCC), TDCC, and/or NK-cell mediated killing, thereby further increasing potency and efficacy. In certain embodiments, a bispecific anti-HBV x anti-CD3 IgM or IgA binding molecule as described herein comprising a modified J-chain can be used for the treatment of a disease or condition caused by, or exacerbated by infection with hepatitis B virus.

**[0162]** In the case of T-cells, cluster of differentiation 3 (CD3) is a multimeric protein complex, known historically as the T3 complex, and is composed of four distinct polypeptide chains (ε, γ, δ, ζ) that assemble and function as three pairs of dimers (εγ, εδ, ζζ). The CD3 complex serves as a T-cell co-receptor that associates non-covalently with the T-cell receptor (TCR). Components of this CD3 complex, especially CD3ε, can be targets for a modified J-chain of a bispecific IgM or IgA binding molecule described herein.

**[0163]** In certain embodiments, a bispecific anti-HBV x anti-CD3 IgM or IgA binding molecule binds to HBV-infected cells or HBV virus particles via the antibody binding domains, while the J-chain is modified to bind to CD3ε.

**[0164]** In certain embodiments the anti- CD3ε binding domain of a modified J-chain described herein is a scFv. The anti CD3ε scFv can be fused at or near the N-terminus of the J-chain, or at or near the C-terminus of the J-chain either directly or indirectly with a synthetic linker introduced in between the scFv and the J-chain sequences, *e.g.*, a $(GGGGS)_3$ linker (SEQ ID NO: 72). In certain embodiments the scFv comprises the VH and VL regions of visilizumab (Nuvion). In certain embodiments the modified J-chain comprises a scFv comprising the VH of visilizumab, a $(GGGGS)_3$ linker, and the VL of visilizumab.

**[0165]** In certain embodiments the modified J-chain comprises a scFv of visilizumab fused to the N-terminus of the human J-chain through a 15-amino acid $(GGGGS)_3$ linker, a modified J-chain referred to herein as V15J. V15J can further include a signal peptide to facilitate transport and assembly into an IgM or IgA binding molecules. The mature V15J protein is presented as SEQ ID NO: 68, the precursor version, comprising a 19-amino acid-immunoglobulin heavy chain signal peptide is presented as SEQ ID NO: 67. In certain embodiments the modified J-chain comprises a scFv of visilizumab fused to the C-terminus of the human J-chain through a 15-amino acid $(GGGGS)_3$ linker, a modified J-chain referred to herein as J15V. J15V can further include a signal peptide to facilitate transport and assembly into an IgM or IgA binding molecules. The mature J15V protein is presented as SEQ ID NO: 71, the precursor version, comprising the 22-amino acid-human J-chain signal peptide is presented as SEQ ID NO: 70. In certain embodiments, other signal peptides can be used. Selection and inclusion of suitable signal peptides to facilitate expression, secretion, and incorporation of a modified J-chain into an anti-HBV IgM or IgA binding molecule as described herein is well within the capabilities of a person of ordinary skill in the art.

Engineered HBV Antigen Binding Domains

**[0166]** In certain embodiments an HBV antigen binding domain as described herein can include as many as six immunoglobulin complementarity determining regions HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3, wherein at least one, at least two, at least three, at least four, at least five, or at least six CDRs are related to, or in some embodiments identical to, the corresponding CDRs of the HBV mAbs set forth in Table 2 below. In certain embodiments an HBV antigen binding domain as described herein can include as many as six immunoglobulin complementarity determining regions HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3, wherein at least one, at least two, at least three, at least four, at least five, or at least six CDRs are related to, or in

some embodiments identical to, the corresponding CDRs of the HBV mAbs KR127, disclosed in U.S. Patent No. 7,115,723. The KR127 antibody and its derivatives are specific for an HBsAg pre-S1 epitope. In certain embodiments an HBV antigen binding domain as described herein can be a humanized version of KR127, *e.g.*, KR127I, where the VH and VL regions comprise the amino acid sequences SEQ ID NOs 1 and 3, respectively, KR127III, where the VH and VL regions comprise the amino acid sequences SEQ ID NOs 1 and 3, respectively, both as disclosed in U.S. Patent No. 7,115,723. In another embodiment, an HBV antigen binding domain as described herein can be a humanized, affinity matured version of KR127 as described in U.S. Patent No. 8,420,353 (VH and VL SEQ ID NOs: 5 and 6, respectively), in Hong *et al.*, Virol., 318:131-141, 2004 (VH and VL SEQ ID NOs 4 and 3, respectively), or in Kim, J.H., *et al.* FEBS Letters 589:193-20, 2015 (VH and VL SEQ ID NOs 47 and 48, respectively.

**[0167]** Methods for genetically engineering cloned variable regions into immunoglobulin domains, and expressing and purifying such constructs are published and within the capability of one of skill in the art. (*See*, for instance, Wu *et al.*, *MAbs*, 1:339–47, 2009, and Wu *et al.*, *Nat. Biotechnol.*, 25:1290–7, 2007).

**[0168]** Table 2 provides the VH and VL amino acid sequences of exemplary, non-limiting HBV binding domains that can be used in a multimeric binding molecule as described herein, as well as the identified epitopes to which binding domain binds. These sequences, or variants, fragments, or derivatives thereof, can be engineered into a standard pentameric or hexameric IgM or an IgA structure.

**Table 2: VH and VL Amino Acid Sequences for Monoclonal Antibodies Specific for HBV**

| Source | Target | VH SEQ ID NO | VH | VL SEQ ID NO | VL |
|---|---|---|---|---|---|
| U.S. Patent No. 7,115,723 | Pre-S1 | 1 | QVQLVQSGAEVVKPGASVKVSCKASG YAFSSSWMNWVRQAPGQGLEWIGRIYP GDGDTNYAQKFQGKATLTADKSTSTA YMELSSLRSEDTAVYFCAREYDEAYW GQGTLVTVSS | 3 | DILMTQTPLSLSVTPGQPASISCKSSQSLLYS NGKTYLNWLLQKPGQSPKRLIYLVSKLDSG VPDRFSGSGSGTDFTLKISRVEAEDVGVYYC VQGTHFPQTFGGGTKVEIKR |
| U.S. Patent No. 7,115,723 | Pre-S1 | 2 | QVQLVQSGAEVKKPGASVKVSCKASG YTFTSSWMNWVRQAPGQGLEWMGRIY PGDGDTNYAQKFQGRVTMTADKSTST VYMELSSLRSEDTAVYYCAREYDEAY WGQGTLVTVSS | 3 | DILMTQTPLSLSVTPGQPASISCKSSQSLLYS NGKTYLNWLLQKPGQSPKRLIYLVSKLDSG VPDRFSGSGSGTDFTLKISRVEAEDVGVYYC VQGTHFPQTFGGGTKVEIKR |
| Hong *et al*., *Virol.*, 318:131-141, 2004 | Pre-S1 | 4 | QVQLVQSGPELAKVGASVKVSCKASG YAFSSSWMNWVRQAPGQGLEWIGRIYP GDGDTNYAQKFQGKATLTADKSTSTA YMELSSLRSEDTAVYFCAREYDEAYW GQGTLVTVSS | 3 | DILMTQTPLSLSVTPGQPASISCKSSQSLLYS NGKTYLNWLLQKPGQSPKRLIYLVSKLDSG VPDRFSGSGSGTDFTLKISRVEAEDVGVYYC VQGTHFPQTFGGGTKVEIKR |
| U.S. Patent No. 8,420,353 | Pre-S1 | 5 | QVQLVQSGAEVKAPGASVKVSCKASG YTFTSAWMNWVRQAPGQGLEWMGRI YPSGGSTSYAQKFQGRVTMTADKSTST VYMELSSLRSEDTAVYYCAREYRVAR WGQGTLVTVSA | 6 | DIVMTQTPLSLSVTPGQPASISCKSSQSLLYS NGKTYLNWLLQKPGQPPQRLIYLVSNRDSG VPDRFSGSGSGTDFTLKISRVEAEDVGVYYC VQGTHFPQTFGGGTKVEIK |
| WO 2011/045079A1 | Pre-S1 | 7 | EVQLVESGGDLVKPGGSLRLSCAASGL TFSNAWMNWVRQAPGKGLEWVGRIKS KSDGGTTDYAAPVEGRFSISRDDSKDTL YLQMNSLKTEDTAVYYCASRLVAEGG FDSWGQGTLVTVSS | 8 | DIVMTQSPDSLAVSLGERATINCKSSQSVLY SSNNRNYLAWYQQKPGQPPKLLIYWASTR DSGVPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQQYYNTPYSFGQGTKLEIK |
| WO 2011/045079A1 | Pre-S1 | 7 | EVQLVESGGDLVKPGGSLRLSCAASGL TFSNAWMNWVRQAPGKGLEWVGRIKS KSDGGTTDYAAPVEGRFSISRDDSKDTL YLQMNSLKTEDTAVYYCASRLVAEGG FDSWGQGTLVTVSS | 9 | DIVMTQSPDSLAVSLGERATINCKSSQSVLY SSNNKNYLAWYQQKPGQPPKLLIYWASTRE SGVPDRFSGSGSGTDFTLTISSLQAEDVAVY YCQQYYSTPYSFGQGTKLEIK |

| Source | Target | VH SEQ ID NO | VH | VL SEQ ID NO | VL |
|---|---|---|---|---|---|
| U.S. Reissue No. RE39586 | HBsAg | 10 | QVQLVESGGGVVRPGRSLRLSCAASGF AFSDYSINWVRQAPGKGLEWVAIISYD GRITYYRDSVKGRFTISRDDSKNTLYLQ MNSLRTEDTAVYYCARQYYDFWSGSS VGRNYDGMDVWGLGTTVTVSS | 11 | DIVMTQSPLSLSVTPGEPASISCRSSQSLLHR SGNNYLDWYLQKPGHSPQLLIYVGSNRASG VPDRFSGSGSGTEYTLKISRVEAEDVGVYY CMQALQTPRTFGQGTKLEIK |
| Walsh *et al*., *Virol.*, 411:132-141 (2011) | HBeAg | 12 | AWVDQTPRTATKETGESLTINCVLRDT SCAFSSTGWYRTKLGSTNEQSISTGGRY VETVNKTSKSISLRISDLRVEDSGTYKC QVYFTPVWDGSCFGILGRTKKGAGTAL TVK | | |
| Walsh *et al*., *Virol.*, 411:132-141 (2011) | HBeAg | 13 | AWVDQTPRTATKETGESLTINCVLRDT SCAFSGTGWYRTKLGSTNEQSISIGGRY VETVSKGSKSISLRISDLRVEDSGTYKC QVYFTPVWDGSCFGILGRTKKGAGTAL TVK | | |
| WO2014048910A1 | HBsAg | 14 | EVQLVESGGGLVQPGGSLRVSCEVSGF TFSNNWMHWVRQAPGKGPVWVSRIST DGMSTSYAEFVKGRFTISRDNARNTLY LQMNSLRDEDTAVYYCVRGSTYYFGS GSLNFWGQGTTVIVSS | 15 | QSALTQPRSVSGSPGQSVTISCTGTNSDIGN YDYVSWYQQHPGKAPRLIIYDVSERPSGVP NRFSGSKSGNTASLTISGLQAEDESDYFCSS YAGTFTYVVFGGGTKLTVL |
| WO2014010890A1 | HBsAg | 16 | QVKLLESGGGLVKPGGSLRLSCSASGFS LTKYKMTWVRQAPGKGLEWVSSISSTS RDIDYADSVKGRFTISRDNAKNSLFLQ MSSLRVDDTAVYYCTRDGWLWGWDV RSNYYYNALDVWGQGTTVTVSS | 21 | ELVMTQSPSSLSASVGDRVTITCRASQGIYN SIAWYQQKPGKAPKLLLYSTSTLLSGVPSRF SGSGSGTDYTLTITNLQPEDFATYYCQQYFV TPETFGQGTKVEIKR |
| WO2014010890A1 | HBsAg | 17 | EVQLVESGGGLVKPGGSLRLSCSASGFS LTKYKMTWVRQAPGKGLEWVSSISSTS RDIDYADSVKGRFTISRDNAKNSLFLQ MSSLRVDDTAVYYCTRDGWLWGWDV RSNYYYNALDVWGQGTTVTVSS | 22 | DIVVTQSPSSLSASVGDRVTITCRASQGIYNS IAWYQQKPGKAPKLLLYSTSTLLSGVPSRFS GSGSGTDYTLTITNLQPEDFATYYCQQYFVT PETFGQGTKLEIKR |

| Source | Target | VH SEQ ID NO | VH | VL SEQ ID NO | VL |
|---|---|---|---|---|---|
| WO2014010890A1 | HBsAg | 18 | QVQLVQSGGEVKKPGALMKVSCKASG YIFTSYGISWVRQAPGQGLEWIGWINTY SGHTNYARKFRGRVTMTWDTSTSTAY MELSSLRSDDTAVYYCARVPTWGIDY WGQGTLVTVSS | 23 | QAGLTQPPSVSVAPGKTARITCGGDNIGRKS VHWYQQKTGQAPVLVVYEDNKRPSGIPERF SGSNSGNTATLTISGTQAMDEADYYCQAW DSSTVVFGGGTKLTVLG |
| WO2014010890A1 | HBsAg | 19 | QVQLVQSGGEVKKPGALMKVSCKASG YIFTSYGISWVRQAPGQGLEWIGWINTY SGHTNYARKFRGRVTMTWDTSTSTAY MELSSLRSDDTAVYYCARVPTWGIDY WGQGTLVTVSS | 24 | EIVLTQSPPSLSASVGDRVTITCQASQDINNN VNWFQQEPGKAPRLLIYDASNLQTGVPSRF SGSGSGTEFTLTISSLQPEDFATYYCQQTSV YPLTFGGGTKVDIKR |
| WO2014010890A1 | HBsAg | 20 | QVQLVQSGGEVKKPGALMKVSCKASG YIFTSYGISWVRQAPGQGLEWIGWINTY SGHTNYARKFRGRVTMTWDTSTSTAY MELSSLRSDDTAVYYCARVPTWGIDY WGQGTLVTVSS | 25 | DIVMTQTPLSLPVTPGEPASISCRSSQSLLHS NGYNYLDWYLQKPGQSPQLLIYLGSKRASG VPDRFSGSGSGTDFTLQISRVEAEDVGVYYC MQSTQFPPYTFGQGTKLEIKR |
| U.S. Patent No. 8,840,895 | HBsAg | 26 | QVQLVQSGGEVKKPGALMKVSCKASG YIFTSYGISWVRQAPGQGLEWIGWINTY SGHTNYARKFRGRVTMTWDTSTSTAY MELSSLRSDDTAVYYCARVPTWGIDY WGQGTLVTVSS | 27 | QAGLTQPPSVSVAPGKTARITCGGDNIGRKS VHWYQQKTGQAPVLVVYEDNKRPSGIPERF SGSNSGNTATLTISGTQAMDEADYYCQAW DSSTVVFGGGTKLTVLG |
| U.S. Patent No. 8,840,895 | HBsAg | 26 | QVQLVQSGGEVKKPGALMKVSCKASG YIFTSYGISWVRQAPGQGLEWIGWINTY SGHTNYARKFRGRVTMTWDTSTSTAY MELSSLRSDDTAVYYCARVPTWGIDY WGQGTLVTVSS | 28 | EIVLTQSPPSLSASVGDRVTITCQASQDINNN VNWFQQEPGKAPRLLIYDASNLQTGVPSRF SGSGSGTEFTLTISSLQPEDFATYYCQQTSV YPLTFGGGTKVDIKR |
| U.S. Patent No. 8,840,895 | HBsAg | 26 | QVQLVQSGGEVKKPGALMKVSCKASG YIFTSYGISWVRQAPGQGLEWIGWINTY SGHTNYARKFRGRVTMTWDTSTSTAY MELSSLRSDDTAVYYCARVPTWGIDY WGQGTLVTVSS | 29 | DIVMTQTPLSLPVTPGEPASISCRSSQSLLHS NGYNYLDWYLQKPGQSPQLLIYLGSKRASG VPDRFSGSGSGTDFTLQISRVEAEDVGVYYC MQSTQFPPYTFGQGTKLEIKR |
| U.S. Patent No. 8,580,256 | HBsAg | 30 | QVQLVESGGGVVQPGGSLRLSCAPSGF VFRSYGMHWVRQTPGKGLEWVSLIWH DGSNRFYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAMYFCARERLIAAPAAF | 31 | SYVLTQPPSVSVAPGKTARISCGGNNIGTKN VHWYQQKPGQAPVLVVYADSDRPSGIPERF SGSNSGNTATLTISRVEVGDEADYYCQVWD SVSYHVVFGGGTTLTVLG |

| Source | Target | VH SEQ ID NO | VH | VL SEQ ID NO | VL |
|---|---|---|---|---|---|
| | | | DLWGQGTLVTVSS | | |
| U.S. Patent No. 8,580,256 | HBsAg | 32 | QVQLVESGGGVVRPGRSLRLSCAASGF AFSDYSINWVRQAPGKGLEWVAIISYD GRITYYRDSVKGRFTISRDDSKNTLYLQ MNSLRTEDTAVYYCARQYYDFWSGSS VGRNYDGMDVWGLGTTVTVSS | 33 | DIVMTQSPLSLSVTPGEPASISCRSSQSLLHR SGNNYLDWYLQKPGHSPQLLIYVGSNRASG VPDRFSGSGSGTEYTLKISRVEAEDVGVYY CMQALQTPRTFGQGTKLEIK |
| U.S. Patent No. 7,435,414 | HBsAg | 34 | QVQLKQSGPGLVKPSQTLSLTCTVSGFS LSTYGVQWVRQPPGKGLEWLGVIWSG GNTDYNAAFISRVTISKDTSKNQVSLKL SSVTAADTAVYYCARARYFDVWGAGT TVTVSS | 35 | QAVVTQEPSLTVSPGGTVTLTCRSSTGAITT NNFANWFQQKPGQAFRGLIGDTNNRVPGV PARFSGSLLGNKAALTITGAQPEDEAEYYC ALWYNNWVFGGGTKLTVLG |
| U.S. Patent No. 7,435,414 | HBsAg | 34 | QVQLKQSGPGLVKPSQTLSLTCTVSGFS LSTYGVQWVRQPPGKGLEWLGVIWSG GNTDYNAAFISRVTISKDTSKNQVSLKL SSVTAADTAVYYCARARYFDVWGAGT TVTVSS | 36 | QAVVTQEPSLTVSPGGTVTLTCRSSTGAITT NNFANWFQQKPGQAFRGLIGDTNNRVPGV PARFSGSLIGDKAALTITGAQPEDEAEYYCA LWYNNWVFGGGTKLTVLG |
| U.S. Reissue Patent No. RE40831 | HBsAg | 37 | QVQLVESGGGVVQPGGSLRLSCAPSGF VFRSYGMHWVRQTPGKGLEWVSLIWH DGSNRFYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAMYFCARERLIAAPAAF DLWGQGTLVTVSS | 38 | SYVLTQPPSVSVAPGKTARISCGGNNIGTKN VHWYQQKPGQAPVLVVYADSDRPSGIPERF SGSNSGNTATLTISRVEVGDEADYYCQVWD SVSYHVVFGGGTTLTVLG |
| U.S. Patent No. 5,565,354 | HBsAg | 39 | MEFGLSWVFLVALLRGVQCQVQLVES GGGVVQPGRSLRLSCAASGFTFSRYGM HWVRQAPGKGLEWVAVISYDGSNKW YADSVKGRFTISRDNSKNTLFLQMHSL RAADTGVYYCAKDQLYFGSQSPGHYW VQGTLVTVSS | 40 | QSQLTQPPSVSVAPGQTARITCGGDNIGSKS VNWFQQKPGQAPVLVVYDDNERPSGISERF SGSNSGNTATLTISRVEAGDEADYYCQVWD SSSDHVVFGGGTKLTVL |
| U.S. Patent No. 5,565,354 | HBsAg | 41 | MEFGLSWVFLVAILEGVQCEVQLVESG GGLVQPGGSLRLSCAASGFTFSRYDMY WVRQATGKGLEWVSAIGPTGDTYYAD SVKGRFTISRENAKNSLYLTMNGLRAG DTAVYYCARDLELWGQGTLVTVSS | 42 | MDTRVPAQLLGLLMLWVPGSSGDVVVTQS PLSLPVTLGQPASISCRSSLSLVDSDGNTYLN WFLQRPGQSPRRLIYQLSSRDSGVPDRFSGS GSGTDFTLKISRVEAEDVGVYYCMQGTHW PITFGQGTRLEIKR |

| Source | Target | VH SEQ ID NO | VH | VL SEQ ID NO | VL |
|---|---|---|---|---|---|
| U.S. Patent No. 5,565,354 | HBsAg | 43 | MKHLWFFLLLVAVPRWVVSQVQLQESGPGLVKAAETLSLTCTVSRGSFSDYFWNWFRQPAGKRLEWLGRVYTSGSVDYNPSLKSRVTVSVDTSKKQFSLRLSSVTVADTAVYYCARGLSGFDYWGQGALVTVSP | 44 | MRPVAQLLGLLLLWFPGSRCDIQMTQSPSSVSASVGDRVTVTCRASQGISSWLAWYQQKPGKAPKLLIHAASSLQSGVPSRFIGSGSGTDFTLTITSLQAEDFATYYCQQADSLPFTFGGGTKVDFKR |
| U.S. Patent No. 5,565,354 | HBsAg | 45 | MGSTAILGLLLAVLQGVCAEVQLVQSGAEVKKPGESLRISCKGSGYSFTSYWISWVRQMPGKGLEWMGRLDPSASSAIFSPSLQGHVTISVDKSMRTAYVQWRSLKASDTAMYYCARHVREKSMVQGVIIKDAFDIWGQGTMVTVSS | 46 | QSQLTQPASVSVSPGQTASITCSGDRLGDEFASWYQQKPGQSPILVIFEDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCLAWASSLWVFGGGTKLTVL |
| Kim, J.H., *et al*. FEBS Letters 589:193-200 (2015) | Pre-S1 | 47 | QVQLQQSGAEVKKPGASVKVSCKASGYTFTSSWMNWVRQAPGQGLEWMGRIYPGDGDTSYAQKFQGRVTMTADKSTSTVYMELSSLRSEDTAVYYCAREYAEAYWGQGTLVTVSS | 48 | DIVMTQTPLSLSVTPGQPASISCKSSQSLLYSNGKTYLNWLLQKPGQPPQRLIYLVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCVQGTHFPQTFGGGTKVEIKR |
| zu Putlitz,J., *et al*. Gene 221 (1), 143-149 (1998) | HBxAg | 49 | EVKLHESGAGLVKPGASVNLSCTASGFNIKDTYMHWVKQRPDQGLEWIGRIDPANGNTKSDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCASYSWGQGTTVTVSS | 50 | DIELTQSPVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPLTFGGGTKLELK |
| Park,O.Y., *et al*. Hybridoma 19 (1), 73-80 (2000) | HBxAg | 51 | QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWIHWVKQRPGQGLEWIGEIDPSDSHANYNQKFKGKATLTVDKSSSTVYMQLSSLTSEDSAVYFCTNGYWGQGTTLTVSSA | 52 | DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGETYLNWLLQRPGQSPKRLIYMVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPFTFGSGTKLEIKR |
| Cerino *et al*. (2015) PLOS one 10(4):e0125704. doi: 10.1371 | HBsAg | 73 | EVQVLESGGGLVQPGGSLRLSCAASGFRFSSYAMSWVRQAPGKGLEWVSGISGTGENTYYADSVKGRFTISRDNSKNTLYVQMNSLRAEDTAVYYCAKDAILGSGHPWYFHVWGRGTLVTVSS | 74 | SYVLTQPPSVSVAPGQTARMTCGGNNIGSESVHWFQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHAVFGGGTQLTVL |

| Source | Target | VH SEQ ID NO | VH | VL SEQ ID NO | VL |
|---|---|---|---|---|---|
| Pizarro, *et al*., *FEBS Letters 509*:463-468 (2001) | Pre-S1 or ay serotype | 75 | EVQLEESGGGLVKPGGSLKLSCAASGF TFSSYAMSWVRQSPEKRLEWVAEVSSD GSYAYYPDTLTGRFTISRDNAKNTLYLE MTSLRSEDTAMYYCASFNWDVAYWG QGTLVTVSAA | 76 | ELVMTQSPSSLAVSVGEKVTMSCRSSQSLL NTRTRKSYLAWFQQKPGQSPKMLIYWAST RESGVPDRFTGSGSGTDFTLTISSVQAEDLA VYYCKQSYSLYTFGGGTKLEIKR |

**[0169]** In certain embodiments the HBV antigen binding domain of a dimeric, hexameric, or pentameric binding molecule as described herein comprises an antibody heavy chain variable region (VH) and an antibody light chain variable region (VL), wherein the VH region, the VL region, or both the VH and VL regions are related to the corresponding VH and VL of HBV monoclonal antibodies disclosed in the references set forth in Table 2, above. In certain embodiments, the binding molecules described herein exhibit greater potency than an IgG antibody comprising the VH and VL of antibodies listed in Table 2. The increased avidity of IgA or IgM forms of anti-HBV can result in a more potent therapeutic antibody that can bind those infected cells with very low density of HBV surface proteins, allowing more efficient clearance of HBV from infected patients. In certain embodiments the VH can comprise an amino acid sequence at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to any one or more of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 26, SEQ ID NO: 26, SEQ ID NO: 26, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 34, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 62, SEQ ID NO: 73, or SEQ ID NO: 75. In certain embodiments the VL can comprise an amino acid sequence at least at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to any one or more of SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 74, or SEQ ID NO: 76. In certain embodiments the VH/VL sequences comprise any one or more of the following pairs of sequences, respectively, SEQ ID NO: 1 and SEQ ID NO: 3, SEQ ID NO: 2 and SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8, SEQ ID NO: 7 and SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 11, SEQ ID NO: 14 and SEQ ID NO: 15, SEQ ID NO: 16 and SEQ ID NO: 21, SEQ ID NO: 17 and SEQ ID NO: 22, SEQ ID NO: 18 and SEQ ID NO: 23, SEQ ID NO: 19 and SEQ ID NO: 24, SEQ ID NO: 20 and SEQ ID NO: 25, SEQ ID NO: 26 and SEQ ID NO: 27, SEQ ID

NO: 26 and SEQ ID NO: 28, SEQ ID NO: 26 and SEQ ID NO: 29, SEQ ID NO: 30 and SEQ ID NO: 31, SEQ ID NO: 32 and SEQ ID NO: 33, SEQ ID NO: 34 and SEQ ID NO: 35, SEQ ID NO: 34 and SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38, SEQ ID NO: 39 and SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44, SEQ ID NO: 45 and SEQ ID NO: 46, SEQ ID NO: 47 and SEQ ID NO: 48, SEQ ID NO: 49 and SEQ ID NO: 50, SEQ ID NO: 51 and SEQ ID NO: 52, SEQ ID NO: 62 and SEQ ID NO: 6, SEQ ID NO: 73 and SEQ ID NO: 74, or SEQ ID NO: 75 and SEQ ID NO: 76.

**[0170]** While a variety of different dimeric, hexameric, and pentameric binding molecules can be contemplated by a person of ordinary skill in the art based on this disclosure, and as such are included in this disclosure, in certain embodiments, a binding molecule as described above is included in which each binding unit comprises two IgM heavy chains each comprising a VH situated amino terminal to the IgM constant region or fragment thereof, and two immunoglobulin light chains each comprising a VL situated amino terminal to an immunoglobulin light chain constant region. In certain embodiments, a binding molecule as described above is included in which each binding unit comprises two IgA heavy chains each comprising a VH situated amino terminal to the IgA constant region or fragment thereof, and two immunoglobulin light chains each comprising a VL situated amino terminal to an immunoglobulin light chain constant region.

**[0171]** Moreover in certain embodiments, at least one binding unit of the binding molecule, or two, three, four, five, or six binding units of the binding molecule, comprises or comprise two of the HBV antigen binding domains as described above. In certain embodiments the two HBV antigen binding domains in the one binding unit of the binding molecule, or two, three, four, five, or six binding units of the binding molecule, can be different from each other, or they can be identical.

**[0172]** In certain embodiments, the two IgA heavy chains within the one binding unit of the binding molecule, or two binding units of the binding molecule, are identical. In certain embodiments, the two IgM heavy chains within the one binding unit of the binding molecule, or two, three, four, five, or six binding units of the binding molecule, are identical.

**[0173]** In certain embodiments, the two light chains within the one binding unit of the binding molecule, or two, three, four, five, or six binding units of the binding molecule, are identical. In certain embodiments, two identical light chains within at least one binding unit, or within at least two, at least three, at least four, at least five, or at least six binding units of the binding molecule

are kappa light chains, *e.g.*, human kappa light chains, or lambda light chains, *e.g.*, human lambda light chains.

**[0174]** In certain embodiments at least one, two, three, four, five, or six binding units of a dimeric, pentameric, or hexameric binding molecule included in this disclosure comprises or each comprise two identical IgA or IgM heavy chains, and two identical light chains. According to this embodiment, the HBV antigen binding domains in the one binding unit of the binding molecule, or two, three, four, five, or six binding units of the binding molecule, can be identical. Further according to this embodiment, a dimeric, pentameric, or hexameric binding molecule as described herein can comprise at least one, two, three, four, five, six, seven, eight, nine, ten, eleven, or twelve copies of an HBV antigen binding domain as described above. In certain embodiments at least two, at least three, at least four, at least five, or at least six of the binding units can be identical and, in certain embodiments the binding units can comprise identical antigen binding domains, *e.g.*, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, or at least twelve HBV antigen binding domains can be identical.

**[0175]** In certain embodiments, a dimeric, hexameric, or pentameric binding molecule includes at least one HBV antigen binding domain comprising a VH and a VL, where the VH region, the VL region, or both the VH and the VL regions are related to corresponding VH and VL regions comprising the amino acid sequences SEQ ID NO: 1 and SEQ ID NO: 3, SEQ ID NO: 2 and SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8, SEQ ID NO: 7 and SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 11, SEQ ID NO: 14 and SEQ ID NO: 15, SEQ ID NO: 16 and SEQ ID NO: 21, SEQ ID NO: 17 and SEQ ID NO: 22, SEQ ID NO: 18 and SEQ ID NO: 23, SEQ ID NO: 19 and SEQ ID NO: 24, SEQ ID NO: 20 and SEQ ID NO: 25, SEQ ID NO: 26 and SEQ ID NO: 27, SEQ ID NO: 26 and SEQ ID NO: 28, SEQ ID NO: 26 and SEQ ID NO: 29, SEQ ID NO: 30 and SEQ ID NO: 31, SEQ ID NO: 32 and SEQ ID NO: 33, SEQ ID NO: 34 and SEQ ID NO: 35, SEQ ID NO: 34 and SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38, SEQ ID NO: 39 and SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44, SEQ ID NO: 45 and SEQ ID NO: 46, SEQ ID NO: 47 and SEQ ID NO: 48, SEQ ID NO: 49 and SEQ ID NO: 50, SEQ ID NO: 51 and SEQ ID NO: 52, SEQ ID NO: 62 and SEQ ID NO: 6, SEQ ID NO: 73 and SEQ ID NO: 74, or SEQ ID NO: 75 and SEQ ID NO: 76, respectively. In certain embodiments, a dimeric, hexameric, or pentameric binding molecule includes at least one HBV antigen binding domain comprising a

VH, where the VH region is related to corresponding VH regions comprising the amino acid sequence SEQ ID NO: 12 or SEQ ID NO: 13.

**[0176]** In certain embodiments, a dimeric, hexameric, or pentameric binding molecule includes at least one HBV antigen binding domain comprising a VH comprising the HCDR1, HCDR2, and HCDR3 regions, or HCDR1, HCDR2, and HCDR3 regions containing one or two single amino acid substitutions, and comprising the LCDR1, LCDR2, and LCDR3 regions, or LCDR1, LCDR2, and LCDR3 containing one or two single amino acid substitutions, of the VH and VL amino acid sequences SEQ ID NO: 1 and SEQ ID NO: 3, SEQ ID NO: 2 and SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8, SEQ ID NO: 7 and SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 11, SEQ ID NO: 14 and SEQ ID NO: 15, SEQ ID NO: 16 and SEQ ID NO: 21, SEQ ID NO: 17 and SEQ ID NO: 22, SEQ ID NO: 18 and SEQ ID NO: 23, SEQ ID NO: 19 and SEQ ID NO: 24, SEQ ID NO: 20 and SEQ ID NO: 25, SEQ ID NO: 26 and SEQ ID NO: 27, SEQ ID NO: 26 and SEQ ID NO: 28, SEQ ID NO: 26 and SEQ ID NO: 29, SEQ ID NO: 30 and SEQ ID NO: 31, SEQ ID NO: 32 and SEQ ID NO: 33, SEQ ID NO: 34 and SEQ ID NO: 35, SEQ ID NO: 34 and SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38, SEQ ID NO: 39 and SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44, SEQ ID NO: 45 and SEQ ID NO: 46, SEQ ID NO: 47 and SEQ ID NO: 48, SEQ ID NO: 49 and SEQ ID NO: 50, SEQ ID NO: 51 and SEQ ID NO: 52, SEQ ID NO: 62 and SEQ ID NO: 6, SEQ ID NO: 73 and SEQ ID NO: 74, or SEQ ID NO: 75 and SEQ ID NO: 76, respectively. In certain embodiments, a dimeric, hexameric, or pentameric binding molecule includes at least one HBV antigen binding domain comprising a VH comprising the HCDR1, HCDR2, and HCDR3 regions, or HCDR1, HCDR2, and HCDR3 regions containing one or two single amino acid substitutions, of the VH amino acid sequence SEQ ID NO: 12 or SEQ ID NO: 13.

**[0177]** In certain embodiments, a dimeric, hexameric, or pentameric binding molecule includes at least one HBV antigen binding domain comprising a VH and a VL, where the VH region, the VL region, or both the VH and the VL regions comprise amino acid sequences at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 1 and SEQ ID NO: 3, SEQ ID NO: 2 and SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8, SEQ ID NO: 7 and SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 11, SEQ ID NO: 14 and SEQ ID NO:

15, SEQ ID NO: 16 and SEQ ID NO: 21, SEQ ID NO: 17 and SEQ ID NO: 22, SEQ ID NO: 18 and SEQ ID NO: 23, SEQ ID NO: 19 and SEQ ID NO: 24, SEQ ID NO: 20 and SEQ ID NO: 25, SEQ ID NO: 26 and SEQ ID NO: 27, SEQ ID NO: 26 and SEQ ID NO: 28, SEQ ID NO: 26 and SEQ ID NO: 29, SEQ ID NO: 30 and SEQ ID NO: 31, SEQ ID NO: 32 and SEQ ID NO: 33, SEQ ID NO: 34 and SEQ ID NO: 35, SEQ ID NO: 34 and SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38, SEQ ID NO: 39 and SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44, SEQ ID NO: 45 and SEQ ID NO: 46, SEQ ID NO: 47 and SEQ ID NO: 48, SEQ ID NO: 49 and SEQ ID NO: 50, SEQ ID NO: 51 and SEQ ID NO: 52, SEQ ID NO: 62 and SEQ ID NO: 6, SEQ ID NO: 73 and SEQ ID NO: 74, or SEQ ID NO: 75 and SEQ ID NO: 76, respectively. In certain embodiments, a dimeric, hexameric, or pentameric binding molecule includes at least one HBV antigen binding domain comprising a VH, where the VH region comprises an amino acid sequence at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 12 or SEQ ID NO: 13.

**[0178]** In certain embodiments the VH and VL can be derived from the HBV pre-S1 mAb described in U.S. Patent No. 7,115,723. For example, the HBV antigen binding domain can comprise a VH amino acid sequence at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 1 or SEQ ID NO: 2, and a VL amino acid sequence at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 3.

**[0179]** In certain embodiments the VH and VL can be derived from the HBV pre-S1 mAb described in Hong *et al.*, *Virol.*, 318:131-141, 2004. For example, the HBV antigen binding domain can comprise a VH amino acid sequence at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 4 and a VL amino acid sequence at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 3.

**[0180]** In certain embodiments the VH and VL can be derived from the HBV mAb described in U.S. Patent No. 8,420,353. For example, the HBV antigen binding domain can comprise a VH amino acid sequence at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 5 and a VL amino acid sequence

at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 6.

**[0181]** In certain embodiments the HBV antigen binding domain can comprise VH and VL amino acid sequences comprising SEQ ID NO: 1 and SEQ ID NO: 3, SEQ ID NO: 2 and SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8, SEQ ID NO: 7 and SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 11, SEQ ID NO: 14 and SEQ ID NO: 15, SEQ ID NO: 16 and SEQ ID NO: 21, SEQ ID NO: 17 and SEQ ID NO: 22, SEQ ID NO: 18 and SEQ ID NO: 23, SEQ ID NO: 19 and SEQ ID NO: 24, SEQ ID NO: 20 and SEQ ID NO: 25, SEQ ID NO: 26 and SEQ ID NO: 27, SEQ ID NO: 26 and SEQ ID NO: 28, SEQ ID NO: 26 and SEQ ID NO: 29, SEQ ID NO: 30 and SEQ ID NO: 31, SEQ ID NO: 32 and SEQ ID NO: 33, SEQ ID NO: 34 and SEQ ID NO: 35, SEQ ID NO: 34 and SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38, SEQ ID NO: 39 and SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44, SEQ ID NO: 45 and SEQ ID NO: 46, SEQ ID NO: 47 and SEQ ID NO: 48, SEQ ID NO: 49 and SEQ ID NO: 50, SEQ ID NO: 51 and SEQ ID NO: 52, SEQ ID NO: 62 and SEQ ID NO: 6, SEQ ID NO: 73 and SEQ ID NO: 74, or SEQ ID NO: 75 and SEQ ID NO: 76, respectively. In certain embodiments the HBV antigen binding domain can comprise a VH amino acid sequence comprising SEQ ID NO: 12 or SEQ ID NO: 13.

**[0182]** In certain embodiments a hexameric or pentameric antibody designated herein as HBV24M is described comprising an IgM heavy chain comprising the amino acid sequence SEQ ID NO: 58 and a kappa light chain comprising the amino acid sequence SEQ ID NO: 59. SEQ ID NOs 58 and 59 are provided here:

>HBV24 IgM Heavy chain (SEQ ID NO: 58)

QVQLVQSGAEVKAPGASVKVSCKASGYTFTSAWMNWVRQAPGQGLEWMG
RIYPSGGSTSYAQKFQGRVTMTADKSTSTVYMELSSLRSEDTAVYYCAR
EYRVARWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP
KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

>HBV24 Kappa Light chain (SEQ ID NO: 59)

DIVMTQTPLSLSVTPGQPASISCKSSQSLLYSNGKTYLNWLLQKPGQPP
QRLIYLVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCVQGTH
FPQTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV
YACEVTHQGLSSPVTKSFNRGEC

**[0183]** In certain embodiments, a humanized heavy chain variable region (VH) comprising the amino acid sequence SEQ ID NO: 62 is provided.

>HBV24M2 IgM Heavy chain (SEQ ID NO: 62)

QVQLVQSGAEVKAPGASVKVSCKASGYTFTSAWMNWVRQAPG
QGLEWMGRIYPSGGSTSYAQKFQGRVTMTADKSTSTVYMELSSL
RSEDTAVYYCAREYDEAYWGQGTLVTVSS

**[0184]** In certain embodiments a hexameric or pentameric antibody designated herein as HBV24M2 is described comprising an IgM heavy chain comprising the amino acid sequence SEQ ID NO: 63 and a kappa light chain comprising the amino acid sequence SEQ ID NO: 59. SEQ ID NO: 63 and 59 are provided here:

>HBV24M2 IgM Heavy chain (SEQ ID NO: 63)

QVQLVQSGAEVKAPGASVKVSCKASGYTFTSAWMNWVRQAPGQGLEWMG
RIYPSGGSTSYAQKFQGRVTMTADKSTSTVYMELSSLRSEDTAVYYCAR
EYDEAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP
KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

>HBV24 Kappa Light chain (SEQ ID NO: 59)

DIVMTQTPLSLSVTPGQPASISCKSSQSLLYSNGKTYLNWLLQKPGQPP
QRLIYLVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCVQGTH
FPQTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV
YACEVTHQGLSSPVTKSFNRGEC

**[0185]** In certain embodiments, a dimeric, pentameric, or hexameric HBV binding molecule as described herein can possess advantageous structural and/or functional properties, or "improved binding characteristics," as compared to other binding molecules, such as a reference single binding unit comprising the same antigen binding domains. For example, the dimeric, pentameric,

or hexameric HBV binding molecule can possess improved activity or potency in a biological assay, either *in vitro* or *in vivo*, relative to a corresponding reference single binding unit, *e.g.*, an IgG1 binding molecule comprising the same VH and VL region sequences as are present in the multimeric binding molecule, as described above. Biological assays include, but are not limited to virus neutralization assays, assays, cell attachment assays, viral egress assays, immunohistochemical assays, direct cytotoxicity assays, complement-mediated cytotoxicity (CDC) assays, T-cell mediated killing (TDCC) assays, NK-cell mediated killing assays, etc. In certain embodiments a dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody as described herein can direct HBV neutralization, or killing of an HBV infected cell, at higher potency than an equivalent amount of a monospecific, single binding unit IgG1 antibody or fragment thereof that specifically binds to the same HBV epitope as the HBV antigen binding domain.

**[0186]** By "potency" or "improved binding characteristics" is meant the least amount of a given binding molecule necessary to achieve a given biological result, *e.g.*, neutralization of 20%, 50%, or 90% of a virus inoculum in a given assay ($EC_{20}$, $EC_{50}$, or $EC_{90}$). Potency can be expressed as a curve in which, for example, % virus neutralization, % killing of infected cells, or other measurable parameter is on the Y axis, and binding molecule concentration (in, *e.g.*, μg/ml or nM) is on the X axis.

**[0187]** In certain embodiments, TDCC can be measured *in vitro* through T-cell activation assays, *e.g.*, by co-culturing HBsAg-expressing cells and engineered CD3-expressing T-cells in the presence of a bispecific anti-HBsAg x anti-CD3 IgM binding molecule as described herein, and measuring T-cell activation through cytokine release, target cell lysis, or other detection method. In certain embodiments TDCC can be measured through T-cell directed target cell killing.

**[0188]** In certain embodiments the HBsAg-expressing cell can be an immortalized cell line, *e.g.*, a hepatocellular carcinoma (HCC) cell line, *e.g.*, PLC/PRF/5 cells, or a cell line, *e.g.*, HEK293, CHO, HepG2, or HepaRG cells, transfected with and expressing an HBV antigen, *e.g.*, HBsAg or HBsAg-L, or HBV-infected cells, *e.g.*, HBV-infected HepaRG cells, or cells producing HBV, *e.g.*, HepG2.2.15 cells. Similar cell lines are known and are easily obtained by a person of ordinary skill in the art. In certain embodiments the HBV antigen-expressing cell line can be derived from a patient suffering from HBV infection, HCC, or a related cancer.

**[0189]** In certain embodiments, the totality of killing of HBV antigen-expressing cells, *e.g.*, by CDC, TDCC, ADCC, and other modes of killing, *e.g.*, apoptosis, can be tested *in vitro* in an assay using isolated T-cells and/or complement or whole blood that includes both T-cells and complement.

**[0190]** In certain embodiments, *e.g.*, where the binding molecule is a pentameric binding molecule comprising five identical binding units each comprising two identical anti-HBsAg binding domains as described herein, tested in a CDC assay using, *e.g.*, the HBsAg-expressing PLC/PRF/5 cell line or HepG2.2.15 cells, the binding molecule can direct complement mediated killing with an $IC_{50}$ at least one-fold, at least two-fold, at least three-fold, at least four-fold, at least five-fold, at least ten-fold, at least 20-fold, at least thirty-fold, at least forty-fold, at least 50-fold, at least 100-fold, at least 150-fold, at least 200-fold or more lower than the $IC_{50}$ of an equivalent amount of an anti-HBsAg monospecific IgG1 antibody with identical anti-HBsAg binding domains (equivalent by weight or by molar concentration) as measured, *e.g.*, in μg/ml or in nM. In certain embodiments, where the HBsAg-expressing cell is a PLC/PRF/5 cell line or an HBsAg-transfected cell, the binding molecule can direct complement-mediated killing with an $IC_{50}$ at least one-fold, at least two-fold, at least three-fold, at least four-fold, at least five-fold, at least ten-fold, at least 20-fold, at least 30-fold, at least 40-fold, at least 50-fold, at least 60-fold, at least 70-fold, at least 80-fold, at least 90-fold, or at least 100-fold lower than the $IC_{50}$ of an equivalent amount of an anti-HBsAg monospecific IgG1 antibody with identical anti-HBsAg binding domains, as measured, *e.g.*, in molar or molecular weight equivalents.

**[0191]** In certain embodiments, a pentameric binding molecule comprising five identical binding units each comprising two identical anti-HBsAg binding domains as described herein, plus a wild-type or modified J-chain as described herein can exhibit increased potency in a CDC assay performed in cells exhibiting lower HBV antigen expression levels. For example, a pentameric anti-HBsAg binding molecule with a wild-type or modified J-chain as described herein, tested in a CDC assay using the HBV-expressing PLC/PRF/5 cells or HepG2.2.15 cells, can direct complement-mediated killing with an $IC_{50}$ at least one-fold, at least two-fold, at least three-fold, at least four-fold, at least five-fold, at least ten-fold, at least twenty-fold, at least thirty-fold, at least forty-fold, at least 50-fold, at least 100-fold, at least 150-fold, at least 200-fold or more lower than the $IC_{50}$ of an equivalent amount of an anti-HBsAg monospecific IgG1 antibody with identical anti-HBsAg binding domains, as measured, *e.g.*, in molar or molecular weight equivalents.

**[0192]** In certain embodiments, a bispecific pentameric binding molecule comprising five identical binding units each comprising two identical anti-HBV binding domains as described herein, plus a modified J-chain capable of binding to human CD3, *e.g.*, V15J or J15V as described herein, can exhibit increased potency in a TDCC assay. For example, a pentameric anti-HBsAg binding molecule with a modified J-chain capable of binding to human CD3, *e.g.*, V15J or J15V as described herein, tested in a T-cell activation assay, *e.g.*, using the HBsAg-expressing PLC/PRF/5 cells or HepG2.2.15 cells co-cultured with engineered Jurkat T-cells, can facilitate T-cell mediated killing with an $IC_{50}$ at least one-fold, at least two-fold, at least three-fold, at least four-fold, at least five-fold, at least ten-fold, at least 20-fold, at least thirty-fold, at least forty-fold, at least 50-fold, at least 100-fold, at least 150-fold, at least 200-fold or more lower than the $IC_{50}$ of an equivalent amount of a bispecific anti-HBsAg IgG1 antibody with identical anti-HBsAg binding domain(s) that binds HBV antigen-expressing cells and T-cells, *e.g.*, a single binding unit bispecific anti-HBsAg x anti-CD3 molecule as measured, *e.g*,. in molar or molecular weight equivalents.

**[0193]** In certain embodiments, a monospecific or bispecific pentameric binding molecule comprising five identical binding units each comprising two identical anti-HBsAg binding domains as described herein, plus a wild-type J-chain or a modified J-chain capable of binding to human CD3, *e.g.*, V15J or J15V as described herein, can exhibit increased potency in a whole-blood *in vitro* cytotoxicity assay. For example, a pentameric anti-HBV binding molecule plus a wild-type or modified J-chain capable of binding to human CD3, *e.g.*, V15J or J15V as described herein, tested in an appropriate *in vitro* cytotoxicity assay using the HBsAg-expressing PLC/PRF/5 cell line co-cultured with Hirudin anti-coagulated human blood can achieve killing of the PLC/PRF/5 cells or HepG2.2.15 cells with an $IC_{50}$ at least one-fold, at least two-fold, at least three-fold, at least four-fold, at least five-fold, at least ten-fold, at least twenty-fold, at least thirty-fold, at least forty-fold, at least 50-fold, at least 100-fold, at least 150-fold, at least 200-fold or more lower than the $IC_{50}$ of an equivalent amount of an anti-HBsAg monospecific IgG1 antibody with identical anti-HBsAg binding domains, as measured, *e.g.*, in molar or molecular weight equivalents, or of a bispecific anti-HBsAg IgG1 antibody with identical anti-HBsAg binding domain(s) that binds HBV antigen-expressing cells and T-cells, *e.g.*, a bispecific single binding unit anti-HBsAg x anti-CD3 molecule, as measured, *e.g.*, in molar or molecular weight equivalents.

**[0194]** In certain embodiments, a monospecific or bispecific pentameric binding molecule comprising five identical binding units each comprising two identical anti-HBsAg binding domains

as described herein, plus a wild-type J-chain or a modified J-chain capable of binding to human CD3, *e.g.*, V15J or J15V as described herein, can exhibit increased HBsAg-expressing or HBV-infected cell killing *in vivo*, for example in a humanized mouse model as described elsewhere herein.

Polynucleotides, Vectors, and Host Cells

**[0195]** The disclosure further includes a polynucleotide, *e.g.*, an isolated, recombinant, and/or non-naturally-occurring polynucleotide, comprising a nucleic acid sequence that encodes a polypeptide subunit of the dimeric, hexameric, or pentameric binding molecule as described above. By "polypeptide subunit" is meant a portion of a binding molecule, binding unit, or antigen binding domain that can be independently translated. Examples include, without limitation, an antibody variable domain, *e.g.*, a VH or a VL, a single chain Fv, an antibody heavy chain, an antibody light chain, an antibody heavy chain constant region, an antibody light chain constant region, and/or any fragment thereof.

**[0196]** In certain embodiments, the polypeptide subunit can comprise an IgM or an IgA heavy chain constant region or fragment thereof, and VH portion of an HBV antigen binding domain. In certain embodiments the polynucleotide can encode a polypeptide subunit comprising a human IgM or IgA constant region or fragment thereof fused to the C-terminal end of a VH, where the VH comprises the HCDR1, HCDR2, and HCDR3 regions, or the HCDR1, HCDR2, and HCDR3 regions containing one or two single amino acid substitutions of a VH comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 26, SEQ ID NO: 26, SEQ ID NO: 26, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 34, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 62, SEQ ID NO: 73, or SEQ ID NO: 75.

**[0197]** In certain embodiments, the polypeptide subunit can comprise an antibody VL portion of an HBV antigen binding domain as described above. In certain embodiments the polypeptide subunit can comprise a human antibody light chain constant region or fragment thereof fused to the C-terminal end of a VL, where the VL comprises LCDR1, LCDR2, and LCDR3 regions, or the LCDR1, LCDR2, and LCDR3 regions containing one or two single amino acid substitutions of a

VL comprising the amino acid sequence SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 74, or SEQ ID NO: 76.

**[0198]** In certain embodiments the polynucleotide can encode a polypeptide subunit comprising a human IgM or IgA constant region or fragment thereof fused to the C-terminal end of a VH, where the VH comprises an amino acid sequence at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to any one or more of the amino acid sequences of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 26, SEQ ID NO: 26, SEQ ID NO: 26, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 34, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 62, SEQ ID NO: 73, or SEQ ID NO: 75

**[0199]** In certain embodiments the polynucleotide can encode a polypeptide subunit comprising a human light chain constant region or fragment thereof fused to the C-terminal end of a VL, where the VL comprises an amino acid sequence at least at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to any one or more of SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 74, or SEQ ID NO: 76.

**[0200]** Thus, to form the antigen binding domains, the variable regions of antibodies that specifically bind to a hepatitis B antigen can be inserted into expression vector templates for IgM and/or IgA structures, thereby creating multimeric binding molecules having at least two bivalent binding units. In brief, nucleic acid sequences encoding the heavy and light chain variable domain sequences can be synthesized or amplified from existing molecules, and inserted into vectors in the proper orientation and in frame such that upon expression, the vector will yield a full length heavy

or light chain. Vectors useful for these purposes are known in the art. Such vectors can also comprise enhancer and other sequences needed to achieve expression of the desired chains. Multiple vectors or single vectors can be used. These vectors are transfected into host cells and then the chains are expressed and purified. Upon expression the chains form fully functional multimeric binding molecules, as has been reported in the literature. The fully assembled multimeric binding molecules can then be purified by standard methods. The expression and purification processes can be performed at commercial scale, if needed.

**[0201]** The disclosure further includes a composition comprising two or more polynucleotides, where the two or more polynucleotides collectively can encode a dimeric, hexameric, or pentameric binding molecule as described above. In certain embodiments the composition can include a polynucleotide encoding an IgM and/or IgA heavy chain or fragment thereof, *e.g.*, a human IgM and/or IgA heavy chain as described above where the IgM and/or IgA heavy chain comprises at least the VH of an HBV antigen binding domain, and a polynucleotide encoding a light chain or fragment thereof, *e.g.*, a human kappa or lambda light chain that comprises at least the VL of an HBV antigen binding domain. A polynucleotide composition as described can further include a polynucleotide encoding a J-chain, *e.g.*, a human J-chain, or a fragment thereof or a variant thereof. In certain embodiments the polynucleotides making up a composition as described herein can be situated on two or three separate vectors, *e.g.*, expression vectors. Such vectors are included in the disclosure. In certain embodiments two or more of the polynucleotides making up a composition as described herein can be situated on a single vector, *e.g.*, an expression vector. Such a vector is included by the disclosure.

**[0202]** The disclosure further includes a host cell, *e.g.*, a prokaryotic or eukaryotic host cell, comprising a polynucleotide or two or more polynucleotides encoding a dimeric, pentameric, or hexameric HBV binding molecule as described herein, or any subunit thereof, a polynucleotide composition as described herein, or a vector or two, three, or more vectors that collectively encode a dimeric, pentameric, or hexameric HBV binding molecule as described herein, or any subunit thereof. In certain embodiments a host cell described by the disclosure can express a dimeric, pentameric, or hexameric HBV binding molecule as included in this disclosure, or a subunit thereof.

**[0203]** In a related embodiment, the disclosure includes a method of producing a dimeric, pentameric, or hexameric HBV binding molecule as included in this disclosure, where the method comprises culturing a host cell as described above, and recovering the binding molecule.

Methods of Use

**[0204]** This disclosure includes improved methods for controlling hepatitis B virus (HBV) proliferation, latency, or maintenance in chronically-infected cells, *e.g.*, controlling viral attachment, infectivity, replication, latency, egress, etc., *e.g.*, across two or more subtypes, using a dimeric IgA-based HBV binding molecule, or pentameric or hexameric IgM-based HBV binding molecule. The methods described below can utilize multimeric binding molecules comprising HBV antigen binding domains derived from any new or existing HBV antibodies, including without limitation, the antibodies and corresponding VH and VL sequences disclosed in the references set forth in Table 2, or variants, derivatives, or analogs thereof, where the dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody can provide improved potency as compared to a corresponding single binding unit antibody, fragment, variant, derivative, or analog, as disclosed and explained above. Based on this disclosure, construction of a dimeric IgA binding molecule, or pentameric or hexameric IgM binding molecule comprising any HBV-specific antigen binding domain of interest is well within the capabilities of a person of ordinary skill in the art. The increased avidity of IgA or IgM forms of anti-HBV antibodies can result in a more potent therapeutic antibody that can bind HBV infected cells with very low density of HBV surface proteins, allowing for improved virus neutralization, improved HBV-infected cell killing, *e.g.*, through complement or T-cell mediated cytotoxicity, prevention diseases or conditions caused by, or exacerbated by infection with HBV, including, but not limited to acute hepatitis, chronic hepatitis, liver inflammation, cirrhosis of the liver, liver failure, hepatocellular carcinoma (HCC), or any combination thereof, and more efficient clearance of HBV from infected patients. The improved binding characteristics of such compositions can, for example, allow a reduced dose to be used, or can result in more effective neutralization and/or clearance of viruses or virus-infected cells resistant to a corresponding single binding unit antibody. By “resistant” is meant any degree of reduced activity of an HBV antibody, on neutralizing HBV, clearing HBV or HBV-infected cells, controlling infectivity, replication, release, etc.

**[0205]** In certain embodiments, this disclosure includes a method of treating a disease or condition caused by or exacerbated by hepatitis B virus (HBV) infection in a patient, comprising administering to a patient infected with HBV or susceptible to HBV infection a dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody as described herein. As described elsewhere herein, the present binding molecules can exhibit increased potency relative to a reference single binding unit antibody comprising equivalent or identical antigen binding domain(s) *e.g.*, a monospecific, single binding unit IgG antibody or fragment thereof that specifically binds to the same HBV epitope, *e.g.*, an epitope on the pre-S1 region of the HBV surface antigen, as the antigen binding domain that comprises a VH with the amino acid sequence SEQ ID NO: 62 and a VL with the amino acid sequence SEQ ID NO: 6, for example. In certain embodiments, the disease or condition is acute hepatitis, chronic hepatitis, liver inflammation, cirrhosis of the liver, liver failure, hepatocellular carcinoma (HCC), or any combination thereof. In certain embodiments a patient to be treated with a binding molecule, *e.g.*, an IgM antibody as described herein can exhibit certain diseases symptoms such as, but not limited to: increased viral load, virus shedding, abdominal pain, dark urine, fever, joint pain, loss of appetite, nausea and vomiting, weakness and fatigue, jaundice, or a combination thereof. In certain embodiments, the disease symptoms can be alleviated or reduced to a greater extent by a binding molecule described herein than by an equivalent single binding unit antibody.

**[0206]** In certain embodiments, this disclosure includes a method for directing improved neutralization of HBV, where the method includes contacting an HBV, or an HBV-infected cell with a dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody as described herein, where the binding molecule can direct virus neutralization at higher potency than an equivalent amount of a reference single binding unit binding molecule, *e.g.*, a monospecific, single binding unit IgG antibody or fragment thereof that specifically binds to the same HBV epitope, *e.g.*, an epitope on the pre-S1 region of the HBV surface antigen, as the antigen binding domain that comprises a VH with the amino acid sequence SEQ ID NO: 62 and a VL with the amino acid sequence SEQ ID NO: 6, for example. For instance, the antigen binding domain can comprise a VH amino acid sequence at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 1 or SEQ ID NO: 2, and a VL amino acid sequence at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 3. In another embodiment,

the antigen binding domain can comprise a VH amino acid sequence at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 5 or SEQ ID NO: 62, and a VL amino acid sequence at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 6. In certain embodiments a dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody as described herein can direct virus neutralization of two or more HBV subtypes at higher potency than an equivalent amount of a monospecific, single binding unit HBV monoclonal antibody, *e.g.*, the corresponding IgG antibody or fragment thereof, where the antibody is, or comprises the same VH and VL regions as, *e.g.*, the VH and VL sequences set forth in Table 2. In certain embodiments, the hexameric or pentameric binding molecule, *e.g.*, an IgM antibody or fragment thereof, comprises a heavy chain comprising the amino acid sequence SEQ ID NO: 58, and a light chain comprising the amino acid sequence SEQ ID NO: 59. In certain embodiments, the hexameric or pentameric binding molecule, *e.g.*, an IgM antibody or fragment thereof, comprises a heavy chain comprising the amino acid sequence SEQ ID NO: 63, and a light chain comprising the amino acid sequence SEQ ID NO: 59.

**[0207]** For instance, methods include screening of various binding molecules whose affinities and/or avidities for infectious HBV viral particles, or other infectious viral particles, have not been determined. The methods described herein can be employed to identify binding molecules that bind to the surface of infectious hepatitis B virus (HBV) viral particles, on the surface if HBV infected cells, or a combination thereof, with greater affinity, greater avidity, or a combination thereof, than binding to HBV subviral particles. The increased avidity of IgA or IgM forms of anti-HBV can result in a more potent therapeutic antibody that can bind those infected cells with very low density of HBV surface proteins, allowing more efficient clearance of HBV from infected patients. Similarly the methods described herein can be employed to identify binding molecules that bind to the surface of other infectious viral particles or virus-infected cells with great affinity, greater avidity, or both, than binding to non-infectious versions of the same virus. Thus, a binding molecule as described herein that possesses the advantageous properties discussed above can be used in a method for binding to infectious HBV or other viral particles. Due to the advantageous properties of a multimeric binding molecule as described herein, binding molecules can be identified that bind infectious HBV particles or other infectious viral particles with a higher avidity or affinity, or combination thereof, than binding to subviral (non-infectious) HBV viral particles or

other non-infectious viral particles. Thus, methods are disclosed wherein such binding molecules with such properties can be identified by detecting binding to infectious and non-infectious viral particles and comparing the binding affinities and/or avidities to identify additional binding molecules possessing advantageous properties. Binding molecules that bind to infectious particles with a higher avidity or affinity, or combination thereof, than binding to subviral (non-infectious) viral particles can be selected by this method.

**[0208]** Such methods can generally be performed by contacting a test binding molecule with an infectious viral particle and measuring the affinity and/or avidity of the test binding molecule for binding to an infectious viral particle. The same test binding molecule is also contacted with a non-infectious HBV subviral particle or other non-infectious viral particle, and the affinity and/or avidity of the test binding molecule for binding to an HBV subviral particle or other non-infectious particle can be detected. The results of these two tests are compared thereby identifying test compounds (binding molecules) in which the affinity and/or avidity measured for binding to infectious HBV particles or other infectious viral particles is higher than the affinity and/or for binding to non-infectious HBV sub-viral particles or other non-infectious particles.

**[0209]** In this manner, additional binding molecules useful in the methods described herein can be identified and utilized.

**[0210]** Similarly, methods are disclosed wherein various test compounds (binding molecules) whose affinities and/or avidities for HBV-infected cells or other viral infected cells have not been determined. The methods described herein can be employed to identify binding molecules that bind to the surface of HBV-infected cells or other viral infected cells with greater affinity, greater avidity, or a combination thereof, than binding to identical cells which are not infected with the virus, or binding to non-infectious viral particles. Thus, a binding molecule possessing the advantageous properties discussed above can be used in a method for preferential binding to HBV-infected cells or other viral infected cells. Due to the advantageous properties of a multimeric binding molecule as described herein, the binding molecule can bind HBV-infected cells or other viral infected cells with a higher avidity and/or affinity, than binding to similar non-infected cells, or to non-infectious viral particles. Thus, methods are disclosed where virus-infected and non-infected cells, as well as non-infectious viral particles, and comparing the binding affinities and/or avidities to identify a difference in binding. Binding molecules which bind to HBV-infected cells or other viral-infected cells with a higher avidity and/or affinity, than binding to similar cells which

are not infected with HBV or other virus, or to non-infectious viral particles can be selected by this method.

**[0211]** This screening method can be accomplished by contacting a test binding molecule with an HBV-infected cell (or other viral infected cell) and measuring the affinity and/or avidity of the test binding molecule for binding to the HBV-or virus-infected cell, and contacting the same test same binding molecule with a cell not infected with HBV or other virus, or to non-infectious viral particles, and measuring the affinity and/or avidity of the test binding molecule for binding to a cell not infected with HBV or other virus, or to non-infectious viral particles, wherein the non-infected cell is identical to the HBV-infected cell except that it is not infected. The binding results for this test compound, or any number of test compounds, can then be compared, thereby identifying a test compound in which the affinity and/or avidity is higher for infected cells than non-infected cells or non-infectious viral particles.

**[0212]** The cells in such methods can be any cell capable of being infected by HBV or other virus, such as a human cell.

**[0213]** In certain embodiments the HBV antigen binding domain of the dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody comprises six immunoglobulin complementarity determining regions HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3, wherein at least one, at least two, at least three, at least four, at least five, or at least six CDRs are related to the corresponding CDRs of any one of the HBV antibodies set forth in Table 2, *e.g.*, those that possess affinity for the hepatitis B epitope HBsAg, *e.g.*, the pre-S1 region.

**[0214]** A dimeric, hexameric or pentameric binding molecule for use in the methods described herein, is a binding molecule with two, five or six "binding units" as defined herein, that can specifically bind to two or more HBV subtypes, *e.g.*, A, B, C, D, E, F, G and/or H. In certain embodiments, a dimeric, pentameric or hexameric binding molecule for use in the methods described herein comprises two, five or six bivalent binding units, respectively, where each binding unit includes two IgA heavy chain constant regions or fragments thereof (for IgA-based binding molecules), or two IgM heavy chain constant regions or fragments thereof (for IgM-based molecules). In certain embodiments, the two IgA or IgM heavy chain constant regions are human heavy chain constant regions.

**[0215]** Dimeric, pentameric, or hexameric HBV binding molecules for use in the methods described herein can possess advantageous structural or functional properties compared to other

binding molecules. For example, a dimeric, pentameric, or hexameric binding molecule for use in the methods described herein can possess improved binding characteristics in a biological assay, as described above, either *in vitro* or *in vivo*, than a corresponding reference single binding unit, *e.g.*, IgG or a variant, analog, or derivative thereof, as also described above. Biological assays include, but are not limited to *in vitro* neutralization assays, hemagglutination inhibition assays, cell attachment assays, viral egress assays, immunohistochemical assays, direct cytotoxicity assays, complement-mediated cytotoxicity assays, etc. *In vivo* efficacy models include, but are not limited to immune-compromised murine models with diminished endogenous liver capacity and re-constituted with human hepatocytes. Alternatively, dimeric, pentameric, or hexameric binding molecules can be tested *in vivo* using non-human primate models of HBV infection to evaluate HBV clearance (see Example 7, below).

Pharmaceutical Compositions and Administration Methods

**[0216]** Methods of preparing and administering a multimeric, *e.g.*, a dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody as described herein to a subject in need thereof are well known to or are readily determined by those skilled in the art in view of this disclosure. The route of administration of a multimeric binding molecule can be, for example, oral, parenteral, by inhalation or topical. The term parenteral as used herein includes, *e.g.*, intravenous, intraarterial, intraperitoneal, intramuscular, subcutaneous, rectal, or vaginal administration. While these forms of administration are contemplated as suitable forms, another example of a form for administration would be a solution for injection, in particular for intravenous or intra-arterial injection or drip. A suitable pharmaceutical composition can comprise a buffer (*e.g.* acetate, phosphate or citrate buffer), a surfactant (*e.g.* polysorbate), and in some embodiments a stabilizer agent (*e.g.* human albumin), etc.

**[0217]** As discussed herein, a dimeric, pentameric, or hexameric HBV binding molecule as described herein can be administered in a pharmaceutically effective amount for the *in vivo* treatment of diseases or disorders in which it is desirable to deplete B cells. In this regard, it will be appreciated that the disclosed multimeric binding molecules can be formulated so as to facilitate administration and promote stability of the active agent. Pharmaceutical compositions accordingly can comprise a pharmaceutically acceptable, non-toxic, sterile carrier such as physiological saline, non-toxic buffers, preservatives and the like. A pharmaceutically effective amount of a dimeric,

pentameric, or hexameric HBV binding molecule as described herein means an amount sufficient to achieve effective binding to a target and to achieve a therapeutic benefit. Suitable formulations are described in Remington's Pharmaceutical Sciences (Mack Publishing Co.) 16th ed. (1980).

**[0218]** Certain pharmaceutical compositions described herein can be orally administered in an acceptable dosage form including, *e.g.*, capsules, tablets, aqueous suspensions or solutions. Certain pharmaceutical compositions also can be administered by nasal aerosol or inhalation. Such compositions can be prepared as solutions in saline, employing benzyl alcohol or other suitable preservatives, absorption promoters to enhance bioavailability, and/or other conventional solubilizing or dispersing agents.

**[0219]** The amount of a dimeric, pentameric, or hexameric HBV binding molecule that can be combined with carrier materials to produce a single dosage form will vary depending, *e.g.*, upon the subject treated and the particular mode of administration. The composition can be administered as a single dose, multiple doses or over an established period of time in an infusion. Dosage regimens also can be adjusted to describe the optimum desired response (*e.g.*, a therapeutic or prophylactic response).

**[0220]** In keeping with the scope of the disclosure, a dimeric, pentameric, or hexameric HBV binding molecule as described herein can be administered to a subject in need of therapy in an amount sufficient to produce a therapeutic effect. A multimeric binding molecule as described herein can be administered to the subject in a conventional dosage form prepared by combining the antibody or antigen-binding fragment, variant, or derivative thereof of the disclosure with a conventional pharmaceutically acceptable carrier or diluent according to known techniques. The form and character of the pharmaceutically acceptable carrier or diluent can be dictated by the amount of active ingredient with which it is to be combined, the route of administration and other well-known variables.

**[0221]** By "therapeutically effective dose or amount" or "effective amount" is intended an amount of a dimeric, pentameric, or hexameric HBV binding molecule, that when administered brings about a positive therapeutic response with respect to treatment of a patient with a disease or condition to be treated.

**[0222]** Therapeutically effective doses of the compositions disclosed herein, for the treatment of a disease or condition caused by, or exacerbated by infection with hepatitis B virus, can vary depending upon many different factors, including means of administration, target site,

physiological state of the patient, whether the patient is human or an animal, other medications administered, and whether treatment is prophylactic or therapeutic. In certain embodiments, the subject or patient is a human, but non-human mammals including transgenic mammals can also be treated. Treatment dosages can be titrated using routine methods known to those of skill in the art to optimize safety and efficacy.

**[0223]** The amount of a dimeric, pentameric, or hexameric binding molecule, *e.g.*, an IgM antibody to be administered is readily determined by one of ordinary skill in the art without undue experimentation given this disclosure. Factors influencing the mode of administration and the respective amount of a multimeric binding molecule include, but are not limited to, the severity of the disease, the history of the disease, and the age, height, weight, health, and physical condition of the individual undergoing therapy. Similarly, the amount of a dimeric, pentameric, or hexameric HBV binding molecule to be administered will be dependent upon the mode of administration and whether the subject will undergo a single dose or multiple doses of this agent.

**[0224]** This disclosure also includes the use of a dimeric, pentameric, or hexameric HBV binding molecule in the manufacture of a medicament for treating, preventing, or managing a disease or condition caused by, or exacerbated by infection with hepatitis B virus.

**[0225]** This disclosure employs, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. (See, for example, Sambrook *et al.*, ed. (1989) Molecular Cloning A Laboratory Manual (2nd ed.; Cold Spring Harbor Laboratory Press); Sambrook *et al.*, ed. (1992) Molecular Cloning: A Laboratory Manual, (Cold Springs Harbor Laboratory, NY); D. N. Glover ed., (1985) DNA Cloning, Volumes I and II; Gait, ed. (1984) Oligonucleotide Synthesis; Mullis *et al.* U.S. Pat. No. 4,683,195; Hames and Higgins, eds. (1984) Nucleic Acid Hybridization; Hames and Higgins, eds. (1984) Transcription And Translation; Freshney (1987) Culture Of Animal Cells (Alan R. Liss, Inc.); Immobilized Cells And Enzymes (IRL Press) (1986); Perbal (1984) A Practical Guide To Molecular Cloning; the treatise, Methods In Enzymology (Academic Press, Inc., N.Y.); Miller and Calos eds. (1987) Gene Transfer Vectors For Mammalian Cells, (Cold Spring Harbor Laboratory); Wu *et al.*, eds., Methods In Enzymology, Vols. 154 and 155; Mayer and Walker, eds. (1987) Immunochemical Methods In Cell And Molecular Biology (Academic Press, London); Weir and Blackwell, eds., (1986) Handbook Of Experimental Immunology, Volumes I-IV; Manipulating the

Mouse Embryo, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1986); and in Ausubel *et al.* (1989) Current Protocols in Molecular Biology (John Wiley and Sons, Baltimore, Md.).

**[0226]** General principles of antibody engineering are set forth in Borrebaeck, ed. (1995) Antibody Engineering (2nd ed.; Oxford Univ. Press). General principles of protein engineering are set forth in Rickwood *et al.*, eds. (1995) Protein Engineering, A Practical Approach (IRL Press at Oxford Univ. Press, Oxford, Eng.). General principles of antibodies and antibody-hapten binding are set forth in: Nisonoff (1984) Molecular Immunology (2nd ed.; Sinauer Associates, Sunderland, Mass.); and Steward (1984) Antibodies, Their Structure and Function (Chapman and Hall, New York, N.Y.). Additionally, standard methods in immunology known in the art and not specifically described can be followed as in Current Protocols in Immunology, John Wiley & Sons, New York; Stites *et al.*, eds. (1994) Basic and Clinical Immunology (8th ed; Appleton & Lange, Norwalk, Conn.) and Mishell and Shiigi (eds) (1980) Selected Methods in Cellular Immunology (W.H. Freeman and Co., NY).

**[0227]** Standard reference works setting forth general principles of immunology include Current Protocols in Immunology, John Wiley & Sons, New York; Klein (1982) J., Immunology: The Science of Self-Nonself Discrimination (John Wiley & Sons, NY); Kennett *et al.*, eds. (1980) Monoclonal Antibodies, Hybridoma: A New Dimension in Biological Analyses (Plenum Press, NY); Campbell (1984) "Monoclonal Antibody Technology" in Laboratory Techniques in Biochemistry and Molecular Biology, ed. Burden *et al.*, (Elsevier, Amsterdam); Goldsby *et al.*, eds. (2000) Kuby Immunology (4th ed.; W.H. Freeman & Co.); Roitt *et al.* (2001) Immunology (6th ed.; London: Mosby); Abbas *et al.* (2005) Cellular and Molecular Immunology (5th ed.; Elsevier Health Sciences Division); Kontermann and Dubel (2001) Antibody Engineering (Springer Verlag); Sambrook and Russell (2001) Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Press); Lewin (2003) Genes VIII (Prentice Hall, 2003); Harlow and Lane (1988) Antibodies: A Laboratory Manual (Cold Spring Harbor Press); Dieffenbach and Dveksler (2003) PCR Primer (Cold Spring Harbor Press).

**[0228]** All of the references cited above, as well as all references cited herein, are incorporated herein by reference in their entireties.

**[0229]** The following examples are offered by way of illustration and not by way of limitation.

# EXAMPLES

## Example 1: Surface antigen preparation

**[0230]** Surface antigens can be prepared as previously reported. (*See*, for instance, Short *et al.*, *J. Mol. Biol.* (2009) 390, 135–141). In one method, HBsAg is isolated from the blood of HBV carriers. Frozen serum containing HBV can be obtained, *e.g.*, from the Diagnostics, Development and Research Division, National Blood Service, Colindale Centre, London, UK. Individual packs are then thawed and centrifuged (3700 x *g* for 20 min) and the supernatant layered over 0.5 ml of 20% sucrose in TBS (in 5.1-ml tubes) and centrifuged (266,000 x *g* for 30 min). The pellets are resuspended in 20 mM Tris chloride (pH 7.4) and 140 mM NaCl (Tris-buffered saline, TBS) (after leaving wetted overnight at 4 °C to soften), pooled and subjected to equilibrium centrifugation with CsCl (0.22 g/ml initial concentration) (266,000 x *g* for 72 h). Fractions (250 µl) are taken from the gradient and monitored by electron microscopy and by DNA extraction and analysis for hepatitis B DNA. The fractions containing the most suitable HBsAg particles, which are also free of hepatitis B DNA (and thus, virus), are taken and dialyzed against TBS for use. Multiple forms of the surface antigen HBsAg (Long, PreS1-PreS2-S; Medium, PreS2-S; Short, S), both native and recombinant as well as peptide fragments, were from commercial sources, as were forms of other HBV proteins.

## Example 2: HBV capsid and virion isolation

**[0231]** Capsid and virion isolation methods are well known in the art and can be conducted by any number of known means. (*See*, for instance, Dryden, *Molecular Cell*, 22:843–850, June 23, 2006, suppl.). In one method of capsid isolation, freshly dissected whole livers are perfused with saline solution. The livers are then homogenized in lysis buffer (for instance, 0.25 M sucrose, 1 mM $MgCl_2$, 5 mM Tris (pH 7.4)) and supplemented with complete protease inhibitor (Roche Applied Science, Indianapolis, IN). The supernatant of each homogenate is obtained by centrifugation for 15 min at 4 °C and 11,000 rpm in an SW40 rotor. An aliquot of the supernatant is removed for the purpose of performing an HBV-specific Southern blot analysis. The remainder is then layered onto a 30% sucrose cushion (0.73 M sucrose in phosphate buffered saline (PBS)), and viral particles are pelleted by centrifugation for 5 hrs at 4 °C and 40,000 rpm in an SW40 rotor. The pellets are then resuspended in 1 ml of CsCl-solution [3.3 g CsCl dissolved in 10 ml PBS-solution (1 x PBS, 20

mM EDTA, and 1 x complete protease inhibitor cocktail)]. The resuspended material is then transferred into quick seal tubes (Beckman Instruments, Palo Alto, CA). The tubes are filled with CsCl solution, sealed, and HBV particles banded by centrifugation for 18 hrs at 11 °C and 60,000 rpm in a TI80 rotor.

**[0232]** The tubes are bottom-punctured, and fractions are collected. Fractions containing capsid are pooled, diluted in PBS and then concentrated. The filtrates are combined, and pelleted an additional 30 min. The sample is then divided and loaded on preformed CsCl gradients (ρ 1.2-1.4). After centrifugation for 3 hrs at 4 °C and 38,000 rpm, fractions (200 µl each) are collected by pipette, their refractive index is measured, and equivalent fractions are pooled.

**[0233]** To remove the CsCl and concentrate the pooled fractions, samples are pelleted and resuspended three times in PBS, twice using, *e.g.*, a TLA100.4 rotor and finally using, *e.g.*, a TLA100.2 rotor, each for 1 hr at 45,000 rpm and 4 °C.

**[0234]** In one method of virion isolation, multiple plasmapheresis units obtained from one or more HBV positive individuals are pooled, filtered through sterile cheesecloth, and virions are purified as described (Kaplan 1973; *J. Virol. 12*,995-1005). Briefly, polycarbonate tubes are loaded with 65 ml of the plasma pool, which is subjected to centrifugation for 3 hrs at 21,000 rpm at 5 °C in an SW30 rotor. The supernatants are decanted, and the tubes are reloaded with another 65 ml of the plasma pool, and the centrifugation is repeated. Two pellets, each from 130 ml of starting material, are resuspended in ~7 ml of PBS each, pooled and subjected to centrifugation for 4 hrs in an SW30 rotor through a 7 ml cushion of 20% (w/w) sucrose in PBS at 30,000 rpm and at 5 °C. The pellet is resuspended in PBS to a final concentration of 50X compared with the original starting material, divided into 50 µl aliquots and frozen at –80 °C.

**[0235]** Alternatively, HBV virions can be produced following methods outlined by Kim (FEBS Letters 2015; 589,193-200). Briefly, viral particles are produced by transient transfection of HepG2 cells (ATCC HB-8065) with a vector containing a full-length HBV genome (*e.g.*, pHBVEcoR1-; Gripon 1995; Virol. 213(2),292-299). The viral particles are then concentrated 50-fold by PEG precipitation (Le Seyed 1999; *J. Virol. 73*(3), 2052-2057). The genotype of the HBV virus will be dependent upon the vector used.

## Example 3: Engineered IgM binding molecules specific for HBV

**[0236]** VH and VL regions of various HBV antibodies described herein can be cloned into IgG and IgM backgrounds by standard methods, or by commercial contractors.

**[0237]** HBV24: The VH and VL of a humanized antibody specific for pre-S1 antigen provided in U.S. Patent No. 8,420,353, presented herein as SEQ ID NO: 5 and SEQ ID NO: 6, respectively, were cloned into appropriate vectors to encode the human IgG and IgM heavy chains comprising the amino acid sequences SEQ ID NO: 84 and SEQ ID NO: 58, respectively, and the kappa light chain comprising SEQ ID NO: 59. SEQ ID NOs 58 and 58 are listed above. The vectors were transfected in to HEK293 cells (with, where appropriate, a vector encoding a human wild-type or modified J-chain as described below) and expression was permitted, producing the IgG molecule HBV24G and the IgM molecule HBV24M.

**[0238]** SEQ ID NO: 84 HBV24G Heavy Chain

QVQLVQSGAEVKAPGASVKVSCKASGYTFTSAWMNWVRQAPG
QGLEWMGRIYPSGGSTSYAQKFQGRVTMTADKSTSTVYMELSSL
RSEDTAVYYCAREYRVARWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

**[0239]** HBV23: The VH and VL of the human antibody specific for the S region of HBsAg provided in Cerino, *et al.*, (2015) *PLOS one 10*(4):e0125704. doi: 10.1371, presented herein as SEQ ID NO: 73 and SEQ ID NO: 74, respectively, were cloned into appropriate vectors to encode the human IgG and IgM heavy chains comprising the amino acid sequences SEQ ID NO: 85 and SEQ ID NO: 80, respectively, and the lambda light chain comprising SEQ ID NO: 81. The vectors were transfected in to HEK293 cells (with, where appropriate, a vector encoding a human wild-type or modified J-chain as described below) and expression was permitted, producing the IgG molecule HBV23G and the IgM molecule HBV23M.

**[0240]** SEQ ID NO: 85 HBV23G Heavy Chain

MDPKGSLSWRILLFLSLAFELSYGEVQVLESGGGLVQPGGSLRLS
CAASGFRFSSYAMSWVRQAPGKGLEWVSGISGTGENTYYADSVK

GRFTISRDNSKNTLYVQMNSLRAEDTAVYYCAKDAILGSGHPWY
FHVWGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPG

**[0241]** SEQ ID 80 HBV23M Heavy Chain

MDPKGSLSWRILLFLSLAFELSYGEVQVLESGGGLVQPGGSLRLS
CAASGFRFSSYAMSWVRQAPGKGLEWVSGISGTGENTYYADSVK
GRFTISRDNSKNTLYVQMNSLRAEDTAVYYCAKDAILGSGHPWY
FHVWGRGTLVTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAQ
DFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQVLLPSKD
VMQGTDEHVVCKVQHPNGNKEKNVPLPVIAELPPKVSVFVPPRD
GFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQA
EAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNAS
SMCVPDQDTAIRVFAIPPSFASIFLTKSTKLTCLVTDLTTYDSVTIS
WTRQNGEAVKTHTNISESHPNATFSAVGEASICEDDWNSGERFTC
TVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESATI
TCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYF
AHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTGKPTL
YNVSLVMSDTAGTCY

**[0242]** SEQ ID 81 HBV23M Light Chain

MSVPTQVLGLLLLWLTDARCSYVLTQPPSVSVAPGQTARMTCGG
NNIGSESVHWFQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNT
ATLTISRVEAGDEADYYCQVWDSSSDHAVFGGGTQLTVLGQPKA
APSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK
AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST
VEKTVAPTECS*

**[0243]** HBV19: The VH and VL of a human antibody specific for the PreS1 region of HBsAg serotype *ay* provided in Pizarro, *et al.*, *FEBS Letters 509*:463-468 (2001), presented herein as SEQ ID NO: 75, and SEQ ID NO: 76, respectively, were cloned into appropriate vectors to encode the human IgG and IgM heavy chains comprising the amino acid sequences SEQ ID NO: 86 and SEQ ID NO: 82, respectively, and the kappa light chain comprising SEQ ID NO: 83. The vectors were transfected in to HEK293 cells (with, where appropriate, a vector encoding a human wild-type or modified J-chain as described below) and expression was permitted, producing the IgG molecule HBV19G and the IgM molecule HBV19M.

**[0244]** SEQ ID NO: 86 HBV19G Heavy Chain

MDPKGSLSWRILLFLSLAFELSYGEVQLEESGGGLVKPGGSLKLS
CAASGFTFSSYAMSWVRQSPEKRLEWVAEVSSDGSYAYYPDTLT
GRFTISRDNAKNTLYLEMTSLRSEDTAMYYCASFNWDVAYWGQ
GTLVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP
KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPG

**[0245]** SEQ ID 82 HBV19M Heavy Chain

MDPKGSLSWRILLFLSLAFELSYGEVQLEESGGGLVKPGGSLKLS
CAASGFTFSSYAMSWVRQSPEKRLEWVAEVSSDGSYAYYPDTLT
GRFTISRDNAKNTLYLEMTSLRSEDTAMYYCASFNWDVAYWGQ
GTLVTVSAGSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSI
TFSWKYKNNSDISSTRGFPSVLRGGKYAATSQVLLPSKDVMQGT
DEHVVCKVQHPNGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNP
RKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESG
PTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPD
QDTAIRVFAIPPSFASIFLTKSTKLTCLVTDLTTYDSVTISWTRQNG
EAVKTHTNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTD
LPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESATITCLVTGF
SPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVS
EEEWNTGETYTCVVAHEALPNRVTERTVDKSTGKPTLYNVSLVM
SDTAGTCY

**[0246]** SEQ ID 83 HBV19M Light Chain

METDTLLLWVLLLWVPGSTGELVMTQSPSSLAVSVGEKVTMSCR
SSQSLLNTRTRKSYLAWFQQKPGQSPKMLIYWASTRESGVPDRFT
GSGSGTDFTLTISSVQAEDLAVYYCKQSYSLYTFGGGTKLEIKRTV
AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG
LSSPVTKSFNRGEC

**[0247]** Two different J-chain variants were constructed with distinct fusion sites incorporating variable regions from the anti-CD3 antibody visilizumab (Nuvion). Shown below are the sequences for two J-chains with the scFv corresponding to visilizumab (V) (VH-$(GGGGS)_3$-VL, double-underlined) fused to the J-chain (italics) through a $(GGGGS)_3$ linker (SEQ ID NO: 72, underlined) containing 15 amino acids in two different orientations – V15J and J15V. Each sequence contains

an N-terminal signal peptide that is shown without underlining or italics. In certain embodiments, other signal peptide sequences can be substituted for the signal peptides shown here.

**[0248]** SEQ ID NO: 67: precursor modified J-chain sequence for V15J (DNA Sequence: SEQ ID NO: 66):

MGWSYIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKAS
GYTFISYTMHWVRQAPGQGLEWMGYINPRSGYTHYNQKLKDKA
TLTADKSASTAYMELSSLRSEDTAVYYCARSAYYDYDGFAYWG
QGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI
TCSASSSVSYMNWYQQKPGKAPKRLIYDTSKLASGVPSRFSGSGS
GTDFTLTISSLQPEDFATYYCQQWSSNPPTFGGGTKLEIKGGGGSG
GGGSGGGGS*QEDERIVLVDNKCKCARITSRIIRSSEDPNEDIVERNIRII*
*VPLNNRENISDPTSPLRTRFVYHLSDLCKKCDPTEVELDNQIVTATQSN*
*ICDEDSATETCYTYDRNKCYTAVVPLVYGGETKMVETALTPDACYPD*

**[0249]** SEQ ID NO: 68: mature modified J-chain sequence for V15J:

QVQLVQSGAEVKKPGASVKVSCKASGYTFISYTMHWVRQAPGQ
GLEWMGYINPRSGYTHYNQKLKDKATLTADKSASTAYMELSSLR
SEDTAVYYCARSAYYDYDGFAYWGQGTLVTVSSGGGGSGGGGS
GGGGSDIQMTQSPSSLSASVGDRVTITCSASSSVSYMNWYQQKPG
KAPKRLIYDTSKLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQWSSNPPTFGGGTKLEIKGGGGSGGGGSGGGGS*QEDERIVLVDN*
*KCKCARITSRIIRSSEDPNEDIVERNIRIIVPLNNRENISDPTSPLRTRFVY*
*HLSDLCKKCDPTEVELDNQIVTATQSNICDEDSATETCYTYDRNKCYT*
*AVVPLVYGGETKMVETALTPDACYPD*

**[0250]** SEQ ID NO: 66:

ATGGGCTGGTCCTACATCATCCTCTTCCTCGTGGCCACAGCCAC
AGGCGTCCATAGCCAGGTGCAGCTGGTGCAGTCCGGCGCCGAA
GTGAAGAAGCCTGGCGCCAGCGTGAAGGTGAGCTGCAAGGCT
TCCGGCTACACCTTCATCTCCTACACCATGCACTGGGTGAGGC
AAGCTCCTGGCCAGGGCCTGGAGTGGATGGGATACATCAACCC
TCGGTCCGGCTATACCCACTACAATCAGAAGCTGAAGGACAAG
GCCACCCTGACCGCTGACAAGTCCGCCTCCACCGCTTACATGG
AGCTGTCCTCCCTGAGGTCCGAGGACACCGCCGTGTACTACTG
TGCCAGGTCCGCCTACTACGACTACGACGGATTCGCTTACTGG
GGCCAGGGCACCCTGGTGACAGTGAGCTCCGGAGGAGGAGGC
AGCGGCGGCGGCGGCAGCGGCGGCGGCGGCAGCGATATCCAG
ATGACCCAGAGCCCTTCCAGCCTGTCCGCTTCCGTGGGCGACA
GGGTGACCATCACCTGCAGCGCTTCCTCCTCCGTGTCCTACATG
AACTGGTACCAGCAGAAGCCTGGCAAGGCCCCCAAGAGGCTG
ATCTACGACACCTCCAAGCTGGCCTCCGGAGTGCCTTCCAGGT
TCAGCGGCTCCGGCTCCGGAACCGACTTCACCCTGACCATTAG
CTCCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCAGCAG

TGGTCCAGCAACCCTCCCACCTTCGGCGGCGGCACAAAGCTGG
AGATCAAGGGAGGAGGAGGATCCGGTGGTGGTGGTTCTGGCG
GAGGTGGATCCCAAGAAGATGAAAGGATTGTTCTTGTTGACAA
CAAATGTAAGTGTGCCCGGATTACTTCCAGGATCATCCGTTCTT
CCGAAGATCCTAATGAGGACATTGTGGAGAGAAACATCCGAA
TTATTGTTCCTCTGAACAACAGGGAGAATATCTCTGATCCCACC
TCACCATTGAGAACCAGATTTGTGTACCATTTGTCTGACCTCTG
TAAAAAATGTGATCCTACAGAAGTGGAGCTGGATAATCAGATA
GTTACTGCTACCCAGAGCAATATCTGTGATGAAGACAGTGCTA
CAGAGACCTGCTACACTTATGACAGAAACAAGTGCTACACAGC
TGTGGTCCCACTCGTATATGGTGGTGAGACCAAAATGGTGGAA
ACAGCCTTAACCCCAGATGCCTGCTATCCTGACTGA

**[0251]** SEQ ID NO: 70: precursor modified J-chain sequence for J15V (DNA sequence: SEQ ID NO: 69):

MKNHLLFWGVLAVFIKAVHVKA*QEDERIVLVDNKCKCARITSRIIRS*
*SEDPNEDIVERNIRIIVPLNNRENISDPTSPLRTRFVYHLSDLCKKCDPT*
*EVELDNQIVTATQSNICDEDSATETCYTYDRNKCYTAVVPLVYGGETK*
*MVETALTPDACYPD*GGGGSGGGGSGGGGSQVQLVQSGAEVKKPG
ASVKVSCKASGYTFISYTMHWVRQAPGQGLEWMGYINPRSGYT
HYNQKLKDKATLTADKSASTAYMELSSLRSEDTAVYYCARSAYY
DYDGFAYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSL
SASVGDRVTITCSASSSVSYMNWYQQKPGKAPKRLIYDTSKLASG
VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQWSSNPPTFGGGTK
LEIK

**[0252]** SEQ ID NO: 71: mature modified J-chain sequence for J15V:

*QEDERIVLVDNKCKCARITSRIIRSSEDPNEDIVERNIRIIVPLNNRENIS*
*DPTSPLRTRFVYHLSDLCKKCDPTEVELDNQIVTATQSNICDEDSATET*
*CYTYDRNKCYTAVVPLVYGGETKMVETALTPDACYPD*GGGGSGGGG
SGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFISYTMHWV
RQAPGQGLEWMGYINPRSGYTHYNQKLKDKATLTADKSASTAY
MELSSLRSEDTAVYYCARSAYYDYDGFAYWGQGTLVTVSSGGG
GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCSASSSVSYMN
WYQQKPGKAPKRLIYDTSKLASGVPSRFSGSGSGTDFTLTISSLQP
EDFATYYCQQWSSNPPTFGGGTKLEIK

**[0253]** SEQ ID NO: 69:

ATGAAGAACCATTTGCTTTTCTGGGGAGTCCTGGCGGTTTTTAT
TAAGGCTGTTCATGTGAAAGCCCAAGAAGATGAAAGGATTGTT
CTTGTTGACAACAAATGTAAGTGTGCCCGGATTACTTCCAGGA
TCATCCGTTCTTCCGAAGATCCTAATGAGGACATTGTGGAGAG
AAACATCCGAATTATTGTTCCTCTGAACAACAGGGAGAATATC
TCTGATCCCACCTCACCATTGAGAACCAGATTTGTGTACCATTT

GTCTGACCTCTGTAAAAAATGTGATCCTACAGAAGTGGAGCTG
GATAATCAGATAGTTACTGCTACCCAGAGCAATATCTGTGATG
AAGACAGTGCTACAGAGACCTGCTACACTTATGACAGAAACA
AGTGCTACACAGCTGTGGTCCCACTCGTATATGGTGGTGAGAC
CAAAATGGTGGAAACAGCCTTAACCCCAGATGCCTGCTATCCT
GACGGAGGAGGAGGATCCGGTGGTGGTGGTTCTGGCGGAGGT
GGATCCCAGGTGCAGCTGGTGCAGTCCGGCGCCGAAGTGAAG
AAGCCTGGCGCCAGCGTGAAGGTGAGCTGCAAGGCTTCCGGCT
ACACCTTCATCTCCTACACCATGCACTGGGTGAGGCAAGCTCC
TGGCCAGGGCCTGGAGTGGATGGGATACATCAACCCTCGGTCC
GGCTATACCCACTACAATCAGAAGCTGAAGGACAAGGCCACC
CTGACCGCTGACAAGTCCGCCTCCACCGCTTACATGGAGCTGT
CCTCCCTGAGGTCCGAGGACACCGCCGTGTACTACTGTGCCAG
GTCCGCCTACTACGACTACGACGGATTCGCTTACTGGGGCCAG
GGCACCCTGGTGACAGTGAGCTCCGGAGGAGGAGGCAGCGGT
GGTGGCGGAAGCGGTGGAGGTGGCAGCGATATCCAGATGACC
CAGAGCCCTTCCAGCCTGTCCGCTTCCGTGGGCGACAGGGTGA
CCATCACCTGCAGCGCTTCCTCCTCCGTGTCCTACATGAACTGG
TACCAGCAGAAGCCTGGCAAGGCCCCCAAGAGGCTGATCTAC
GACACCTCCAAGCTGGCCTCCGGAGTGCCTTCCAGGTTCAGCG
GCTCCGGCTCCGGAACCGACTTCACCCTGACCATTAGCTCCCT
GCAGCCCGAGGACTTCGCCACCTACTACTGCCAGCAGTGGTCC
AGCAACCCTCCCACCTTCGGAGGCGGCACAAAGCTGGAGATCA
AGTGA

**[0254]** The mature constructs each have a molecular weight of about 45 kD and can bind to soluble epsilon chain of CD3 (Sino Biological), or T-cells (data not shown).

**[0255]** The DNA constructs corresponding to the various anti-HBsAg heavy and light chains as well as those corresponding to either the wild-type (wt) J-chain, V15J or J15V J-chain sequences were co-transfected into HEK293 cells, and proteins were expressed and purified according to standard methods. See, *e.g.*, PCT Publication No. WO 2015/153912, which is incorporated herein by reference in its entirety. HEK293 cells transfected with IgG or IgM+J versions of HBV19, HBV23, and HBV24 antibodies produced sufficient protein to allow purification by standard methods.

**[0256]** Agarose-Acrylamide Hybrid Gel. IgM Constructs were separated by non-reducing SDS-PAGE adapted from a previously described method (Chugai Seiyaki Kabushiki Kaisha, 2010, Pub. No.: US 2010/0172899 A1). Briefly, the hybrid gel was mixed with 40% Acrylamide / Bis-Acrylamide, 37.5:1 (Sigma-Aldrich) and Ultrapure Agarose (Invitrogen) to final concentrations of 3.6% and 0.5%, respectively, in 0.375 M Tris Buffer, pH 8.8 and 15% glycerol. The resulting

mixture was heated to 50 ºC and polymerization was initiated with the addition of 0.08% TEMED and 0.08% of ammonium persulfate. The resulting solution was poured between two plates and the acrylamide was allowed to polymerize at 37 ºC for 1 hour and then left at room temperature for 30 min to ensure complete polymerization. Protein samples were loaded into the resulting hybrid gel and the gel was run in Tris-Acetate SDS Running Buffer (Novex) for 800 Vh. The gel was then fixed in 40% methanol, 10% acetic for 10 minutes, stained using a Colloidal Blue Staining Kit (Novex) for at least 3 hours and subsequently de-stained in water.

**[0257]** Non-Reducing SDS-Native-PAGE. Protein samples were loaded into a NativePAGE 3-12% Bis-Tris gel (Novex). Tris-Acetate SDS Running Buffer (Novex) was added and the gel was run at 40V for 15 min and then at 90V for 2 hours. The gel was then fixed in 40% methanol, 10% acetic acid for 10 minutes, stained using a Colloidal Blue Staining Kit (Novex) for at least 3 hours and subsequently de-stained in water.

**[0258]** Expression and assembly of HBV24, as measured by non-reducing SDS native-PAGE is shown in **FIG. 2A**. Expression and assembly of HBV23 is shown in **FIG. 2B**. Expression and assembly of HBV19 is shown in **FIG. 2C**. The heavy and light chains of each IgG expressed well and assembled into IgG antibodies (HBV24, not shown; HBV23, FIG 2B, Lane 2; HBV19, FIG 2C, Lane 2).

**[0259]** The heavy and light chains of HBV24M expressed well, but when co-expressed with a human J chain, did not properly assemble into IgM pentamers (**FIG. 2A**, "Hu/Hu"). On the other hand, the light chain comprising SEQ ID NO: 59, when combined with a chimeric HBV24 with a murine IgM heavy chain constant region, did assemble properly (**FIG. 2A**, "Ch/Hu").

**[0260]** An IgM heavy chain variable region related to SEQ ID NO: 5 was constructed via site-directed mutagenesis of certain amino acids, resulting in a heavy chain variable region comprising the amino acid sequence SEQ ID NO: 62. SEQ ID 62 was cloned into the appropriate vector according the method described above to encode the IgM heavy chain comprising the amino acid sequence SEQ ID NO: 63. This vector was co-transfected in to HEK293 cells a vector comprising the kappa light chain comprising the amino acid sequence SEQ ID NO: 59 and a vector encoding the human J-chain (SEQ ID NO: 54) or a vector encoding the modified J-chain V15J (SEQ ID NO: 68), and expression was permitted, producing the IgM molecules HBV24M2J and HBV24M2V15J. Both expression products properly assembled into a pentameric IgM molecules. The bispecific binding molecule HBV24M2V15J is shown in **FIG. 2A** ("M2/Hu").

## Example 4: Binding Assays

**[0261]** HBV24M2V15J and HBV23MJ were evaluated for binding to the full-length HBsAg-L (preS1, preS2, and S) by an ELISA assay. For HBV24M2V15J, binding was compared with the humanized IgG antibody specific for pre-S1 antigen provided in U.S. Patent No. 8,420,353, and for HBV23MJ binding was compared with the human IgG antibody provided in Cerino *et al.* (2015) PLOS one 10(4):e0125704. doi: 10.1371.

**[0262]** The assays were carried out by the following method. For HBV24, 96-well polystyrene MaxiSorp ELISA plates (Nunc) were coated with 1 μg/mL HBsAg-L antigen (Beacle, BCL-AG-001) in 100 μL coating buffer (100 mM bicarbonate, pH 9.5) overnight at 4 °C. For HBV23, plates were coated with HBsAg (Prospec HBS-872). Plates were then washed with 0.05% PBS-Tween and blocked with 2% BSA-PBS. After blocking, 100 μL of the serial diluted samples (purified protein or cell culture supernatant) were added to the wells and incubated at room temperature for 1 hour. The plates were then washed and incubated with HRP conjugated mouse anti-human kappa antibody (Southern Biotech, 9230-05. 1:6000 diluted in 2% BSA-PBS) for the HBV24 antibodies, and with HRP conjugated mouse anti-human Lambda (Southern Biotech, Cat 9180-05. 1:6000 diluted in 2% BSA-PBS) for the HBV23 antibodies, for 1 hour. After 5 final washes using 0.05% PBS-Tween, 100 μL TMB substrate (BD Biosciences, 555214) was added to each well and incubated in dark for 15 min. The reaction was then stopped by adding 50 μL of 2N HCl per well. A450 data was then collected and analyzed with GraphPad Prism using a 4-parameter logistic model.

**[0263]** The results for HBV24 are shown in **FIG. 3A**, comparing IgM vs. IgG by molar concentrations. HBV24M2V15J exhibited more effective binding than the IgG counterpart (HBV24G), exhibiting an EC50 of 26 pM vs 57 pM for the IgG supernatant and 61 pM for the purified IgG.

**[0264]** The results for HBV23 are shown in **FIG. 3B**, comparing IgM vs. IgG by weight concentrations. HBV23MJ exhibited more effective binding than the IgG counterpart (HBV23G), exhibiting an EC50 of 64 ng/ml vs 30 ng/ml for the IgG. The capacity of HBV23 MJ binding, as measured by maximum A450, was also much higher than for HBV23G.

**[0265]** HBV24M2V15J, HBV24G, HBV23MJ, and HBV23G were further evaluated for binding to PLC cells, a hepatocellular carcinoma cell line that expresses HBsAg on the cell surface, by the following method.

**[0266]** Alexander hepatoma cells (PLC/PRF/5; ATCC CRL-8024) were cultured in DMEM (Gibco, cat#11965-084) with 10% HI FBS (Gibco, cat#10082-147), and cells were replenished with fresh media the day before staining. On the day of staining, the cells were dislodged using Cell Dissociation Buffer (Gibco, cat#131510-14). After aspirating off all the media, the cells were rinsed with 10 mL of PBS without calcium or magnesium. After aspirating off the PBS, the cells were incubated with 10 ml of Cell Dissociation Buffer for 20~30 min at 37°C. The cells were then dislodged by tapping the flask to create a single cell suspension. Cell Dissociation Buffer was neutralized by adding an equal amount of media, and live cell counts were determined using Trypan Blue exclusion on a cell counter (BioRad TC20). The density of the cells was adjusted to 1.5 x 10e4 cells per 60 µL of FACS 2% FBS buffer (BD Pharmingen, cat# 554656), and 60 µL were added to "v" bottom 96 well plates. All antibodies were tested at final concentrations of 30 µg/mL, 10 µg/mL, 3 µg/mL, and 1 µg/mL; and 50 µL of the each antibody was added to the respective wells. The plates were then incubated for 30 min at 4°C. After washing the cells with 150 µL of FACS 2% FBS buffer, the plates were centrifuged (Sorvall Legend XIR centrifuge) at 1200 rpm for 5 min. and supernatants were gently aspirated without disturbing the cell pellets. Antibody binding was detected by incubating the cells with the appropriate AlexaFluor-647-labeled secondary antibody, anti-human kappa light chain (BioLegend, cat#316514) or AF647 anti-human lambda light chain (BioLegend, cat#316614), at 4°C for 30 min. The wash step was repeated as above and the cells were resuspended in 60 µL of FACS 2% FBS with 1:100 7_AAD (BD Pharm, cat#51-68981E). One thousand events were acquired for each sample on a FACSCalibur™ (Becton Dickinson) and the data analysis was done in FlowJo, from FlowJo LLC. For each study, antibody binding was compered to unstained cells and cells stained with the appropriate human isotype control antibody.

**[0267]** Binding of HBV24G and HBV23G could not be detected by FACS analysis. On the other hand, HBV23MJ and the bispecific HBV24M2V15J showed detectable binding (**FIG. 4**).

## Example 5: Screening for antibodies that bind preferentially to infectious virions and/or HBV-infected cells.

**[0268]** In this example, a library is screened for binding molecules that bind to cells infected by a virus of interest, or infectious versions of that virus to a greater extent, *e.g.*, affinity, avidity, or other characteristics. A binding molecule library, *e.g.*, an antibody library (phage/hybridoma/etc) is created, *e.g.*, a library of VH and VL regions derived from B cells of a virus-infected mammal, *e.g.*, an HBV-infected mammal. The library is then contacted with virus-infected cells, *e.g.*, HBV-infected cells, *e.g.*, a Hepatocellular carcinoma (HCC) cell line, or infectious viral particles, *e.g.*, HBV particles, on a solid support, *e.g.*, adherent to 96-well plate or beads to enrich those antibodies that bind to infected cells (will include all such antibodies, whether or not they also bind to non-infectious particles). Antibodies that bind to the infected cells are harvested and amplified. The recovered antibodies are then put in contact with non-infectious viral particles, *e.g.*, HBV subviral particles, and/or to non-infected cells of the same type as the earlier-used virus-infected cells, where the non-infectious particles and/or cells are attached to a solid support such as a plate, beads, column, etc. Antibodies that do not bind to the non-infectious viral particles or non-infected cells are recovered and amplified. This step is repeated one or more times to enrich for those antibodies that preferentially bind to virus-infected cells or infectious virus particles. The enriched/selectively depleted library is again recovered and amplified. Finally, antibodies of interest are recovered, clone purified, and further characterized.

## Example 6: Virus Neutralization Assays

**[0269]** *In vitro* HBV virus neutralization assays can be conducted using a variety of standard techniques, such as those described by Maeng *et al.*, *Virology* 270:9-16, 2000. Briefly, human hepatocytes (prepared by enzymatic dissociation of non-cancerous liver fragments) are seeded at a density of $10^6$ cells per well containing 2 ml of normal growth medium and are infected 3 days later with HBV particles (about 3 x $10^7$ viral genomic equivalents).

**[0270]** For the neutralization assay, the virus particles are pre-incubated with various concentrations of the antibody (as well as appropriate controls) at room temperature for 1 h and inoculated onto the cultured hepatocytes. The hepatocytes are covered with 1 ml of the serum-free

culture medium containing 4% polyethylene glycol (PEG). The infected cells are washed with the growth medium and further incubated for 17 days, with the medium renewed every 2 days.

**[0271]** On Day 17 post-infection, an aliquot of the culture medium is removed and diluted 10-fold, and the concentration of an HBV antigen (*e.g.*, HBsAg) is determined using an appropriate assay kit, *e.g.*, for HBsAg, a radioimmunoassay kit (Abbott Laboratories, Chicago, IL).

**[0272]** Alternatively, HBV virus neutralization studies can be conducted as described by Kim (FEBS Letters 2015; 589,193-200). Briefly, HepaRG cells (*e.g.*, ThermoFisher HPRGC10) are seeded at a density of $6x10^4$ cells per well (containing 100 µL of culture medium) and are cultured for 6 days. Viral particles (5 µL) are then preincubated with 5 µL of antibody at various concentrations at room temperature for 30 min and then incubated with the cultured HepaRG cells for 24 h in the absence or presence of 4% PEG 8000. The infected cells are washed with the medium and further incubated for 10 days, with the medium changed every 2 days. On day 10 post infection, the culture supernatant are diluted in order to remain in the quantitative range of the assay and the HBsAg concentration is determined with an ELISA kit (Bio-Rad).

## Example 7: *In Vivo* Models

**[0273]** Dimeric, pentameric, or hexameric binding molecules described herein can be tested *in vivo* in mouse models including, without limitation, uPA/RAG-2 mouse (Dandri Hepatology 2001; 33 (4): 981-988), immunodeficient urokinase-type plasminogen activator (uPA)/recombinant activation gene-2 (RAG-2) mice. The mice can be repopulated with human hepatocytes and infected with HBV, to test the binding molecules for efficacy *in vivo*. The trimera mouse model (llan Hepatology 1999; 29: 553-562) involves lethally irradiated mice, radioprotected with SCID mouse bone marrow cells. The Fah-/-Rag2-/-Il2rg-/- model (Grompe Nat Biotech 2007; 25 (8): 903-910; Verma PNAS 2007; 104 (51):20507-20511) involves immunodeficient, fumaryl acetoacetate hydrolase-deficient (fah(-/-)) mice with a regulatable system for repopulating the liver with human hepatocytes. The TK-NOG based humanized mouse model (Kosaka Biochem Biophys Res Commun. 2013 Nov 8;441(1):230-5) involves super immunodeficient NOG mouse with transgenic expression of thymidine kinase under control of liver-restricted albumin promoter. The MUP-uPA/SCID/Bg model (Tesfave PLoS ONE 2013; 8(10):e77298) involves mice carrying the uPA gene driven by the major urinary protein promoter on a SCID/Beige background. Dimeric,

pentameric, or hexameric binding molecules can be tested *in vivo* in non-human primates. The As/HSG-hu HSC/Hep mouse model (Bility PLoS ONE 2014; 10(3):e1004032) involves mice repopulated with both human immune and liver cells and supports persistent HBV infection.

## Example 8: Complement Dependent Cytotoxicity of HBV antibodies

**[0274]** Antibodies of the IgM phenotype are particularly well-suited to use the efficient engagement of complement protein C1q to affect complement dependent cytotoxicity (CDC) activity on target cells. To measure CDC, hepatocellular carcinoma cells expressing HBsAg (*e.g.* Alexander hepatoma cells (PLC/PRF/5; ATCC CRL-8024)) or recombinant cells expressing HBsAg-L are used. The target cells are washed and resuspended in CDC assay medium (RPMI 1640, 10% heat-inactivated FBS) at a density of 1.0 x $10^6$ cells/mL and 10 µL/well is added to a Nunc 384-well tissue culture-treated white polystyrene plate. Serial 3-fold dilutions of test antibodies are prepared in assay medium, 10 µL/well is added to the assay plate, and the plate is incubated for 2 hr at 37 °C in a 5% $CO_2$ incubator to allow opsonization to occur. Normal human serum complement (Quidel) is diluted to 30% in assay medium, and 10 µL/well is added to the assay plate. The plate is incubated for 4 hr at 37 °C in a 5% $CO_2$ incubator. Cell Titer-Glo reagent (Promega) is thawed for use and 15 µL/well is added to the assay plate. The plate is gently mixed for 2 min on a plate shaker to lyse the cells and then for another 10 min at room temperature before measuring luminescence on an EnVision plate reader (Perkin-Elmer). After subtracting background signal, percent viability is plotted against antibody concentration and EC50 values are determined using GraphPad Prism.

## Example 9: T-Cell Activation by HBVXCD3 Bispecific antibodies

**[0275]** To demonstrate whether a bispecific anti-HBsAg/anti-CD3 antibody can activate T cells upon binding to the HBsAg target the following assay is performed. Engineered Jurkat T cells (Promega CS176403) and either hepatocellular carcinoma cells expressing HBsAg (*e.g.*, Alexander hepatoma cells (PLC/PRF/5; ATCC CRL-8024)) or recombinant cells expressing HBsAg-L are cultured in RPMI (Invitrogen) supplemented with 10% Fetal Bovine Serum (Invitrogen). Serial dilutions of purified bispecific and monospecific anti-HBV antibodies are incubated with HBsAg-expressing cells in 20 µL in a white 384 well assay plate for 2h at 37 °C with 5% $CO_2$. The

engineered Jurkat cells (25000) are added to the mixture to a final volume of 40 µL. The mixture is incubated for 5h at 37 ºC with 5% $CO_2$. The cell mixtures are then mixed with 20 µL lysis buffer containing luciferin (Promega, Cell Titer Glo) to measure luciferase reporter activity. Light output is measured by EnVision plate reader. EC50 is determined by 4 parameter curve fit using Prism software.

## Example 10: T-cell Directed B-Cell Killing – LDH Release Assay

**[0276]** In order to demonstrate whether bispecific HBV x CD3 IgM binding molecules can kill target cells in the presence of CD8+ T-cell acute lymphoblastic leukemia (TALL) cells, co-culture experiments can be performed. HBsAg-expressing cells (about 6 x $10^3$ cells), *e.g.*, hepatocellular carcinoma cells such as Alexander hepatoma cells (PLC/PRF/5; ATCC CRL-8024) or recombinant cells expressing HBsAg-L, are co-cultured with 3 x $10^4$ TALL cells (ATCC CRL-11386) in the presence of different concentrations of test compounds in 45 µL total volume of RPMI 1640 media supplemented with 10% heat-inactivated FBS per well on a 384-well black tissue culture plate. After 24 hours of incubation at 37 °C in a 5% $CO_2$ incubator, 15 µL of CytoTox-ONE substrate reagent (Promega, G7891) is added to each well to measure the level of LDH released from dead cells. The plates are shaken briefly to mix the reagents, and then incubated at room temperature for 90 min before measuring fluorescence signal (485 nm for excitation and 615 nm for emission) on an EnVision plate reader (Perkin-Elmer). The data is then analyzed with GraphPad Prism to determine the $EC_{50}$.

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**[0277]** The breadth and scope of the disclosure should not be limited by any of the above-described exemplary embodiments, but should be defined in accordance with the following claims and their equivalents.

[0277A] Certain statements that appear herein are broader than what appears in the statements of the invention. These statements are provided in the interests of providing the reader with a better understanding of the invention and its practice. The reader is directed to the accompanying claim set which defines the scope of the invention.

[0277B] In this specification where reference has been made to patent specifications, other external documents, or other sources of information, this is generally for the purpose of providing a context

for discussing the features of the invention. Unless specifically stated otherwise, reference to such external documents is not to be construed as an admission that such documents, or such sources of information, in any jurisdiction, are prior art, or form part of the common general knowledge in the art.

WHAT IS CLAIMED IS:

1. A multimeric antibody comprising at least two bivalent binding units, or functional variants or functional fragments thereof;

wherein each binding unit comprises two IgM or IgA antibody heavy chain constant regions or functional fragments thereof, each associated with an antigen binding domain;

wherein the antigen binding domains specifically bind to a hepatitis B virus (HBV) antigen expressed on the surface of infectious viral particles, on the surface of HBV infected cells, or a combination thereof, and

wherein the multimeric antibody is more potent in inhibiting HBV proliferation, enhancing HBV clearance, controlling HBV infectivity and/or controlling HBV growth than a reference IgG antibody comprising the antigen binding domain that specifically binds to the HBV antigen.

2. The multimeric antibody of claim 1, wherein the HBV antigen is a hepatitis B surface antigen (HBsAg), a precore antigen, a core antigen, or an X-antigen.

3. The antibody of claim 2, wherein the HBsAg comprises the S region, the S and pre-S2 regions, or the S, pre-S2, and pre-S1 regions.

4. The multimeric antibody of any one of claim 1 to 3, which is a dimeric antibody comprising two bivalent IgA binding units, or functional variants or functional fragments thereof, and a J-chain or functional fragment thereof or functional variant thereof, wherein each binding unit comprises two IgA heavy chain constant regions or functional fragments thereof each associated with a VH situated amino terminal to the IgA constant region, and two immunoglobulin light chains each comprising a VL situated amino terminal to an immunoglobulin light chain constant region, wherein the IgA heavy chain constant regions each comprise a Cα1 domain, a Cα2 domain, and a Cα3-tp domain.

5. The multimeric antibody of any one of claims 1 to 3, which is a pentameric or a hexameric antibody comprising five or six bivalent IgM binding units, respectively, wherein each binding unit comprises two IgM heavy chain constant regions or functional fragments thereof each associated with a VH situated amino terminal to the IgM constant region, and two immunoglobulin

light chains each comprising a VL situated amino terminal to an immunoglobulin light chain constant region, and wherein the IgM heavy chain constant regions each comprise a Cμ1 domain, a Cμ2 domain, a Cμ3 domain, and a Cμ4-tp domain.

6. The multimeric antibody of claim 5, wherein the IgM heavy chain constant regions are human IgM constant regions.

7. The multimeric antibody of any one of claims 1 to 6, wherein the antigen binding domains comprise an antibody heavy chain variable region (VH) and an antibody light chain variable region (VL), wherein the VH and VL comprise, respectively, HCDR1, HCDR2, and HCDR3 regions and LCDR1, LCDR2, and LCDR3 regions of the VH and VL amino acid sequences SEQ ID NO: 1 and SEQ ID NO: 3, SEQ ID NO: 2 and SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8, SEQ ID NO: 7 and SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 11, SEQ ID NO: 14 and SEQ ID NO: 15, SEQ ID NO: 16 and SEQ ID NO: 21, SEQ ID NO: 17 and SEQ ID NO: 22, SEQ ID NO: 18 and SEQ ID NO: 23, SEQ ID NO: 19 and SEQ ID NO: 24, SEQ ID NO: 20 and SEQ ID NO: 25, SEQ ID NO: 26 and SEQ ID NO: 27, SEQ ID NO: 26 and SEQ ID NO: 28, SEQ ID NO: 26 and SEQ ID NO: 29, SEQ ID NO: 30 and SEQ ID NO: 31, SEQ ID NO: 32 and SEQ ID NO: 33, SEQ ID NO: 34 and SEQ ID NO: 35, SEQ ID NO: 34 and SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38, SEQ ID NO: 39 and SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44, SEQ ID NO: 45 and SEQ ID NO: 46, SEQ ID NO: 47 and SEQ ID NO: 48, SEQ ID NO: 49 and SEQ ID NO: 50, SEQ ID NO: 51 and SEQ ID NO: 52, SEQ ID NO: 62 and SEQ ID NO: 6, SEQ ID NO: 73 and SEQ ID NO: 74, or SEQ ID NO: 75 and SEQ ID NO: 76, respectively.

8. The multimeric antibody of claim 7, wherein the antigen binding domains comprise an antibody heavy chain variable region (VH) and an antibody light chain variable region (VL), wherein the VH and VL comprise, respectively, amino acid sequences that are at least 80%, at least 85%, at least 90%, at least 95% or 100% identical to SEQ ID NO: 1 and SEQ ID NO: 3, SEQ ID NO: 2 and SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8, SEQ ID NO: 7 and SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 11, SEQ ID NO: 14 and SEQ ID NO: 15, SEQ ID NO: 16 and SEQ ID NO: 21, SEQ ID NO: 17 and SEQ ID NO: 22, SEQ ID NO: 18 and SEQ ID NO: 23, SEQ ID NO: 19 and SEQ ID NO: 24, SEQ ID NO: 20 and

SEQ ID NO: 25, SEQ ID NO: 26 and SEQ ID NO: 27, SEQ ID NO: 26 and SEQ ID NO: 28, SEQ ID NO: 26 and SEQ ID NO: 29, SEQ ID NO: 30 and SEQ ID NO: 31, SEQ ID NO: 32 and SEQ ID NO: 33, SEQ ID NO: 34 and SEQ ID NO: 35, SEQ ID NO: 34 and SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38, SEQ ID NO: 39 and SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44, SEQ ID NO: 45 and SEQ ID NO: 46, SEQ ID NO: 47 and SEQ ID NO: 48, SEQ ID NO: 49 and SEQ ID NO: 50, SEQ ID NO: 51 and SEQ ID NO: 52, SEQ ID NO: 62 and SEQ ID NO: 6, SEQ ID NO: 73 and SEQ ID NO: 74, or SEQ ID NO: 75 and SEQ ID NO: 76.

9. The multimeric antibody of any one of claims 1 to 3 or 5 to 8, comprising an IgM heavy chain comprising the amino acid sequence SEQ ID NO: 58 and a light chain comprising the amino acid sequence SEQ ID NO: 59, or comprising an IgM heavy chain comprising the amino acid sequence SEQ ID NO: 63 and a light chain comprising the amino acid sequence SEQ ID NO: 59.

10. The multimeric antibody of any one of claims 1 to 3 or 5 to 9, which is pentameric, and further comprises a J-chain or functional fragment thereof or functional variant thereof.

11. An isolated IgM antibody or functional fragment thereof comprising a J-chain or functional fragment thereof or functional variant thereof and five binding units, each comprising two heavy chains and two light chains, wherein each heavy chain comprises a human Mu constant region or functional fragment thereof, and the heavy chain variable region amino acid sequence SEQ ID NO: 62, and wherein each light chain comprises a human kappa constant region and the light chain variable region amino acid sequence SEQ ID NO: 6; wherein the antibody or functional fragment thereof can assemble into a pentameric IgM antibody that can specifically bind to the pre-S1 region of HBV surface antigen.

12. The multimeric antibody of claim 4 or claim 10, or the isolated IgM antibody or functional fragment thereof of claim 11, and wherein the J-chain or functional fragment thereof or functional variant thereof comprises the amino acid sequence SEQ ID NO: 54.

13. The multimeric antibody of any one of claims 4, 10, or 12, or the isolated IgM antibody or functional fragment thereof of claim 11 or claim 12, wherein the J-chain or functional fragment thereof or functional variant thereof is a modified J-chain further comprising a heterologous polypeptide, wherein the heterologous polypeptide is directly or indirectly fused to the J-chain or functional fragment thereof or functional variant thereof.

14. The multimeric antibody of claim 13 or the isolated IgM antibody or functional fragment thereof of claim 13, wherein the heterologous polypeptide is fused to the N-terminus of the J-chain or

functional fragment thereof or functional variant thereof, the C-terminus of the J-chain or functional fragment thereof or functional variant thereof, or to both the N-terminus and C-terminus of the J-chain or functional fragment thereof or functional variant thereof.

15. The multimeric antibody of claim 13 or claim 14, or the isolated IgM antibody or functional fragment thereof of claim 13 or claim 14, wherein the heterologous polypeptide comprises a scFv antibody fragment.

16. The multimeric antibody of any one of claims 13 to 15, or the isolated IgM antibody or functional fragment thereof of any one of claims 13 to 15, wherein the heterologous polypeptide can specifically bind to CD3ε.

17. A polynucleotide comprising a nucleic acid sequence that encodes at least one polypeptide subunit of the multimeric antibody of any one of claims 1 to 10 or 12 to 16, or the isolated IgM antibody or functional fragment thereof of any one of claims 11 to 16, wherein the polypeptide subunit comprises the IgM heavy chain constant region and at least the antibody VH portion of an antibody binding domain that specifically binds to a hepatitis B virus (HBV) antigen expressed on the surface of infectious viral particles, on the surface of HBV-infected cells, or a combination thereof, and/or the polypeptide subunit comprises the antibody VL portion of an antibody binding domain that specifically binds to a hepatitis B virus (HBV) antigen expressed on the surface of infectious viral particles, on the surface of HBV-infected cells, or a combination thereof.

18. A composition comprising:

(a) a first polynucleotide comprising a nucleic acid sequence that encodes the IgM heavy chain constant region and at least the antibody VH portion of the antibody binding domain of the multimeric antibody of any one of claims 1 to 10 or 12 to 16, or the isolated IgM antibody or functional fragment thereof of any one of claims 11 to 16; and

(b) a second polynucleotide comprising a nucleic acid sequence that encodes the VL portion of the antibody binding domain of the multimeric antibody of any one of claims 1 to 10 or 12 to 16, or the isolated IgM antibody or functional fragment thereof of any one of claims 11 to 16.

19. The composition of claim 18, further comprising a third polynucleotide comprising a nucleic acid sequence encoding a J-chain, or functional fragment thereof, or functional variant thereof.

20. The composition of claim 19, wherein the polynucleotides are situated on a single vector.

21. The composition of claim 19, wherein the polynucleotides are on at least two separate vectors.

22. A host cell comprising the composition of any one of claims 18 to 21, wherein the host cell can express the multimeric antibody of any one of claims 1 to 10 or 12 to 16, or the isolated IgM antibody or functional fragment thereof of any one of claims 11 to 16.

23. A method of producing the multimeric antibody of any one of claims 1 to 10 or 12 to 16, or the isolated IgM antibody or functional fragment thereof of any one of claims 11 to 16, comprising culturing the host cell of claim 22, and recovering the multimeric antibody or the isolated IgM antibody or functional fragment thereof.

24. A method of controlling hepatitis B virus (HBV) proliferation, latency, or maintenance in chronically-infected cells, comprising contacting a mixture of HBV and HBV-susceptible cells with the multimeric antibody of any one of claims 1 to 10 or 12 to 16, or the isolated IgM antibody or functional fragment thereof of any one of claims 11 to 16, wherein the multimeric antibody or isolated IgM antibody or functional fragment thereof is more potent than a reference IgG antibody comprising the antigen binding domain that specifically binds to the HBV antigen.

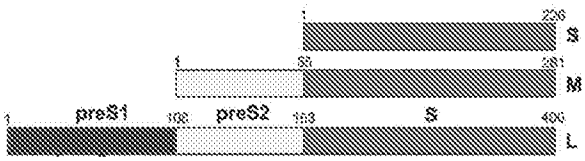
25. A method of treating a disease or condition caused by or exacerbated by hepatitis B virus (HBV) infection in a patient, comprising administering to a patient infected with HBV or susceptible to HBV infection the multimeric antibody of any one of claims 1 to 10 or 12 to 16, or the isolated IgM antibody or functional fragment thereof of any one of claims 11 to 16, wherein multimeric antibody or isolated IgM antibody or functional fragment thereof is more potent than a reference IgG antibody comprising the antigen binding domain that specifically binds to the HBV antigen.

26. The method of claim 25, wherein the disease or condition is acute hepatitis, chronic hepatitis, liver inflammation, cirrhosis of the liver, liver failure, hepatocellular carcinoma (HCC), or any combination thereof.

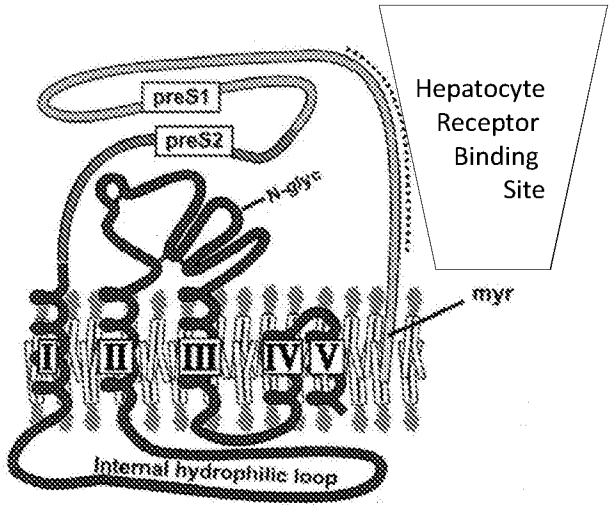
27. The method of claim 25 or claim 26, wherein the patient exhibits an HBV disease symptom, and wherein the symptom is increased viral load, virus shedding, abdominal pain, dark urine, fever, joint pain, loss of appetite, nausea and vomiting, weakness and fatigue, jaundice, or a combination thereof.

Figure 1

A




B




Adapted from Chi 2007 & Glebe 2005

FIGURE 2A

Hu = HBV24 mu or kappa
Ch = Chimeric HBV24 mu or kappa
K1 = HBV24K1 kappa mutant
M2 = HBV24M2 mu mutant
+ = IgM positive control

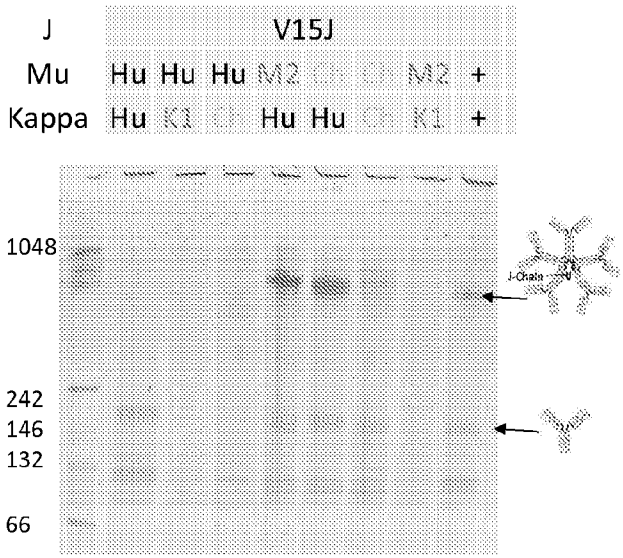


Figure 2B

1 Native markers
2 HBV23G anti-S hIgG1
3 HBV23MJ anti-S-hIgM+J

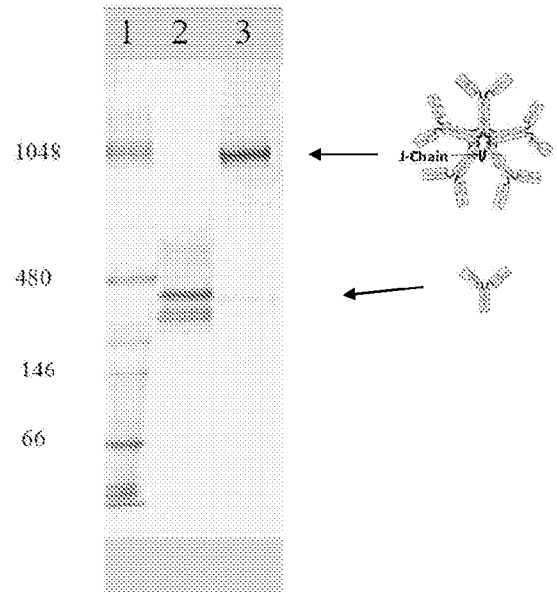
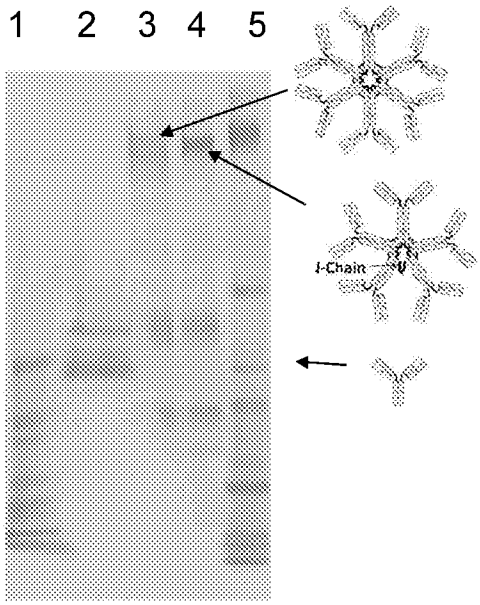


FIGURE 2C Expression & Assembly of 5a19 IgM




1 LMW Marker
2 HBV19 IgG
3 HBV19 IgM
4 HBV19 IgM+J
5 Native Markers

Figure 3A

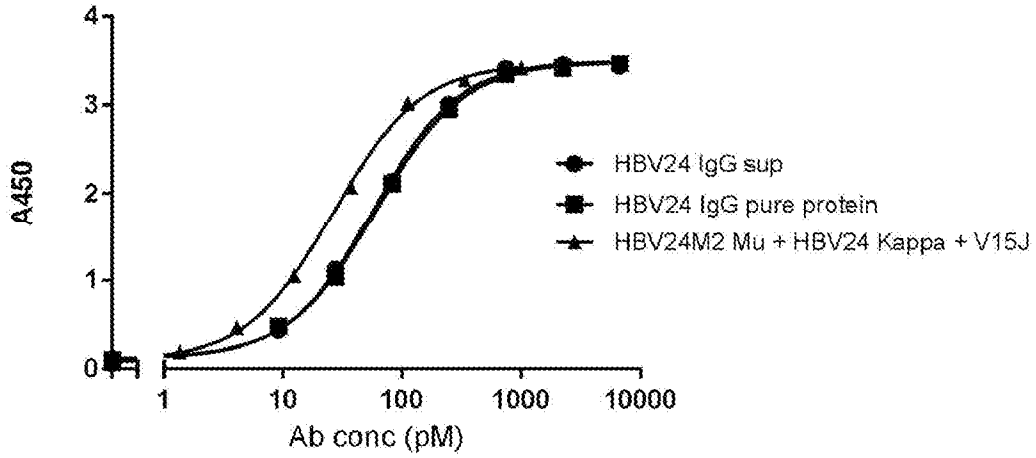

A450
4
3
2
1
0
1
10
100
1000
10000
Ab conc (pM)
HBV24 IgG sup
HBV24 IgG pure protein
HBV24M2 Mu + HBV24 Kappa + V15J

Figure 3B

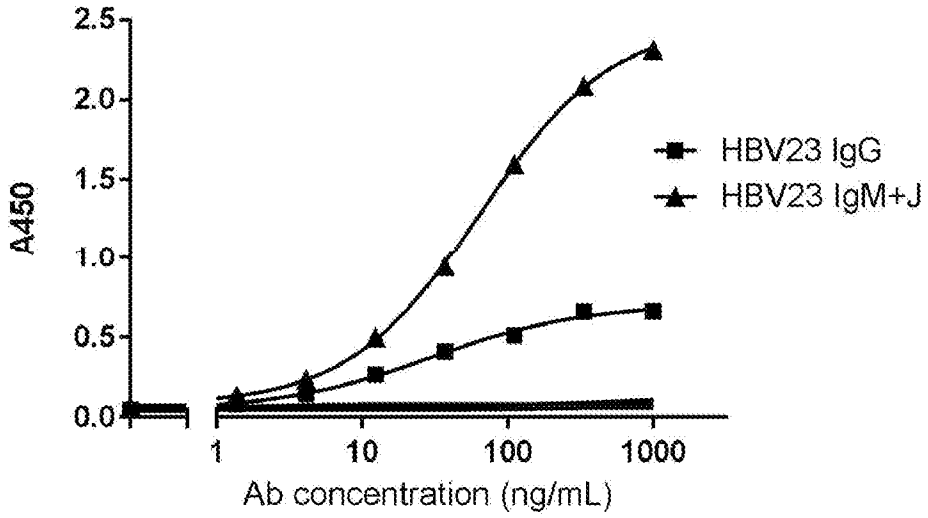
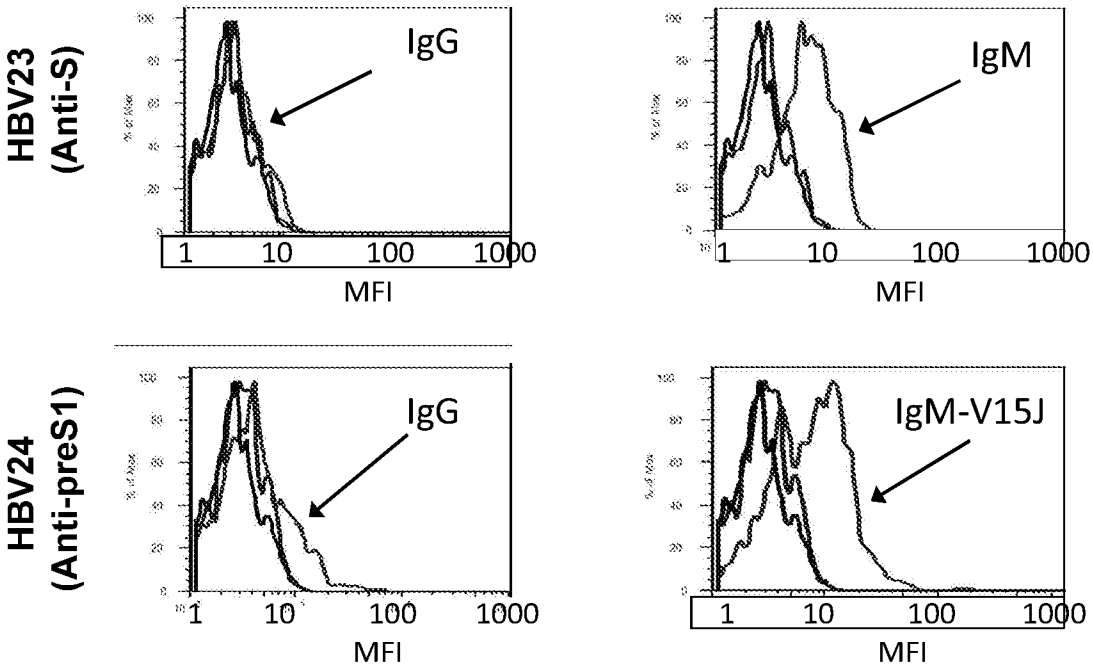

2.5
2.0
1.5
1.0
0.5
0.0
A450
1
10
100
1000
Ab concentration (ng/mL)
HBV23 IgG
HBV23 IgM+J

FIGURE 4


HBV23
(Anti-S)
IgG
IgM
1
10
100
1000
MFI
HBV24
(Anti-preS1)
IgG
IgM-V15J
1
10
100
1000
MFI