

ANTIBODIES THAT NEUTRALIZE HEPATITIS B VIRUS
AND USES THEREOF

5 STATEMENT REGARDING SEQUENCE LISTING

The Sequence Listing associated with this application is provided in text format in lieu of a paper copy, and is hereby incorporated by reference into the specification. The name of the text file containing the Sequence Listing is

930485_402WO_SEQUENCE_LISTING.txt. The text file is 109 KB, was created on
10 December 16, 2019, and is being submitted electronically via EFS-Web.

The present disclosure relates to the field of immunotherapy for hepatitis B virus (HBV) and against hepatitis delta virus (HDV), and uses thereof. Anti-hepatitis B binding proteins described herein, e.g., antibodies and antigen binding fragments
15 thereof, are capable of binding to an epitope located in the antigenic loop region of the S domain of the HBV envelope proteins (HBsAg). In certain embodiments, anti-hepatitis B binding proteins can bind to any or all of the known HBsAg genotypes, as well as HBsAg variants, and can neutralize HBV infection. Nucleic acids that encode, and host cells that express, such binding proteins are also provided herein. In addition,
20 the present disclosure provides methods of using the antibodies and antibody fragments described herein in the diagnosis, prophylaxis, and treatment of diseases, as well as in methods of screening.

By way of background, HBV consists of (i) an envelope containing three related surface
25 proteins (hepatitis B surface antigen, HBsAg) and lipid and (ii) an icosahedral nucleocapsid enclosing the viral DNA genome and DNA polymerase. The HBV capsid is formed in the cytosol of the infected cell during packaging of an RNA pregenome replication complex and gains the ability to bud during synthesis of the viral DNA genome by reverse transcription of the pregenome in the lumen of the particle. The
30 three HBV envelope proteins S-HBsAg, M-HBsAg, and L-HBsAg shape a complex transmembrane fold at the endoplasmic reticulum, and form disulfide-linked homo- and heterodimers. During budding at an intracellular membrane, a short linear domain in

the cytosolic preS region interacts with binding sites on the capsid surface. The virions are subsequently secreted into the blood. In addition, the surface proteins can bud in the absence of capsids and form subviral particles (SVPs) which are also secreted in 3–4 log excess over virions. High level of HBsAg can exhaust HBsAg-specific T-cell response, and is proposed as an important factor for viral immunotolerance in patients with chronic hepatitis B (CHB) (Chisari FV, Isogawa M, Wieland SF, *Pathologie Biologie*, 2010;58:258–66).

Hepatitis B virus causes potentially life-threatening acute and chronic liver infections. Acute hepatitis B is characterized by viremia, with or without symptoms, with the risk of fulminant hepatitis occurrence (Liang TJ, Block TM, McMahon BJ, Ghany MG, Urban S, Guo JT, Locarnini S, Zoulim F, Chang KM, Lok AS. Present and future therapies of hepatitis B: From discovery to cure. *Hepatology*. 2015 Aug 3. doi: 10.1002/hep.28025. [Epub ahead of print]). Despite an efficacious vaccine against hepatitis B being available since 1982, WHO reports that 240 million people are chronically infected with hepatitis B and more than 780,000 people die every year due to hepatitis B complications. Approximately one third of chronic hepatitis B (CHB) patients develop cirrhosis, liver failure and hepatocellular carcinoma, accounting for 600,000 deaths per year (Liang TJ, Block TM, McMahon BJ, Ghany MG, Urban S, Guo JT, Locarnini S, Zoulim F, Chang KM, Lok AS. Present and future therapies of hepatitis B: From discovery to cure. *Hepatology*. 2015 Aug 3. doi: 10.1002/hep.28025. [Epub ahead of print]).

For patients infected with HBV, severe complications can develop as a result of coinfection or superinfection with HDV. According to the WHO, hepatitis D infects about 15 million people worldwide. HDV is considered a subviral satellite because it can propagate only in the presence of HBV. HDV is one of the smallest known animal viruses (40 nm), whereby its genome is only 1.6 kb and encodes for S and L HDAG. All other proteins needed for genome replication of HDV, including the RNA polymerase, are provided by the host cell, and the HDV envelope is provided by HBV. When introduced into permissive cells, the HDV RNA genome replicates and associates with multiple copies of the HDV-encoded proteins to assemble a ribonucleoprotein

(RNP) complex. The RNP is exported from the cell by the HBV envelope proteins, which are able to assemble lipoprotein vesicles that bud into the lumen of a pre-Golgi compartment before being secreted. Moreover, the HBV envelope proteins also provide a mechanism for the targeting of HDV to an uninfected cell, thereby ensuring the spread of HDV.

Complications caused by HDV include a greater likelihood of experiencing liver failure in acute infections and a rapid progression to liver cirrhosis, with an increased chance of developing liver cancer in chronic infections. In combination with hepatitis B virus, hepatitis D has the highest fatality rate of all the hepatitis infections, at 20% (Fattovich G, Giustina G, Christensen E, Pantalena M, Zagni I, Realdi G, Schalm SW. Influence of hepatitis delta virus infection on morbidity and mortality in compensated cirrhosis type B. Gut. 2000 Mar;46(3):420-6). The only approved therapy for chronic HDV infection is interferon-alpha. However, treatment of HDV with interferon-alpha is relatively inefficient and is not well-tolerated. Treatment with interferon-alpha results in sustained virological response six months post-treatment in one-fourth of the patients. Also, nucleos(t)ide analogs (NAs) have been widely tested in hepatitis delta, but they appear to be ineffective. Combination treatment using NAs with interferon also proved to be disappointing (Zaigham Abbas, Minaam Abbas Management of hepatitis delta: Need for novel therapeutic Options. World J Gastroenterol 2015 August 28; 21(32): 9461-9465). Accordingly, new therapeutic options are needed.

BRIEF DESCRIPTION OF THE DRAWINGS

The figures provided herein are intended to illustrate subject matter included in the present disclosure in more detail. The figures are not intended to limit the disclosure in any way.

Figure 1 shows binding of HBC34-V7 and two engineered antibodies of the present disclosure ("HBC34-V34"; "HBC34-V35") at the indicated concentrations to HBsAg adw (top panel) and HBsAg adr (bottom panel), as determined in direct antigen-based ELISA assays. All antibodies were produced as IgG1 (g1m17, 1 allotype).

Figures 2A-2K show binding of HBC34-V7, HBC34-V34, and HBC34-V35 to all known HBsAg genotypes ((A)-(J), respectively) and to mock control (K). Genotype-representative sequences representing the HBsAg antigenic outer loop, as shown in
 5 Example 5 of PCT Publication No. WO 2017/060504, were used. Staining was performed by FACS. Antibody concentrations were as indicated on the x-axis of the graphs.

Figures 3A-3V show *in vitro* binding (3A-3R) and neutralization (3S-3V) of certain
 10 HBC antibodies to HBsAg. Figures 3A and 3B show binding of HBC34-V7 and HBC34-V35 with wild type or variant Fc regions to HBsAg adw in a direct antigen-based ELISA assay (2 experiments; data from "Experiment 1" is shown in Figure 3A, and data from "Experiment 2" is shown in Figure 3B). Antigen-binding curves are shown in the top panel of each Figure. EC₅₀ values (determined by fitting the curves
 15 using Graphpad prism) are shown in the middle panel of each Figure. Binding to uncoated plates (control) is shown in the bottom panel of each Figure. Fc regions: "HBC34v7" and "HBC34-V35" = wild-type Fc; "HBC34-V35-MLNS" = Fc with M428L/N434S. "HBC34-V35-MLNS-GAALIE" = Fc with M428L/N434S/G236A/A330L/I332E. Three lots of HBC34-V35 were tested. Two
 20 lots of HBC34-V35-MLNS, and two lots of HBC34-v35-MLNS-GAALIE were tested. One lot of HBC34-V7 was used. Figures 3C-3H show binding of HBC34-V35, HBC34-V35-MLNS, and HBC34-V35-MLNS-GAALIE to Expi293 cells expressing HBsAg from all ten known HBV genotypes or mock control. Binding was determined by flow cytometry. Data are expressed as the mean fluorescence intensity (y-axis) of
 25 the transfected populations as defined by gating out the signal obtained with mock-transfected cells. For each HbsAg, serial dilutions of the three test articles were tested (12 points, 1 in 3, starting from 10 µg/ml). Figures 3I-3R show binding of HBC34-V35, HBC34-V35-MLNS, and HBC34-V35-MLNS-GAALIE to Expi293 cells expressing HBsAg from nineteen (19) HBsAg variants or mock control. Binding was
 30 determined by flow cytometry. Data are expressed as the mean fluorescence intensity of the transfected populations as defined by gating out the signal obtained with mock-transfected cells. For each HBsAg, serial dilutions of the three test articles were tested

(12 points, 1 in 3, starting from 10 µg/ml). Antibody concentration was as shown on the x-axis. Figures 3S and 3U show neutralizing capacity of the indicated HBC antibodies against HBV genotype D as assessed by measuring levels of HBsAg (top) and HbeAg (bottom) in the cell culture supernatant of HBVD-infected HepG2 cells expressing NTCP. Data represent the means $\pm$ SD from one of two independent experiments. Figures 3T and 3V show EC₅₀ values. The geometric mean and range (in brackets) of EC₅₀ values were determined from two independent experiments.

Figure 4 shows neutralization (EC₅₀ value), by HBC34-V35-MLNS-GAALIE, of individual HBV genotypes using an HDV pseudotyping system.

Figures 5-8 show the effect of HBC34-V35 on serum HBsAg levels in an *in vivo* mouse model of HBV infection. HBV genotype C-infected SCID mice were transplanted with primary human hepatocytes and administered HBC34-V35 at 1, 5, or 15 mg/kg, or PBS (control), as described in Example 5. Figure 5 shows serum HBV DNA concentration before and after treatment. Figure 6 shows serum HBsAg concentration before and after treatment. Figure 7 shows serum HBeAg concentration before and after treatment. Figure 8 shows serum HBcrAg concentration before and after treatment. "Tmt" = Treatment.

Figures 9A-9F show binding of HBC34-V35-MLNS and HBC34-V35-MLNS-GAALIE to human FcRs. (A)-(E) Binding to FcγRs, as assessed by biolayer interferometry (BLI). His-tagged human FcγRs ((A) FcγRIIa allele H131; (B) FcγRIIa allele R131; (C) FcγRIIIa allele F158; (D) FcγRIIIa allele V158; (E) FcγRIIb) at 2 µg/ml were captured onto anti-penta-His sensors for 6 minutes. FcγR-loaded sensors were then exposed for 5 minutes to a solution of kinetics buffer (pH 7.1) containing 2 µg/ml of each mAb (left part of the plot) in the presence 1 µg/ml of affiniPure F(ab')₂ Fragment Goat Anti-Human IgG, F(ab')₂ fragment specific (to cross-link human mAbs through the Fab fragment), followed by a dissociation step in the same buffer for additional 4 minutes (right part of the plot). Association and dissociation profiles were measured in real time as change in the interference pattern using an Octet® RED96 (FortéBio). (F) *In vitro* binding of HBC34 antibodies to FcRn at different pHs, as

determined using Bio-Layer interferometry (BLI). The time point 0 seconds represents switch from base line buffer to buffer containing antibodies. Time point 300 seconds (dotted vertical line) represents switch to blank buffer at the corresponding pH. Curves indicate association and dissociation profiles of change in the interference patterns.

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Figure 10 shows binding of HBC34-V35-MLNS and HBC34-V35-MLNS-GAALIE to human C1q, as measured by Octet®. Anti-human Fab (CH1) sensors were used to capture, through the Fab fragment, the full IgG1 of HBC34v35-MLNS and HBC34-V35-MLNS-GAALIE mAbs at 10 µg/ml for 10 minutes. IgG-loaded sensors were then exposed for 4 minutes to a solution of kinetics buffer (pH 7.1) containing 3 µg/ml of purified human C1q (left part of the plot), followed by a dissociation step in the same buffer for additional 4 minutes (right part of the plot). Association and dissociation profiles were measured in real time as change in the interference pattern using an Octet® RED96 (FortéBio).

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Figures 11A and 11B show *in vitro* activation of human FcγRIIIa using receptor-linked activation of a NFAT-mediated Luciferase reporter in engineered Jurkat cells. FcγRIIIa activation was tested using a validated, commercially available bioreporter assay in which recombinant HBsAg (Engerix B) is used as target antigen. Serial dilutions of HBC34-V35-MLNS and HBC34-V35-MLNS-GAALIE and a control (Ctr) mAb were incubated with 0.2 µg/ml of HBsAg at 37 °C for 25 min. Jurkat effector cells (Promega) expressing either FcγRIIIa low affinity allele F158 (A) or FcγRIIIa high affinity allele V158 (B) were resuspended in assay buffer and then added to assay plates. After incubation at 37 °C for 24 hours, Bio-Glo™ Luciferase Assay Reagent (Promega) was added, and luminescence was quantified using luminometer (Bio-Tek).

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Figures 12A and 12B show *in vitro* activation of human FcγRIIa using receptor-linked activation of a NFAT-mediated luciferase reporter in engineered Jurkat cells. Activation of human FcγRIIa was determined using a validated, commercially available bioreporter assay in which recombinant HBsAg (Engerix B) was used as target antigen. Serial dilutions of HBC34v35-MLNS and HBC34-V35-MLNS-GAALIE and a control mAb (Ctr) were incubated with 2 µg/ml (A) or 0.2 µg/ml (B) of HBsAg at 37 °C for 25

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min. Jurkat effector cells (Promega) expressing FcγRIIa high affinity allele H131 were resuspended in assay buffer and then added to assay plates. After incubation at 37 °C for 23 hours, Bio-Glo™ Luciferase Assay Reagent (Promega) was added, and luminescence was quantified using luminometer (Bio-Tek).

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Figures 13A-13B show *in vitro* activation of human FcγRIIb using receptor-linked activation of a NFAT-mediated luciferase reporter in engineered Jurkat cells. Activation of human FcγRIIb was tested using a validated, commercially available bioreporter assay in which recombinant HBsAg (Engerix B) is used as target antigen. Serial dilutions of HBC34-V35-MLNS and HBC34-V35-MLNS-GAALIE and a control mAb (Ctr) were incubated with 1 µg/ml of HBsAg at 37 °C for 15 min. Jurkat effector cells (Promega) expressing FcγRIIb were resuspended in assay buffer and then added to assay plates. After incubation at 37 °C for 20 hours, Bio-Glo™ Luciferase Assay Reagent (Promega) was added, and luminescence was quantified using luminometer (Bio-Tek). In Figure 13B, the control mAb from Figure 13A is designated "Ctr mAb1". A second control mAb, designated "Ctr mAb2", is a version of HBC34-V35 including IgG1 Fc with the following mutations that enhance binding to FcγRIIb: G237D/P238D/H268D/P271G/A330R (Mimoto *et al.*, *Prot Eng Des Sel.* 26(10):589-598 (2013)).

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Figures 14A and 14B show *in vitro* killing of PLC/PRF/5 human hepatoma cells by human primary NK cells in the presence of HBC34-V35-MLNS and HBC34-V35-MLNS-GAALIE. (A) ADCC was tested using freshly isolated NK cells from one donor previously genotyped for expressing heterozygous high (V158) and low (F158) affinity FcγRIIIa (F/V). Serial dilutions of HBC34-V35, HBC34-V35-MLNS, HBC34-V35-MLNS-GAALIE, anti-HBV mAb 17.1.41, and a control mAb were added to the HBsAg-secreting hepatoma cell line PLC/PRF/5 (also referred to as Alexander cells). PLC/PRF/5 cells were incubated together with antibodies at room temperature for 10 min. NK cells were added to assay plates (effector cells to target cells ratio of 10:1) and incubated at 37 °C for 4 hours. Cell death was determined by measuring lactate dehydrogenase (LDH) release. (B) Staining of PLC/PRF/5 human hepatoma cells by HBC34-V35 and 17.1.41 mAbs as assessed by flow cytometry. Cells were extensively

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washed, fixed with formaldehyde (4%) or fixed and permeabilized (saponin 0.5%) before staining with different concentrations of HBC34-V35 and 17.1.41 mAbs. Binding of these human (in the case of HBC34-V35, engineered human) mAbs was detected by flow-cytometry using an Alexa Fluor® 647 AffiniPure F(ab')₂ Fragment
5 Goat Anti-Human IgG, Fcγ Fragment Specific antibody.

Figures 15A and 15B show *in vitro* activation of primary human NK cells in the presence of HBC34-V35-MLNS and HBC34-V35-MLNS-GAALIE and HBsAg. Activation of NK cells was tested using freshly isolated cells from two donors
10 previously genotyped for expressing (A) homozygous high (V158) or (B) low (F158) affinity FcγRIIIa. Serial dilutions of HBC34-V35, HBC34-V35-MLNS-GAALIE, and HBC34v35-LALA mAbs were incubated with NK cells for 4 hours. Activation of NK cells was measured by flow cytometry by staining NK cells with anti-CD107a mAb, as a functional marker for the identification of NK cell activity.
15 CD107a, also known as LAMP-1, is a marker for degranulation of NK cells.

Figure 16 shows results from *in vitro* drug interaction studies between HBC34-V35-MLNS-GAALIE and polymerase/reverse transcriptase inhibitor Entecavir (ETV).

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DETAILED DESCRIPTION

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art.

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Throughout this disclosure, unless the context requires otherwise, the term "comprise," and variations thereof, such as "comprises," and "comprising," is used synonymously with, *e.g.* "having," "has," "including," "includes," or the like, and will be understood to imply the inclusion of a stated member, ratio, integer (including, where appropriate, a
30 fraction thereof, *e.g.*, one tenth and one hundredth of an integer), concentration, or step but not the exclusion of any other non-stated member, ratio, integer, concentration, or step. Any concentration range, percentage range, ratio range, or integer range is to be

understood to include the value of any integer within the recited range and, when appropriate, fractions thereof (such as one tenth and one hundredth of an integer), unless otherwise indicated. Also, any number range recited herein relating to any physical feature, such as polymer subunits, size or thickness, are to be understood to include any integer within the recited range, unless otherwise indicated. The term "consists of" refers to an embodiment of the term "comprise," wherein any other non-stated member, integer or step is excluded. In the context of the present disclosure, the term "comprise" encompasses the term "consist of". The term "consisting essentially of" is not equivalent to "comprising" and refers to the specified materials or steps of a claim, or to those that do not materially affect the basic characteristics of a claimed subject matter.

In addition, it should be understood that the individual compounds, or groups of compounds, derived from the various combinations of the structures and substituents described herein, are disclosed by the present application to the same extent as if each compound or group of compounds was set forth individually. Thus, selection of particular structures or particular substituents is within the scope of the present disclosure.

The terms "a" and "an" and "the" and similar reference used in the context of describing the disclosure (including in the context of the claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. The use of the alternative (*e.g.*, "or") should be understood to mean either one, both, or any combination of the alternatives. Recitation of ranges of values herein is intended to serve as a shorthand method of referring individually to each separate value falling within the range. Unless otherwise indicated herein, each individual value is incorporated into the disclosure as if it were individually recited herein. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the subject matter disclosed herein.

The word "substantially" does not exclude "completely"; *e.g.*, a composition which is "substantially free" from Y may be completely free from Y. In certain embodiments, "substantially" refers to a given amount, effect, or activity of a composition, method, or

use of the present disclosure as compared to that of a reference composition, method, or use, and describes a reduction in the amount, effect, or activity of no more than 50%, such as no more than 40%, 30%, 25%, 20%, 15%, 10%, 5%, or 1%, or less, of the amount, effect, or activity of the reference composition, method, or use.

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As used herein, the term "about" means $\pm$ 20% of the indicated range, value, or structure, unless otherwise indicated.

"Optional" or "optionally" means that the subsequently described element, component, event, or circumstance may or may not occur, and that the description includes instances in which the element, component, event, or circumstance occurs and instances in which they do not.

The term "disease" as used herein is intended to be generally synonymous, and is used interchangeably with, the terms "disorder" and "condition" (as in medical condition), in that all reflect an abnormal condition of the human or animal body or of one of its parts that impairs normal functioning, is typically manifested by distinguishing signs and symptoms, and causes the affected human or animal to have a reduced duration or quality of life.

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As used herein, reference to "treatment" of a subject or patient is intended to include prevention, prophylaxis, attenuation, amelioration and therapy. Benefits of treatment include improved clinical outcome; lessening or alleviation of symptoms associated with a disease; decreased occurrence of symptoms; improved quality of life; longer disease-free status; diminishment of extent of disease; stabilization of disease state; delay of disease progression; remission; survival; prolonged survival; or any combination thereof. The terms "subject" or "patient" are used interchangeably herein to mean all mammals, including humans. Examples of subjects include humans, cows, dogs, cats, horses, goats, sheep, pigs, and rabbits. In one embodiment, the patient is a human.

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As used herein, "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, *e.g.*,
5 hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, *i.e.*, an α -carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, *e.g.*, homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (*e.g.*, norleucine) or modified
10 peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function in a manner similar to a naturally occurring amino acid.

15 As used herein, the terms "peptide," "polypeptide," and "protein," and variations of these terms, refer to a molecule that comprises at least two amino acids joined to each other by a (normal or modified) peptide bond. For example, a peptide, polypeptide or protein may comprise or be composed of a plurality of amino acids selected from the 20 amino acids defined by the genetic code or an amino acid analog or mimetic, each being
20 linked to at least one other by a peptide bond. A peptide, polypeptide or protein can comprise or be composed of L-amino acids and/or D-amino acids (or analogs or mimetics thereof). The terms "peptide", "polypeptide," "protein" also include "peptidomimetics" which are defined as peptide analogs containing non-peptidic structural elements, which peptides are capable of mimicking or antagonizing the
25 biological action(s) of a natural parent peptide. In certain embodiments, a peptidomimetic lacks characteristics such as enzymatically scissile peptide bonds.

A peptide, polypeptide or protein may comprise amino acids other than the 20 amino acids defined by the genetic code in addition to these amino acids, or it can be
30 composed of amino acids other than the 20 amino acids defined by the genetic code. In certain embodiments, a peptide, polypeptide or protein in the context of the present disclosure can comprise amino acids that are modified by natural processes, such as

post-translational maturation processes, or by chemical processes (*e.g.*, synthetic processes), which are known in the art and include those described herein. Such modifications can appear anywhere in the polypeptide; *e.g.*, in the peptide skeleton; in the amino acid chain; or at the carboxy- or amino-terminal ends. A peptide or polypeptide can be branched, such as following an ubiquitination, or may be cyclic, with or without branching. The terms "peptide", "polypeptide", and "protein" also include modified peptides, polypeptides and proteins. For example, peptide, polypeptide or protein modifications can include acetylation, acylation, ADP-ribosylation, amidation, covalent fixation of a nucleotide or of a nucleotide derivative, covalent fixation of a lipid or of a lipidic derivative, the covalent fixation of a phosphatidylinositol, covalent or non-covalent cross-linking, cyclization, disulfide bond formation, demethylation, glycosylation including pegylation, hydroxylation, iodization, methylation, myristoylation, oxidation, proteolytic processes, phosphorylation, prenylation, racemization, seneloylation, sulfatation, amino acid addition such as arginylation or ubiquitination. Such modifications have been described in the literature (*see* Proteins Structure and Molecular Properties (1993) 2nd Ed., T. E. Creighton, New York; Post-translational Covalent Modifications of Proteins (1983) B. C. Johnson, Ed., Academic Press, New York; Seifter et al. (1990) Analysis for protein modifications and nonprotein cofactors, Meth. Enzymol. 182: 626-646 and Rattan et al., (1992) Protein Synthesis: Post-translational Modifications and Aging, Ann NY Acad Sci, 663: 48-62). Accordingly, the terms "peptide", "polypeptide", "protein" can include for example lipopeptides, lipoproteins, glycopeptides, glycoproteins and the like. Variants of proteins, peptides, and polypeptides of this disclosure are also contemplated. In certain embodiments, variant proteins, peptides, and polypeptides comprise or consist of an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 99.9% identical to an amino acid sequence of a defined or reference amino acid sequence as described herein.

As used herein, "(poly)peptide" and "protein" may be used interchangeably in reference to a polymer of amino acid residues, such as a plurality of amino acid monomers linked by peptide bonds.

- "Nucleic acid molecule" or "polynucleotide" or "nucleic acid" refers to a polymeric compound including covalently linked nucleotides, which can be made up of natural subunits (*e.g.*, purine or pyrimidine bases) or non-natural subunits (*e.g.*, morpholine ring). Purine bases include adenine, guanine, hypoxanthine, and xanthine, and pyrimidine bases include uracil, thymine, and cytosine. Nucleic acid monomers can be linked by phosphodiester bonds or analogs of such linkages. Analogs of phosphodiester linkages include phosphorothioate, phosphorodithioate, phosphoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phosphoranilidate, phosphoramidate, or the like.
- 5
- 10 Nucleic acid molecules include polyribonucleic acid (RNA), polydeoxyribonucleic acid (DNA), which includes cDNA, genomic DNA, and synthetic DNA, any of which may be single or double-stranded. If single-stranded, the nucleic acid molecule may be the coding strand or non-coding (anti-sense strand). Polynucleotides (including oligonucleotides), and fragments thereof may be generated, for example, by polymerase
- 15 chain reaction (PCR) or by *in vitro* translation, or generated by any of ligation, scission, endonuclease action, or exonuclease action.

A nucleic acid molecule encoding an amino acid sequence includes all nucleotide sequences that encode the same amino acid sequence. Some versions of the nucleotide sequences may also include intron(s) to the extent that the intron(s) may be removed through co- or post-transcriptional mechanisms. Different nucleotide sequences may encode the same amino acid sequence as the result of the redundancy or degeneracy of the genetic code, or by splicing, or both.

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Variants of nucleic acid molecules of this disclosure are also contemplated. Variant nucleic acid molecules are at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.9% identical a nucleic acid molecule of a defined or reference polynucleotide as described herein, or that hybridize to a polynucleotide under stringent hybridization conditions of 0.015M sodium chloride, 0.0015M sodium citrate at about 65-68°C or 0.015M sodium chloride, 0.0015M sodium citrate, and 50% formamide at about 42°C. Nucleic acid molecule variants retain the capacity to encode a fusion

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protein or a binding domain thereof having a functionality described herein, such as specifically binding a target molecule.

As used herein, the term "sequence variant" refers to any sequence having one or more alterations in comparison to a reference sequence, whereby a reference sequence is any published sequence and/or of the sequences listed in the "Table of Sequences and SEQ ID Numbers" (sequence listing), *i.e.* SEQ ID NO: 1 to SEQ ID NO: 139. Thus, the term "sequence variant" includes nucleotide sequence variants and amino acid sequence variants. In certain embodiments, a sequence variant in the context of a nucleotide sequence, the reference sequence is also a nucleotide sequence, whereas in certain embodiments for a sequence variant in the context of an amino acid sequence, the reference sequence is also an amino acid sequence. A "sequence variant" as used herein can be at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the reference sequence.

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"Percent sequence identity" refers to a relationship between two or more sequences, as determined by comparing the sequences. Methods to determine sequence identity can be designed to give the best match between the sequences being compared. For example, the sequences may be aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment). Further, non-homologous sequences may be disregarded for comparison purposes. The percent sequence identity referenced herein is calculated over the length of the reference sequence, unless indicated otherwise. Methods to determine sequence identity and similarity can be found in publicly available computer programs. Sequence alignments and percent identity calculations may be performed using a BLAST program (*e.g.*, BLAST 2.0, BLASTP, BLASTN, or BLASTX). The mathematical algorithm used in the BLAST programs can be found in Altschul et al., Nucleic Acids Res. 25:3389-3402, 1997. Within the context of this disclosure, it will be understood that where sequence analysis software is used for analysis, the results of the analysis are based on the "default values" of the program

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referenced. "Default values" mean any set of values or parameters which originally load with the software when first initialized.

A "sequence variant" in the context of a nucleic acid (nucleotide) sequence has an altered sequence in which one or more of the nucleotides in the reference sequence is deleted, or substituted, or one or more nucleotides are inserted into the sequence of the reference nucleotide sequence. Nucleotides are referred to herein by the standard one-letter designation (A, C, G, or T). Due to the degeneracy of the genetic code, a "sequence variant" of a nucleotide sequence can either result in a change in the respective reference amino acid sequence, *i.e.* in an amino acid "sequence variant" or not. In certain embodiments, a nucleotide sequence variant does not result in an amino acid sequence variant (*e.g.*, a silent mutation). In some embodiments, a nucleotide sequence variant that results in one or more "non-silent" mutation is contemplated. In some embodiments, a nucleotide sequence variant of the present disclosure encodes an amino acid sequence that is at least 80%, at least 85 %, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a reference amino acid sequence. Nucleotide and amino sequences as disclosed herein refer also to codon-optimized versions of a reference or wild-type nucleotide or amino acid sequence. In any of the embodiments described herein, a polynucleotide of the present disclosure may be codon-optimized for a host cell containing the polynucleotide (*see, e.g.* Scholten et al., Clin. Immunol. 119:135-145 (2006). Codon optimization can be performed using known techniques and tools, *e.g.*, using the GenScript® OptimumGene™ tool, or the GeneArt Gene Synthesis Tool (Thermo Fisher Scientific). Codon-optimized sequences include sequences that are partially codon-optimized (*i.e.*, at least one codon is optimized for expression in the host cell) and those that are fully codon-optimized.

A "sequence variant" in the context of an amino acid sequence has an altered sequence in which one or more of the amino acids is deleted, substituted, or inserted in comparison to a reference amino acid sequence. As a result of the alterations, such a sequence variant has an amino acid sequence which is at least 80%, at least 85 %, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least

96%, at least 97%, at least 98%, or at least 99% identical to the reference amino acid sequence. For example, per 100 amino acids of the reference sequence a variant sequence that has no more than 10 alterations, *i.e.* any combination of deletions, insertions or substitutions, is "at least 90% identical" to the reference sequence.

5

A "conservative substitution" refers to amino acid substitutions that do not significantly affect or alter binding characteristics of a particular protein. Generally, conservative substitutions are ones in which a substituted amino acid residue is replaced with an amino acid residue having a similar side chain. Conservative substitutions include a
10 substitution found in one of the following groups: Group 1: Alanine (Ala or A), Glycine (Gly or G), Serine (Ser or S), Threonine (Thr or T); Group 2: Aspartic acid (Asp or D), Glutamic acid (Glu or Z); Group 3: Asparagine (Asn or N), Glutamine (Gln or Q); Group 4: Arginine (Arg or R), Lysine (Lys or K), Histidine (His or H); Group 5: Isoleucine (Ile or I), Leucine (Leu or L), Methionine (Met or M), Valine (Val or V); and
15 Group 6: Phenylalanine (Phe or F), Tyrosine (Tyr or Y), Tryptophan (Trp or W). Additionally or alternatively, amino acids can be grouped into conservative substitution groups by similar function, chemical structure, or composition (*e.g.*, acidic, basic, aliphatic, aromatic, or sulfur-containing). For example, an aliphatic grouping may include, for purposes of substitution, Gly, Ala, Val, Leu, and Ile. Other conservative
20 substitutions groups include: sulfur-containing: Met and Cysteine (Cys or C); acidic: Asp, Glu, Asn, and Gln; small aliphatic, nonpolar or slightly polar residues: Ala, Ser, Thr, Pro, and Gly; polar, negatively charged residues and their amides: Asp, Asn, Glu, and Gln; polar, positively charged residues: His, Arg, and Lys; large aliphatic, nonpolar residues: Met, Leu, Ile, Val, and Cys; and large aromatic residues: Phe, Tyr, and Trp.
25 Additional information can be found in Creighton (1984) Proteins, W.H. Freeman and Company.

Amino acid sequence insertions can include amino- and/or carboxyl-terminal fusions ranging in length from one residue to polypeptides containing a hundred or more
30 residues, as well as intrasequence insertions of single or multiple amino acid residues. Examples of terminal insertions include the fusion to the N- or C-terminus of an amino acid sequence to a reporter molecule or an enzyme.

In general, alterations in the sequence variants do not abolish or significantly reduce a desired functionality of the respective reference sequence. For example, it is preferred that a variant sequence of the present disclosure does not significantly reduce or completely abrogate the functionality of a sequence of an antibody, or antigen binding fragment thereof, to bind to the same epitope and/or to sufficiently neutralize infection of HBV and HDV as compared to antibody or antigen binding fragment having (or encoded by) the reference sequence. Guidance in determining which nucleotides and amino acid residues, respectively, may be substituted, inserted or deleted without abolishing a desired structure or functionality can be found by using, e.g., known computer programs.

As used herein, a nucleic acid sequence or an amino acid sequence "derived from" a designated nucleic acid, peptide, polypeptide or protein refers to the origin of the nucleic acid, peptide, polypeptide or protein. A nucleic acid sequence or amino acid sequence which is derived from a particular sequence may have an amino acid sequence that is essentially identical to that sequence or a portion thereof, from which it is derived, whereby "essentially identical" includes sequence variants as defined above. A nucleic acid sequence or amino acid sequence which is derived from a particular peptide or protein, may be derived from the corresponding domain in the particular peptide or protein. In this context, "corresponding" refers to possession of a same functionality or characteristic of interest. For example, an "extracellular domain" corresponds to another "extracellular domain" (of another protein), or a "transmembrane domain" corresponds to another "transmembrane domain" (of another protein). "Corresponding" parts of peptides, proteins and nucleic acids are thus easily identifiable to one of ordinary skill in the art. Likewise, a sequence "derived from" another (*e.g.*, "source") sequence can be identified by one of ordinary skill in the art as having its origin in the source sequence.

A nucleic acid sequence or an amino acid sequence derived from another nucleic acid, peptide, polypeptide or protein may be identical to the starting nucleic acid, peptide, polypeptide or protein (from which it is derived). However, a nucleic acid sequence or

an amino acid sequence derived from another nucleic acid, peptide, polypeptide or protein may also have one or more mutations relative to the starting nucleic acid, peptide, polypeptide or protein (from which it is derived), in particular a nucleic acid sequence or an amino acid sequence derived from another nucleic acid, peptide, polypeptide or protein may be a functional sequence variant as described above of the starting nucleic acid, peptide, polypeptide or protein (from which it is derived). For example, in a peptide/protein, one or more amino acid residues may be substituted with other amino acid residues, or one or more amino acid residue insertions or deletions may occur.

10

As used herein, the term "mutation" relates to a change in a nucleic acid sequence and/or in an amino acid sequence in comparison to a reference sequence, *e.g.* a corresponding genomic, wild type, or reference sequence. A mutation, *e.g.* in comparison to a reference genomic sequence, may be, for example, a (naturally occurring) somatic mutation, a spontaneous mutation, an induced mutation, *e.g.* induced by enzymes, chemicals or radiation, or a mutation obtained by site-directed mutagenesis (molecular biology methods for making specific and intentional changes in the nucleic acid sequence and/or in the amino acid sequence). Thus, the terms "mutation" or "mutating" shall be understood to also include physically making or inducing a mutation, *e.g.* in a nucleic acid sequence or in an amino acid sequence. A mutation includes substitution, deletion and insertion of one or more nucleotides or amino acids as well as inversion of several successive nucleotides or amino acids. To achieve a mutation in an amino acid sequence, a mutation may be introduced into the nucleotide sequence encoding said amino acid sequence in order to express a (recombinant) mutated polypeptide. A mutation may be achieved, for example, by altering (*e.g.*, by site-directed mutagenesis) a codon (*e.g.*, by alternating one, two, or three nucleotide bases therein) of a nucleic acid molecule encoding one amino acid to provide a codon that encodes a different amino acid, or that encodes a same amino acid, or by synthesizing a sequence variant.

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The term "introduced" in the context of inserting a nucleic acid molecule into a cell, means "transfection", or "transformation" or "transduction" and includes reference to

the incorporation of a nucleic acid molecule into a eukaryotic or prokaryotic cell wherein the nucleic acid molecule may be incorporated into the genome of a cell (*e.g.*, chromosome, plasmid, plastid, or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (*e.g.*, transfected mRNA).

5

The term "recombinant", as used herein (*e.g.* a recombinant antibody, a recombinant protein, a recombinant nucleic acid, or the like, refers to any molecule (antibody, protein, nucleic acid, or the like) which is prepared, expressed, created or isolated by recombinant means, and which is not naturally occurring. "Recombinant" can be used
10 synonymously with "engineered" or "non-natural" and can refer to to an organism, microorganism, cell, nucleic acid molecule, or vector that includes at least one genetic alteration or has been modified by introduction of an exogenous nucleic acid molecule, wherein such alterations or modifications are introduced by genetic engineering (*i.e.*, human intervention). Genetic alterations include, for example, modifications
15 introducing expressible nucleic acid molecules encoding proteins, fusion proteins or enzymes, or other nucleic acid molecule additions, deletions, substitutions or other functional disruption of a cell's genetic material. Additional modifications include, for example, non-coding regulatory regions in which the modifications alter expression of a polynucleotide, gene or operon.

20 As used herein, "heterologous" or "non-endogenous" or "exogenous" refers to any gene, protein, compound, nucleic acid molecule, or activity that is not native to a host cell or a subject, or any gene, protein, compound, nucleic acid molecule, or activity native to a host cell or a subject that has been altered. Heterologous, non-endogenous, or exogenous includes genes, proteins, compounds, or nucleic acid molecules that have
25 been mutated or otherwise altered such that the structure, activity, or both is different as between the native and altered genes, proteins, compounds, or nucleic acid molecules. In certain embodiments, heterologous, non-endogenous, or exogenous genes, proteins, or nucleic acid molecules may not be endogenous to a host cell or a subject, but instead nucleic acids encoding such genes, proteins, or nucleic acid molecules may have been
30 added to a host cell by conjugation, transformation, transfection, electroporation, or the like, wherein the added nucleic acid molecule may integrate into a host cell genome or

can exist as extra-chromosomal genetic material (*e.g.*, as a plasmid or other self-replicating vector). The term "homologous" or "homolog" refers to a gene, protein, compound, nucleic acid molecule, or activity found in or derived from a host cell, species, or strain. For example, a heterologous or exogenous polynucleotide or gene
5 encoding a polypeptide may be homologous to a native polynucleotide or gene and encode a homologous polypeptide or activity, but the polynucleotide or polypeptide may have an altered structure, sequence, expression level, or any combination thereof. A non-endogenous polynucleotide or gene, as well as the encoded polypeptide or activity, may be from the same species, a different species, or a combination thereof.

10 As used herein, the term "endogenous" or "native" refers to a polynucleotide, gene, protein, compound, molecule, or activity that is normally present in a host cell or a subject.

As used herein, the terms "cell," "cell line," and "cell culture" are used interchangeably
15 and all such designations include progeny. Thus, the words "transformants" and "transformed cells" include the primary subject cell and cultures derived therefrom without regard for the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. Variant progeny that have the same or substantially the same function, phenotype, or
20 biological activity as screened for in the originally transformed cell are included. Where distinct designations are intended, it will be clear from the context.

The present disclosure provides, in part, on antibodies, antigen binding fragments, and
25 fusion proteins that are capable of neutralizing hepatitis B and hepatitis delta viruses. Embodiments of the antibodies, antigen binding fragments, and fusion proteins according to the present description may be used in methods of preventing, treating, or attenuating, or diagnosing HBV and HDV. In particular embodiments, the antibodies, antigen binding fragments, and fusion proteins described herein bind to two or more
30 different genotypes of hepatitis B virus surface antigen and to two or more different infectious mutants of hepatitis B virus surface antigen. In specific embodiments, the

antibodies, antigen binding fragments, and fusion proteins described herein bind to all known genotypes of hepatitis B virus surface antigen and to all known infectious mutants of hepatitis B virus surface antigen.

5 Antibodies and antigen-binding fragments

In one aspect, the present disclosure provides an isolated antibody, or an antigen binding fragment thereof, that is capable of binding to the antigenic loop region of HBsAg and is capable of neutralizing infection with hepatitis B virus and hepatitis delta
10 virus.

As used herein, and unless the context clearly indicates otherwise, "antibody" refers to an intact antibody comprising at least two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds (though it will be understood that heavy chain
15 antibodies, which lack light chains, are still encompassed by the term "antibody"), as well as any antigen-binding portion or fragment of an intact antibody that has or retains the ability to bind to the antigen target molecule recognized by the intact antibody, such as, for example, a scFv, Fab, or F(ab')₂ fragment. Thus, the term "antibody" herein is used in the broadest sense and includes polyclonal and monoclonal antibodies,
20 including intact antibodies and functional (antigen-binding) antibody fragments thereof, including fragment antigen-binding (Fab) fragments, F(ab')₂ fragments, Fab' fragments, Fv fragments, recombinant IgG (rIgG) fragments, single chain antibody fragments, including single chain variable fragments (scFv), and single domain antibodies (*e.g.*, sdAb, sdFv, nanobody) fragments. The term encompasses genetically engineered
25 and/or otherwise modified forms of immunoglobulins, such as intrabodies, peptibodies, chimeric antibodies, fully human antibodies, humanized antibodies, and heteroconjugate antibodies, multispecific, *e.g.*, bispecific, antibodies, diabodies, triabodies, and tetrabodies, tandem di-scFv, tandem tri-scFv. Unless otherwise stated, the term "antibody" should be understood to encompass functional antibody fragments
30 thereof. The term also encompasses intact or full-length antibodies, including antibodies of any class or sub-class thereof, including IgG and sub-classes thereof, IgM, IgE, IgA, and IgD.

As used herein, the terms "antigen binding fragment," "fragment, " and "antibody fragment" are used interchangeably to refer to any fragment of an antibody of the disclosure that retains the antigen-binding activity of the antibody. Examples of
5 antibody fragments include, but are not limited to, a single chain antibody, Fab, Fab', F(ab')₂, Fv or scFv.

Human antibodies are known (e.g., van Dijk, M. A., and van de Winkel, J. G., *Curr. Opin. Chem. Biol.* 5 (2001) 368-374). Human antibodies can be produced in transgenic
10 animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire or a selection of human antibodies in the absence of endogenous immunoglobulin production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge (see, e.g., Jakobovits, A., et al., *Proc. Natl. Acad. Sci. USA* 90 (1993) 2551-
15 2555; Jakobovits, A., et al., *Nature* 362 (1993) 255-258; Bruggemann, M., et al., *Year Immunol.* 7 (1993) 3340). Human antibodies can also be produced in phage display libraries (Hoogenboom, H. R., and Winter, G., *J. Mol. Biol.* 227 (1992) 381-388; Marks, J. D., et al., *J. Mol. Biol.* 222 (1991) 581-597). The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal
20 antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985); and Boerner, P., et al., *J. Immunol.* 147 (1991) 86-95). Human monoclonal antibodies may be prepared by using improved EBV-B cell immortalization as described in Traggiai E, Becker S, Subbarao K, Kolesnikova L, Uematsu Y, Gismondo MR, Murphy BR, Rappuoli R, Lanzavecchia A. (2004): An efficient method to make
25 human monoclonal antibodies from memory B cells: potent neutralization of SARS coronavirus. *Nat Med.* 10(8):871-5. The term "human antibody" as used herein also comprises such antibodies which are modified, e.g., in the variable region, to generate properties according to the antibodies and antibody fragments of the present disclosure.

30 As used herein, the term "variable region" (variable region of a light chain (V_L), variable region of a heavy chain (V_H)) denotes each variable region polypeptide of the

pair of light and heavy chains which, in most instances, is involved directly in binding the antibody to the antigen.

Antibodies according to the present disclosure can be of any isotype (*e.g.*, IgA, IgG, IgM, IgE, IgD; *i.e.*, comprising a α , γ , μ , ϵ , or δ heavy chain). Within the IgG isotype, for example, antibodies may be IgG1, IgG2, IgG3 or IgG4 subclass. In specific embodiments, an antibody of the present disclosure is an IgG1 antibody. Antibodies or antigen binding fragments provided herein may include a κ or a λ light chain. In certain embodiments, HBsAg-specific antibodies described herein are of the IgG isotype and may block the release of HBV and HBsAg from infected cells. Accordingly, in certain embodiments, an antibody according to the present description can bind intracellularly and thereby block the release of HBV virions and HBsAg.

The terms "VL" and "VH" refer to the variable binding region from an antibody light and heavy chain, respectively. The variable binding regions are made up of discrete, well-defined sub-regions known as "complementarity determining regions" (CDRs) and "framework regions" (FRs). The terms "complementarity determining region" and "CDR" are synonymous with "hypervariable region" or "HVR," and are known in the art to refer to sequences of amino acids within TCR or antibody variable regions, which confer antigen specificity and/or binding affinity and are separated by framework sequence. In general, there are three CDRs in each variable region of an immunoglobulin binding protein; *e.g.*, for antibodies, the VH and VL regions comprise six CDRs HCDR1, HCDR2, HCDR3; LCDR1, LCDR2, LCDR3; also referred to herein as CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3, respectively). As used herein, a "variant" of a CDR refers to a functional variant of a CDR sequence having up to 1-3 amino acid substitutions, deletions, or combinations thereof.

Immunoglobulin sequences can be aligned to a numbering scheme (*e.g.*, Kabat, EU, International Immunogenetics Information System (IMGT) and Aho), which can allow equivalent residue positions to be annotated and for different molecules to be compared using Antigen receptor Numbering And Receptor Classification (ANARCI) software tool (2016, Bioinformatics 15:298-300). It will be understood that in certain

embodiments, an antibody or antigen binding fragment of the present disclosure can comprise all or part of a heavy chain (HC), a light chain (LC), or both. For example, a full-length intact IgG antibody monomer typically includes a VH, a CH1, a CH2, a CH3, a VL, and a CL. Fc components are described further herein. In certain

5 embodiments, an antibody or antigen binding fragment of the present disclosure comprises a CDRH1, a CDRH2, a CDRH3, a CDRL1, a CDRL2, and a CDRL3 according to any one of the presently disclosed VH and VL sequences, respectively.

Table 1 shows the amino acid sequences of heavy chain variable regions (VH), light chain variable regions (VL), CDRs, heavy chains (HC), and light chains (LC) of certain

10 exemplary antibodies according to the present disclosure.

Antibody sequence description	SEQ ID NO:	Amino acid sequence
HBC34-V35 VH; HBC34-V34 VH; HBC23-LC40A VH; HBC23-LC40S VH; HBC34-LC40A VH; HBC34-LC40S VH	41	ELQLVESGGGWVQPGGSQRLSCAAS GRIFRSFYMSWVRQAPGKGLEWVATI NQDGSEKLYVDSVKGRFTISRDNACKN SLFLQMNNLRVEDTAVYYCAAWSGN SGGMDVWGQGTTVSVSS
HBC34v31_LC40A VH HBC34v31_LC40S VH HBC34v32_LC40A VH HBC34v32_LC40S VH HBC34v33_LC40A VH HBC34v32_LC40S VH	67	EVQLVESGGGLVQPGGSLRLSCAASG RIFRSFYMSWVRQAPGKGLEWVANIN QDGSEKLYVDSVKGRFTISRDNACKNS LFLQMNNLRVEDTAVYYCAAWSGNS GGMDVWGQGTTVTVSS
HBC34-V35 VL	89	SYELTQPPSVSVSPGQTVSIPCSGDKL GNKNVAWFQHKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEAAYFCQTFDSTTVVFGGGTRLTV L
HBC34-V34 VL	90	SYELTQPPSVSVSPGQTVSIPCSGDKL

Antibody sequence description	SEQ ID NO:	Amino acid sequence
		GNKNVSWFQHKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEAAYFCQTFDSTTVVFGGGTRLTV L
HBC34-V23-VL_C40S	110	SYELTQPPSVSVSPGQTASITCSGDKL GNKNASWYQQKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEADYYCQTFDSTTVVFGGGTKLT VL
HBC34-V23-VL_C40A	111	SYELTQPPSVSVSPGQTASITCSGDKL GNKNAAWYQQKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEADYYCQTFDSTTVVFGGGTKLT VL
HBC34-V31-VL_C40S	112	SYELTQPPSVSVSPGQTVSIPCSGDKL GNKNVSWFQHKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEAAYFCQTDSTTVVFGGGTRLT VL
HBC34-V31-VL_C40A	113	SYELTQPPSVSVSPGQTVSIPCSGDKL GNKNVAWFQHKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEAAYFCQTDSTTVVFGGGTRLT VL
HBC34-V32-VL_C40S	114	SYELTQPPSVSVSPGQTVSIPCSGDKL GNKNVSWFQHKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEAAYFCQTFDSTTVVFGGGTRLTV L
HBC34-V32-VL_C40A	115	SYELTQPPSVSVSPGQTVSIPCSGDKL

Antibody sequence description	SEQ ID NO:	Amino acid sequence
		GNKNVAWFQHKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEAAYFCQTFDSTTVVFGGGTRLTV L
HBC34-V33-VL_C40S	116	SYELTQPPSVSVSPGQTASITCSGDKL GNKNASWYQQKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEADYYCQTFDSTTVVFGGGTKLTVL
HBC34-V33-VL_C40A	117	SYELTQPPSVSVSPGQTASITCSGDKL GNKNAAWYQQKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEADYYCQTFDSTTVVFGGGTKLTVL
HBC34-VL_C40S	118	SYELTQPPSVSVSPGQTVSIPCSGDKL GNKNVSWFQHKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEAAYFCQTDSTTVVFGGGTRLTVL
HBC34-VL_C40A	119	SYELTQPPSVSVSPGQTVSIPCSGDKL GNKNVAWFQHKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEAAYFCQTDSTTVVFGGGTRLTVL
HBC34-V35 CDRH1; HBC34-V34 CDRH1; HBC34-V23_LC40S CDRH1; HBC34-V23_LC40A CDRH1; HBC34-V31_LC40S CDRH1; HBC34-V31_LC40A CDRH1;	34	GRIFRSFY

Antibody sequence description	SEQ ID NO:	Amino acid sequence
HBC34-V32_LC40S CDRH1; HBC34-V32_LC40A CDRH1; HBC34-V33_LC40S CDRH1; HBC34-V33_LC40A CDRH1; HBC34_LC40S CDRH1; HBC34_LC40A CDRH1		
HBC34-V35 CDRH2; HBC34-V34 CDRH2; HBC34-V23_LC40S CDRH2; HBC34-V23_LC40A CDRH2; HBC34-V31_LC40S CDRH2; HBC34-V31_LC40A CDRH2; HBC34-V32_LC40S CDRH2; HBC34-V32_LC40A CDRH2; HBC34-V33_LC40S CDRH2; HBC34-V33_LC40A CDRH2; HBC34_LC40S CDRH2; HBC34_LC40A CDRH2 (short CDRH2)	35	NQDGSEK
HBC34-V35 CDRH2; HBC34-V34 CDRH2; HBC34-V23_LC40S CDRH2; HBC34-V23_LC40A CDRH2; HBC34-V31_LC40S CDRH2; HBC34-V31_LC40A CDRH2; HBC34-V32_LC40S CDRH2; HBC34-V32_LC40A CDRH2; HBC34-V33_LC40S CDRH2; HBC34-V33_LC40A CDRH2; HBC34_LC40S CDRH2;	66	INQDGSEK

Antibody sequence description	SEQ ID NO:	Amino acid sequence
HBC34_LC40A CDRH2 (long CDRH2)		
HBC34-V35 CDRH3; HBC34-V34 CDRH3; HBC34-V23_LC40S CDRH3; HBC34-V23_LC40A CDRH3; HBC34-V31_LC40S CDRH3; HBC34-V31_LC40A CDRH3; HBC34-V32_LC40S CDRH3; HBC34-V32_LC40A CDRH3; HBC34-V33_LC40S CDRH3; HBC34-V33_LC40A CDRH3; HBC34_LC40S CDRH3; HBC34_LC40A CDRH3	36	AAWSGNSGGMDV
HBC34-V35 CDRL1; HBC34-V34 CDRL1; HBC34-V23_LC40S CDRL1; HBC34-V23_LC40A CDRL1; HBC34-V31_LC40S CDRL1; HBC34-V31_LC40A CDRL1; HBC34-V32_LC40S CDRL1; HBC34-V32_LC40A CDRL1; HBC34-V33_LC40S CDRL1; HBC34-V33_LC40A CDRL1; HBC34_LC40S CDRL1; HBC34_LC40A CDRL1	37	KLGNKN
HBC34-V35 CDRL2; HBC34-V34 CDRL2; HBC34-V23_LC40S CDRL2; HBC34-V23_LC40A CDRL2;	38	EVK

Antibody sequence description	SEQ ID NO:	Amino acid sequence
HBC34-V31_LC40S CDRL2; HBC34-V31_LC40A CDRL2; HBC34-V32_LC40S CDRL2; HBC34-V32_LC40A CDRL2; HBC34-V33_LC40S CDRL2; HBC34-V33_LC40A CDRL2; HBC34_LC40S CDRL2; HBC34_LC40A CDRL2 (short CDRL2)		
HBC34-V35 CDRL2; HBC34-V34 CDRL2; HBC34-V23_LC40S CDRL2; HBC34-V23_LC40A CDRL2; HBC34-V31_LC40S CDRL2; HBC34-V31_LC40A CDRL2; HBC34-V32_LC40S CDRL2; HBC34-V32_LC40A CDRL2; HBC34-V33_LC40S CDRL2; HBC34-V33_LC40A CDRL2; HBC34_LC40S CDRL2; HBC34_LC40A CDRL2 (long LCDRL2)	39	VIYEVKYRP
HBC34-V35 CDRL3; HBC34-V34 CDRL3; HBC34-V23_LC40S CDRL3; HBC34-V23_LC40A CDRL3; HBC34-V32_LC40S CDRL3; HBC34-V32_LC40A CDRL3; HBC34-V33_LC40S CDRL3; HBC34-V33_LC40A CDRL3;	58	QTFDSTTVV

Antibody sequence description	SEQ ID NO:	Amino acid sequence
HBC34_LC40S CDRL3; HBC34_LC40A CDRL3; HBC34-V31_LC40S CDRL3; HBC34-V31_LC40A CDRL3;	40	QTWDSTTVV
HC of HBC34-V35-MLNS-GAALIE and HBC34-V34-MLNS-GAALIE (g1M17, 1)	91	ELQLVESGGGWVQPGGSQRLSCAAS GRIFRSFYMSWVRQAPGKGLEWVATI NQDGSEKLYVDSVKGRFTISRDNACKN SLFLQMNNLRVEDTAVYYCAAWSGN SGGMDVWGQGTTVSVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPA PELLAGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPLPEEKTI SKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSGDSFFLYSKLTVDK SRWQQGNVFSCSVLHEALHSHYTQKS LSLSPGK
HC of HBC34-V35-MLNS and HBC34-V34-MLNS	92	ELQLVESGGGWVQPGGSQRLSCAAS GRIFRSFYMSWVRQAPGKGLEWVATI NQDGSEKLYVDSVKGRFTISRDNACKN SLFLQMNNLRVEDTAVYYCAAWSGN SGGMDVWGQGTTVSVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHK

Antibody sequence description	SEQ ID NO:	Amino acid sequence
		PSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVLHEALHSHYTQKS LSLSPGK
LC of HBC34-V35	93	SYELTQPPSVSVSPGQTVSIPCSGDKL GNKNVAWFQHKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEAAYFCQTFDSTTVVFGGGTRLTV LGQPKAAPSVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPTE CS
LC of HBC34-V34	94	SYELTQPPSVSVSPGQTVSIPCSGDKL GNKNVSWFQHKPGQSPVLVIYEVKY RPSGIPERFSGSNSGNTATLTISGTQA MDEAAYFCQTFDSTTVVFGGGTRLTV LGQPKAAPSVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPTE CS
HBC24 VH	95	EVQLLES GGGLVQPGGSLRLSCAASG STFTKYAMSWVRQAPGKGLEWVASI

Antibody sequence description	SEQ ID NO:	Amino acid sequence
		SGSVPGFGIDTYYADSVKGRFTISRDT SKNTLYLQMNSLRAEDTALYYCAKD VGVIGSYYYYAMDVWGQGTAVTVSS
HBC24 VL	96	EIVLTQSPGTLSPGERATLSCRASQ GLSSSYLAWYQQKPGQAPRLLIYSAS TRATGIPDRFSGSGSGTDFTLTISRLEP EDFAVYYCQQYAYSPRWTFGQGTKV EIK
HBC24 CDRH1	97	GSTFTKYA
HBC24 CDRH2	98	ISGSVPGF
HBC24 CDRH3	99	LYYCAKDVGIVIGSYYYYAMDV
HBC24 CDRL1	100	QGLSSSY
HBC24 CDRL2	101	SAS
HBC24 CDRL3	102	QQYAYSPRWT
HBC34-V7, HBC34-V34, HBC34-V35 HC (VH-hinge-CH1-CH2-CH3) (wild-type)	129	ELQLVESGGGWVQPGGSQRLSCAAS GRIFRSFYMSWVRQAPGKGLEWVATI NQDGSEKLYVDSVKGRFTISRDNACKN SLFLQMNNLRVEDTAVYYCAAWSGN SGGMDVWGQGTTSVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDK

Antibody sequence description	SEQ ID NO:	Amino acid sequence
		SRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
WT hIgG1 Fc	137	APELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSRDELTKN QVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSGDSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQ KLSLSLSPGK
HBC34-V7, HBC34-V23, HBC34-V34, HBC34-V35, HBC34_C40S, HBC34_C40A, HBC34-V23_C40S, HBC34-V23_C40A HC with GAALIE mutation in hIgG1 Fc	138	ELQLVESGGGWVQPGGSQRLSCAAS GRIFRSFYMSWVRQAPGKGLEWVATI NQDGSEKLYVDSVKGRFTISRDNANK SLFLQMNNLRVEDTAVYYCAAWSGN SGGMDVWGQGTTSVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPA PELLAGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPLPEEKTI SKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSGDSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK

Fragments of the antibodies described herein can be obtained from the antibodies by methods that include digestion with enzymes, such as pepsin or papain, and/or by cleavage of disulfide bonds by chemical reduction. Alternatively, fragments of the antibodies can be obtained by cloning and expression of part of the sequences of the heavy or light chains. The present disclosure encompasses single-chain Fv fragments (scFv) derived from the heavy and light chains of an antibody as described herein, including, for example, an scFv comprising the CDRs from an antibody according to the present description, heavy or light chain monomers and dimers, single domain heavy chain antibodies, single domain light chain antibodies, as well as single chain antibodies, in which the heavy and light chain variable domains are joined by a peptide linker.

In certain embodiments, an antibody according to the present disclosure, or an antigen binding fragment thereof, comprises a purified antibody, a monoclonal antibody, a single chain antibody, Fab, Fab', F(ab')₂, Fv or scFv.

Antibodies and antigen binding fragments of the present disclosure may, in embodiments, be multispecific (e.g., bispecific, trispecific, tetraspecific, or the like), and may be provided in any multispecific format, as disclosed herein. In certain embodiments, an antibody or antigen-binding fragment of the present disclosure is a multispecific antibody, such as a bispecific or trispecific antibody. Formats for bispecific antibodies are disclosed in, for example, Spiess et al., *Mol. Immunol.* 67(2):95 (2015), and in Brinkmann and Kontermann, *mAbs* 9(2):182-212 (2017), which bispecific formats and methods of making the same are incorporated herein by reference and include, for example, Bispecific T cell Engagers (BiTEs), DARTs, Knobs-Into-Holes (KIH) assemblies, scFv-CH3-KIH assemblies, KIH Common Light-Chain antibodies, TandAbs, Triple Bodies, TriBi Minibodies, Fab-scFv, scFv-CH-CL-scFv, F(ab')₂-scFv₂, tetravalent HCabs, Intrabodies, CrossMabs, Dual Action Fabs (DAFs) (two-in-one or four-in-one), DutaMabs, DT-IgG, Charge Pairs, Fab-arm Exchange, SEEDbodies, Triomabs, LUZ-Y assemblies, Fcabs, $\kappa\lambda$ -bodies, orthogonal Fabs, DVD-IgGs, IgG(H)-scFv, scFv-(H)IgG, IgG(L)-scFv, scFv-(L)IgG, IgG(L,H)-Fv,

IgG(H)-V, V(H)-IgG, IgG(L)-V, V(L)-IgG, KIH IgG-scFab, 2scFv-IgG, IgG-2scFv, scFv4-Ig, Zybody, and DVI-IgG (four-in-one). A bispecific or multispecific antibody may comprise a HBV- and/or HDV-specific binding domain of the instant disclosure in combination with another HBV- and/or HDV-specific binding domain of the instant disclosure, or in combination with a different binding domain that specifically binds to HBV and/or HDV (*e.g.*, at a same or a different epitope), or with a binding domain that specifically binds to a different antigen.

Antibody fragments of the disclosure may impart monovalent or multivalent interactions and be contained in a variety of structures as described above. For instance, scFv molecules may be synthesized to create a trivalent "triabody" or a tetravalent "tetraabody". The scFv molecules may include a domain of the Fc region resulting in bivalent minibodies. In addition, the sequences of the disclosure may be a component of multispecific molecules in which the sequences of the disclosure target the epitopes of the disclosure and other regions of the molecule bind to other targets. Exemplary molecules include, but are not limited to, bispecific Fab2, trispecific Fab3, bispecific scFv, and diabodies (Holliger and Hudson, 2005, *Nature Biotechnology* 9: 1126-1136).

Antibodies or antigen-binding fragments thereof such as those described herein, including but not limited to scFv, may, in certain embodiments, be comprised in a fusion protein that is capable of specifically binding to an antigen as described herein. As used herein, "fusion protein" refers to a protein that, in a single chain, has at least two distinct domains or motifs, wherein the domains or motifs are not naturally found together, or in the given arrangement, in a protein. A polynucleotide encoding a fusion protein may be constructed using PCR, recombinantly engineered, or the like, or such fusion proteins can be synthesized.

In some embodiments, a fusion protein is capable of expression at a surface of a host cell, *e.g.*, a T cell, NK cell, or NK-T cell. In certain embodiments, a fusion protein comprises (i) an extracellular component comprising the antibody or antigen binding fragment thereof (*e.g.*, a scFv); (ii) a transmembrane component (*e.g.*, a transmembrane

domain from CD4, CD8, CD27, CD28, or a functional variant or portion thereof, or any combination thereof); and (iii) an intracellular component comprising a signaling domain from a costimulatory protein, or a functional variant or portion thereof (*e.g.*, a signaling domain from from CD27, CD28, 4-1BB (CD137), OX40 (CD134), CD2, 5 CD5, ICAM-1 (CD54), LFA-1 (CD11a/CD18), ICOS (CD278), GITR, CD30, CD40, BAFF-R, HVEM, LIGHT, MKG2C, SLAMF7, NKp80, CD160, B7-H3, a ligand that specifically binds with CD83, or a functional variant thereof, or any combination thereof), and/or an effector domain (*e.g.*, from CD3 ϵ , CD3 δ , CD3 ζ , CD25, CD79A, CD79B, CARD11, DAP10, FcR α , FcR β , FcR γ , Fyn, HVEM, ICOS, Lck, LAG3, LAT, 10 LRP, NKG2D, NOTCH1, NOTCH2, NOTCH3, NOTCH4, Wnt, ROR2, Ryk, SLAMF1, Slp76, pT α , TCR α , TCR β , TRIM, Zap70, PTCH2, or any combination thereof).

In certain embodiments, a fusion protein comprising an antibody or antigen binding 15 fragment comprises a chimeric antigen receptor molecule (CAR), which may be expressed on a cell surface of a host cell such as a T cell, a NK cell, or a NK-T cell for use in a cellular immunotherapy. CAR molecules and principles of design are described in, for example: Sadelain et al., *Cancer Discov.*, 3(4):388 (2013); Harris and Kranz, *Trends Pharmacol. Sci.*, 37(3):220 (2016); Stone et al., *Cancer Immunol.* 20 *Immunother.*, 63(11):1163 (2014); Xu et al., 2018 *Oncotarget* 9:13991; Androulla et al., 2018 *Curr. Pharm. Biotechnol.* Volume 19 (April 2018); Wu et al., 2016 *Expert Opin. Biol. Ther.* 16:1469; Ren et al., 2017 *Protein Cell* 8:634; which CAR molecules, CAR designs, and CAR design principles are herein incorporated by reference in their entirety.

25

Throughout this disclosure, antibodies, antigen binding fragments thereof, and fusion proteins may individually or collectively (*e.g.*, in any combination) be referred to as "binding proteins"

30 Binding proteins according to the present disclosure may be provided in purified form. For example, an antibody may be present in a composition that is substantially free of

other polypeptides *e.g.*, where less than 90% (by weight), usually less than 60% and more usually less than 50% of the composition is made up of other polypeptides.

Binding proteins according to the present disclosure may be immunogenic in human and/or in non-human (or heterologous) hosts; *e.g.*, in mice. For example, an antibody may have an idiotope that is immunogenic in non-human hosts, but not in a human host. Antibodies of the disclosure for human use include those that are not typically isolated from hosts such as mice, goats, rabbits, rats, non-primate mammals, or the like, and in some instances are not obtained by humanization or from xeno-mice. Also contemplated herein are variant forms of the disclosed antibodies, which are engineered so as to reduce known or potential immunogenicity and/or other potential liabilities, or to confer a desired structure and/or functionality of the antibody in a non-human animal, such as a mouse (*e.g.*, a "murinized " antibody wherein one or more human amino acid residue, sequence, or motif is replaced by a residue, sequence, or motif that has reduced or abrogated immunogenicity or other liability, or has a desired structure and/or function, in a mouse; *e.g.*, for model studies using a mouse).

Amino acid sequences of exemplary murinized antibodies of the present disclosure are provided in **Table 2**.

20

Murinized antibody sequence description	SEQ ID NO.	Amino acid sequence
HBC34-V7-mu (IgG2a) HC	122	ELQLVESGGGWVQPGGSQRLSCAASGRIFRSFY MSWVRQAPGKGLEWVATINQDGSEKLYVDSV KGRFTISRDNANKSLFLQMNNLRVEDTAVYYC AAWSGNSGGMDVWGQGTTSVSSAKTTAPSV YPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSS TWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPC PPCKCPAPNLLGGPSVFIFPPKIKDVLMSISPIV

		TCVVVDVSEDDPDVQISWVFNNEVHTAQTQT HREDYNSTLRVVSALPIQHQDWMSGKEFKCKV NNKDLPAPIERTISKPKGSVRAPQVYVLPPEEE MTKKQVTLTCMVTDFMPEDIYVEWTNNGKTE LNYKNTEPVLDSGDSYFMYSKLRVEKKNWVE RNSYSCSVVHEGLHNHHTTKSFSRTPGK
HBC34-V7-mu (IgG2a) LC	123	SYELTQPPSVSVSPGQTVSIPCSGDKLGKNVC WFQHKPGQSPVLVIYEVKYRPSGIPERFSGSNS GNTATLTISGTQAMDEAAYFCQTFDSTTVVFG GGTRLTVLGQPKSSPSVTLFPPSSEELETNKATL VCTITDFYPGVVTVDWKVDGTPVTQGMETTQP SKQSNNKYMASSYLTLTARAWERHSSYSCQVT HEGHTVEKSLSRADCS
HBC34-V35-mu (IgG2a) HC	124	ELQLVESGGGWVQPGGSQRLSCAASGRIFRSFY MSWVRQAPGKGLEWVATINQDGSEKLYVDSV KGRFTISRDNANKSLFLQMNNLRVEDTAVYYC AAWSGNSGGMDVWGQGTTVSVSSAKTTAPSV YPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSS TWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPC PPCKCPAPNLLGGPSVFIFPPKIKDVLMSLSPIV TCVVVDVSEDDPDVQISWVFNNEVHTAQTQT HREDYNSTLRVVSALPIQHQDWMSGKEFKCKV NNKDLPAPIERTISKPKGSVRAPQVYVLPPEEE MTKKQVTLTCMVTDFMPEDIYVEWTNNGKTE LNYKNTEPVLDSGDSYFMYSKLRVEKKNWVE RNSYSCSVVHEGLHNHHTTKSFSRTPGK
HBC34-V35-mu (IgG2a) LC	125	SYELTQPPSVSVSPGQTVSIPCSGDKLGKNVA WFQHKPGQSPVLVIYEVKYRPSGIPERFSGSNS GNTATLTISGTQAMDEAAYFCQTFDSTTVVFG GGTRLTVLGQPKSSPSVTLFPPSSEELETNKATL

		VCTITDFYPGVVTVDWKVDGTPVTQGMETTQP SKQSNNKYMASSYLTLTARAWERHSSYSCQVT HEGHTVEKSLSRADCS
HBC24-mu (IgG2a) HC	126	EVQLLESGGGLVQPGGSLRLSCAASGSTFTKYA MSWVRQAPGKGLEWVASISGSPGFGIDTYYA DSVKGRFTISRDTSKNTLYLQMNSLRAEDTAL YYCAKDVGVISSYYYAMDVWGQGTAVTVS SAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKG YFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTL SSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIE PRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDV LMISLSPIVTCVVVDVSEDDPDVQISWVFNVE VHTAQTQTHREDYNSTLRVVSALPIQHQQDWMS GKEFKCKVNNKDLPAPIERTISKPKGSVRAPQV YVLPPEEEMTKKQVTLTCMVTDMPEDIYVE WTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNNSYSCSVVHEGLHNHHTTKSFSR TPGK
HBC24-mu (IgG2a) LC	127	EIVLTQSPGTLSPGERATLSCRASQGLSSSYL AWYQQKPGQAPRLLIYSASTRATGIPDRFSGSG SGTDFTLTISRLEPEDFAVYYCQQYAYSPTWTF GQGTEVEIKADAAPTVSIFPPSSEQLTSGGASV VCFLNNFYPKDINVKKIDGSERQNGVLNSWT DQDSKDSTYSMSSTLTTLTKDEYERHNSYTCEA THKTSTSPIVKSFNRNEC

As used herein, a "neutralizing antibody" (or antigen binding fragment, or fusion protein) is one that can neutralize, *i.e.*, prevent, inhibit, reduce, impede or interfere with, the ability of a pathogen to initiate and/or perpetuate an infection in a host (*e.g.*, host
5 organism or host cell). The terms "neutralizing antibody" and "an antibody that neutralizes" or "antibodies that neutralize" are used interchangeably herein. These antibodies can be used alone, or in combination (*e.g.*, two or more of the presently

disclosed antibodies in a combination, or an antibody of the present disclosure in combination with another agent, which may or may not be an antibody agent, including an antibody that is capable of neutralizing an HBV B and/or D infection), as prophylactic or therapeutic agents upon appropriate formulation, in association with
5 active vaccination, as a diagnostic tool, or as a production tool as described herein.

As used herein, "specifically binds" or "specific for" refers to an association or union of a binding protein (*e.g.*, an antibody or antigen binding fragment thereof) or a binding domain to a target molecule with an affinity or K_a (*i.e.*, an equilibrium association
10 constant of a particular binding interaction with units of $1/M$) equal to or greater than $10^5 M^{-1}$ (which equals the ratio of the on-rate $[K_{on}]$ to the off rate $[K_{off}]$ for this association reaction), while not significantly associating or uniting with any other molecules or components in a sample. Binding proteins or binding domains may be classified as "high-affinity" binding proteins or binding domains or as "low-affinity"
15 binding proteins or binding domains. "High-affinity" binding proteins or binding domains refer to those binding proteins or binding domains having a K_a of at least $10^7 M^{-1}$, at least $10^8 M^{-1}$, at least $10^9 M^{-1}$, at least $10^{10} M^{-1}$, at least $10^{11} M^{-1}$, at least $10^{12} M^{-1}$, or at least $10^{13} M^{-1}$. "Low-affinity" binding proteins or binding domains refer to those binding proteins or binding domains having a K_a of up to $10^7 M^{-1}$, up to $10^6 M^{-1}$, or up to $10^5 M^{-1}$. Alternatively, affinity may be defined as an equilibrium dissociation constant (K_d) of a particular binding interaction with units of M (*e.g.*, $10^{-5} M$ to $10^{-13} M$). The terms "binding" and "specifically binding" and similar references do not encompass non-specific sticking.

25 Binding of a binding protein can be determined or assessed using an appropriate assay, such as, for example, Surface Plasmon Resonance (SPR) methods, *e.g.*, a Biacore™ system; kinetic exclusion assays such as KinExA®; and BioLayer interferometry (*e.g.*, using the ForteBio® Octet platform); isothermal titration calorimetry (ITC), or the like, an antigen-binding ELISA (*e.g.*, direct or indirect) with imaging by, *e.g.*, optical density
30 at 450nm, or by flow cytometry, or the like.

In certain embodiments, binding proteins according to the present disclosure can bind to the antigenic loop region of HBsAg. The envelope of the hepatitis B virus generally contains three "HBV envelope proteins" (also known as "HBsAg", "hepatitis B surface antigen"): S protein (for "small", also referred to as S-HBsAg), M protein (for "middle", also referred to as M-HBsAg) and L protein (for "large", also referred to as L-HBsAg). S-HBsAg, M-HBsAg and L-HBsAg share the same C-terminal extremity (also referred to as "S domain", 226 amino acids), which corresponds to the S protein (S-HBsAg) and which is crucial for virus assembly and infectivity. S-HBsAg, M-HBsAg and L-HBsAg are synthesized in the endoplasmic reticulum (ER), assembled, and secreted as particles through the Golgi apparatus. The S domain comprises four predicted transmembrane (TM) domains, whereby both the N-terminus as well as the C-terminus of the S domain are exposed to the lumen. The transmembrane domains TM1 and TM2 are both believed necessary for cotranslational protein integration into the ER membrane and the transmembrane domains TM3 and TM4 are located in the C-terminal third of the S domain. The "antigenic loop region" of HBsAg is located between the predicted TM3 and TM4 transmembrane domains of the S domain of HBsAg, whereby the antigenic loop region comprises amino acids 101 – 172 of the S domain, which contains 226 amino acids in total (Salisse J. and Sureau C., 2009, Journal of Virology 83: 9321-9328). A determinant of infectivity resides in the antigenic loop region of HBV envelope proteins. In particular, residues between 119 and 125 of the HBsAg contain a CXXC motif, which is considered to be important for the infectivity of HBV and HDV (Jaoude GA, Sureau C, Journal of Virology, 2005;79:10460–6).

When positions in the amino acid sequence of the S domain of HbsAg are referred to herein, such positions are made with reference to the amino acid sequence as set forth in SEQ ID NO: 3 (shown below) or to natural or artificial sequence variants thereof.

MENITSGFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGTTVCLGQNSQS
 PTSNHSPTSCPPTCPGYRWMCLRRFIIFLLCLIFLLVLLDYQGMLPVCPLIPG
SSTTSTGPCRTCMTTAQGTSMPSCCCTKPSDGNCTCIPISSWAFGKFLWEWA
SARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPFLPLLPIFF
 CLWVYI

(SEQ ID NO: 3; amino acids 101 – 172 are shown underlined)

For example, the expression "amino acids 101 – 172 of the S domain" refers to the amino acid residues from positions 101 – 172 of the polypeptide according to SEQ ID NO: 3. However, a person skilled in the art understands that mutations or variations (including, but not limited to, substitution, deletion and/or addition, for example, HBsAg of a different genotype or a different HBsAg mutant as described herein) may occur naturally in the amino acid sequence of the S domain of HBsAg or be introduced artificially into the amino acid sequence of the S domain of HBsAg without affecting its biological properties. Therefore, as used herein, the term "S domain of HBsAg" encompasses all such polypeptides including, for example, the polypeptide according to SEQ ID NO: 3 and its natural or artificial mutants. In addition, when sequence fragments of the S domain of HBsAg are described herein (e.g. amino acids 101 – 172 or amino acids 120 -130 of the S domain of HBsAg), they include not only the corresponding sequence fragments of SEQ ID NO: 3, but also the corresponding sequence fragments of its natural or artificial mutants. For example, the phrase "amino acid residues from positions 101 – 172 of the S domain of HBsAg" encompasses amino acid residues from positions 101 – 172 of SEQ ID NO: 3 and the corresponding fragments of its mutants (natural or artificial mutants). As used herein, the phrases "corresponding sequence fragments" and "corresponding fragments" refer to fragments that are located in equal positions of sequences when the sequences are subjected to optimized alignment, namely, the sequences are aligned to obtain a highest percentage of identity.

The M protein (M-HBsAg) corresponds to the S protein extended by an N-terminal domain of 55 amino acids called "pre-S2". The L protein (L-HBsAg) corresponds to the M protein extended by an N-terminal domain of 108 amino acids called "pre-S1" (genotype D). The pre-S1 and pre-S2 domains of the L protein can be present either at the inner face of viral particles (on the cytoplasmic side of the ER), and is believed to play a crucial role in virus assembly, or on the outer face (on the luminal side of the ER), available for the interaction with target cells and important for viral infectivity. Moreover, HBV surface proteins (HBsAg) are not only incorporated into virion

envelopes but also can spontaneously bud from ER-Golgi intermediate compartment membranes to form empty "subviral particles" (SVPs) that are released from the cell by secretion.

- 5 In some embodiments, an antibody, antigen binding fragment, or fusion protein binds to the antigenic loop region of HBsAg, and is capable of binding to all of S-HBsAg, M-HBsAg and L-HBsAg.

In some embodiments, an antibody, an antigen binding fragment, or fusion protein
10 neutralizes infection with hepatitis B virus and hepatitis delta virus. In some embodiments, the antibody, or the antigen binding fragment thereof, reduces viral infectivity of hepatitis B virus and hepatitis delta virus.

To study and quantitate virus infectivity (or "neutralization") in the laboratory, standard
15 "neutralization assays" may be utilized. For a neutralization assay, animal viruses are typically propagated in cells and/or cell lines. A neutralization assay wherein cultured cells are incubated with a fixed amount of HBV or HDV in the presence (or absence) of the antibody (or antigen-binding fragment or fusion protein) to be tested may be used. In such an assay, the levels of hepatitis B surface antigen (HBsAg) or hepatitis B e
20 antigen (HBeAg) secreted into the cell culture supernatant may be used and/or HBcAg staining may be assessed to provide a readout. For HDV, for example, delta antigen immunofluorescence staining may be assessed.

In a particular embodiment of an HBV neutralization assay, cultured cells, for example
25 HepaRG cells, such as differentiated HepaRG cells, are incubated with a fixed amount of HBV in the presence or absence of the antibody to be tested. In such an embodiment, incubation may be carried out, for example, for 16 hours at 37°C. That incubation may be performed in a medium (e.g. supplemented with 4% PEG 8000). After incubation, cells may be washed and further cultivated. To measure virus
30 infectivity, the levels of hepatitis B surface antigen (HBsAg) and hepatitis B e antigen (HBeAg) secreted into the culture supernatant, e.g. from day 7 to day 11 post-infection, may be determined by enzyme-linked immunosorbent assay (ELISA). Additionally,

HBcAg staining may be assessed in an immunofluorescence assay. In an embodiment of a HDV neutralization assay, essentially the same assay as for HBV may be used, with the difference that sera from HDV carriers may be used as HDV infection inoculum on differentiated HepaRg cells (instead of HBV). For detection, delta antigen immunofluorescence staining may be used as a readout.

Embodiments of the binding proteins of the disclosure have high neutralizing potency. In certain embodiments, the concentration of an antibody as described herein required for 50% neutralization of hepatitis B virus (HBV) and hepatitis delta virus (HDV), is, for example, about 10 µg/ml or less. In other embodiments, the concentration of a binding protein required for 50% neutralization of HBV and HDV is about 5 µg/ml. In other embodiments, the concentration of a binding protein as described herein required for 50% neutralization of HBV and HDV is about 1 µg/ml. In still other embodiments, the concentration of a binding protein required for 50% neutralization of HBV and HDV is about 750 ng/ml. In yet further embodiments, the concentration of a binding protein as described herein required for 50% neutralization of HBV and HDV is 500 ng/ml or less. In such embodiments, the concentration of a binding protein as described herein required for 50% neutralization of HBV and HDV may be selected from 450 ng/ml or less, 400 ng/ml or less, 350 ng/ml or less, 300 ng/ml or less, 250 ng/ml or less, 200 ng/ml or less, 175 ng/ml or less, 150 ng/ml or less, 125 ng/ml or less, 100 ng/ml or less, 90 ng/ml or less, 80 ng/ml or less, 70 ng/ml or less, 60 ng/ml or less or 50 ng/ml or less.

Antibodies or antigen binding fragments according to the present disclosure, which can neutralize both HBV and HDV, are useful in the prevention and treatment of hepatitis B and hepatitis D. Infection with HDV typically occurs simultaneously with or subsequent to infection by HBV (*e.g.*, inoculation with HDV in the absence of HBV does not cause hepatitis D since HDV requires the support of HBV for its own replication) and hepatitis D is typically observed in chronic HBV carriers.

Embodiments of the disclosed binding proteins promote clearance of HBsAg and HBV. In particular embodiments, binding proteins promote clearance of both HBV and

subviral particles of hepatitis B virus (SVPs). Clearance of HBsAg or of subviral particles may be assessed by measuring the level of HBsAg for example in a blood sample, *e.g.* from a hepatitis B patient. Similarly, clearance of HBV may be assessed by measuring the level of HBV for example in a blood sample, *e.g.* from a hepatitis B
5 patient.

In the sera of patients infected with HBV, in addition to infectious particles (HBV), there is typically an excess (typically 1,000- to 100,000-fold) of empty subviral particles (SVP) composed solely of HBV envelope proteins (HBsAg) in the form of
10 relatively smaller spheres and filaments of variable length. Subviral particles have been shown to strongly enhance intracellular viral replication and gene expression of HBV (Bruns M. et al. 1998 J Virol 72(2): 1462–1468). This is also relevant in the context of infectivity of sera containing HBV, since the infectivity depends not only on the number of viruses but also on the number of SVPs (Bruns M. et al. 1998 J Virol 72(2):
15 1462–1468). Moreover, an excess of subviral particles can serve as a decoy by absorbing neutralizing antibodies and therefore delay the clearance of infection. Achievement of hepatitis B surface antigen (HBsAg) loss is considered in some instances to be an ideal endpoint of treatment and the closest outcome to cure chronic hepatitis B (CHB).

20

Embodiments of binding proteins of the present disclosure may promote clearance of HbsAg. In certain embodiments, the binding proteins may promote clearance of subviral particles of hepatitis B virus. In some embodiments, the binding proteins may be used to treat chronic hepatitis B.

25

In any of the presently disclosed embodiments, a binding protein of the present disclosure is capable of binding an HBsAg of a genotype selected from the HBsAg genotypes A, B, C, D, E, F, G, H, I, and J, or any combination thereof.

30 In certain embodiments, binding proteins of the present disclosure are capable of binding to 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 of the HBsAg genotypes A, B, C, D, E, F, G, H, I, and J. Examples of different HBsAg genotypes of include the following: GenBank

accession number J02203 (HBV-D, ayw3); GenBank accession number FJ899792.1 (HBV-D, adw2); GenBank accession number AM282986 (HBV-A); GenBank accession number D23678 (HBV-B1 Japan); GenBank accession number AB117758 (HBV-C1 Cambodia); GenBank accession number AB205192 (HBV-E Ghana);
5 GenBank accession number X69798 (HBV-F4 Brazil); GenBank accession number AF160501 (HBV-G USA); GenBank accession number AY090454 (HBV-H Nicaragua); GenBank accession number AF241409 (HBV-I Vietnam); and GenBank accession number AB486012 (HBV-J Borneo). Exemplary amino acid sequences of the antigenic loop region of the S domain of HBsAg of different genotypes are described
10 herein (*e.g.*, SEQ ID NOs: 5 – 15).

In some embodiments, a binding protein is capable of binding to one or more, and in some cases at least 6 of the 10 HBsAg genotypes A, B, C, D, E, F, G, H, I, and J. In certain embodiments, a binding protein is capable of binding to at least 8 of the 10
15 HBsAg genotypes A, B, C, D, E, F, G, H, I, and J. In some embodiments, a binding protein is capable of binding to all 10 of the 10 HBsAg genotypes A, B, C, D, E, F, G, H, I, and J. HBV is differentiated into several genotypes, according to genome sequence. To date, eight well-known genotypes (A-H) of the HBV genome have been defined. Moreover, two other genotypes, I and J, have also been identified (Sunbul M.,
20 2014, World J Gastroenterol 20(18): 5427–5434). The genotype is known to affect the progression of the disease and differences between genotypes in response to antiviral treatment have been determined.

In some embodiments, a binding protein according to the present disclosure is capable
25 of binding to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or 18 of the HBsAg mutants having mutations in the antigenic loop region, with such mutant(s) being selected from one or more of HBsAg Y100C/P120T, HBsAg P120T, HBsAg P120T/S143L, HBsAg C121S, HBsAg R122D, HBsAg R122I, HBsAg T123N, HBsAg Q129H, HBsAg Q129L, HBsAg M133H, HBsAg M133L, HBsAg M133T, HBsAg
30 K141E, HBsAg P142S, HBsAg S143K, HBsAg D144A, HBsAg G145R and HBsAg N146A. These mutants are naturally occurring mutants based on the S domain of

HBsAg Genotype D, Genbank accession no. FJ899792 (SEQ ID NO: 4). The mutated amino acid residue(s) in each of the mutants noted herein are indicated in the name.

SEQ ID NO: 4:

- 5 MENVTSGFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGTTVCLGQNSQ
 SPTSNHSPTSCPPTCPGYRWMCLRRFIIFLLFILLCLIFLLVLLDYQGMLPVCPLIP
GSSTTGTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPISSWAFGKFLWEW
ASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSTLSPFLPLLPI
 FFCLWVYI
- 10 (the antigenic loop region, *i.e.* amino acids 101 – 172, is shown underlined).

Amino acid sequences of the antigenic loop region of the S domain of HBsAg of different mutants are shown in SEQ ID NOs: 16 – 33.

- 15 In certain embodiments, a binding protein as disclosed herein is capable of binding to at one or more, and in some cases at least 12 infectious HBsAg mutants selected from HBsAg Y100C/P120T, HBsAg P120T, HBsAg P120T/S143L, HBsAg C121S, HBsAg R122D, HBsAg R122I, HBsAg T123N, HBsAg Q129H, HBsAg Q129L, HBsAg M133H, HBsAg M133L, HBsAg M133T, HBsAg K141E, HBsAg P142S, HBsAg
- 20 S143K, HBsAg D144A, HBsAg G145R and HBsAg N146A. In some such embodiments, a binding protein is capable of binding to at least 15 infectious HBsAg mutants selected from HBsAg Y100C/P120T, HBsAg P120T, HBsAg P120T/S143L, HBsAg C121S, HBsAg R122D, HBsAg R122I, HBsAg T123N, HBsAg Q129H, HBsAg Q129L, HBsAg M133H, HBsAg M133L, HBsAg M133T, HBsAg K141E,
- 25 HBsAg P142S, HBsAg S143K, HBsAg D144A, HBsAg G145R and HBsAg N146A. In some embodiments, a binding protein is capable of binding to each of the following infectious HBsAg mutants: HBsAg Y100C/P120T; HBsAg P120T; HBsAg P120T/S143L; HBsAg C121S; HBsAg R122D; HBsAg R122I; HBsAg T123N; HBsAg Q129H; HBsAg Q129L; HBsAg M133H; HBsAg M133L; HBsAg M133T; HBsAg
- 30 K141E; HBsAg P142S; HBsAg S143K; HBsAg D144A; HBsAg G145R; and HBsAg N146A.

In certain embodiments, the binding protein (e.g., including an antibody or antigen binding fragment thereof) is capable of reducing a serum concentration of HBV DNA in a mammal having an HBV infection. In certain embodiments, the binding protein is capable of reducing a serum concentration of HBsAg in a mammal having an HBV infection. In certain embodiments, binding protein is capable of reducing a serum concentration of HBeAg in a mammal having an HBV infection. In certain embodiments, the binding protein is capable of reducing a serum concentration of HBcrAg in a mammal having an HBV infection. In some embodiments, the binding protein is capable of reducing the serum concentration of HBV DNA, HBsAg, HBeAg, and/or HBcrAg in the mammal for about 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more days following a single administration of the binding protein.

The term "epitope" or "antigenic epitope" includes any molecule, structure, amino acid sequence, or protein determinant that is recognized and specifically bound by a cognate binding molecule, such as an immunoglobulin, chimeric antigen receptor, or other binding molecule, domain or protein. Epitopic determinants generally contain chemically active surface groupings of molecules, such as amino acids or sugar side chains, and can have specific three dimensional structural characteristics, as well as specific charge characteristics.

20

In some embodiments, a binding protein is capable of binding to an epitope comprising at least one, at least two, at least three, or at least four amino acids of the antigenic loop region of HbsAg. In certain embodiments, a binding protein is capable of binding at least two amino acids selected from amino acids 115 – 133 of the S domain of HbsAg, amino acids 120 – 133 of the S domain of HbsAg, or amino acids 120 – 130 of the S domain of HbsAg. In certain embodiments, a binding protein is capable of binding at least three amino acids selected from amino acids 115 – 133 of the S domain of HbsAg, amino acids 120 – 133 of the S domain of HbsAg, or amino acids 120 – 130 of the S domain of HbsAg. In some embodiments, a binding protein is capable of binding at least four amino acids selected from amino acids 115 – 133 of the S domain of HbsAg, amino acids 120 – 133 of the S domain of HbsAg, or amino acids 120 – 130 of the S domain of HbsAg. As used herein, the position of the amino acids (e.g. 115 – 133, 120

– 133, 120 - 130) refers to the S domain of HBsAg as described above, which is present in all three HBV envelope proteins S-HBsAg, M-HBsAg, and L-HBsAg, whereby S-HBsAg typically corresponds to the S domain of HBsAg.

- 5 The term "formed by" as used herein in the context of an epitope, means that the epitope to which binding protein binds to may be linear (continuous) or conformational (discontinuous). A linear or a sequential epitope is an epitope that is recognized by an antibody according to its linear sequence of amino acids, or primary structure. A conformational epitope may be recognized according to a three-dimensional shape and
- 10 protein structure. Accordingly, if the epitope is a linear epitope and comprises more than one amino acid located at positions selected from amino acid positions 115 – 133 or from amino acid positions 120 – 133 of the S domain of HBsAg, the amino acids comprised by the epitope may be located in adjacent positions of the primary structure (*e.g.*, are consecutive amino acids in the amino acid sequence). In the case of a
- 15 conformational epitope (3D structure), the amino acid sequence typically forms a 3D structure as epitope and, thus, the amino acids forming the epitope may be or may be not located in adjacent positions of the primary structure (*i.e.* maybe or may be not consecutive amino acids in the amino acid sequence).
- 20 In certain embodiments, an epitope to which a binding protein binds to a conformational epitope. In some embodiments, a binding protein binds to an epitope comprising at least two amino acids of the antigenic loop region of HBsAg, wherein the at least two amino acids are selected from amino acids 120 – 133 or from from amino acids 120 – 130, of the S domain of HbsAg, and wherein the at least two amino acids
- 25 are not located in adjacent positions (of the primary structure). In certain embodiments, a binding protein binds to an epitope comprising at least three amino acids of the antigenic loop region of HBsAg, wherein the at least three amino acids are selected from amino acids 120 – 133 or from from amino acids 120 – 130, of the S domain of HbsAg, and wherein at least two of the three amino acids are not located in adjacent
- 30 positions (of the primary structure). In some embodiments, a binding protein binds to an epitope comprising at least four amino acids of the antigenic loop region of HBsAg, wherein the at least four amino acids are selected from amino acids 120 – 133 or from

from amino acids 120 – 130, of the S domain of HbsAg, and wherein at least two of the four amino acids are not located in adjacent positions (of the primary structure).

Amino acids to which a presently disclosed antibody, antigen binding fragment, or fusion protein binds (*i.e.* the amino acids forming the epitope), which are not located in adjacent positions of the primary structure, are in some cases spaced apart by one or more amino acids, to which the antibody, antigen binding fragment, or fusion protein does not bind. In some embodiments, at least one, at least two, at least three, at least four, or at least five amino acids may be located between two of the amino acids not located in adjacent positions comprised by the epitope.

In certain embodiments, a binding protein binds to an epitope comprising at least amino acids P120, C121, R122 and C124 of the S domain of HBsAg. In other embodiments, a binding protein of the present disclosure binds to an epitope comprising an amino acid sequence according to SEQ ID NO: 88:

PCRXC

wherein X is any amino acid or no amino acid; X is any amino acid; X is T, Y, R, S, or F; X is T, Y or R; or X is T or R.

In other embodiments, a binding protein of the present disclosure binds to an epitope comprising an amino acid sequence according to SEQ ID NO: 80:

TGPCRTC

or to an amino acid sequence sharing at least 80%, at least 90%, or at least 95% sequence identity with SEQ ID NO: 80.

25

In other embodiments, a binding protein of the present disclosure binds to an epitope comprising an amino acid sequence according to SEQ ID NO: 85:

STTSTGPCRTC

or to an amino acid sequence sharing at least 80%, at least 90% or at least 95% sequence identity with SEQ ID NO: 85.

In certain embodiments, a binding protein of the present disclosure binds to an epitope comprising an amino acid sequence comprising at least amino acids 145 – 151 of the S domain of HBsAg:

GNCTCIP

5 (SEQ ID NO: 81).

In still other embodiments, a binding protein of the present disclosure binds to an epitope comprising an amino acid sequence according to SEQ ID NO: 80 and an amino acid sequence according to SEQ ID NO: 81.

10

In other embodiments, a binding protein of the present disclosure binds to an epitope comprising an amino acid sequence according to SEQ ID NO: 85 and/or an amino acid sequence according to SEQ ID NO: 87.

15 As described above, an epitope to which a binding protein of the present disclosure binds may be linear (continuous) or conformational (discontinuous). In some embodiments, a binding protein of the disclosure binds to a conformational epitope, and in certain such embodiments, the conformational epitope is present only under non-reducing conditions.

20

In certain embodiments, binding protein of the present disclosure, binds to a linear epitope. In certain such embodiments, the the linear epitope is present under both, non-reducing conditions and reducing conditions.

25 In particular embodiments, a binding protein of the present disclosure binds to an epitope in the antigenic loop of HBsAg formed by an amino acid sequence according to SEQ ID NO: 1:

X₁ X₂ X₃ TC X₄ X₅ X₆A X₇G

30 wherein X₁, X₂, X₃, X₄, X₅, X₆ and X₇ may be any amino acid (SEQ ID NO: 1).

In some embodiments, X₁, X₂, X₃, X₄, X₅, X₆ and X₇ are amino acids, which are conservatively substituted in comparison to amino acids 120 – 130 of SEQ ID NO: 3. In some embodiments, X₁, X₂, X₃, X₄, X₅, X₆ and X₇ are amino acids, which are conservatively substituted in comparison to amino acids 20 – 30 of any of SEQ ID NOs 5 – 33.

In specific embodiments, X₁ of SEQ ID NO: 1 X₁ is a small amino acid. A "small" amino acid, as used herein, refers to any amino acid selected from the group consisting of alanine, aspartic acid, asparagine, cysteine, glycine, proline, serine, threonine and valine. In certain such embodiments, X₁ is proline, serine or threonine.

In certain embodiments, X₂ of SEQ ID NO: 1 X₂ is a small amino acid. In certain embodiments, X₂ may be selected from cysteine or threonine.

15 In some embodiments, X₃ of SEQ ID NO: 1 is a charged amino acid or an aliphatic amino acid. A "charged" amino acid, as used herein, refers to any amino acid selected from the group consisting of arginine, lysine, aspartic acid, glutamic acid and histidine. A "aliphatic" amino acid, as used herein, refers to any amino acid selected from the group consisting of alanine, glycine, isoleucine, leucine, and valine. In certain
20 embodiments, X₃ is selected from arginine, lysine, aspartic acid or isoleucine.

In some embodiments, X₄ of SEQ ID NO: 1 is a small amino acid and/or a hydrophobic amino acid. A "hydrophobic" amino acid, as used herein, refers to any amino acid selected from the group consisting of alanine, isoleucine, leucine, phenylalanine, valine, tryptophan, tyrosine, methionine, proline and glycine. In certain embodiments, X₄ is
25 selected from methionine or threonine.

In some embodiments, X₅ of SEQ ID NO: 1 X₅ is a small amino acid and/or a hydrophobic amino acid. In certain embodiments, X₅ is selected from threonine, alanine
30 or isoleucine.

In some embodiments, X₆ of SEQ ID NO: 1 is a small amino acid and/or a hydrophobic amino acid. In certain embodiments, X₆ is selected from threonine, proline or leucine.

- 5 In some embodiments, X₇ of SEQ ID NO: 1 is a polar amino acid or an aliphatic amino acid. A "polar" amino acid, as used herein, refers to any amino acid selected from the group consisting of aspartic acid, asparagine, arginine, glutamic acid, histidine, lysine, glutamine, tryptophan, tyrosine, serine, and threonine. In certain such embodiments, X₇ is glutamine, histidine or leucine.

10

In some embodiments, a binding protein according to the present disclosure binds to an epitope in the antigenic loop of HBsAg formed by an amino acid sequence according to SEQ ID NO: 2:

- 15 X₁ X₂ X₃ TC X₄ X₅ X₆A X₇G

wherein X₁ is P, T or S,
X₂ is C or S,
X₃ is R, K, D or I,
X₄ is M or T,
20 X₅ is T, A or I,
X₆ is T, P or L, and
X₇ is Q, H or L

(SEQ ID NO: 2).

- 25 With regard to the epitopes formed by the amino acid sequences according to SEQ ID NO: 1 or 2, it is noted that the term "formed by" as used herein is not intended to imply that a disclosed binding protein necessarily binds to each and every amino acid of SEQ ID NO: 1 or 2. In particular, a binding protein may bind only to some of the amino acids of SEQ ID NO: 1 or 2, whereby other amino acid residues may act as "spacers".

30

In particular embodiments, a binding protein according to the present disclosure binds to an epitope in the antigenic loop of HBsAg formed by one or more, two or more, three

or more, or four or more amino acids of an amino acid sequence selected from SEQ ID NOs 5 – 33 shown below in Table 3.

In some embodiments, binding protein according to the present disclosure binds to an antigenic loop region of HBsAg having an amino acid sequence according to any one or more of SEQ ID NOs 5 – 33 shown below in Table 3, or to a sequence variant thereof. In certain embodiments, a binding protein according to the present disclosure binds to all of the antigenic loop variants of HBsAg having an amino acid sequence according to any of SEQ ID NOs 5 – 33 shown below in Table 3.

Table 3: Exemplary amino acid sequences of the antigenic loop region of the S domain of HBsAg (residues 101-172 of the S domain of HBsAg – except for SEQ ID NO: 16, which refers to residues 100-172 of the S domain of HBsAg in order to include the relevant mutation) of the different genotypes and mutants as used herein.

Name	SEQ ID NO.	Amino acid sequence
J02203 (D, ayw3)	5	QGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTS MYPSCCCTKPSDGNCTCIIPSSWAFGKFLWE WASARFSW
FJ899792 (D, adw2)	6	QGMLPVCPLIPGSSTTGTGPCRTCCTTP AQGTSMYPSCCCTKPSDGNCTCIIPS SWAFGKFLWEWASARFSW
AM282986 (A)	7	QGMLPVCPLIPGTTTTSTGPCKTCTTPAQGNS MFPSCCCTKPSDGNCTCIIPSSWAFAYLWE WASVRFSW
D23678 (B1)	8	QGMLPVCPLIPGSSTTSTGPCKTCTTPAQGTS MFPSCCCTKPTDGNCTCIIPSSWAFAYLWE WASVRFSW
AB117758 (C1)	9	QGMLPVCPLLPGTSTTSTGPCKTCTIPAQGTS MFPSCCCTKPSDGNCTCIIPSSWAFARFLWE WASVRFSW

Name	SEQ ID NO.	Amino acid sequence
AB205192 (E)	10	QGMLPVCPLIPGSSTTSTGPCRTCTTLAQGTS MFPSCCCSKPSDGNCTCIIPSSWAFGKFLWE WASARFSW
X69798 (F4)	11	QGMLPVCPLLPGSTTTSTGPCKTCTTLAQGTS MFPSCCCSKPSDGNCTCIIPSSWALGKYLWE WASARFSW
AF160501 (G)	12	QGMLPVCPLIPGSSTTSTGPCKTCTTPAQGNS MYPSCCCTKPSDGNCTCIIPSSWAFKYLWE WASVRFSW
AY090454 (H)	13	QGMLPVCPLLPGSTTTSTGPCKTCTTLAQGTS MFPSCCCTKPSDGNCTCIIPSSWAFGKYLWE WASARFSW
AF241409 (I)	14	QGMLPVCPLIPGSSTTSTGPCKTCTTPAQGNS MYPSCCCTKPSDGNCTCIIPSSWAFKYLWE WASARFSW
AB486012 (J)	15	QGMLPVCPLLPGSTTTSTGPCRTCTTITAQGTS MFPSCCCTKPSDGNCTCIIPSSWAFKFLWE WASVRFSW
HBsAg Y100C/P120T	16	CQGMLPVCPLIPGSSTTGTGTCRTCTTPAQGT SMYPSCCCTKPSDGNCTCIIPSSWAFGKFLW EWASARFSW
HBsAg P120T	17	QGMLPVCPLIPGSSTTGTGTCRTCTTPAQGTS MYPSCCCTKPSDGNCTCIIPSSWAFGKFLWE WASARFSW
HBsAg P120T/S143L	18	QGMLPVCPLIPGSSTTGTGTCRTCTTPAQGTS MYPSCCCTKPLDGNCTCIIPSSWAFGKFLWE WASARFSW
HBsAg C121S	19	QGMLPVCPLIPGSSTTGTGPSRTCTTPAQGTS MYPSCCCTKPSDGNCTCIIPSSWAFGKFLWE WASARFSW

Name	SEQ ID NO.	Amino acid sequence
HBsAg R122D	20	QGMLPVCPLIPGSSTTGTGPCDTCTTPAQGTS MYPSCCCTKPSDGNCTCIIPSSWAFGKFLWE WASARFSW
HBsAg R122I	21	QGMLPVCPLIPGSSTTGTGPCITCTTPAQGTS YPSCCCTKPSDGNCTCIIPSSWAFGKFLWE ASARFSW
HBsAg T123N	22	QGMLPVCPLIPGSSTTGTGPCRNCTTPAQGTS MYPSCCCTKPSDGNCTCIIPSSWAFGKFLWE WASARFSW
HBsAg Q129H	23	QGMLPVCPLIPGSSTTGTGPCRTCTTPAHGTS MYPSCCCTKPSDGNCTCIIPSSWAFGKFLWE WASARFSW
HBsAg Q129L	24	QGMLPVCPLIPGSSTTGTGPCRTCTTPALGTS MYPSCCCTKPSDGNCTCIIPSSWAFGKFLWE WASARFSW
HBsAg M133H	25	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTS HYPSCCCTKPSDGNCTCIIPSSWAFGKFLWE WASARFSW
HBsAg M133L	26	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTS YPSCCCTKPSDGNCTCIIPSSWAFGKFLWE ASARFSW
HBsAg M133T	27	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTST YPSCCCTKPSDGNCTCIIPSSWAFGKFLWE ASARFSW
HBsAg K141E	28	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTS MYPSCCCTEPSDGNCTCIIPSSWAFGKFLWE WASARFSW
HBsAg P142S	29	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTS MYPSCCCTKSSDGNCTCIIPSSWAFGKFLWE WASARFSW

Name	SEQ ID NO.	Amino acid sequence
HBsAg S143K	30	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTS MYPSCCCTKPKDGNCTCIPISSWAFGKFLWE WASARFSW
HBsAg D144A	31	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTS MYPSCCCTKPSAGNCTCIPISSWAFGKFLWE WASARFSW
HBsAg G145R	32	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTS MYPSCCCTKPSDRNCTCIPISSWAFGKFLWE WASARFSW
HBsAg N146A	33	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTS MYPSCCCTKPSDGACTCIPISSWAFGKFLWE WASARFSW

In certain aspects, the present disclosure provides an isolated antibody, or an antigen binding fragment thereof, comprising: (i) a heavy chain variable region (V_H) comprising at least 90% (*i.e.*, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more) identity to the amino acid sequence according to SEQ ID NO:41 or 67; and (ii) a light chain variable region (V_L) comprising at least 90% identity to the amino acid sequence according to any one of SEQ ID NOs:42; 59; 65; 89, 90, or 111-120, provided that the amino acid at position 40 of the V_L according to IMGT numbering is not a cysteine, wherein the antibody or antigen binding fragment thereof binds to the antigenic loop region of HBsAg and neutralizes infection with hepatitis B virus and hepatitis delta virus.

In further embodiments, (i) the V_H comprises at least 95% identity to the amino acid sequence according to SEQ ID NO:41 or 67; and/or (ii) the V_L comprises at least 95% identity to the amino acid sequence according to any one of SEQ ID NOs:42, 59, 65, 89, 90, or 111-120.

In certain embodiments, the amino acid at position 40 of the V_L is alanine. In other embodiments, the amino acid at position 40 of the V_L is serine. In still other embodiments, the amino acid at position 40 of the V_L is glycine.

- 5 In any of the embodiments disclosed herein, the antibody or antigen binding fragment can comprise CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 sequences according to SEQ ID NOs: (i) 34-36, 37, 38, and 40, respectively; (ii) 34, 66, 36, 37, 38, and 40, respectively; (iii) 34-36, 37, 39, and 40, respectively; (iv) 34, 66, 36, 37, 39, and 40, respectively; (v) 34-36, 37, 38, and 58, respectively; (vi) 34, 66, 36, 37, 38, and 58,
10 respectively; (vii) 34-36, 37, 39, and 58, respectively; or (viii) 34, 66, 36, 37, 39, and 58, respectively.

In some embodiments, the V_L of the antibody or antigen binding fragment comprises or consists of the amino acid sequence according to SEQ ID NO:89. In some
15 embodiments, the V_L of the antibody or antigen binding fragment comprises or consists of the amino acid sequence according to SEQ ID NO:90. In other embodiments, the V_L of the antibody or antigen binding fragment comprises or consists of the amino acid sequence according to any one of SEQ ID NOs: 111-120. In certain embodiments, the V_H comprises or consists of the amino acid sequence according to SEQ ID NO:41. In
20 other embodiments, the V_H comprises or consists of the amino acid sequence according to SEQ ID NO:67.

In particular embodiments, the V_H comprises or consists of the amino acid sequence according to SEQ ID NO:41 and the V_L comprises or consists of the amino acid
25 sequence according to SEQ ID NO:89. In other embodiments, the V_H comprises or consists of the amino acid sequence according to SEQ ID NO:41 and the V_L comprises or consists of the amino acid sequence according to SEQ ID NO:90. In certain embodiments, the V_H comprises or consists of the amino acid sequence according to SEQ ID NO:41 and the V_L comprises or consists of the amino acid sequence according
30 to any one of SEQ ID NOs:111-120. In other embodiments, the V_H comprises or consists of the amino acid sequence according to SEQ ID NO:67 and the V_L comprises

or consists of the amino acid sequence according to any one of SEQ ID NOs:89, 90, and 111-120.

In another aspect, the present disclosure provides an isolated antibody, or an antigen binding fragment thereof, comprising: (i) a heavy chain variable region (V_H) comprising at least 90% identity to the amino acid sequence according to SEQ ID NO:95; and (ii) a light chain variable region (V_L) comprising at least 90% identity to the amino acid sequence according to SEQ ID NO:96, wherein the antibody or antigen binding fragment thereof binds to the antigenic loop region of HBsAg and neutralizes infection with hepatitis B virus and hepatitis delta virus.

In further embodiments, (i) the V_H comprises at least 95% identity to the amino acid sequence according to SEQ ID NO:95; and/or (ii) the V_L comprises at least 95% identity to the amino acid sequence according to SEQ ID NO:96.

15

In certain embodiments, the antibody or antigen binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 sequences according to SEQ ID NOs:97-102, respectively.

20 In particular embodiments, the V_H comprises or consists of the amino acid sequence according to SEQ ID NO:95; and the V_L comprises or consists of the amino acid sequence according to SEQ ID NO:96.

Fc Moiety

25 In some embodiments, a binding protein (*e.g.*, antibody or an antigen binding fragment thereof) of the present disclosure comprises an Fc moiety. In certain embodiments, the Fc moiety may be derived from human origin, *e.g.*, from human IgG1, IgG2, IgG3, and/or IgG4, or from another Ig class or isotype. In specific embodiments, an antibody or antigen binding fragments can comprise an Fc moiety derived from human IgG1.

30

As used herein, the term "Fc moiety" refers to a sequence comprising, consisting, consisting essentially of, or derived from a portion of an immunoglobulin heavy chain

- beginning in the hinge region just upstream of the papain cleavage site (*e.g.*, residue 216 in native IgG, taking the first residue of heavy chain constant region to be 114) and ending at the C-terminus of the immunoglobulin heavy chain. Accordingly, an Fc moiety may be a complete Fc moiety or a portion (*e.g.*, a domain) thereof. In certain
- 5 embodiments, a complete Fc moiety comprises a hinge domain, a CH2 domain, and a CH3 domain (*e.g.*, EU amino acid positions 216-446). An additional lysine residue (K) is sometimes present at the extreme C-terminus of the Fc moiety, but is often cleaved from a mature antibody. Amino acid positions within an Fc moiety have been numbered according to the EU numbering system of Kabat, *see e.g.*, Kabat *et al.*, "Sequences of
- 10 Proteins of Immunological Interest", U.S. Dept. Health and Human Services, 1983 and 1987. Amino acid positions of an Fc moiety can also be numbered according to the IMGT numbering system (including unique numbering for the C-domain and exon numbering) and the Kabat numbering system.
- 15 In some embodiments, an Fc moiety comprises at least one of: a hinge (*e.g.*, upper, middle, and/or lower hinge region) domain, a CH2 domain, a CH3 domain, or a variant, portion, or fragment thereof. In some embodiments, an Fc moiety comprises at least a hinge domain, a CH2 domain or a CH3 domain. In further embodiments, the Fc moiety is a complete Fc moiety. The amino acid sequence of an exemplary Fc moiety of human
- 20 IgG1 isotype is provided in SEQ ID NO:137. The Fc moiety may also comprise one or more amino acid insertions, deletions, or substitutions relative to a naturally occurring Fc moiety. For example, at least one of a hinge domain, CH2 domain, or CH3 domain, or a portion thereof, may be deleted. For example, an Fc moiety may comprise or consist of: (i) hinge domain (or a portion thereof) fused to a CH2 domain (or a portion
- 25 thereof), (ii) a hinge domain (or a portion thereof) fused to a CH3 domain (or a portion thereof), (iii) a CH2 domain (or a portion thereof) fused to a CH3 domain (or a portion thereof), (iv) a hinge domain (or a portion thereof), (v) a CH2 domain (or a portion thereof), or (vi) a CH3 domain or a portion thereof.
- 30 An Fc moiety of the present disclosure may be modified such that it varies in amino acid sequence from the complete Fc moiety of a naturally occurring immunoglobulin molecule, while retaining or enhancing at least one desirable function conferred by the

naturally occurring Fc moiety, and/or reducing an undesired function of a naturally occurring Fc moiety. Such functions include, for example, Fc receptor (FcR) binding, antibody half-life modulation (e.g., by binding to FcRn), ADCC function, protein A binding, protein G binding, and complement binding. Portions of naturally occurring Fc moieties which are involved with such functions have been described in the art.

For example, to activate the complement cascade, the C1q protein complex can bind to at least two molecules of IgG1 or one molecule of IgM when the immunoglobulin molecule(s) is attached to the antigenic target (Ward, E. S., and Ghetie, V., *Ther. Immunol.* 2 (1995) 77-94). Burton, D. R., described (*Mol. Immunol.* 22 (1985) 161-206) that the heavy chain region comprising amino acid residues 318 to 337 is involved in complement fixation. Duncan, A. R., and Winter, G. (*Nature* 332 (1988) 738-740), using site directed mutagenesis, reported that Glu318, Lys320 and Lys322 form the binding site to C1q. The role of Glu318, Lys320 and Lys 322 residues in the binding of C1q was confirmed by the ability of a short synthetic peptide containing these residues to inhibit complement mediated lysis.

For example, FcR binding can be mediated by the interaction of the Fc moiety (of an antibody) with Fc receptors (FcRs), which are specialized cell surface receptors on cells including hematopoietic cells. Fc receptors belong to the immunoglobulin superfamily, and shown to mediate both the removal of antibody-coated pathogens by phagocytosis of immune complexes, and the lysis of erythrocytes and various other cellular targets (e.g. tumor cells) coated with the corresponding antibody, via antibody dependent cell mediated cytotoxicity (ADCC; Van de Winkel, J. G., and Anderson, C. L., *J. Leukoc. Biol.* 49 (1991) 511-524). FcRs are defined by their specificity for immunoglobulin classes; Fc receptors for IgG antibodies are referred to as Fc γ R, for IgE as Fc ϵ R, for IgA as Fc α R and so on and neonatal Fc receptors are referred to as FcRn. Fc receptor binding is described for example in Ravetch, J. V., and Kinet, J. P., *Annu. Rev. Immunol.* 9 (1991) 457-492; Capel, P. J., et al., *Immunomethods* 4 (1994) 25-34; de Haas, M., et al., *J Lab. Clin. Med.* 126 (1995) 330-341; and Gessner, J. E., et al., *Ann. Hematol.* 76 (1998) 231-248.

Cross-linking of receptors by the Fc domain of native IgG antibodies (FcγR) triggers a wide variety of effector functions including phagocytosis, antibody-dependent cellular cytotoxicity, and release of inflammatory mediators, as well as immune complex clearance and regulation of antibody production. Fc moieties providing cross-linking of
5 receptors (e.g., FcγR) are contemplated herein. In humans, three classes of FcγR have been characterized to-date, which are: (i) FcγRI (CD64), which binds monomeric IgG with high affinity and is expressed on macrophages, monocytes, neutrophils and eosinophils; (ii) FcγRII (CD32), which binds complexed IgG with medium to low affinity, is widely expressed, in particular on leukocytes, is believed to be a central
10 player in antibody-mediated immunity, and which can be divided into FcγRIIA, FcγRIIB and FcγRIIC, which perform different functions in the immune system, but bind with similar low affinity to the IgG-Fc, and the ectodomains of these receptors are highly homologous; and (iii) FcγRIII (CD16), which binds IgG with medium to low affinity and has been found in two forms: FcγRIIIA, which has been found on NK cells,
15 macrophages, eosinophils, and some monocytes and T cells, and is believed to mediate ADCC; and FcγRIIB, which is highly expressed on neutrophils.

FcγRIIA is found on many cells involved in killing (e.g. macrophages, monocytes, neutrophils) and seems able to activate the killing process. FcγRIIB seems to play a role
20 in inhibitory processes and is found on B-cells, macrophages and on mast cells and eosinophils. Importantly, it has been shown that 75% of all FcγRIIB is found in the liver (Ganesan, L. P. et al., 2012: "FcγRIIb on liver sinusoidal endothelium clears small immune complexes," Journal of Immunology 189: 4981–4988). FcγRIIB is abundantly expressed on Liver Sinusoidal Endothelium, called LSEC, and in Kupffer cells in the
25 liver and LSEC are the major site of small immune complexes clearance (Ganesan, L. P. et al., 2012: FcγRIIb on liver sinusoidal endothelium clears small immune complexes. Journal of Immunology 189: 4981–4988).

In some embodiments, the antibodies disclosed herein and the antigen binding
30 fragments thereof comprise an Fc moiety for binding to FcγRIIB, in particular an Fc region, such as, for example IgG-type antibodies. Moreover, it is possible to engineer the Fc moiety to enhance FcγRIIB binding by introducing the mutations S267E and

L328F as described by Chu, S. Y. et al., 2008: Inhibition of B cell receptor-mediated activation of primary human B cells by coengagement of CD19 and FcγRIIb with Fc-engineered antibodies. *Molecular Immunology* 45, 3926–3933. Thereby, the clearance of immune complexes can be enhanced (Chu, S., et al., 2014: Accelerated
5 Clearance of IgE In Chimpanzees Is Mediated By Xmab7195, An Fc-Engineered Antibody With Enhanced Affinity For Inhibitory Receptor FcγRIIb. *Am J Respir Crit, American Thoracic Society International Conference Abstracts*). In some embodiments, the antibodies of the present disclosure, or the antigen binding fragments thereof, comprise an engineered Fc moiety with the mutations S267E and L328F, in particular
10 as described by Chu, S. Y. et al., 2008: Inhibition of B cell receptor-mediated activation of primary human B cells by coengagement of CD19 and FcγRIIb with Fc-engineered antibodies. *Molecular Immunology* 45, 3926–3933.

On B cells, FcγRIIB seems to function to suppress further immunoglobulin production
15 and isotype switching to, for example, the IgE class. On macrophages, FcγRIIB is thought to inhibit phagocytosis as mediated through FcγRIIA. On eosinophils and mast cells, the B form may help to suppress activation of these cells through IgE binding to its separate receptor.

20 Regarding FcγRI binding, modification in native IgG of at least one of E233-G236, P238, D265, N297, A327 and P329 reduces binding to FcγRI. IgG2 residues at positions 233-236, substituted into corresponding positions IgG1 and IgG4, reduces binding of IgG1 and IgG4 to FcγRI by 10³-fold and eliminated the human monocyte response to antibody-sensitized red blood cells (Armour, K. L., et al. *Eur. J. Immunol.*
25 29 (1999) 2613-2624).

Regarding FcγRII binding, reduced binding for FcγRIIA is found, e.g., for IgG mutation of at least one of E233-G236, P238, D265, N297, A327, P329, D270, Q295, A327, R292 and K414.

30

Two allelic forms of human FcγRIIA are the "H131" variant, which binds to IgG1 Fc with high affinity, and the "R131" variant, which binds to IgG1 Fc with low affinity. *See, e.g., Bruhns et al., Blood 113:3716-3725 (2009).*

- 5 Regarding FcγRIII binding, reduced binding to FcγRIIIA is found, e.g., for mutation of at least one of E233-G236, P238, D265, N297, A327, P329, D270, Q295, A327, S239, E269, E293, Y296, V303, A327, K338 and D376. Mapping of the binding sites on human IgG1 for Fc receptors, the above-mentioned mutation sites, and methods for measuring binding to FcγRI and FcγRIIA, are described in Shields, R. L., et al., *J. Biol.*
10 *Chem.* 276 (2001) 6591-6604.

Two allelic forms of human FcγRIIIA are the "F158" variant, which binds to IgG1 Fc with low affinity, and the "V158" variant, which binds to IgG1 Fc with high affinity. *See, e.g., Bruhns et al., Blood 113:3716-3725 (2009).*

15

- Regarding binding to FcγRII, two regions of native IgG Fc appear to be involved in interactions between FcγRIIs and IgGs, namely (i) the lower hinge site of IgG Fc, in particular amino acid residues L, L, G, G (234 – 237, EU numbering), and (ii) the adjacent region of the CH2 domain of IgG Fc, in particular a loop and strands in the
20 upper CH2 domain adjacent to the lower hinge region, e.g. in a region of P331 (Wines, B.D., et al., *J. Immunol.* 2000; 164: 5313 – 5318). Moreover, FcγRI appears to bind to the same site on IgG Fc, whereas FcRn and Protein A bind to a different site on IgG Fc, which appears to be at the CH2-CH3 interface (Wines, B.D., et al., *J. Immunol.* 2000; 164: 5313 – 5318).

25

- Also contemplated are mutations that increase binding affinity of an Fc moiety of the present disclosure to a (*i.e.*, one or more) Fcγ receptor (*e.g.*, as compared to a reference Fc moiety or antibody containing the same that does not comprise the mutation(s)). *See, e.g., Delillo and Ravetch, Cell 161(5):1035-1045 (2015) and Ahmed et al., J. Struc.*
30 *Biol.* 194(1):78 (2016), the Fc mutations and techniques of which are incorporated herein by reference.

In any of the herein disclosed embodiments, a binding protein can comprise a Fc moiety comprising a mutation selected from G236A; S239D; A330L; and I332E; or a combination comprising any two or more of the same; *e.g.*, S239D/I332E; S239D/A330L/I332E; G236A/S239D/I332E; G236A/A330L/I332E (also referred to
5 herein as "GAALIE"); or G236A/S239D/A330L/I332E. In some embodiments, the Fc moiety does not comprise S239D.

In certain embodiments, the Fc moiety may comprise or consist of at least a portion of an Fc moiety that is involved in binding to FcRn binding. In certain embodiments, the
10 Fc moiety comprises one or more amino acid modifications that improve binding affinity for (*e.g.*, enhance binding to) FcRn (*e.g.*, at a pH of about 6.0) and, in some embodiments, thereby extend *in vivo* half-life of a molecule comprising the Fc moiety (*e.g.*, as compared to a reference Fc moiety or antibody that is otherwise the same but does not comprise the modification(s)). In certain embodiments, the Fc moiety
15 comprises or is derived from a IgG Fc and a half-life-extending mutation comprises any one or more of: M428L; N434S; N434H; N434A; N434S; M252Y; S254T; T256E; T250Q; P257I Q311I; D376V; T307A; E380A (EU numbering). In certain embodiments, a half-life-extending mutation comprises M428L/N434S (also referred to herein as "MLNS"). In certain embodiments, a half-life-extending mutation comprises
20 M252Y/S254T/T256E. In certain embodiments, a half-life-extending mutation comprises T250Q/M428L. In certain embodiments, a half-life-extending mutation comprises P257I/Q311I. In certain embodiments, a half-life-extending mutation comprises P257I/N434H. In certain embodiments, a half-life-extending mutation comprises D376V/N434H. In certain embodiments, a half-life-extending mutation
25 comprises T307A/E380A/N434A.

In some embodiments, a binding protein includes a Fc moiety that comprises the substitution mutations M428L/N434S. In some embodiments, a binding protein includes a Fc moiety that comprises the substitution mutations G236A/A330L/I332E.
30 In certain embodiments, a binding protein includes a (*e.g.*, IgG) Fc moiety that comprises a G236A mutation, an A330L mutation, and a I332E mutation (GAALIE), and does not comprise a S239D mutation (*e.g.*, comprises a native S at position 239).

In particular embodiments, a binding protein includes an Fc moiety that comprises the substitution mutations: M428L/N434S and G236A/A330L/I332E, and optionally does not comprise S239D. In certain embodiments, a binding protein includes a Fc moiety that comprises the substitution mutations: M428L/N434S and
5 G236A/S239D/A330L/I332E.

In certain embodiments, a binding protein of the present disclosure comprises: CDRs and/or a variable domain and/or a heavy chain and/or a light chain according to any one of the exemplary anti-HBV antibodies disclosed herein and/or in PCT Publication No.
10 WO 2017/060504 (including antibodies HBC34, HBC34-V7, HBC34-V23, HBC34-V31, HBC34-V32, HBC34-V33, HBC34-V34, HBC34-V35, (including herein disclosed variants of HBC antibodies which comprise a substitution mutation at position 40 in the light chain (e.g., a substitution of a native cysteine with an alanine, a serine, or the like) and HBC24); and a Fc moiety comprising a G236A mutation, an
15 A330L mutation, and a I332E (GAALIE) mutation, wherein the Fc moiety optionally further comprises a M428L/N434S (MLNS) mutation. In certain embodiments, the Fc moiety does not comprise S239D.

In certain embodiments, a binding protein comprises: a CDRH1 amino acid sequence
20 according to SEQ ID NO:34, a CDRH2 amino acid sequence according to SEQ ID NO:35 or 66, a CDRH3 amino acid sequence according to SEQ ID NO:36, a CDRL1 amino acid sequence according to SEQ ID NO:37, a CDRL2 amino acid sequence according to SEQ ID NO:38 or 39, and CDRL3 amino acid sequence according to SEQ ID NO:58 or 40; and a Fc moiety comprising a GAALIE mutation. In certain embodiments, the Fc
25 moiety does not comprise a S239D mutation. In certain embodiments, the Fc moiety further comprises a MLNS mutation.

In certain embodiments, a binding protein comprises: a heavy chain variable domain (VH) amino acid sequence according to any one of SEQ ID NOs:41 or 67 and a light
30 chain variable domain (VL) amino acid sequence according to any one of SEQ ID NOs:42, 59, 65, 89, 90, and 111-120; and a Fc moiety comprising a GAALIE mutation. In certain embodiments, the Fc moiety further comprises a MLNS mutation.

In certain embodiments, a binding protein comprises a heavy chain amino acid sequence according to SEQ ID NO:138 or 91 or 92 and/or a light chain amino acid sequences according to any one of SEQ ID NOs:93 or 94. In certain embodiments, a binding protein comprises a heavy chain amino acid sequence according to SEQ ID NO: 91 and a light chain amino acid sequences according to SEQ ID NOs:93. In certain embodiments, a binding protein comprises a heavy chain amino acid sequence according to SEQ ID NO: 91 and a light chain amino acid sequences according to SEQ ID NOs:94. In certain embodiments, a binding protein comprises a heavy chain amino acid sequence according to SEQ ID NO: 92 and a light chain amino acid sequences according to SEQ ID NOs:93. In certain embodiments, a binding protein comprises a heavy chain amino acid sequence according to SEQ ID NO: 92 and a light chain amino acid sequences according to SEQ ID NOs:94.

In certain embodiments, a binding protein comprises: a CDRH1 amino acid sequence according to SEQ ID NO:97, a CDRH2 amino acid sequence according to SEQ ID NO:98, a CDRH3 amino acid sequence according to SEQ ID NO:99, a CDRL1 amino acid sequence according to SEQ ID NO:100, a CDRL2 amino acid sequence according to SEQ ID NO:100, and CDRL3 amino acid sequence according to SEQ ID NO:102; and a Fc moiety comprising a GAALIE mutation. In certain embodiments, the Fc moiety further comprises a MLNS mutation.

In certain embodiments, a binding protein comprises: a heavy chain variable domain (VH) amino acid sequence according to SEQ ID NO:95 and a light chain variable domain (VL) amino acid sequence according to SEQ ID NO:96; and a Fc moiety comprising a GAALIE mutation. In certain embodiments, the Fc moiety further comprises a MLNS mutation.

In any of the presently disclosed embodiments, a binding protein of the present disclosure includes a Fc moiety comprising a GAALIE mutation and has enhanced binding to a human FcγRIIa and/or a human FcγRIIIa, as compared to a reference

polypeptide (*i.e.*, a polypeptide, which may be a binding protein, that includes a Fc moiety that does not comprise the GAALIE mutation).

In certain embodiments, the reference polypeptide includes a Fc moiety that is a wild-type Fc moiety (e.g., of the same isotype) or is a Fc moiety that comprises one or more substitution mutation (or insertion or deletion), provided that the substitution mutation is not or does not comprise GAALIE. In certain embodiments, a binding protein comprises HBC34-V35 antibody with a GAALIE mutation (and optionally other substitution mutations, such as, for example, MLNS), and a reference polypeptide is HBC34-V35 (including a wild-type Fc moiety). In certain embodiments, the reference polypeptide does not comprise a substitution mutation that is known or believed to affect binding to a human FcγRIIa and/or to a human FcγRIIIa.

Binding between polypeptides, such as binding between a Fc moiety (or a binding protein comprising the same) and a human Fcγ Receptor, such as human FcγRIIa, human FcγRIIIa, or human Fc FcγRIIB, or a complement protein, such as C1q, can be determined or detected using methods known in the art. For example, a biolayer interferometry (BLI) assay can be performed using an Octet® RED96 (ForteBio, Fremont, California USA) instrument according to manufacturer's instructions to determine real-time association and dissociation between a first polypeptide of interest (e.g., HBC34v35 comprising a GAALIE mutation) and a second polypeptide of interest (e.g., a FcγRIIa (H131), a FcγRIIa (R131), a FcγRIIIa (F158), a FcγRIIIa (V158), or a FcγRIIb) that is captured on a sensor substrate.

In certain embodiments, a binding protein includes a Fc moiety comprising a GAALIE mutation and has enhanced binding to a human FcγRIIa (H131), a human FcγRIIa (R131), a human FcγRIIIa (F158), a human FcγRIIIa (V158), or any combination thereof, as compared to a reference polypeptide that includes a Fc moiety that does not comprise the GAALIE mutation. In certain embodiments, enhanced binding is determined by an increase (e.g., one or more of: a higher peak signal; a greater rate of association; a slower rate of dissociation; a greater area under the curve) in signal shift versus the reference binding protein in a BLI assay. In certain embodiments, the BLI

assay comprises use of Octet^(R) RED96 (ForteBio, Fremont, California USA) instrument. In further embodiments, the BLI assay comprises a tagged human FcγR captured onto an anti-penta-tag sensor and exposed to the binding protein. In some embodiments, the binding protein comprises a IgG Fab and the BLI assay further
5 comprises exposing the captured human FcγR to the binding protein in the presence of an anti-IgG Fab binding fragment to cross-link the binding proteins through the Fab fragment.

In certain embodiments, a binding protein includes a Fc moiety comprising a GAALIE
10 mutation and has enhanced binding to a human FcγRIIA (H131), a human FcγRIIA (R131), a human FcγRIIA (F158), and/or a human FcγRIIA (V158) as compared to a reference polypeptide, wherein the enhanced binding can comprise a signal shift (nanometers) in a BLI assay of 1.5, 2, 2.5, 3, or more times greater than the signal shift observed using the reference binding protein.

15 In certain embodiments, a binding protein includes a Fc moiety comprising a GAALIE mutation and has enhanced binding to a human FcγRIIA (H131), a human FcγRIIA (R131), a human FcγRIIA (F158), and a human FcγRIIA (V158), as compared to a reference polypeptide.

20 In any of the presently disclosed embodiments, a binding protein includes a Fc moiety comprising a GAALIE mutation and has reduced binding to a human FcγRIIB, as compared to a reference polypeptide. In certain embodiments, a binding protein includes a Fc moiety comprising a GAALIE mutation and does not bind to a human
25 FcγRIIB, as determined, for example, by the absence of a statistically significant signal shift versus baseline in a BLI assay.

In any of the presently disclosed embodiments, a binding protein includes a Fc moiety comprising a GAALIE mutation and has reduced binding to a human C1q (complement
30 protein), as compared to a reference polypeptide. In certain embodiments, a binding protein includes a Fc moiety comprising a GAALIE mutation and does not bind to a

human C1q, as determined by the absence of a statistically significant signal shift versus baseline in a BLI assay.

In any of the presently disclosed embodiments, a binding protein includes a Fc moiety comprising a GAALIE mutation and activates a human FcγRIIA, a human FcγRIIIA, or both, to a greater degree than does a reference polypeptide. (*i.e.*, a polypeptide, which may be a HbsAg-specific binding protein, that includes a Fc moiety that does not comprise the GAALIE mutation). In certain embodiments, the reference polypeptide includes a Fc moiety that is a wild-type Fc moiety or that comprises one or more substitution mutation, provided that the substitution mutation is not GAALIE. In certain embodiments, a binding protein comprises HBC34-V35 antibody with a GAALIE mutation (and optionally other substitution mutations, such as, for example, MLNS), and a reference polypeptide is HBC34-V35 with a wild-type Fc moiety.

Activation of a human FcγR can be determined or detected using methods known in the art. For example, a well-validated, commercially available bioreporter assay involves incubating a HBsAg-specific binding protein with a recombinant HBsAg (Engerix B, GlaxoSmithKline) in the presence of Jurkat effector cells (Promega; Cat. no: G9798) stably expressing (i) a FcγR of interest and (ii) firefly luciferase reporter under the control of a NFAT response element. Binding of Fc to cell surface-expressed FcγR drives NFAT-mediated expression of luciferase reporter gene. Luminescence is then measured with a luminometer (*e.g.*, Bio-Tek) using the Bio-Glo™ Luciferase Assay Reagent (Promega) according to the manufacturer's instructions. Activation is expressed as the average of relative luminescence units (RLU) over the background by applying the following formula: (RLU at concentration [x] of binding protein (*e.g.*, mAbs) – RLU of background).

In certain embodiments, a binding protein includes a Fc moiety comprising a GAALIE mutation activates a human FcγRIIA (H131), a human FcγRIIA (R131), a human FcγRIIIA (F158), and/or a human FcγRIIIA (V158) to a greater degree than does a reference polypeptide. In certain embodiments, a greater degree of activation refers to

a higher peak luminescence and/or a greater luminescence area under the curve, as determined using a luminescence bioreporter assay as described herein. In certain embodiments, a binding protein includes a Fc moiety comprising a GAALIE mutation and activates a human FcγRIIA (H131), a human FcγRIIA (R131), and a human FcγRIIA (F158) to a greater degree than does a reference polypeptide, wherein the greater degree of activation comprises to a peak RLU that is 1.5, 2, 2.5, 3, or more times greater than the peak RLU observed using the reference binding protein.

In any of the presently disclosed embodiments, a binding protein includes a Fc moiety comprising a GAALIE mutation does not activate a human FcγRIIB, as determined by the absence of a statistically significant and/or measurable RLU in a luminescence bioreporter assay as described above.

In any of the presently disclosed embodiments, a binding protein includes a Fc moiety comprising a GAALIE mutation and activates a human natural killer (NK) cell in the presence of HBsAg to a greater degree than does a reference polypeptide. In certain embodiments, activation of a NK cell is determined by CD107a expression (*e.g.*, by flow cytometry). In certain embodiments, the NK cell comprises a cell that comprises V158/V158 homozygous, a F158/F158 homozygous, or a V158/F158 heterozygous FcγRIIIa genotype.

It will be appreciated that any binding protein including a Fc moiety comprising a GAALIE mutation according to the present disclosure can perform or possess any one or more of the features described herein; *e.g.*, enhanced binding to a human FcγRIIA and/or a human FcγRIIA as compared to a reference polypeptide; reduced binding to a human FcγRIIB as compared to a reference polypeptide (and/or no binding to a human FcγRIIB); reduced binding to a human C1q as compared to a reference polypeptide (and/or no binding to a human C1q); activates a FcγRIIA, a human FcγRIIA, or both, to a greater degree than does a reference polypeptide; does not activate a human FcγRIIB; and/or activates a human natural killer (NK) cell in the presence of HBsAg to

a greater degree than does a reference polypeptide (*e.g.*, an antibody that is specific for HBsAg and includes a Fc moiety that does not comprise a GAALIE mutation).

In certain embodiments, a binding protein of the present disclosure includes a Fc moiety comprising a GAALIE mutation and: (i) has enhanced binding to a human FcγRIIA, a
5 human FcγRIIIA, or both, as compared to a reference polypeptide that includes a Fc moiety that does not comprise G236A/A330L/I332E, wherein the human FcγRIIA is optionally H131 or R131, and/or the human FcγRIIIA is optionally F158 or V158; (ii) has reduced binding to a human FcγRIIB, as compared to a reference polypeptide that includes a Fc moiety that does not comprise G236A/A330L/I332E; (iii) does not bind
10 to a human FcγRIIB; (iv) has reduced binding to a human C1q, as compared to a reference polypeptide that includes a Fc moiety that does not comprise G236A/A330L/I332E; (v) does not bind to a human C1q; (vi) activates a FcγRIIA, a human FcγRIIIA, or both, to a greater degree than does a reference polypeptide that includes a Fc moiety that does not comprise G236A/A330L/I332E, wherein the human
15 FcγRIIA is optionally H131 or R131, and/or the human FcγRIIIA is optionally F158 or V158; (vii) does not activate a human FcγRIIB; (viii) activates a human natural killer (NK) cell in the presence of HBsAg to a greater degree than does a reference polypeptide that includes a Fc moiety that does not comprise G236A/A330L/I332E, wherein the reference polypeptide is optionally an antibody that binds to an HB Ag, optionally an HBsAg; (ix) has an HBsAg EC₅₀ of from about 12.75 ng/mL to about
20 19.9 ng/mL, or from about 12.75 ng/mL to about 12.84 ng/mL, or about 12.79 ng/mL, or from about 16.22 ng/mL to about 19.9 ng/mL, or about 17.97 ng/mL, and/or (b) has an HBeAg EC₅₀ about from about 10.78 ng/mL to about 13.72 ng/mL, or from about 10.78 ng/mL to about 10.93 ng/mL, or about 10.85 ng/mL, or from about 11.59 ng/mL
25 to about 13.72 ng/mL, or about 12.61 ng/mL, wherein the HBV is optionally HBV Genotype D, and wherein the EC₅₀ is optionally determined *in vitro* by measuring HBsAg or HBeAg, respectively, secreted by HepG2 cells overexpressing NTCP and infected with the HBV, at day 7 following administration of the antibody or antigen binding fragment to the HepG2 cells; (x) has an HBsAg EC₅₀ of from about 10.43
30 ng/mL to about 22.41 ng/mL, or about 13.81 ng/mL to about 16.56 ng/mL, or about 15.12 ng/mL, or from about 12.24 ng/mL to about 22.41 ng/mL, or about 16.56 ng/mL, or from about 10.43 ng/mL to about 20.08 ng/mL, or about 14.47 ng/mL, and/or (b)

- has an HBeAg EC_{50} about from about 10.39 ng/mL to about 13.99 ng/mL, or from about 10.63 ng/mL to about 10.66 ng/mL, or about 10.64 ng/mL, or from about 10.39 ng/mL to about 10.60 ng/mL, or about 10.49 ng/mL, or from about 13.25 ng/mL to about 13.99 ng/mL, or about 13.61 ng/mL, wherein the HBV is optionally HBV
- 5 Genotype D, and wherein the EC_{50} is optionally determined *in vitro* by measuring HBsAg or HBeAg, respectively, secreted by HepG2 cells overexpressing NTCP and infected with the HBV, at day 7 following administration of the antibody or antigen binding fragment to the HepG2 cells; (xi) is capable of binding to an HBsAg variant comprising HBsAg-Y100C/P120T, HBsAg-P120T, HBsAg-P120S/S143L, HBsAg-
- 10 C121S, HBsAg-R122D, HBsAg-R122I, HBsAg-T123N, HBsAg-Q129H, HBsAg-Q129L, HBsAg-M133H, HBsAg-M133L, HBsAg-M133T, HBsAg-K141E, HBsAg-P142S, HBsAg-S143K, HBsAg-D144A, HBsAg-G145R, HBsAg-N146A, or any combination thereof; (xii) has improved binding to an HBsAg variant comprising HBsAg-Y100C/P120T, HBsAg-P120T, HBsAg-P120S/S143L, HBsAg-C121S,
- 15 HBsAg-R122D, HBsAg-R122I, HBsAg-T123N, HBsAg-Q129H, HBsAg-Q129L, HBsAg-M133H, HBsAg-M133L, HBsAg-M133T, HBsAg-K141E, HBsAg-P142S, HBsAg-S143K, HBsAg-D144A, HBsAg-G145R, HBsAg-N146A, or any combination thereof, as compared to a reference antibody or antigen binding fragment that binds to HBsAg and that includes a Fc moiety that does not comprise G236A/A330L/I332E;
- 20 and/or (xiii) is capable of neutralizing (a) an HBV of genotype A with an EC_{50} of about 2.34 ng/mL; (b) an HBV of genotype B with an EC_{50} of about 2.22 ng/mL; (c) an HBV of genotype C with an EC_{50} of about 0.92 ng/mL; (d) an HBV of genotype D with an EC_{50} of about 1.10 ng/mL; (e) an HBV of genotype E with an EC_{50} of about 1.12 ng/mL; (f) an HBV of genotype F with an EC_{50} of about 1.93 ng/mL; (g) an HBV of
- 25 genotype G with an EC_{50} of about 1.43 ng/mL; and/or (h) an HBV of genotype H with an EC_{50} of about 1.93 ng/mL, wherein the EC_{50} is optionally determined using a recombinant HDV engineered to express an HBsAg of the HBV genotype.

Alternatively or additionally, the Fc moiety of a binding protein of the disclosure can

30 comprise at least a portion known in the art to be required for Protein A binding; and/or the Fc moiety of an antibody of the disclosure comprises at least the portion of an Fc

molecule known in the art to be required for protein G binding. In some embodiments, a retained function comprises the clearance of HBsAg and HBVg. Accordingly, in certain embodiments, an Fc moiety comprises at least a portion known in the art to be required for Fc γ R binding. As outlined above, an Fc moiety may thus at least comprise (i) the lower hinge site of native IgG Fc, in particular amino acid residues L, L, G, G (234 – 237, EU numbering), and (ii) the adjacent region of the CH2 domain of native IgG Fc, in particular a loop and strands in the upper CH2 domain adjacent to the lower hinge region, e.g. in a region of P331, for example a region of at least 3, 4, 5, 6, 7, 8, 9, or 10 consecutive amino acids in the upper CH2 domain of native IgG Fc around P331, e.g. between amino acids 320 and 340 (EU numbering) of native IgG Fc.

In some embodiments, a binding protein according to the present disclosure comprises an Fc region. As used herein, the term "Fc region" refers to the portion of an immunoglobulin formed by two or more Fc moieties of antibody heavy chains. For example, an Fc region may be monomeric or "single-chain" Fc region (i.e., a scFc region). Single chain Fc regions are comprised of Fc moieties linked within a single polypeptide chain (e.g., encoded in a single contiguous nucleic acid sequence). Exemplary scFc regions are disclosed in WO 2008/143954 A2, and are incorporated by reference herein. The Fc region can be or comprise a dimeric Fc region. A "dimeric Fc region" or "dcFc" refers to the dimer formed by the Fc moieties of two separate immunoglobulin heavy chains. The dimeric Fc region may be a homodimer of two identical Fc moieties (e.g., an Fc region of a naturally occurring immunoglobulin) or a heterodimer of two non-identical Fc moieties (e.g., one Fc monomer of the dimeric Fc region comprises at least one amino acid modification (e.g., substitution, deletion, insertion, or chemical modification) that is not present in the other Fc monomer, or one Fc monomer may be truncated as compared to the other).

Particular embodiments include those antibodies and antigen binding fragments having a heavy chain (e.g., VH-hinge-CH1-CH2-CH3) according to SEQ ID NO:91 or SEQ ID NO:92 or SEQ ID NO:138, and those having a light chain (i.e., VL-CL) according to SEQ ID NO:93 or SEQ ID NO:94. In certain embodiments, an antibody or antigen binding fragment comprises a heavy chain according to SEQ ID NO:91 and a light

chain according to SEQ ID NO:93. In other embodiments, an antibody or antigen binding fragment comprises a heavy chain according to SEQ ID NO:92 and a light chain according to SEQ ID NO:94. In other embodiments, an antibody or antigen binding fragment comprises a heavy chain according to SEQ ID NO:91 and a light chain according to SEQ ID NO:94. In other embodiments, an antibody or antigen binding fragment comprises a heavy chain according to SEQ ID NO:92 and a light chain according to SEQ ID NO:93. In some embodiments, an antibody or antigen binding fragment comprises or consists of a heavy chain according to SEQ ID NO:129. In some embodiments, an antibody or antigen binding fragment comprises or consists of a heavy chain according to SEQ ID NO:138, and optionally a light chain according to any one of SEQ ID NOs:93 or 94. These sequences are provided in the Sequence Listing.

Presently disclosed Fc moieties may comprise Fc sequences or regions of the same or different class and/or subclass. For example, Fc moieties may be derived from an immunoglobulin (*e.g.*, a human immunoglobulin) of an IgG1, IgG2, IgG3 or IgG4 subclass, or from any combination thereof. In certain embodiments, the Fc moieties of Fc region are of the same class and subclass. However, the Fc region (or one or more Fc moieties of an Fc region) may also be chimeric, whereby a chimeric Fc region may comprise Fc moieties derived from different immunoglobulin classes and/or subclasses. For example, at least two of the Fc moieties of a dimeric or single-chain Fc region may be from different immunoglobulin classes and/or subclasses. In certain embodiments, a dimeric Fc region can comprise sequences from two or more different isotypes or subclasses; *e.g.*, a SEEDbody ("strand-exchange engineered domains"), see Davis *et al.*, *Protein Eng. Des. Sel.* 23(4):195 (2010).

Additionally or alternatively, chimeric Fc regions may comprise one or more chimeric Fc moieties. For example, the chimeric Fc region or moiety may comprise one or more portions derived from an immunoglobulin of a first subclass (*e.g.*, an IgG1, IgG2, or IgG3 subclass) while the remainder of the Fc region or moiety is of a different subclass. For example, an Fc region or moiety of an Fc polypeptide may comprise a CH2 and/or CH3 domain derived from an immunoglobulin of a first subclass (*e.g.*, an IgG1, IgG2 or

IgG4 subclass) and a hinge region from an immunoglobulin of a second subclass (e.g., an IgG3 subclass). For example, the Fc region or moiety may comprise a hinge and/or CH2 domain derived from an immunoglobulin of a first subclass (e.g., an IgG4 subclass) and a CH3 domain from an immunoglobulin of a second subclass (e.g., an IgG1, IgG2, or IgG3 subclass). For example, the chimeric Fc region may comprise an Fc moiety (e.g., a complete Fc moiety) from an immunoglobulin for a first subclass (e.g., an IgG4 subclass) and an Fc moiety from an immunoglobulin of a second subclass (e.g., an IgG1, IgG2 or IgG3 subclass). For example, the Fc region or moiety may comprise a CH2 domain from an IgG4 immunoglobulin and a CH3 domain from an IgG1 immunoglobulin. For example, the Fc region or moiety may comprise a CH1 domain and a CH2 domain from an IgG4 molecule and a CH3 domain from an IgG1 molecule. For example, the Fc region or moiety may comprise a portion of a CH2 domain from a particular subclass of antibody, e.g., EU positions 292-340 of a CH2 domain. For example, an Fc region or moiety may comprise amino acids a positions 292-340 of CH2 derived from an IgG4 moiety and the remainder of CH2 derived from an IgG1 moiety (alternatively, 292-340 of CH2 may be derived from an IgG1 moiety and the remainder of CH2 derived from an IgG4 moiety).

It will also be appreciated that any antibody, antigen-binding fragment, or Fc region or moiety of the present disclosure can be of any allotype and/or haplotype. For example, human Immunoglobulin G allotypes include those disclosed in Jefferis and LeFranc, *mAbs* 1(4):1-7 (2009), which allotypes (including G1m (1(a); 2(x); 3(f); and 17(z)); G2m (23(n)); G3m (21(g1); 28(g5); 11(b0); 5(b2); 13(b3); 14(b4); 10(b5); 15(s); 16(t); 6(c3); 24(c5); 26(u); and 27(v)); A2m (1 and 2); and Km (1; 2; and 3) and haplotypes, and resultant amino acid sequences, and combinations thereof, are incorporated herein by reference. In certain embodiments, an antibody, antigen-binding fragment, or Fc region or moiety of the present disclosure comprises a IgG1 allotype g1m17, k1.

Moreover, an Fc region or moiety may (additionally or alternatively) for example comprise a chimeric hinge region. For example, the chimeric hinge may be derived, e.g. in part, from an IgG1, IgG2, or IgG4 molecule (e.g., an upper and lower middle hinge sequence) and, in part, from an IgG3 molecule (e.g., an middle hinge sequence). In

another example, an Fc region or moiety may comprise a chimeric hinge derived, in part, from an IgG1 molecule and, in part, from an IgG4 molecule. In another example, the chimeric hinge may comprise upper and lower hinge domains from an IgG4 molecule and a middle hinge domain from an IgG1 molecule. Such a chimeric hinge
5 may be made, for example, by introducing a proline substitution (Ser228Pro) at EU position 228 in the middle hinge domain of an IgG4 hinge region. In another embodiment, the chimeric hinge can comprise amino acids at EU positions 233-236 are from an IgG2 antibody and/or the Ser228Pro mutation, wherein the remaining amino acids of the hinge are from an IgG4 antibody (*e.g.*, a chimeric hinge of the sequence
10 ESKYGPPCPPCPAPPVAGP). Further chimeric hinges which may be used in the Fc moiety of the antibody according to the present disclosure are described in US 2005/0163783 A1.

In some embodiments of the binding proteins disclosed herein, the Fc moiety, or the Fc
15 region, comprises or consists of an amino acid sequence derived from a human immunoglobulin sequence (*e.g.*, from an Fc region or Fc moiety from a human IgG molecule). However, polypeptides may comprise one or more amino acids from another mammalian species. For example, a primate Fc moiety or a primate binding site may be included in the subject polypeptides. Alternatively, one or more murine amino acids
20 may be present in the Fc moiety or in the Fc region.

Nucleic acid molecule

In another aspect, the disclosure provides a nucleic acid molecule comprising a
25 polynucleotide encoding an antibody, antigen binding fragment, or fusion protein according to the present disclosure

Table 4 shows exemplary V_H-, V_L-, CH-, CL-, HC-, and LC-encoding nucleotide sequences according to the present disclosure:

Antibody nucleotide acid sequence description	SEQ ID NO:	nucleotide sequence
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Antibody nucleotide acid sequence description	SEQ ID NO:	nucleotide sequence
V _H of HBC34-V7, HBC34-V35, and HBC34-V34 (codon optimized)	103	GAGCTGCAGCTGGTGGAGTCCGGCGGC GGCTGGGTGCAGCCTGGCGGCTCCCAGA GGCTGAGCTGTGCCGCTTCTGGCAGGAT CTTCCGGTCCTTTTACATGTCTTGGGTGC GGCAGGCTCCAGGCAAGGGCCTGGAGT GGGTGGCTACCATCAACCAGGACGGCTC CGAGAAGCTGTATGTGGATAGCGTGAA GGGCAGATTCACAATCTCTCGCGACAAC GCCAAGAAGTCCCTGTTTCTGCAGATGA ACAATCTGAGGGTGGAGGATACCGCCGT GTACTATTGCGCCGCTTGGTCTGGCAAT AGCGGCGGCATGGACGTGTGGGGACAG GGCACCAACCGTGTCCGTGTCCAGC
HBC34-V34 V _L (codon optimized)	104	AGCTACGAGCTGACACAGCCCCCTTCCG TGTCCGTGTCCCCTGGACAGACCGTGTC CATCCCATGCAGCGGCGACAAGCTGGGC AACAAGAACGTGTCCTGGTTTCAGCATA AGCCTGGCCAGTCCCCCGTGCTGGTCAT CTACGAGGTGAAGTATAGGCCAGCGG CATCCCTGAGCGGTTCTCTGGCTCCAAC AGCGGCAATACAGCCACCCTGACAATCT CTGGCACACAGGCTATGGACGAGGCCG CTTATTTCTGCCAGACCTTTGATTCCACC ACAGTGGTGTTCGGCGGCGGCACCAGAC TGACAGTGCTG
HBC34-V35 V _L (codon optimized)	105	AGCTACGAGCTGACACAGCCCCCTTCCG TGTCCGTGTCCCCTGGACAGACCGTGTC CATCCCATGCAGCGGCGACAAGCTGGGC AACAAGAACGTGGCCTGGTTTCAGCATA

Antibody nucleotide acid sequence description	SEQ ID NO:	nucleotide sequence
		AGCCTGGCCAGTCCCCCGTGCTGGTCAT CTACGAGGTGAAGTATAGGCCAGCGG CATCCCTGAGCGGTTCTCTGGCTCCAAC AGCGGCAATACAGCCACCCTGACAATCT CTGGCACACAGGCTATGGACGAGGCCG CTTATTTCTGCCAGACCTTTGATTCCACC ACAGTGGTGTTCGGCGGCGGCACCAGAC TGACAGTGCTG
HBC34-V7 V _L (codon optimized)	110	AGCTACGAGCTGACACAGCCCCCTTCCG TGTCCGTGTCCCCTGGACAGACCGTGTC CATCCCATGCAGCGGCGACAAGCTGGGC AACAAGAACGTGTGCTGGTTTCAGCATA AGCCTGGCCAGTCCCCCGTGCTGGTCAT CTACGAGGTGAAGTATAGGCCAGCGG CATCCCTGAGCGGTTCTCTGGCTCCAAC AGCGGCAATACAGCCACCCTGACAATCT CTGGCACACAGGCTATGGACGAGGCCG CTTATTTCTGCCAGACCTTTGATTCCACC ACAGTGGTGTTCGGCGGCGGCACCAGAC TGACAGTGCTG
HBC24 V _H (wild type)	106	gaggtgcagttgttgagctctgggggaggcttggtacagcctgg ggggtccctgagactctcctgtgcagcctctGGATCCACT TTTACCAAATATGCCatgagctgggtccgtcaggct ccagggaaggggctggagtggtcgcaagtATTAGTGG AAGTgttcctggttttGGTATTGACACAtactacgca gactccgttaagggccggttcaccatctccagagacactccaag aacaccctgtatctgcaaatgaacagcctgagagccgaggacac ggccttatattactgtGCGAAAGATGTCTGGGGTTA TCGGGTCATACTATTACTACGCTATGGA

Antibody nucleotide acid sequence description	SEQ ID NO:	nucleotide sequence
		CGTCtggggtaa
HBC24 V _L (wild type)	107	aaattgtgtgacgcagctccaggcacccctgtcttfgtctcagggaagagccaccctctcctgcagggccagtCAGGGTCTTAGCAGCAGTTACtagcctggtaccagcagaaacctggccaggctcccaggctcctcatctatAGTGCGTCCaccaggccactggcatccagacaggttcagtggcagtggtctgggacagactcactctcaccatcagcagactggagcctgaagatttgcagtgtattactgtCAACAGTATGCTTACTCACCTCGGTGGACGttcgccaagggaaccaaggtggagatcaaac
HBC24 V _H (codon optimized)	108	GAGGTGCAGCTGCTGGAAAGCGGCGGC GGCCTGGTGCAGCCCGGCGGCTCCCTGAGGCTGTCTTGCGCCGCCTCTGGCAGCAC CTTCACAAAGTATGCAATGTCTTGGGTG CGCCAGGCACCAGGCAAGGGCCTGGAG TGGGTGGCCTCCATCTCTGGCAGCGTGC CTGGCTTCGGCATCGACACCTACTATGC CGATTCCGTGAAGGGCCGGTTTACAATC AGCAGAGACACCTCCAAGAACACACTG TATCTGCAGATGAATTCTCTGCGGGCCG AGGACACCGCCCTGTACTATTGTGCCAA GGATGTGGGCGTGATCGGCAGCTACTAT TACTATGCAATGGACGTGTGGGGACAGG GAACAGCAGTGACAGTGAGCTCC
HBC24 V _L (codon optimized)	109	GAGATCGTGCTGACCCAGTCTCCTGGCA CACTGTCCCTGTCCCCTGGAGAGAGAGC CACCCTGTCTGCAGAGCCTCTCAGGGC CTGAGCTCCTCTTACCTGGCCTGGTATC AGCAGAAGCCTGGACAGGCCCTCGGCT

Antibody nucleotide acid sequence description	SEQ ID NO:	nucleotide sequence
		GCTGATCTACTCTGCCTCCACCAGAGCA ACAGGCATTCCTGACCGCTTCTCCGGAT CTGGAAGCGGCACAGACTTCACCCTGAC AATCAGCCGGCTGGAGCCTGAGGACTTC GCCGTGTACTATTGTCAGCAGTACGCCT ATTCCCCAAGGTGGACCTTTGGCCAGGG CACAAAGGTGGAGATCAAG
HBC34-V7, HBC34-V34, HBC34-V35 CH1-hinge-CH2-CH3 (codon-optimized)	130	GCCTCCACAAAGGGCCCAAGCGTGTTC CACTGGCTCCCTCTTCCAAGTCTACCTCC GGCGGCACAGCCGCTCTGGGATGTCTGG TGAAGGATTACTTCCCAGAGCCCGTGAC CGTGTCTTGGAACCTCCGGCGCCCTGACC AGCGGAGTGCATACATTTCAGCTGTGC TGCAGAGCTCTGGCCTGTACTCTCTGTC CAGCGTGGTGACCGTGCCCTCTTCCAGC CTGGGCACCCAGACATATATCTGCAACG TGAATCACAAGCCAAGCAATAACAAAGG TGGACAAGAAGGTGGAGCCCAAGTCTT GTGATAAGACCCATACATGCCCTCCATG TCCAGCTCCAGAGCTGCTGGGCGGCCCA AGCGTGTTCTGTTTCCACCCAAGCCTA AGGATACCCTGATGATCTCCAGAACCCC CGAGGTGACATGCGTGGTGGTGGACGTG AGCCACGAGGATCCTGAGGTGAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGC ATAATGCTAAGACCAAGCCCAGGGAGG AGCAGTACAACCTCTACCTATCGGGTGGT GTCCGTGCTGACAGTGCTGCACCAGGAT TGGCTGAACGGCAAGGAGTATAAGTGC

Antibody nucleotide acid sequence description	SEQ ID NO:	nucleotide sequence
		AAGGTGTCTAATAAGGCCCTGCCCGCTC CTATCGAGAAGACCATCTCCAAGGCCAA GGGCCAGCCTAGAGAGCCACAGGTGTA CACACTGCCTCCATCTCGCGATGAGCTG ACCAAGAACCAGGTGTCCCTGACATGTC TGGTGAAGGGCTTCTATCCTTCCGACAT CGCTGTGGAGTGGGAGAGCAATGGCCA GCCAGAGAACAATTACAAGACCACACC CCCTGTGCTGGACAGCGATGGCTCTTTC TTTCTGTATAGCAAGCTGACCGTGGACA AGTCTCGCTGGCAGCAGGGCAACGTGTT TAGCTGTTCTGTGATGCATGAGGCCCTG CACAATCATTATACACAGAAGTCCCTGA GCCTGTCTCCTGGCAAG
HBC34-V7, HBC34-V34, HBC34-V35 HC (VH-CH1-hinge-CH2- CH3) (codon-optimized)	131	GAGCTGCAGCTGGTGGAGTCCGGCGGC GGCTGGGTGCAGCCTGGCGGCTCCCAGA GGCTGAGCTGTGCCGCTTCTGGCAGGAT CTTCCGGTCCTTTTACATGTCTTGGGTGC GGCAGGCTCCAGGCAAGGGCCTGGAGT GGGTGGCTACCATCAACCAGGACGGCTC CGAGAAGCTGTATGTGGATAGCGTGAA GGGCAGATTACAATCTCTCGCGACAAC GCCAAGAAGTCCCTGTTTCTGCAGATGA ACAATCTGAGGGTGGAGGATACCGCCGT GTACTATTGCGCCGCTTGGTCTGGCAAT AGCGGCGGCATGGACGTGTGGGGACAG GGCACCACCGTGTCCGTGTCCAGCGCCT CCACAAAGGGCCCAAGCGTGTTCCTACT GGCTCCCTCTTCCAAGTCTACCTCCGGC

Antibody nucleotide acid sequence description	SEQ ID NO:	nucleotide sequence
		GGCACAGCCGCTCTGGGATGTCTGGTGA AGGATTACTTCCCAGAGCCCGTGACCGT GTCTTGGAACCTCCGGCGCCCTGACCAGC GGAGTGCATACATTTCCAGCTGTGCTGC AGAGCTCTGGCCTGTACTCTCTGTCCAG CGTGGTGACCGTGCCCTCTTCCAGCCTG GGCACCCAGACATATATCTGCAACGTGA ATCACAAGCCAAGCAATACAAAGGTGG ACAAGAAGGTGGAGCCCAAGTCTTGTG ATAAGACCCATACATGCCCTCCATGTCC AGCTCCAGAGCTGCTGGGCGGCCCAAGC GTGTTCTGTGTTCCACCCAAGCCTAAGG ATACCCTGATGATCTCCAGAACCCCCGA GGTGACATGCGTGGTGGTGGACGTGAGC CACGAGGATCCTGAGGTGAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGCATA ATGCTAAGACCAAGCCCAGGGAGGAGC AGTACAACCTCTACCTATCGGGTGGTGTC CGTGCTGACAGTGCTGCACCAGGATTGG CTGAACGGCAAGGAGTATAAGTGCAAG GTGTCTAATAAGGCCCTGCCCGCTCCTA TCGAGAAGACCATCTCCAAGGCCAAGG GCCAGCCTAGAGAGCCACAGGTGTACA CACTGCCTCCATCTCGCGATGAGCTGAC CAAGAACCAGGTGTCCCTGACATGTCTG GTGAAGGGCTTCTATCCTTCCGACATCG CTGTGGAGTGGGAGAGCAATGGCCAGC CAGAGAACAATTACAAGACCACACCCC CTGTGCTGGACAGCGATGGCTCTTTCTTT

Antibody nucleotide acid sequence description	SEQ ID NO:	nucleotide sequence
		CTGTATAGCAAGCTGACCGTGGACAAGT CTCGCTGGCAGCAGGGCAACGTGTTTAG CTGTTCTGTGATGCATGAGGCCCTGCAC AATCATTATACACAGAAGTCCCTGAGCC TGTCTCCTGGCAAGTGATGAGGTACCGT GCGACGGCCGGCAAGCCCCCGCTCCCCG GGCTCTCGCGGTCTGACGAGGAAAGCTT
HBC34-V7 CL (codon-optimized)	132	GGACAGCCAAAGGCTGCTCCATCTGTGA CCCTGTTTCCACCCTCTTCCGAGGAGCT GCAGGCCAACAAGGCCACCCTGGTGTGC CTGATCTCTGACTTCTACCCTGGAGCTGT GACAGTGGCTTGGAAGGCTGATAGCTCT CCCGTGAAGGCTGGCGTGGAGACAACA ACCCCTAGCAAGCAGTCTAACAATAAGT ACGCCGCTTCCAGCTATCTGTCTCTGAC ACCAGAGCAGTGGAAGTCCCACCGCTCT TATTCCTGCCAGGTGACCCATGAGGGCA GCACCGTGGAGAAGACAGTGGCCCCCA CCGAGTGTCT
HBC34-V7 LC (VL-CL) (codon-optimized)	133	AGCTACGAGCTGACACAGCCCCCTCCG TGTCCGTGTCCCCTGGACAGACCGTGTC CATCCCATGCAGCGGCGACAAGCTGGGC AACAAGAACGTGTGCTGGTTTCAGCATA AGCCTGGCCAGTCCCCCGTGCTGGTCAT CTACGAGGTGAAGTATAGGCCAGCGG CATCCCTGAGCGGTTCTCTGGCTCCAAC AGCGGCAATACAGCCACCCTGACAATCT CTGGCACACAGGCTATGGACGAGGCCG CTTATTTCTGCCAGACCTTTGATTCCACC

Antibody nucleotide acid sequence description	SEQ ID NO:	nucleotide sequence
		ACAGTGGTGTTCGGCGGCGGCACCAGAC TGACAGTGCTGGGACAGCCAAAGGCTG CTCCATCTGTGACCCTGTTTCCACCCTCT TCCGAGGAGCTGCAGGCCAACAAGGCC ACCCTGGTGTGCCTGATCTCTGACTTCTA CCCTGGAGCTGTGACAGTGGCTTGGAAG GCTGATAGCTCTCCCGTGAAGGCTGGCG TGGAGACAACAACCCCTAGCAAGCAGT CTAACAATAAGTACGCCGCTTCCAGCTA TCTGTCTCTGACACCAGAGCAGTGGAAG TCCCACCGCTCTTATTCCTGCCAGGTGA CCCATGAGGGCAGCACCGTGGAGAAGA CAGTGGCCCCCACCAGAGTGTCT
HBC34-V34, HBC34-V35 CL (codon-optimized)	134	GGACAGCCAAAGGCTGCTCCATCTGTGA CCCTGTTTCCACCCTCTTCCGAGGAGCT GCAGGCCAACAAGGCCACCCTGGTGTGC CTGATCTCTGACTTCTACCCTGGAGCTGT GACAGTGGCTTGGAAGGCTGATAGCTCT CCCGTGAAGGCTGGCGTGGAGACAACA ACCCCTAGCAAGCAGTCTAACAATAAGT ACGCCGCTTCCAGCTATCTGTCTCTGAC ACCAGAGCAGTGGAAGTCCCACCGCTCT TATTCCTGCCAGGTGACCCATGAGGGCA GCACCGTGGAGAAGACAGTGGCCCCCA CCGAGTGTCT
HBC34-V34 LC (VL-CL) (codon-optimized)	135	AGCTACGAGCTGACACAGCCCCCTTCCG TGTCCGTGTCCCCTGGACAGACCGTGTC CATCCCATGCAGCGGCGACAAGCTGGGC AACAAGAACGTGTCCTGGTTTCAGCATA

Antibody nucleotide acid sequence description	SEQ ID NO:	nucleotide sequence
		AGCCTGGCCAGTCCCCCGTGCTGGTCAT CTACGAGGTGAAGTATAGGCCAGCGG CATCCCTGAGCGGTTCTCTGGCTCCAAC AGCGGCAATACAGCCACCCTGACAATCT CTGGCACACAGGCTATGGACGAGGCCG CTTATTTCTGCCAGACCTTTGATTCCACC ACAGTGGTGTTCGGCGGCGGCACCAGAC TGACAGTGCTGGGACAGCCAAAGGCTG CTCCATCTGTGACCCTGTTTCCACCCTCT TCCGAGGAGCTGCAGGCCAACAAGGCC ACCCTGGTGTGCCTGATCTCTGACTTCTA CCCTGGAGCTGTGACAGTGGCTTGGAAG GCTGATAGCTCTCCCGTGAAGGCTGGCG TGGAGACAACAACCCCTAGCAAGCAGT CTAACAATAAGTACGCCGCTTCCAGCTA TCTGTCTCTGACACCAGAGCAGTGGAAG TCCCACCGCTCTTATTCCTGCCAGGTGA CCCATGAGGGCAGCACCGTGGAGAAGA CAGTGGCCCCCACCAGTGTTCT
HBC34-V35 LC (VL-CL) (codon- optimized)	136	AGCTACGAGCTGACACAGCCCCCTTCG TGTCCGTGTCCCCTGGACAGACCGTGTC CATCCCATGCAGCGGCGACAAGCTGGGC AACAAGAACGTGGCCTGGTTTCAGCATA AGCCTGGCCAGTCCCCCGTGCTGGTCAT CTACGAGGTGAAGTATAGGCCAGCGG CATCCCTGAGCGGTTCTCTGGCTCCAAC AGCGGCAATACAGCCACCCTGACAATCT CTGGCACACAGGCTATGGACGAGGCCG CTTATTTCTGCCAGACCTTTGATTCCACC

Antibody nucleotide acid sequence description	SEQ ID NO:	nucleotide sequence
		ACAGTGGTGTTCGGCGGCGGCACCAGAC TGACAGTGCTGGGACAGCCAAAGGCTG CTCCATCTGTGACCCTGTTTCCACCCTCT TCCGAGGAGCTGCAGGCCAACAAGGCC ACCCTGGTGTGCCTGATCTCTGACTTCTA CCCTGGAGCTGTGACAGTGGCTTGGAAG GCTGATAGCTCTCCCGTGAAGGCTGGCG TGGAGACAACAACCCCTAGCAAGCAGT CTAACAATAAGTACGCCGCTTCCAGCTA TCTGTCTCTGACACCAGAGCAGTGGAAG TCCCACCGCTCTTATTCCTGCCAGGTGA CCCATGAGGGCAGCACCGTGGAGAAGA CAGTGGCCCCCACCAGAGTGTCT

Due to the redundancy of the genetic code, the present disclosure also comprises sequence variants of these nucleic acid sequences and in particular such sequence variants, which encode the same amino acid sequences.

In certain embodiments, a polynucleotide or nucleic acid molecule comprises a nucleotide sequence sharing at least 80% identity to the nucleotide sequence according to any one of SEQ ID NOs: 103-110 and 130-136, wherein the nucleotide sequence is codon optimized for expression by a host cell.

In particular embodiments, a nucleic acid molecule according to the present disclosure comprises or consists of a nucleic acid sequence according to any one of SEQ ID NOs: 103-110 and 130-136.

In certain embodiments, a polynucleotide comprises a V_H -encoding nucleotide sequence according to SEQ ID NO:103 and a V_L -encoding nucleotide sequence

according to SEQ ID NO:105. In other embodiments, a polynucleotide comprises a V_H-encoding nucleotide sequence according to SEQ ID NO:103, and a V_L-encoding nucleotide sequence according to SEQ ID NO:104. In other embodiments, a polynucleotide comprises a V_H-encoding nucleotide sequence according to SEQ ID NO: 108, and a V_L-encoding nucleotide sequence according to SEQ ID NO: 109.

Also provided herein are polynucleotides that encode an antibody or antigen binding fragment, wherein the polynucleotide comprises or consists of a V_H-encoding nucleotide sequence according to SEQ ID NO:103 and a V_L-encoding nucleotide sequence according to SEQ ID NO:110, wherein the encoded antibody or antigen binding fragment binds to the antigenic loop region of HBsAg and neutralizes infection with hepatitis B virus and hepatitis delta virus.

In any of the presently disclosed embodiments, a polynucleotide can comprise a CH1-hinge-CH2-CH3-encoding nucleotide sequence according to SEQ ID NO:130, and/or comprises a HC (VH-CH1-hinge-CH3-CH3)-encoding nucleotide sequence according to SEQ ID NO:131. In some embodiments, a polynucleotide comprises a CL-encoding nucleotide sequence according to SEQ ID NO:132 and/or comprises a LC (VL-CL)-encoding nucleotide sequence according to SEQ ID NO:133. In other embodiments, a polynucleotide comprises a CL-encoding nucleotide sequence according to SEQ ID NO:134 and/or comprises a LC (VL-CL)-encoding nucleotide sequence according to SEQ ID NO:135 or SEQ ID NO:136.

Vectors

Further included within the scope of the disclosure are vectors, for example, expression vectors, that comprise a nucleic acid molecule according to the present disclosure.

The term "vector" refers to a construct comprising a nucleic acid molecule. A vector in the context of the present disclosure is suitable for incorporating or harboring a desired nucleic acid sequence. Such vectors may be storage vectors, expression vectors, cloning vectors, transfer vectors etc. A storage vector is a vector which allows the convenient

storage of a nucleic acid molecule. Thus, the vector may comprise a sequence corresponding, e.g., to a desired antibody or antibody fragment thereof according to the present description.

5 As used herein, "expression vector" refers to a DNA construct containing a nucleic acid molecule that is operably linked to a suitable control sequence capable of effecting the expression of the nucleic acid molecule in a suitable host. Such control sequences include a promoter (*e.g.*, a heterologous promoter) to effect transcription, an optional operator sequence to control such transcription, a sequence encoding suitable mRNA
10 ribosome binding sites, and sequences which control termination of transcription and translation. Any of the elements of an expression vector that contribute to transcription of a nucleic acid molecule of interest may be heterologous to the vector. The vector may be a plasmid, a phage particle, a virus, or simply a potential genomic insert. Once transformed into a suitable host, the vector may replicate and function independently of
15 the host genome, or may, in some instances, integrate into the genome itself. In the present specification, "plasmid," "expression plasmid," "virus" and "vector" are often used interchangeably.

A cloning vector is typically a vector that contains a cloning site, which may be used to
20 incorporate nucleic acid sequences into the vector. A cloning vector may be, *e.g.*, a plasmid vector or a bacteriophage vector.

A transfer vector may be a vector which is suitable for transferring nucleic acid molecules into cells or organisms, for example, viral vectors. A vector in the context of
25 the present disclosure may be, *e.g.*, an RNA vector or a DNA vector. A vector may be a DNA molecule. For example, a vector in the sense of the present application comprises a cloning site, a selection marker, such as an antibiotic resistance factor, and a sequence suitable for multiplication of the vector, such as an origin of replication. In some embodiments, a vector in the context of the present application is a plasmid vector. In
30 certain such embodiments, a vector comprises a lentiviral vector or a retroviral vector.

Cells

In a further aspect, the present disclosure also provides a cell (also referred to as a "host cell") expressing an antibody, antigen binding fragment, or fusion protein according to the present disclosure; or comprising a vector or polynucleotide according the present
5 disclosure.

Examples of such cells include but are not limited to, eukaryotic cells, *e.g.*, yeast cells, animal cells, insect cells, plant cells; and prokaryotic cells, including *E. coli*. In some embodiments, the cells are mammalian cells. In certain such embodiments, the cells are
10 a mammalian cell line such as CHO cells (*e.g.*, DHFR- CHO cells (Urlaub *et al.*, *PNAS* 77:4216 (1980), CHO-KSV), human embryonic kidney cells (*e.g.*, HEK293T cells), PER.C6 cells, Y0 cells, Sp2/0 cells. NS0 cells, human liver cells, *e.g.* Hepa RG cells, myeloma cells or hybridoma cells. Other examples of mammalian host cell lines include mouse sertoli cells (*e.g.*, TM4 cells); monkey kidney CV1 line transformed by
15 SV40 (COS-7); baby hamster kidney cells (BHK); African green monkey kidney cells (VERO-76); monkey kidney cells (CV1); human cervical carcinoma cells (HELA); human lung cells (W138); human liver cells (Hep G2); canine kidney cells (MDCK; buffalo rat liver cells (BRL 3A); mouse mammary tumor (MMT 060562); TRI cells; *MRC 5* cells; and FS4 cells. Mammalian host cell lines suitable for antibody
20 production also include those described in, for example, Yazaki and Wu, *Methods in Molecular Biology*, Vol. 248 (B. K. C. Lo, ed., Humana Press, Totowa, N.J.), pp. 255-268 (2003).

In certain embodiments, a host cell is a prokaryotic cell, such as an *E. coli*. The
25 expression of peptides in prokaryotic cells such as *E. coli* is well established (*see, e.g.*, Pluckthun, A. *Bio/Technology* 9:545-551 (1991). For example, antibodies may be produced in bacteria, in particular when glycosylation and Fc effector function are not needed. For expression of antibody fragments and polypeptides in bacteria, *see, e.g.*, U.S. Pat. Nos. 5,648,237; 5,789,199; and 5,840,523.

30

Insect cells useful expressing a binding protein of the present disclosure are known in the art and include, for example, *Spodoptera frugiperma* Sf9 cells, *Trichoplusia ni* BTI-

TN5B1-4 cells, and *Spodoptera frugiperda* SfSWT01 “MimicTM” cells. See, e.g., Palmberger *et al.*, *J. Biotechnol.* 153(3-4):160-166 (2011). Numerous baculoviral strains have been identified which may be used in conjunction with insect cells, particularly for transfection of *Spodoptera frugiperda* cells.

5

Eukaryotic microbes such as filamentous fungi or yeast are also suitable hosts for cloning or expressing protein-encoding vectors, and include fungi and yeast strains with “humanized” glycosylation pathways, resulting in the production of an antibody with a partially or fully human glycosylation pattern. See Gerngross, *Nat. Biotech.* 22:1409-

10 1414 (2004); Li *et al.*, *Nat. Biotech.* 24:210-215 (2006).

Plant cells can also be utilized as hosts for expressing a binding protein of the present disclosure. For example, PLANTIBODIESTM technology (described in, for example, U.S. Pat. Nos. 5,959,177; 6,040,498; 6,420,548; 7,125,978; and 6,417,429) employs

15 transgenic plants to produce antibodies.

In some embodiments, a fusion protein is expressed at a cell surface by an immune cell, e.g., a T cell, NK cell, or NK-T cell, or any subtype thereof.

20 Any protein expression system compatible with the disclosure may be used to produce the disclosed binding proteins. Suitable expression systems include transgenic animals described in Gene Expression Systems, Academic Press, eds. Fernandez et al., 1999.

In particular embodiments, the cell may be transfected with a vector according to the

25 present description with an expression vector. The term “transfection” refers to the introduction of nucleic acid molecules, such as DNA or RNA (e.g. mRNA) molecules, into cells, such as into eukaryotic cells. In the context of the present description, the term “transfection” encompasses any method known to the skilled person for introducing nucleic acid molecules into cells, such as into eukaryotic cells, including30 into mammalian cells. Such methods encompass, for example, electroporation, lipofection, e.g., based on cationic lipids and/or liposomes, calcium phosphate precipitation, nanoparticle based transfection, virus based transfection, or transfection

based on cationic polymers, such as DEAE-dextran or polyethylenimine etc. In certain embodiments, the introduction is non-viral.

Moreover, cells of the present disclosure may be transfected stably or transiently with the vector according to the present description, e.g. for expressing an antibody, or an antigen binding fragment thereof, according to the present description. In such embodiments, the cells are stably transfected with the vector as described herein encoding a binding protein. Alternatively, cells may be transiently transfected with a vector according to the present disclosure encoding a binding protein according to the present description. In any of the presently disclosed embodiments, a polynucleotide may be heterologous to the host cell.

In a related aspect, the present disclosure provides methods for producing an antibody, antigen binding fragment, or fusion protein, wherein the methods comprise culturing a host cell of the present disclosure under conditions and for a time sufficient to produce the antibody, antigen binding fragment, or fusion protein.

Accordingly, the present disclosure also provides recombinant host cells that heterologously express an antibody, antigen binding fragment, or fusion protein of the present disclosure. For example, the cell may be of a species that is different to the species from which the antibody was fully or partially obtained (*e.g.*, CHO cells expressing a human antibody or an engineered human antibody). In some embodiments, the cell type of the host cell does not express the antibody or antigen binding fragment in nature. Moreover, the host cell may impart a post-translational modification (PTM; *e.g.*, glycosylation or fucosylation) on the antibody or antigen binding fragment that is not present in a native state of the antibody or antigen binding fragment (or in a native state of a parent antibody from which the antibody or antigen binding fragment was engineered or derived). Such a PTM may result in a functional difference (*e.g.*, reduced immunogenicity). Accordingly, an antibody or antigen binding fragment of the present disclosure that is produced by a host cell as disclosed herein may include one or more post-translational modification that is distinct from the antibody (or parent antibody) in its native state (*e.g.*, a human antibody produced by a

CHO cell can comprise a more post-translational modification that is distinct from the antibody when isolated from the human and/or produced by the native human B cell or plasma cell,

5 Optional additional features of the antibodies, antigen binding fragments, or fusion proteins

Antibodies, antigen binding fragments, and fusion proteins of the disclosure may be coupled, for example, to a drug for delivery to a treatment site or coupled to a
10 detectable label to facilitate imaging of a site comprising cells of interest. Methods for coupling antibodies to drugs and detectable labels are well known in the art, as are methods for imaging using detectable labels. Labeled antibodies may be employed in a wide variety of assays, employing a wide variety of labels. Detection of the formation of an antibody-antigen complex between an antibody (or antigen binding fragment or
15 fusion protein) of the disclosure and an epitope of interest on HBsAg, in particular on the antigenic loop region of HBsAg, can be facilitated by attaching a detectable substance to the antibody. Suitable detection means include the use of labels such as radionuclides, enzymes, coenzymes, fluorescers, chemilumescers, chromogens, enzyme substrates or co-factors, enzyme inhibitors, prosthetic group complexes, free
20 radicals, particles, dyes, and the like. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material is luminol; examples
25 of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S , or ^3H . Such labeled reagents may be used in a variety of well-known assays, such as radioimmunoassays, enzyme immunoassays, e.g., ELISA, fluorescent immunoassays, and the like. Labeled
30 antibodies, antigen binding fragments, and fusion proteins according to the present disclosure may be thus be used in such assays for example as described in US 3,766,162; US 3,791,932; US 3,817,837; and US 4,233,402.

An antibody, antigen binding fragment, or fusion protein according to the present disclosure may be conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent, or a radioactive metal ion or radioisotope. Examples of radioisotopes include, 5 but are not limited to, I-131, I-123, I-125, Y-90, Re-188, Re-186, At-211, Cu-67, Bi-212, Bi-213, Pd-109, Tc-99, In-111, and the like. Such antibody conjugates can be used for modifying a given biological response; the drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may 10 include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin.

Techniques for conjugating such therapeutic moiety to antibodies are well known. See, for example, Arnon et al. (1985) "Monoclonal Antibodies for Immunotargeting of 15 Drugs in Cancer Therapy, " in Monoclonal Antibodies and Cancer Therapy, ed. Reisfeld et al. (Alan R. Liss, Inc.), pp. 243-256; ed. Hellstrom et al. (1987) "Antibodies for Drug Delivery, " in Controlled Drug Delivery, ed. Robinson et al. (2d ed; Marcel Dekker, Inc.), pp. 623-653; Thorpe (1985) "Antibody Carriers of Cytotoxic Agents in Cancer Therapy: A Review," in Monoclonal Antibodies '84: Biological and Clinical 20 Applications, ed. Pinchera et al. pp. 475-506 (Editrice Kurtis, Milano, Italy, 1985); "Analysis, Results, and Future Prospective of the Therapeutic Use of Radiolabeled Antibody in Cancer Therapy, " in Monoclonal Antibodies for Cancer Detection and Therapy, ed. Baldwin et al. (Academic Press, New York, 1985), pp. 303-316; and Thorpe et al. (1982) Immunol. Rev. 62:119-158.

25 Alternatively, an antibody, antibody fragment, or fusion protein, can be conjugated to a second antibody, or antibody fragment thereof, (or second fusion protein) to form a heteroconjugate as described in US 4,676,980. In addition, linkers may be used between the labels and the antibodies of the description, *e.g.*, as described in US 30 4,831,175. Antibodies, antigen-binding fragments, and fusion proteins may be directly labeled with radioactive iodine, indium, yttrium, or other radioactive particle known in the art, *e.g.*, as described in US 5,595,721. Treatment may consist of a combination of

treatment with conjugated and non-conjugated antibodies, antigen binding fragments, and/or fusion proteins, administered simultaneously or subsequently e.g., as described in WO00/52031; WO00/52473.

- 5 Antibodies, antigen binding fragments, and fusion proteins as described herein may also be attached to a solid support. Additionally, the antibodies of the present disclosure, functional antibody fragments thereof, or fusion proteins, can be chemically modified by covalent conjugation to a polymer to, for example, increase their circulating half-life. Examples of polymers, and methods to attach them to peptides, are shown in US
10 4,766,106; US 4,179,337; US 4,495,285 and US 4,609,546. In some embodiments, the polymers may be selected from polyoxyethylated polyols and polyethylene glycol (PEG). PEG is soluble in water at room temperature and has the general formula: $R(O-CH_2-CH_2)_nO-R$, wherein R can be hydrogen, or a protective group such as an alkyl or alkanol group. In certain embodiments, the protective group may have between 1 and 8
15 carbons. For example, the protective group may be methyl. The symbol n is a positive integer. In one embodiment, n is between 1 and 1,000. In another embodiment n is between 2 and 500. In some embodiments, the PEG has an average molecular weight selected from between 1,000 and 40,000, between 2,000 and 20,000, and between 3,000 and 12,000. Furthermore, PEG may have at least one hydroxy group, for example the
20 PEG may have a terminal hydroxy group. For example, it is the terminal hydroxy group which is activated to react with a free amino group on the inhibitor. However, it will be understood that the type and amount of the reactive groups may be varied to achieve a covalently conjugated PEG/antibody of the present description.
- 25 Water-soluble polyoxyethylated polyols may also be utilized in the context of the antibodies and antigen binding fragments described herein. They include polyoxyethylated sorbitol, polyoxyethylated glucose, polyoxyethylated glycerol (POG), and the like. In one embodiment, POG is used. Without being bound by any theory, because the glycerol backbone of polyoxyethylated glycerol is the same backbone
30 occurring naturally in, for example, animals and humans in mono-, di-, triglycerides, this branching would not necessarily be seen as a foreign agent in the body. POG may have a molecular weight in the same range as PEG. Another drug delivery system that

can be used for increasing circulatory half-life is the liposome. Methods of preparing liposome delivery systems are known to one of skill in the art. Other drug delivery systems are known in the art and are described in, for example, referenced in Poznansky et al. (1980) and Poznansky (1984).

5

Antibodies, antigen binding fragments, and fusion proteins of the disclosure may be provided in purified form. Typically, the antibody, binding fragment, or fusion protein will be present in a composition that is substantially free of other polypeptides *e.g.*, where less than 90% (by weight), usually less than 60% and more usually less than 50% of the composition is made up of other polypeptides.

10

Antibodies, fusion proteins, or antigen binding fragments of the disclosure may be immunogenic in non-human (or heterologous) hosts *e.g.*, in mice. In particular, the antibodies, antigen binding fragments, or fusion proteins may have an idiotope that is immunogenic in non-human hosts, but not in a human host. In particular, such molecules of the disclosure for human use include those that cannot be easily isolated from hosts such as mice, goats, rabbits, rats, non-primate mammals, etc. and cannot generally be obtained by humanization or from xeno-mice.

15

20 **Production of antibodies, antigen binding fragments, and fusion proteins**

Antibodies, antigen binding fragments, and fusion proteins according to the disclosure can be made by any method known in the art. For example, the general methodology for making monoclonal antibodies using hybridoma technology is well known (Kohler, G. and Milstein, C., 1975; Kozbar et al. 1983). In one embodiment, the alternative EBV immortalization method described in WO2004/076677 is used.

25

In one embodiment, antibodies are produced using a method described in WO 2004/076677. In such methods, B cells producing the antibody are transformed with EBV and a polyclonal B cell activator. Additional stimulants of cellular growth and differentiation may optionally be added during the transformation step to further enhance the efficiency. These stimulants may be cytokines such as IL-2 and IL-15. In

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one aspect, IL-2 is added during the immortalization step to further improve the efficiency of immortalization, but its use is not essential. The immortalized B cells produced using these methods can then be cultured using methods known in the art and antibodies isolated therefrom.

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Another method for producing antibodies is described in WO 2010/046775. In such a method, plasma cells are cultured in limited numbers, or as single plasma cells in microwell culture plates. Antibodies can be isolated from the plasma cell cultures. Further, from the plasma cell cultures, RNA can be extracted and PCR can be performed using methods known in the art. The VH and VL regions of the antibodies can be amplified by RT-PCR (reverse transcriptase PCR), sequenced and cloned into an expression vector that is then transfected into HEK293T cells or other host cells. The cloning of nucleic acid in expression vectors, the transfection of host cells, the culture of the transfected host cells and the isolation of the produced antibody can be done using any methods known to one of skill in the art.

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The antibodies may be further purified, if desired, using filtration, centrifugation and various chromatographic methods such as HPLC or affinity chromatography. Techniques for purification of antibodies, *e.g.*, monoclonal antibodies, including techniques for producing pharmaceutical-grade antibodies, are well known in the art.

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Standard techniques of molecular biology may be used to prepare DNA sequences encoding the antibodies, antibody fragments, or fusion proteins of the present description. Desired DNA sequences may be synthesized completely or in part using oligonucleotide synthesis techniques. Site-directed mutagenesis and polymerase chain reaction (PCR) techniques may be used as appropriate.

25

Any suitable host cell/vector system may be used for expression of the DNA sequences encoding the antibody or fusion protein molecules of the present disclosure or fragments thereof. Bacterial, for example *E. coli*, and other microbial systems may be used, in part, for expression of antibody fragments such as Fab and F(ab')₂ fragments, and especially Fv fragments and single chain antibody fragments, for example, single

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chain Fvs. Eukaryotic, *e.g.*, mammalian, host cell expression systems may be used for production of larger antibody molecules, including complete antibody molecules. Suitable mammalian host cells include, but are not limited to, those exemplary host cells and cell lines disclosed herein.

5

The present disclosure also provides a process for the production of an antibody, antigen binding fragment, or fusion protein molecule according to the present disclosure comprising culturing a host cell comprising a vector encoding a nucleic acid of the present disclosure under conditions suitable for expression of protein from DNA
10 encoding the antibody molecule of the present description, and isolating the antibody molecule.

An antibody molecule or antibody fragment may comprise only a heavy or light chain polypeptide, in which case only a heavy chain or light chain polypeptide coding
15 sequence needs to be used to transfect the host cells. For production of products comprising both heavy and light chains, the cell line may be transfected with two vectors, a first vector encoding a light chain polypeptide and a second vector encoding a heavy chain polypeptide. Alternatively, a single vector may be used, the vector including sequences encoding light chain and heavy chain polypeptides.

20

Alternatively, antibodies, antigen binding fragments, and fusion proteins according to the disclosure may be produced by (i) expressing a nucleic acid sequence according to the disclosure in a host cell, *e.g.* by use of a vector according to the present description, and (ii) isolating the expressed desired product. Additionally, the method may include
25 (iii) purifying the isolated antibody, antigen binding fragment, or fusion protein. Transformed B cells and cultured plasma cells may be screened for those producing antibodies, antigen binding fragments, or fusion proteins of the desired specificity or function.

30 Screening may be carried out by any immunoassay, *e.g.*, ELISA, by staining of tissues or cells (including transfected cells), by neutralization assay or by one of a number of other methods known in the art for identifying desired specificity or function. The assay

may select on the basis of simple recognition of one or more antigens, or may select on the additional basis of a desired function *e.g.*, to select neutralizing antibodies rather than just antigen-binding antibodies, to select antibodies that can change characteristics of targeted cells, such as their signaling cascades, their shape, their growth rate, their capability of influencing other cells, their response to the influence by other cells or by other reagents or by a change in conditions, their differentiation status, or the like.

Individual transformed B cell clones may then be produced from the positive transformed B cell culture. The cloning step for separating individual clones from the mixture of positive cells may be carried out using limiting dilution, micromanipulation, single cell deposition by cell sorting or another method known in the art.

Nucleic acid from the cultured plasma cells can be isolated, cloned and expressed in HEK293T cells or other known host cells using methods known in the art.

The immortalized B cell clones or the transfected host-cells of described herein can be used in various ways *e.g.*, as a source of monoclonal antibodies, as a source of nucleic acid (DNA or mRNA) encoding a monoclonal antibody of interest, for research, etc.

20 Pharmaceutical Compositions

The present disclosure also provides a pharmaceutical composition comprising an antibody, antigen binding fragment, or fusion protein, according to the present disclosure, a nucleic acid according to the present disclosure, a vector according to the present disclosure and/or a cell according to the present disclosure.

Pharmaceutical compositions may also contain a pharmaceutically acceptable carrier, diluent and/or excipient. Although the carrier or excipient may facilitate administration, it should not itself induce the production of antibodies harmful to the individual receiving the composition. Nor should it be toxic. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polypeptides, liposomes, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino

acid copolymers and inactive virus particles. In general, pharmaceutically acceptable carriers in a pharmaceutical composition according to the present disclosure may be active components or inactive components.

- 5 Pharmaceutically acceptable salts can be used, for example mineral acid salts, such as hydrochlorides, hydrobromides, phosphates and sulphates, or salts of organic acids, such as acetates, propionates, malonates and benzoates.

10 Pharmaceutically acceptable carriers in a pharmaceutical composition may additionally contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents or pH buffering substances, may be present in such compositions. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries and suspensions, for ingestion by the subject.

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Pharmaceutical compositions of the disclosure may be prepared in various forms. For example, the compositions may be prepared as injectables, either as liquid solutions or suspensions. Solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared (*e.g.*, a lyophilized composition, similar to Synagis™ and Herceptin™, for reconstitution with sterile water containing a preservative). The composition may be prepared for topical administration *e.g.*, as an ointment, cream or powder. The composition may be prepared for oral administration *e.g.*, as a tablet or capsule, as a spray, or as a syrup (optionally flavored). The composition may be prepared for pulmonary administration *e.g.*, as an inhaler, using a fine powder or a spray. The composition may be prepared as a suppository or pessary. The composition may be prepared for nasal, aural or ocular administration *e.g.*, as drops. The composition may be in kit form, designed such that a combined composition is reconstituted just prior to administration to a subject. For example, a lyophilized antibody may be provided in kit form with sterile water or a sterile buffer.

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In particular embodiments, the active ingredient in a composition according to the present disclosure is an antibody molecule, an antibody fragment or variant or

derivative thereof, in particular the active ingredient in the composition is an antibody, an antibody fragment, a fusion protein, or variants and derivatives thereof, as described herein. As such, it may be susceptible to degradation in the gastrointestinal tract. Thus, if the composition is to be administered by a route using the gastrointestinal tract, the composition may contain agents which protect the antibody from degradation but which release the antibody once it has been absorbed from the gastrointestinal tract.

A thorough discussion of pharmaceutically acceptable carriers is available in Gennaro (2000) Remington: The Science and Practice of Pharmacy, 20th edition, ISBN: 0683306472.

Pharmaceutical compositions of the disclosure may have a pH between 5.5 and 8.5, and in some embodiments this may be between 6 and 8. In other embodiments, the pH of a pharmaceutical composition as described herein may be about 7. The pH may be maintained by the use of a buffer. The composition may be sterile and/or pyrogen free. The composition may be isotonic with respect to humans. In certain embodiments, pharmaceutical compositions of the disclosure are supplied in hermetically sealed containers.

Within the scope of the disclosure are compositions present in several forms of administration; the forms include, but are not limited to, those forms suitable for parenteral administration, e.g., by injection or infusion, for example by bolus injection or continuous infusion. Where the product is for injection or infusion, it may take the form of a suspension, solution or emulsion in an oily or aqueous vehicle and it may contain formulatory agents, such as suspending, preservative, stabilizing and/or dispersing agents. Alternatively, the antibody molecule may be in dry form, for reconstitution before use with an appropriate sterile liquid. A vehicle is typically understood to be a material that is suitable for storing, transporting, and/or administering a compound, such as a pharmaceutically active compound, in particular the antibodies according to the present description. For example, the vehicle may be a physiologically acceptable liquid, which is suitable for storing, transporting, and/or administering a pharmaceutically active compound, in particular the antibodies

according to the present description. Once formulated, the compositions of the present disclosure can be administered directly to the subject. In one embodiment the compositions are adapted for administration to mammalian, e.g., human subjects.

5 The pharmaceutical compositions described herein may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intraperitoneal, intrathecal, intraventricular, transdermal, transcutaneous, topical, subcutaneous, intranasal, enteral, sublingual, intravaginal or rectal routes. Hyposprays may also be used to administer the pharmaceutical
10 compositions of the description. In specific embodiments, the pharmaceutical composition may be prepared for oral administration, e.g. as tablets, capsules and the like, for topical administration, or as injectable, e.g. as liquid solutions or suspensions. Solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be utilized, e.g. that the pharmaceutical composition is in lyophilized form.

15

For injection, e.g. intravenous, cutaneous or subcutaneous injection, or injection at the site of affliction, the active ingredient can be provided be in the form of a parenterally acceptable aqueous solution which is pyrogen-free and has suitable pH, isotonicity and stability. Preservatives, stabilizers, buffers, antioxidants and/or other additives may be
20 included, as required.

Whether it is a polypeptide, peptide, or nucleic acid molecule, cell, or other pharmaceutically useful compound according to the present disclosure that is to be given to an individual, administration is generally in a "prophylactically effective
25 amount" or a "therapeutically effective amount" or an "effective amount" (as the case may be), this being sufficient to show a benefit to the individual (e.g., improved clinical outcome; lessening or alleviation of symptoms associated with a disease; decreased occurrence of symptoms; improved quality of life; longer disease-free status; diminishment of extent of disease, stabilization of disease state; delay of disease
30 progression; remission; survival; or prolonged survival in a statistically significant manner). The actual amount administered, and rate and time-course of administration, will depend on the nature and severity of what is being treated. For injection, the

pharmaceutical composition according to the present disclosure may be provided for example in a pre-filled syringe.

Pharmaceutical compositions as disclosed herein may also be administered orally in any orally acceptable dosage form including, but not limited to, capsules, tablets, aqueous suspensions or solutions. In the case of tablets for oral use, carriers commonly used include lactose and corn starch. Lubricating agents, such as magnesium stearate, are also typically added. For oral administration in a capsule form, useful diluents include lactose and dried cornstarch. When aqueous suspensions are required for oral use, the active ingredient, i.e. the inventive transporter cargo conjugate molecule as defined above, is combined with emulsifying and suspending agents. If desired, certain sweetening, flavoring or coloring agents may also be added.

The pharmaceutical compositions according to the present description may also be administered topically, especially when the target of treatment includes areas or organs readily accessible by topical application, *e.g.*, including diseases of the skin or of any other accessible epithelial tissue. Suitable topical formulations are readily prepared for each of these areas or organs. For topical applications, the pharmaceutical composition may be formulated in a suitable ointment, containing the inventive pharmaceutical composition, particularly its components as defined above, suspended or dissolved in one or more carriers. Carriers for topical administration include, but are not limited to, mineral oil, liquid petrolatum, white petrolatum, propylene glycol, polyoxyethylene, polyoxypropylene compound, emulsifying wax and water. Alternatively, the pharmaceutical composition can be formulated in a suitable lotion or cream. In the context of the present description, suitable carriers include, but are not limited to, mineral oil, sorbitan monostearate, polysorbate 60, cetyl esters wax, cetearyl alcohol, 2-octyldodecanol, benzyl alcohol and water.

Doses may be expressed in relation to the bodyweight. Thus, a dose which is expressed as [g, mg, or other unit]/kg (or g, mg etc.) usually refers to [g, mg, or other unit] "per kg (or g, mg etc.) bodyweight", even if the term "bodyweight" is not explicitly mentioned.

In specific embodiments, in a single dose, *e.g.* a daily, weekly or monthly dose, the amount of the antibody, or the antigen binding fragment thereof, in the pharmaceutical composition does not exceed 1 g. In certain such embodiments, the single dose does not exceed a dose selected from 500 mg, 250 mg, 100 mg, and 50 mg.

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In some embodiments, a composition or kit as described herein further comprises (i) a polymerase inhibitor, wherein the polymerase inhibitor optionally comprises Lamivudine, Adefovir, Entecavir, Telbivudine, Tenofovir, or any combination thereof; (ii) an interferon, wherein the interferon optionally comprises IFNbeta and/or IFNalpha; 10 (iii) a checkpoint inhibitor, wherein the checkpoint inhibitor optionally comprises an anti-PD-1 antibody or antigen binding fragment thereof, an anti-PD-L1 antibody or antigen binding fragment thereof, and/or an anti-CTLA4 antibody or antigen binding fragment thereof; (iv) an agonist of a stimulatory immune checkpoint molecule; or (v) any combination of (i)-(iv). In some embodiments, a kit comprises a composition or 15 combination as described herein, and further comprises instructions for using the component to prevent, treat, attenuate, and/or diagnose a hepatitis B infection and/or a hepatitis D infection.

In certain embodiments, a composition of the present disclosure (*e.g.*, antibody, 20 antigen-binding fragment, host cell, nucleic acid, vector, or pharmaceutical composition) is used in combination with a PD-1 inhibitor, for example a PD-1-specific antibody or binding fragment thereof, such as pidilizumab, nivolumab, pembrolizumab, MEDI0680 (formerly AMP-514), AMP-224, BMS-936558 or any combination thereof.

25 In certain embodiments, a composition of the present disclosure is used in combination with a PD-L1 specific antibody or binding fragment thereof, such as BMS-936559, durvalumab (MEDI4736), atezolizumab (RG7446), avelumab (MSB0010718C), MPDL3280A, or any combination thereof.

30 In certain embodiments, an a composition of the present disclosure is used in combination with a LAG3 inhibitor, such as LAG525, IMP321, IMP701, 9H12, BMS-986016, or any combination thereof.

In certain embodiments, a composition of the present disclosure is used in combination with an inhibitor of CTLA4. In particular embodiments, an a composition of the present disclosure is used in combination with a CTLA4 specific antibody or binding
5 fragment thereof, such as ipilimumab, tremelimumab, CTLA4-Ig fusion proteins (e.g., abatacept, belatacept), or any combination thereof.

In certain embodiments, a composition of the present disclosure is used in combination with a B7-H3 specific antibody or binding fragment thereof, such as enoblituzumab
10 (MGA271), 376.96, or both. A B7-H3 antibody binding fragment may be a scFv or fusion protein thereof, as described in, for example, Dangaj et al., Cancer Res. 73:4820, 2013, as well as those described in U.S. Patent No. 9,574,000 and PCT Patent Publication Nos. WO /201640724A1 and WO 2013/025779A1.

15 In certain embodiments, a composition of the present disclosure is used in combination with an inhibitor of CD244.

In certain embodiments, a composition of the present disclosure is used in combination with an inhibitor of BLTA, HVEM, CD160, or any combination thereof. Anti CD-160
20 antibodies are described in, for example, PCT Publication No. WO 2010/084158.

In certain embodiments, a composition of the present disclosure is used in combination with an inhibitor of TIM3.

25 In certain embodiments, a composition of the present disclosure is used in combination with an inhibitor of Gal9.

In certain embodiments, a composition of the present disclosure is used in combination with an inhibitor of adenosine signaling, such as a decoy adenosine receptor.
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In certain embodiments, a composition of the present disclosure is used in combination with an inhibitor of A2aR.

In certain embodiments, a composition of the present disclosure is used in combination with an inhibitor of KIR, such as lirilumab (BMS-986015).

- 5 In certain embodiments, a composition of the present disclosure is used in combination with an inhibitor of an inhibitory cytokine (typically, a cytokine other than TGF β) or Treg development or activity.

In certain embodiments, a composition of the present disclosure is used in combination
10 with an IDO inhibitor, such as levo-1-methyl tryptophan, epacadostat (INCB024360; Liu *et al.*, *Blood* 115:3520-30, 2010), ebselen (Terentis *et al.*, *Biochem.* 49:591-600, 2010), indoximod, NLG919 (Mautino *et al.*, American Association for Cancer Research 104th Annual Meeting 2013; Apr 6-10, 2013), 1-methyl-tryptophan (1-MT)-tira-
pazamine, or any combination thereof.

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In certain embodiments, a composition of the present disclosure is used in combination with an arginase inhibitor, such as N(omega)-Nitro-L-arginine methyl ester (L-NAME), N-omega-hydroxy-nor-l-arginine (nor-NOHA), L-NOHA, 2(S)-amino-6-borono-hexanoic acid (ABH), S-(2-boronoethyl)-L-cysteine (BEC), or any combination
20 thereof.

In certain embodiments, a composition of the present disclosure is used in combination with an inhibitor of VISTA, such as CA-170 (Curis, Lexington, Mass.).

- 25 In certain embodiments, a composition of the present disclosure is used in combination with an inhibitor of TIGIT such as, for example, COM902 (Compugen, Toronto, Ontario Canada), an inhibitor of CD155, such as, for example, COM701 (Compugen), or both.

- 30 In certain embodiments, a composition of the present disclosure is used in combination with an inhibitor of PVRIG, PVRL2, or both. Anti-PVRIG antibodies are described in,

for example, PCT Publication No. WO 2016/134333. Anti-PVRL2 antibodies are described in, for example, PCT Publication No. WO 2017/021526.

In certain embodiments, a composition of the present disclosure is used in combination
5 with a LAIR1 inhibitor.

In certain embodiments a composition of the present disclosure is used in combination with an inhibitor of CEACAM-1, CEACAM-3, CEACAM-5, or any combination thereof.

10

In certain embodiments, a composition of the present disclosure is used in combination with an agent that increases the activity (*i.e.*, is an agonist) of a stimulatory immune checkpoint molecule. For example, a composition of the present disclosure can be used in combination with a CD137 (4-1BB) agonist (such as, for example, urelumab), a
15 CD134 (OX-40) agonist (such as, for example, MEDI6469, MEDI6383, or MEDI0562), lenalidomide, pomalidomide, a CD27 agonist (such as, for example, CDX-1127), a CD28 agonist (such as, for example, TGN1412, CD80, or CD86), a CD40 agonist (such as, for example, CP-870,893, rhuCD40L, or SGN-40), a CD122 agonist (such as, for example, IL-2) an agonist of GITR (such as, for example,
20 humanized monoclonal antibodies described in PCT Patent Publication No. WO 2016/054638), an agonist of ICOS (CD278) (such as, for example, GSK3359609, mAb 88.2, JTX-2011, Icos 145-1, Icos 314-8, or any combination thereof). In any of the embodiments disclosed herein, a method may comprise administering a composition of the present disclosure with one or more agonist of a stimulatory immune checkpoint
25 molecule, including any of the foregoing, singly or in any combination.

An antibody, antigen binding fragment, or fusion protein according to the present disclosure can be present either in the same pharmaceutical composition as the additional active component or, the antibody, antigen binding fragment, or fusion
30 protein according to the present disclosure may be included in a first pharmaceutical composition and the additional active component may be included in a second pharmaceutical composition different from the first pharmaceutical composition.

Uses

- In a further aspect, the present disclosure provides methods for the use of an antibody,
5 an antigen binding fragment, a fusion protein, a nucleic acid, a vector, a cell or a
pharmaceutical composition, or kit according to the present disclosure in the (i)
prophylaxis, treatment or attenuation of hepatitis B and/or hepatitis D; or in (ii)
diagnosis of hepatitis B and/or hepatitis D (e.g., in a human subject).
- 10 Methods of diagnosis (*e.g., in vitro, ex vivo*) may include contacting an antibody,
antibody fragment (e.g., antigen binding fragment), or fusion protein with a sample.
Such samples may be isolated from a subject, for example an isolated tissue sample
taken from, for example, nasal passages, sinus cavities, salivary glands, lung, liver,
pancreas, kidney, ear, eye, placenta, alimentary tract, heart, ovaries, pituitary, adrenals,
15 thyroid, brain, skin or blood. The methods of diagnosis may also include the detection
of an antigen/antibody or antigen/fusion protein complex, in particular following the
contacting of an antibody, antibody fragment, or fusion protein with a sample. Such a
detection step is typically performed at the bench, i.e. without any contact to the human
or animal body. Examples of detection methods are well-known to the person skilled in
20 the art and include, e.g., ELISA (enzyme-linked immunosorbent assay).

- The disclosure also provides the use of (i) an antibody, an antibody fragment, fusion
protein, or variants and derivatives thereof according to the disclosure, (ii) host cell
(which can be an immortalized B cell) according to the disclosure, (iii) a nucleic acid or
25 a vector according to the present disclosure or (iv) a pharmaceutical composition of the
disclosure in (a) the manufacture of a medicament for the prevention, treatment or
attenuation of hepatitis B and/or hepatitis D or for (b) diagnosis of hepatitis B and/or
hepatitis D.
- 30 The disclosure also provides an antibody, antigen binding fragment, or fusion protein
according to the present disclosure, a nucleic acid according to the present disclosure, a
vector according to the present disclosure, a cell according to the present disclosure or

the pharmaceutical composition according to the present disclosure for use as a medicament for the prevention or treatment of hepatitis B and/or hepatitis D. It also provides the use of an antibody, antigen binding fragment, or fusion protein of the disclosure in the manufacture of a medicament for treatment of a subject and/or
5 diagnosis in a subject. It also provides a method for treating a subject (*e.g.*, a human subject), comprising administering to the subject an effective amount of a composition as described herein. In some embodiments, the subject may be a human. One way of checking efficacy of therapeutic treatment involves monitoring disease symptoms after administration of the composition. Treatment can be a single dose schedule or a
10 multiple dose schedule.

In one embodiment, an antibody, antibody fragment, fusion protein, host cell (*e.g.*, immortalized B cell clone, or T cell, NK-T cell, or NK cell that expresses a fusion protein), or pharmaceutical composition according to the disclosure is administered to a
15 subject in need of such treatment. Such a subject includes, but is not limited to, one who is particularly at risk of or susceptible to hepatitis B and/or hepatitis D.

Antibodies, antigen binding fragments, fusion proteins, polynucleotides, vectors, host cells, pharmaceutical compositions, and combinations of the same, according to the
20 present disclosure may also be used in a kit for the prevention, treatment, attenuation, and/or diagnosis of hepatitis B and/or hepatitis D. In some embodiments, a kit further comprises instructions for using the component to prevent, treat, attenuate, and/or diagnose a hepatitis B infection and/or a hepatitis D infection. Further, the epitope in the antigenic loop region of HBsAg, which is capable of binding an antibody, antigen
25 binding fragment, or fusion protein of the disclosure as described herein may be used in a kit for monitoring the efficacy of application procedures by detecting the presence or determining the titer of protective anti-HBV antibodies.

In certain embodiments, a composition or a kit of this disclosure further comprises: a
30 polymerase inhibitor, wherein the polymerase inhibitor optionally comprises Lamivudine, Adefovir, Entecavir, Telbivudine, Tenofovir, or any combination thereof; (ii) an interferon, wherein the interferon optionally comprises IFNbeta and/or IFNalpha;

- (iii) a checkpoint inhibitor, wherein the checkpoint inhibitor optionally comprises an anti-PD-1 antibody or antigen binding fragment thereof, an anti-PD-L1 antibody or antigen binding fragment thereof, and/or an anti-CTLA4 antibody or antigen binding fragment thereof; (iv) an agonist of a stimulatory immune checkpoint molecule; or
- 5 (v) any combination of (viii)-(xii).

In some embodiments, an antibody, an antigen binding fragment, or fusion protein according to the present disclosure, a nucleic acid according to the present disclosure, the vector according to the present disclosure, the cell according to the present disclosure or the pharmaceutical composition according to the present disclosure is used

10 in treatment or attenuation of chronic hepatitis B infection.

In particular embodiments, an antibody, antigen binding fragment, or fusion protein according to the present disclosure (i) neutralizes HBV infection, (ii) binds to L-HBsAg

15 (the large HBV envelope protein, which is present in infectious HBV particles), thereby preventing spreading of HBV, (iii) binds to S-HBsAg, thereby promoting clearance of subviral particles (SVP) and/or (iv) can induce seroconversion, i.e. an active immune response to the virus.

20 In particular embodiments, antibody, antigen binding fragment, or fusion protein according to the present disclosure, a nucleic acid according to the present disclosure, a vector according to the present disclosure, a cell according to the present disclosure, or a pharmaceutical composition according to the present disclosure, may be used in prevention of hepatitis B (re-)infection after liver transplantation in particular for

25 hepatitis B induced liver failure.

In further embodiments an antibody, antigen binding fragment thereof, or fusion protein according to the present disclosure, a nucleic acid according to the present disclosure, a vector according to the description provided herein, a cell according to the present disclosure, or a pharmaceutical composition according to the present disclosure, may be

30 used in prevention/prophylaxis of hepatitis B in non-immunized subjects. This is for example in case of (an assumed) accidental exposure to HBV (post-exposure

prophylaxis). The term "non-immunized subjects" includes subjects, who never received a vaccination and are, thus, not immunized, and subjects, who did not show an immune response (e.g., no measurable anti-hepatitis B antibodies) after vaccination.

- 5 In some embodiments, an antibody, antigen binding fragment, or fusion protein according to the present disclosure, the nucleic acid according to the present disclosure, a vector according to the present disclosure, a cell according to the present disclosure, or a pharmaceutical composition according to the present disclosure, is used in prophylaxis of hepatitis B in haemodialysed patients.

10

- In some embodiments, an antibody, an antigen binding fragment, or fusion protein according to the present disclosure, a nucleic acid according to the present disclosure, a vector according to the present disclosure, a cell according to the present disclosure or a pharmaceutical composition according to the present disclosure is used in prevention of hepatitis B in a newborn. In such embodiments, an antibody, or an antigen binding fragment thereof, according to the present disclosure, a nucleic acid according to the present disclosure, a vector according to the present disclosure, a cell according to the present disclosure or a pharmaceutical composition according to the present disclosure may be administered at birth or as soon as possible after birth. The administration may be repeated until seroconversion following vaccination.
- 15
20

- Moreover, the present disclosure also provides the use of an antibody, antigen binding fragment, or fusion protein according to the present disclosure, a nucleic acid according to the present disclosure, a vector according to the present disclosure, a cell according to the present disclosure or a pharmaceutical composition according to the present disclosure in the diagnosis (*e.g. in vitro, ex vivo, or in vivo*) of hepatitis B and/or hepatitis D.
- 25

- In addition, the use of an antibody, antigen binding fragment, or fusion protein according to the present disclosure, a nucleic acid according to the present disclosure, a vector according to the present disclosure, a cell according to the present disclosure or a pharmaceutical composition according to the present disclosure in determining whether
- 30

an isolated blood sample is infected with hepatitis B virus and/or hepatitis delta virus is provided.

As described above, methods of diagnosis may include contacting an antibody,
5 antibody fragment, or fusion protein with a sample. Such samples may be isolated from a subject, for example an isolated tissue sample taken from, for example, nasal passages, sinus cavities, salivary glands, lung, liver, pancreas, kidney, ear, eye, placenta, alimentary tract, heart, ovaries, pituitary, adrenals, thyroid, brain, skin or blood. The methods of diagnosis may also include the detection of an antigen/antibody
10 complex, in particular following the contacting of an antibody or an antibody fragment with a sample. Such a detection step is typically performed at the bench, i.e. without any contact to the human or animal body. Examples of detection methods are well-known to the person skilled in the art and include, e.g., ELISA (enzyme-linked immunosorbent assay).

15

The present disclosure also provides a method of treating, preventing and/or attenuating hepatitis B and/or hepatitis D in a subject, wherein the method comprises administering to the subject an antibody, antigen binding fragment, or fusion protein according to the present disclosure, a nucleic acid according to the present disclosure, a vector according
20 to the present disclosure, a cell according to the present disclosure or a pharmaceutical composition according to the present disclosure. In certain embodiments, a method further comprises administering to the subject one or more of: (vii) a polymerase inhibitor, wherein the polymerase inhibitor optionally comprises Lamivudine, Adefovir, Entecavir, Telbivudine, Tenofovir, or any combination thereof; (viii) an interferon,
25 wherein the interferon optionally comprises IFNbeta and/or IFNalpha; (ix) a checkpoint inhibitor, wherein the checkpoint inhibitor optionally comprises an anti-PD-1 antibody or antigen binding fragment thereof, an anti-PD-L1 antibody or antigen binding fragment thereof, and/or an anti-CTLA4 antibody or antigen binding fragment thereof; (x) an agonist of a stimulatory immune checkpoint molecule; or (xi) any combination of
30 (vii)-(x).

In some embodiments, the hepatitis B infection is a chronic hepatitis B infection. In some embodiments, the subject has received a liver transplant. In some embodiments, the subject is non-immunized against hepatitis B. In certain embodiments, the subject is a newborn. In some embodiments, the subject is undergoing or has undergone
5 hemodialysis.

The present disclosure also provides a method of treating a subject who has received a liver transplant comprising administering to the subject who has received the liver transplant an effective amount of an antibody, an antigen binding fragment, or fusion
10 protein according to the present disclosure, a nucleic acid according to the present disclosure, a vector according to the present disclosure, a cell according to the present disclosure or a pharmaceutical composition according to the present disclosure.

Also provided herein are methods for detecting the presence or absence of an epitope in
15 a correct conformation in an anti-hepatitis-B and/or an anti-hepatitis-D vaccine, wherein the methods comprise: (i) contacting the vaccine with an antibody, antigen-binding fragment, or fusion protein of any one of the present disclosure; and (ii) determining whether a complex comprising an antigen and the antibody, or comprising an antigen and the antigen binding fragment, or comprising an antigen and the fusion
20 protein, has been formed.

The term "vaccine" as used herein is typically understood to be a prophylactic or therapeutic material providing at least one antigen, such as an immunogen. The antigen or immunogen may be derived from any material that is suitable for vaccination. For
25 example, the antigen or immunogen may be derived from a pathogen, such as from bacteria particles, virus particles, a tumor (including a solid or liquid tumor), or other cancerous tissue. The antigen or immunogen stimulates the body's adaptive immune system to provide an adaptive immune response. In certain embodiments, an "antigen" or an "immunogen" refers to a substance which may be recognized by the immune
30 system, *e.g.* by the adaptive immune system, and which is capable of triggering an antigen-specific immune response, *e.g.* by formation of antibodies and/or antigen-specific T cells as part of an adaptive immune response. In some embodiments, an

antigen may be or may comprise a peptide or protein which may be presented by an MHC complex (*e.g.*, MHC class I; MHC class II) to T cells. In certain embodiments, the antigen comprises a HBV and/or HBD antigen; *e.g.*, an HBsAg antigen.

- 5 In some instances, elements of the of the antibodies, antibody fragments, fusion proteins, nucleic acids, cells, compositions, uses, and methods provided herein are described or listed with reference to embodiments or examples. However, it should be understood that the examples and embodiments described herein may be combined in various ways to create additional embodiments.

10

EXAMPLES

- In the following, particular examples illustrating various embodiments and aspects of the disclosure are presented. However, the present disclosure shall not to be limited in scope by the specific embodiments described herein.
- 15

Example 1: Generation and Testing of Engineered Antibodies

- Analysis of some HBC34 antibody variants from PCT Publication No. WO 2017/060504 revealed a cysteine amino acid at position 40 (IMGT numbering) in the light chain variable region that is unpaired and represents a potential liability. Without wishing to be bound by theory, unpaired cysteine residues are potentially reactive and can potentially trigger aggregation through intramolecular scrambling or intermolecular disulfide formation. Variants of HBC34-V7 (WO 2017/060504) were engineered in which the cysteine amino acid at position 40 of the light chain variable region was substituted with a serine (thereby generating "HBC34-V34") or with an alanine (thereby generating "HBC34-V35"). The nucleotide sequences encoding these additional variant antibodies were codon-optimized, and antibodies were expressed as IgG1 (g1m17, 1 allotype) in ExpiCHOTM cells (ThermoFisher). Codon-optimized nucleotide sequences encoding the VH and VL domains of HBC34-V35 are provided in SEQ ID NOS: 103 and 104, respectively.
- 20
- 25
- 30

The ability of HBC34-V34 and HBC34-V35 to bind antigen was investigated using a direct antigen-binding ELISA. HBC34-V7 was used as a comparator. As shown in Figure 1, both HBC34-V34 and HBC34-V35 bound effectively to two recombinant HBsAg antigens ("adw", top panel; "adr", bottom panel), and HBC34-V35 had very
5 similar binding as the parent HBC34-V7.

The variant antibodies were examined for binding to all known HBsAg genotypes ((A)-(J)). Briefly, human epithelial cells (Hep2 cells) were transfected with plasmids expressing the HBsAg of each of the 10 HBV genotypes A, B, C, D, E, F, G, H, I, and
10 J. All antibodies were tested at multiple concentrations for staining of transiently transfected permeabilized cells. Two days after transfection, Hep2 cells were collected, fixed and permeabilized with saponin for immunostaining with HBC34 and the five selected variants. HBC34-V7 was included as a comparator. Binding of antibodies to transfected cells was analysed using a Becton Dickinson FACSCanto2™ (BD
15 Biosciences) with FlowJo software (TreeStar). As shown in Figures 2A-2J, HBC34-V34 and HBC34-V35 recognized all 10 HBV HBsAg genotypes. HBC34-V35 showed somewhat stronger staining than HBC34-V34.

These data show that the antibody variants HBC34-V34 and HBC34-V35 broadly
20 recognize and bind to HBsAG at levels comparable to HBC34-V7.

Example 2: Anti-HBsAg Antibodies with Modified Fc Regions Efficiently Bind to Antigen

25 Modifications in the Fc region may provide advantages to a therapeutic antibody. HBC34-V35 was expressed as IgG1 with wild-type Fc, or with Fc containing a "MLNS" mutation (M428L/N434S) or with Fc containing MLNS in combination with a "GAALIE" mutation (G239A/A330L/I332E). Each construct was tested for binding to recombinant HBsAg (adw) in two separate antigen-binding ELISA experiments. Three
30 (3) lots of HBC34-v35 (wild-type Fc) were tested. Two (2) lots of HBC34-V35-MLNS and two (2) lots of HBC34-V35-MLNS- GAALIE were tested. HBC34v7 (one lot) was tested as a comparator.

As shown in Figures 3A and 3B, the introduced Fc mutations did not affect antigen-binding activity of HBC34-V35. EC₅₀ values varied somewhat between the various constructs and the two experiments, and were generally low.

5

Binding of HBC34-V35 with MLNS or MLNS and GAALIE mutations to EXP1293 cells expressing HBsAg genotypes (A)-(J) or HBsAg variants was assessed. HBC34-V35 with wild-type IgG1 Fc was used as a comparator. Data showing binding to HBsAg genotypes are shown in Figures 3C-3H. Data showing binding to HBsAg variants are shown in Figures 3I-3R.

10

Example 3: In Vitro Neutralization Activity of Antibodies

The neutralizing capacity of HBC34, HBC34-V35, HBC34-V35-MLNS, and HBC34-V35-MLNS-GAALIE was compared by measuring the levels of HBsAg (A) and HBeAg (B) in the cell culture supernatant of HBV infected HepG2 cells expressing NTCP. Data are shown in Figures 3S-3V, and represent the means $\pm$ SD from one of two independent experiments.

15

Example 4: Pan-Genotype Neutralization Capacity of HBC34-V35 MLNS-GAALIE Assessed in an HDV Pseudosystem

20

To confirm the breadth of neutralization of HBC34-V35-MLNS-GAALIE against HBV virus, neutralization assays were conducted with HBC34-V35-MLNS-GAALIE against eight prevalent human HBV genotypes. An *in vitro* system that takes advantage of hepatitis D virus (HDV) engineered to express HBV HBsAg representing different genotypes was employed. Briefly, as both HBV and HDV share the same envelope proteins, their viral entry pathway via heparan sulfate proteoglycans and NTCP is identical, and HDV can be used as a model system to study HBsAg-mediated viral entry (Tu 2018; Lempp 2016). Further, HDV can be enveloped/pseudotyped with HBsAg of different HBV genotypes and subsequently be used in infection studies (Freitas 2014).

25

30

HBC34-V35-MLNS-GAALIE showed neutralizing capacity for all tested genotypes with similar EC₅₀ values, ranging from 0.92 ng/mL (genotype C) to 2.34 ng/mL (genotype A). These results show that HBC34-V35-MLNS-GAALIE is able to neutralize infectious virus carrying HBsAg from all eight HBV genotypes tested, supporting *in vivo* pan-genotypic neutralization activity of HBC34-V35-MLNS-GAALIE (Figure 4).

Example 5: Clearance of HB Antigens and Viral Entry Inhibition in an *In Vivo* Model

10

An immune-deficient mouse having transplanted human hepatocytes was used to test the effectiveness of anti-HBV antibodies of the present disclosure in clearing HBsAg. Briefly, primary human hepatocytes were transplanted into SCID mice for which mouse hepatocytes had previously been destroyed enzymatically. The mice were T- and B-cell deficient. This model is useful for studying HBV infection including entry, spreading, cccDNA regulation, hepatocyte-intrinsic immune responses, and viral integration into host genome.

Mice were inoculated via tail vein injection with HBV, genotype C, at 1.0×10^7 viral genomes per mouse at Day -28. Treatments at Day 0 following initial measurement of HBV. HBV-infected mice ($n=4$ per treatment group) were administered PBS (control) or HBC34-V35 (1, 5, or 15 mg/kg i.p., 2x/week). Antibodies were murinized with the exception of the antigen-binding Fab regions.

Plasma and serum samples were collected periodically throughout the study, and viral loads, HBV DNA (by PCR), and HB Ag (HBsAg, HBeAg, HBcrAg) were measured. Mice were sacrificed at week 6.

As shown in Figures 5-8, treatment with the highest tested dose of HBC34-V35 reduced viral load and viral entry into hepatocytes.

Example 6: In Vitro Effector Function Studies

In vitro studies were performed to examine the ability of HBC34 antibodies with modified Fc to: (1) bind to human FcRs and to complement; (2) activate FcγRIIa, FcγRIIb, and FcγRIIIa; and (3) promote ADCC and activate human Natural Killer (NK) cells. Test articles, cell lines, and reagents used were as described in Tables 5-7, below. The following abbreviations are used in this Example: GLP = Good Laboratory Practice; ADCC = Antibody-dependent cellular cytotoxicity; ADCP = Antibody-dependent cellular phagocytosis; Fc = Fragment crystallizable; HBsAg = Hepatitis B surface Antigen; mAb = Monoclonal antibody; PBS = Phosphate-buffered saline; UHPL-SEC = Ultra-high performance liquid size-exclusion chromatography; ATCC = American Type Culture Collection; FcγRs = Fc gamma receptor(s); CHO cells = Chinese hamster ovary cells; RLU = Relative luminescence units; BLI = Bio-layer interferometry.

Table 5. Test Articles.

Test Article	HBC34-V35-MLNS
• Isotype	• IgG1λ
• Relative molecular weight	• ≈150 kDa
• Concentration	• 3.47 mg/ml
• Source	• In-house
• Handling and storage conditions	• 4°C short term, -80°C long term storage
• Formulation buffer	• PBS, pH 7.2
Test Article	HBC34-V35-MLNS-GAALIE
• Isotype	• IgG1λ
• Relative molecular weight	• ≈150 kDa
• Concentration	• 2.1 mg/ml / 0.86 mg/ml

• Source	• In-house
• Handling and storage conditions	• 4°C short term, -80°C long term storage
• Formulation buffer	• PBS, pH 7.2
Test Article	HBC34-V35-LALA
• Isotype	• IgG1 λ
• Relative molecular weight	• $\approx$ 150 kDa
• Concentration	• 1.2 mg/ml
• Source	• In-house
• Handling and storage conditions	• 4°C short term, -80°C long term storage
• Formulation buffer	• PBS, pH 7.2
Test Article	mAb 17.1.41
• Isotype	• IgG1 κ
• Relative molecular weight	• $\approx$ 150 kDa
• Concentration	• 4.4 mg/ml
• Source	• In-house
• Handling and storage conditions	• 4°C short term, -80°C long term storage
• Formulation buffer	• PBS, pH 7.2

Table 6. Cell Lines

Cell Line	PLC/PRF/5
• Catalogue number	• #4325-FC-050
• Concentration	• 100 μ g/ml
• Source	• R&D Systems, mouse myeloma cell line, NS0-derived, with a

	C-terminal 6-His tag
Stability	Stable at -20 to 80°C
Handling and storage conditions	Store at -80°C until use, 1 month, 2 to 8°C under sterile conditions after reconstitution
Formulation buffer	PBS
Cell Line	Jurkat-FcγRIIIA (F158)
Tissue origin	Immortalized line of human T lymphocyte cells; Jurkat cells stably expressing the FcγRIIIa receptor, F158 (low affinity) variant, and an NFAT response element driving expression of firefly luciferase as effector cells
Source	Promega (Cat. Nr.: G9798)
Assay media	RPMI1640 supplemented with 4% low IgG serum
Cell line	Jurkat-FcγRIIIA (V158)
Tissue origin	Immortalized line of human T lymphocyte cells; Jurkat cells stably expressing the FcγRIIIa receptor, V158 (high affinity) variant, and an NFAT response element driving expression of firefly luciferase as effector cells
Source	Promega (Cat. Nr.: G7018)
Assay media	RPMI1640 supplemented with 4% low IgG serum
Cell line	Jurkat-FcγRIIA (H131)
Tissue origin	Immortalized line of human T lymphocyte cells; Jurkat cells stably expressing the FcγRIIa receptor, H131 (high affinity) variant, and an NFAT response element driving expression of

	firefly luciferase as effector cells
• Source	• Promega (Cat. Nr.: G9995)
• Assay media	• RPMI1640 supplemented with 4% low IgG fetal bovine serum
Cell line	Jurkat-FcγRIIB
• Tissue origin	• Immortalized line of human T lymphocyte cells; Jurkat cells stably expressing the FcγRIIb receptor, and an NFAT response element driving expression of firefly luciferase as effector cells
• Source	• Promega (Cat. Nr.: CS1781E02)
• Assay media	• RPMI1640 supplemented with 4% low IgG fetal bovine serum
Cell line	Freshly isolated human NK cells
• Tissue origin	• Whole blood (EDTA) from donor HM_WB019 (genotyped for FcγRIIIa F/V), purified with MACSxpress® NK Isolation Kit from Miltenyi Biotec (#130-098-185)
• Source	• In-house
• Assay media	• AIM-V
• Growth media	• RPMI1640 supplemented with 10% low IgG fetal bovine serum, Glutamax
• Growth conditions	• 37°C, 5% CO ₂
Cell line	Freshly isolated human NK cells
• Tissue origin	• Whole blood (EDTA) from donor HM_WB002 (genotyped for FcγRIIIa V/V), purified with MACSxpress® NK Isolation Kit from Miltenyi Biotec (#130-

	098-185)
• Source	• In-house
• Assay media	• AIM-V
• Growth media	• RPMI1640 supplemented with 10% low IgG fetal bovine serum, Glutamax
• Growth conditions	• 37°C, 5% CO ₂
Cell line	Freshly isolated human NK cells
• Tissue origin	• Whole blood (EDTA) from donor HM_WB018 (genotyped for FcγRIIIa F/F), purified with MACSxpress® NK Isolation Kit from Miltenyi Biotec (#130-098-185)
• Source	• In-house
• Assay media	• AIM-V
• Growth media	• RPMI1640 supplemented with 10% low IgG fetal bovine serum, Glutamax
• Growth conditions	• 37°C, 5% CO ₂

Table 7. Other Reagents

Reagent	Recombinant human FcγRIIIa (V158)
• Catalogue number	• #4325-FC-050
• Concentration	• 100 µg/ml
• Source	• R&D Systems, mouse myeloma cell line, NS0-derived, with a C-terminal 6-His tag
• Stability	• Stable at -20 to 80°C

• Handling and storage conditions	• Store at -80°C until use, 1 month, 2 to 8°C under sterile conditions after reconstitution
• Formulation buffer	• PBS
Reagent	Recombinant human FcγRIIIa (F158)
• Catalogue number	• 10389-H08H
• Concentration	• 200 µg/ml (when reconstituted)
• Source	• Sino Biological, HEK293-derived, with a C-terminal 6-His tag
• Stability	• Stable at -20 to 80°C
• Handling and storage conditions	• Store at -80°C until use
• Formulation buffer	• PBS
Reagent	Recombinant human FcγRIIa (H131)
• Catalogue number	• 10374-H08C1
• Concentration	• 200 µg/ml (when reconstituted)
• Source	• Sino Biological, CHO-derived, with a C-terminal 6-His tag
• Stability	• Stable at -20 to 80°C
• Handling and storage conditions	• Store at -80°C until use
• Formulation buffer	• PBS
Reagent	Recombinant human FcγRIIa (H131)
• Catalogue number	• 10374-H08B
• Concentration	• 200 µg/ml (when reconstituted)
• Source	• Sino Biological, insect cells-derived, with a C-terminal 6-His tag

• Stability	• Stable at -20 to 80°C
• Handling and storage conditions	• Store at -80°C until use
• Formulation buffer	• PBS
Reagent	Recombinant human FcγRIIb
• Catalogue number	• 10259-H08C
• Concentration	• 200 µg/ml (when reconstituted)
• Source	• Sino Biological, CHO-derived, with a C-terminal 6-His tag
• Stability	• Stable at -20 to 80°C
• Handling and storage conditions	• Store at -80°C until use
Reagent	Human complement component C1q
• Catalogue number	• 204873
• Concentration	• 1.17 mg/ml
• Source	• Sigma-Aldrich, prepared from human serum
• Stability	• Stable at -80°C
• Handling and storage conditions	• Store at -80°C until use
• Formulation buffer	• 10 mM HEPES with 0.3 M NaCl, pH 7.2
Reagent	Source
PBS	Sigma-Aldrich Chemie GmbH, Switzerland
AIM-V media	Gibco
Ham's F-12K Medium	Gibco
MACSxpress® NK Isolation Kit	Miltenyi Biotec GmbH, Germany
Cytotoxicity Detection Kit (LDH)	Roche Diagnostics GmbH, Switzerland

96-well round bottom plates	Corning
white flat bottom 96-well plate	PerkinElmer
384-well round bottom plates	Corning
384-well flat bottom plates	Corning
Spectrophotometer	Bio-Tek
RMPI medium	Gibco
DMEM High Glucose with stable Glutamine	Bioconcept
FBS	GE Healthcare
Glutamax	Gibco
Trypsin-EDTA (0.05%), phenol red	Gibco
Prism7 Software Graph	Pad Software, Inc., La Jolla, CA
Triton X-100	Sigma
ADCC Assay buffer	Promega
Bio-Glo-TM Luciferase Assay Reagent	Promega
ADCC Bioassay	Promega
Wash buffer	PBS, 1% FBS
Formaldehyde solution, conc. 37%	Sigma (Cat. Nr.: F1635-500ML)
Saponin	Sigma (Cat. Nr.: S7900-100G)
Permeabilization buffer	0.5% saponin, PBS, 1% FBS
Alexa Fluor® 647 secondary Ab	AffiniPure F(ab') ₂ Fragment Goat Anti-Human IgG, Fcγ Fragment Specific (Jackson ImmunoResearch, Cat. Nr.: 109-606-098)
Anti-CD107 PE secondary Ab	Anti-CD107 PE (BioLegend, Cat. Nr.: 328608, Clone H4A3, Mouse IgG1, kappa)

Experimental Procedures

Measurement of binding to human Fc-receptors

5 Binding of HBC34-V35-MLNS and HBC34-V35-MLNS-GAALIE to human FcγRs was measured on an Octet® instrument (BLI, biolayer interferometry; FortéBio). Briefly, His-tagged human FcγRs (FcγRIIa allele H131, FcγRIIa allele R131, FcγRIIAa allele F158, FcγRIIIa allele V158 and FcγRIIb) at 2 µg/ml were captured onto anti-penta-His sensors for 6 minutes. FcγR-loaded sensors were then exposed for 4 minutes
10 to a solution of kinetics buffer (pH 7.1) containing 2 µg/ml of each mAb in the presence 1 µg/ml of affiniPure F(ab')₂ Fragment Goat Anti-Human IgG, F(ab')₂ fragment-specific (to cross-link human mAbs through the Fab fragment), followed by a dissociation step in the same buffer for 4 additional minutes (right part of the plot). Association and dissociation profiles were measured in real time as change in the
15 interference pattern using an Octet® RED96 (FortéBio). Binding of HBC34-V35-MLNS-GAALIE, HBC34-V35-MLNS, or HBC34-V35 in solution to immobilized human FcRn was measured by Octet in real time at pH=6.0 or pH=7.4.

Measurement of binding to human complement protein C1q

20 Binding of HBC34-V35-MLNS and HBC34-V35-MLNS-GAALIE to human complement was measured on an Octet® instrument (BLI, biolayer interferometry; FortéBio). Briefly, anti-human Fab (CH1-specific) sensors were used to capture, through the Fab fragment, the full IgG1 of HBC34-V35-MLNS and HBC34-V35-
25 MLNS-GAALIE mAbs at 10 µg/ml for 10 minutes. IgG-loaded sensors were then exposed for 4 minutes to a solution of kinetics buffer (pH 7.1) containing 3 µg/ml of purified human C1q (left part of the plot), followed by a dissociation step in the same buffer for 4 additional minutes (right part of the plot). Association and dissociation profiles were measured in real time as change in the interference pattern using an
30 Octet® RED96 (FortéBio).

Preparation of Human NK cells from whole blood

NK cells were freshly isolated from whole EDTA blood using the MACSxpress® NK isolation Kit following the manufacturer's instruction. Briefly, anticoagulated blood
5 was mixed in a 50 ml tube with 15 ml of the NK isolation cocktail and incubated for 5 minutes at room temperature using a rotator at approximately 12 rounds per minute. The tube was then placed in the magnetic field of the MACSxpress® Separator for 15 minutes. The magnetically labeled cells adhere to the wall of the tube while the aggregated erythrocytes sediment to the bottom. The target NK cells were then
10 collected from the supernatant while the tube was still inside the MACSxpress® Separator. NK cells were centrifuged, treated with distilled water to remove residual erythrocytes, centrifuged again and finally resuspended in AIM-V medium.

Determination of Antibody-Dependent NK cell killing

15 MAbs were serially diluted 10-fold in AIM-V medium from 100 µg/ml to 0.001 µg/ml. Target cells (PLC/PRF/5; MacNab, et al., British Journal of Cancer, 34(5), 1976) were added in a round bottom 384-well plate at 7.5×10^3 cells/well in 23 µl, then serially diluted antibodies were added to each well (23 µl per well), and the antibody/cell
20 mixture was incubated for 10 minutes at room temperature. Following incubation, human NK cells were added at a cell density of 7.5×10^4 /well in 23 µl, yielding an effector to target ratio of 10:1. Control wells were also included that were used to measure maximal lysis (containing target cells with 23 µl of 3% Triton x-100) and spontaneous lysis (containing target cells and effector cells without antibody). Plates
25 were incubated for 4 hours at 37°C with 5% CO₂. Cell death was determined by measuring lactate dehydrogenase (LDH) release using a LDH detection kit according to the manufacturer's instructions. In brief, plates were centrifuged for 4 minutes at 400 x g, and 35 µl of supernatant was transferred to a flat 384-well plate. LDH reagent was prepared and 35 µl were added to each well. Using a kinetic protocol, the absorbance at
30 490 nm and 650 nm was measured once every 2 minutes for 8 minutes. The percent specific lysis was determined by applying the following formula: (specific release – spontaneous release) / (maximum release - spontaneous release) x 100.

Determination of Antibody-Dependent NK cell activation

Activation of primary NK cells was tested using freshly isolated cells from two donors
5 that had been previously genotyped for expressing homozygous high (V158 allele) or
low (F158 allele) affinity FcγRIIIa. Serial dilutions of mAbs (serially diluted 10-fold in
AIM-V medium from 100 µg/ml to 0.0001 µg/ml) were incubated with NK cells for 4
hours. Activation of NK cell was measured by flow cytometry by staining NK cells
with anti-CD107a mAb (anti-CD107 PE, BioLegend®, used diluted 1/35) as a
10 functional marker for NK cell activity.

Determination of Antibody-Dependent Activation of Human FcγRIIIa

HBC34-V35-MLNS and HBC34-V35-MLNS-GAALIE were serially diluted 4-fold in
15 ADCC Assay buffer from 5 µg/ml to 0.076 µg/ml. Target antigen (HBsAg from
Engerix B, Glaxo SmithKline) was added in a white flat bottom 96-well plate at 0.6
µg/ml in 25 µl, then serially diluted antibodies were added to each well (25 µl per well),
and the antibody/cell mixture was incubated for 10 minutes at room temperature.
Effector cells for the ADCC Bioassay were thawed and added at a cell density of $7.5 \times$
20 10^4 /well in 25 µl (final HBsAg concentration was 0.2 µg/ml). Control wells were also
included that were used to measure antibody-independent activation (containing HBsAg
and effector cells but no antibody) and spontaneous luminescence of the plate (wells
containing the ADCC Assay buffer only). Plates were incubated for 24 hours at 37°C
with 5% CO₂. Activation of human FcγRIIIa (V158 or F158 variants) in this bioassay
25 results in NFAT-mediated expression of the luciferase reporter gene. Luminescence
was measured with a luminometer using the Bio-Glo™ Luciferase Assay Reagent
according to the manufacturer's instructions. The data (*i.e.*, specific FcγRIIIa
activation) are expressed as the average of relative luminescence units (RLU) over the
background by applying the following formula: (RLU at concentration x of mAbs –
30 RLU of background).

Determination of Antibody-Dependent Activation of Human FcγRIIa

HBC34-V35-MLNS and HBC34-V35-MLNS-GAALIE were serially diluted 5-fold in ADCP Assay buffer from 50 µg/ml to 0.00013 µg/ml. Target antigen (HBsAg from Engerix B) was added in a white flat-bottom 96-well plate at 0.6 or 6 µg/ml in 25 µl, then serially diluted antibodies were added to each well (25 µl per well), and the antigen/antibody was incubated for 25 minutes at room temperature. Effector cells for the FcγRIIa activation bioassay were thawed and added at a cell density of 50.0×10^4 /well in 25 µl (final HBsAg concentration was 0.2 or 2 µg/ml, respectively). Control wells were also included that were used to measure antibody-independent activation (containing HBsAg and effector cells but no antibody) and spontaneous luminescence of the plate (wells containing the ADCP Assay buffer only). Plates were incubated for 23 hours at 37°C with 5% CO₂. Activation of human FcγRIIa (H131 variants) in this bioassay results in NFAT-mediated expression of the luciferase reporter gene. Luminescence was measured with a luminometer using the Bio-Glo™ Luciferase Assay Reagent according to the manufacturer's instructions. The data (*i.e.*, specific FcγRIIa activation) are expressed as the average of relative luminescence units (RLU) over the background by applying the following formula: (RLU at concentration [x] of mAbs – RLU of background).

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Determination of Antibody-Dependent Activation of Human FcγRIIb

HBC34-V35-MLNS and HBC34-V35-MLNS-GAALIE were serially diluted 5-fold in ADCP Assay buffer from 100 µg/ml to 0.00026 µg/ml. Target antigen (HBsAg from Engerix B) was added in a white flat bottom 96-well plate at 3 µg/ml in 25 µl, then serially diluted antibodies were added to each well (25 µl per well), and the antigen/antibody was incubated for 15 minutes at room temperature. Effector cells for the FcγRIIb activation bioassay were thawed and added at a cell density of 75.0×10^4 /well in 25 µl (the final HBsAg concentration was 1 µg/ml). Control wells were also included that were used to measure antibody-independent activation (containing HBsAg and effector cells but no antibody) and spontaneous luminescence of the plate (wells containing the ADCP Assay buffer only). Plates were incubated for 20 hours at 37°C

with 5% CO₂. Activation of human FcγRIIb in this bioassay results in NFAT-mediated expression of the luciferase reporter gene. Luminescence was measured with a luminometer using the Bio-Glo-™ Luciferase Assay Reagent according to the manufacturer's instructions. The data (*i.e.*, specific FcγRIIb activation) are expressed as the average of relative luminescence units (RLU) over the background by applying the following formula: (RLU at concentration [x] of mAbs – RLU of background).

Determination of Antibody binding to human hepatoma cell line PLC/PRF/5

PLC/PRF/5 cells were trypsinized for 5 min at 37°C, transferred in 7 ml growing medium, centrifugated at 400 x g, 4 min, 4°C, and extensively washed at 4°C in PBS. Some cells were fixed with 4% formaldehyde (20 minutes at 4°C); others were fixed and then permeabilized with permeabilization buffer (20 minutes at 4°C). The cellular pellet was resuspended in 2.64 ml of wash buffer (fixed cells) or permeabilization buffer (fix&perm cells) (Table 7) and dispensed at 200 µl/well into 96-well round bottom plates (corresponding to 100'000 cells/well). The plate was centrifugated at 400g , 4 min, 4°C. Serial 1:5 5-points dilutions of the test antibodies starting from a final concentration of 10 µg/ml were added to cell-containing wells and incubated 30 minutes on ice. After 2 washes at 4°C, 400 x g, 4 min in wash buffer (fix cells) or permeabilization buffer (fix&perm cells), 50 µl/well of Alexa Fluor® 647-labelled secondary antibody (Table 7) was added to cells and incubated for 20 min on ice. Cells were washed 2 more times with wash buffer (fix cells) or permeabilization buffer (fix&perm cells), resuspended in 200 µl/well of wash buffer (fix cells) or permeabilization buffer (fix&perm cells) and signal (MFI, mean fluorescence intensity) was quantified with a cytofluorimeter (BD FACSCanto™ II).

Results

Direct antiviral mechanisms are important for neutralizing HBV *in vivo*. Indirect, Fc-dependent mechanisms of action mediated by the interaction of the Fc region with Fc gamma receptors (FcγRs) on immune cells may also have important contributions to *in vivo* efficacy and to mediate endogenous immune responses. FcγR-dependent

mechanisms can be assessed *in vitro* by measuring binding to FcγRs as well as in antibody-dependent activation of human FcγRs (Hsieh, Y.-T., et al., Journal of Immunological Methods, 441(C), 56–66. doi.org/10.1016/j.jim.2016.12.002). The ability of the antibody to bind to FcRn and to complement are other factors of interest.

5

In one set of experiments, HBC34-V35-MLNS and HBC34-V35-MLNS-GAALIE were compared side-by-side for their ability to bind to the full set of human FcγRs (FcγRIIIa V158 and F158 alleles, FcγRIIa H131 and R131 alleles, and FcγRIIb) using biolayer interferometry (BLI Octet® System, ForteBio). As shown in Figures 9A-9E, Fc bearing MLNS-GAALIE mutations have altered interactions with FcγRs; specifically, Fc bearing both of these mutations, as opposed to Fc bearing MLNS alone, have enhanced binding to FcγRIIIa and FcγRIIa, and reduced binding to FcγRIIb.

As shown in Figure 9F, antibodies bearing the MLNS Fc mutation have increased binding to FcRn at pH 6.0 relative to antibody with wild-type Fc, but little to no measurable binding to FcRn at pH 7.4, which is comparable to antibody with wild-type Fc.

Also, binding of HBC34-V35-MLNS-GAALIE to C1q was abolished, as measured by biolayer interferometry (Figure 10).

HBC34-V35-MLNS and HBC34-V35-MLNS-GAALIE were also tested for their ability to activate human FcγRIIIa and FcγRIIa using cell-based reporter bioassays. These assays utilize Jurkat cells engineered with a NFAT-mediated luciferase reporter to reflect activation of human FcγRs. While HBC34-V35-MLNS poorly activated or did not activate human FcγRIIIa and FcγRIIa in the presence of HBsAg, HBC34-V35-MLNS-GAALIE showed dose-dependent activation of all tested FcγRs (Figures 11A, 11B, 12A-12B). HBC34-V35-MLNS-GAALIE did not activate FcγRIIb, even when tested at 100 µg/ml (Figures 13A-13B).

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ADCC activity was also measured using natural killer cells (NK) isolated from human peripheral blood mononuclear cells of one donor who was previously genotyped for

expressing heterozygous high (V158) and low (F158) affinity FcγRIIIa (F/V). Isolated NK cells were used to measure the killing of the hepatoma cell line PLC/PR/5 upon exposure to HBC34-V35; HBC34-V35-MLNS; HBC34-V35-MLNS-GAALIE; or another mAb (17.1.41, targeting another epitope on the antigenic loop of the HBsAg; *see* Eren, R., et al., Hepatology, doi.org/10.1053/jhep.2000.9632; Galun, E., et al., Hepatology, doi.org/10.1053/jhep.2002.31867). Killing in the presence of the HBsAg-specific mAbs HBC34-V35, HBC34-V35-MLNS, HBC34-V35-MLNS-GAALIE and 17.1.41 was not observed (Figure 14A). The observed lack of antibody-dependent killing of PLC/PR/5 cells might be related to the poor expression of HBsAg on the surface of these cells (Figure 14B), which, without wishing to be bound by theory, may not be sufficient to trigger killing by NK cells. Conversely, high levels of HBsAg were detected with HBC34v35 and 17.1.41 when PLC/PR/5 cells were fixed and permeabilized, indicating that most of the HBsAg is found either intracellularly or in secreted forms (*i.e.* subviral particles) (Figure 14B).

Activation of primary human NK cells (V/F) in the presence of HBC34v35-MLNS or HBC34-V35-MLNS-GAALIE and HBsAg was also examined using anti-CD107a mAb. Data are shown in Figures 15A and 15B.

These *in vitro* data show that HBV-specific binding proteins of the present disclosure bearing the GAALIE Fc mutation bind to and activate low affinity activating FcγRIIa and FcγRIIIa more effectively than the non-GAALIE Fc parental antibody. GAALIE-bearing binding proteins also do not bind to and or activate low affinity inhibitory FcγRIIb. GAALIE-bearing binding proteins also do not bind to C1q. Furthermore, GAALIE-bearing binding proteins do not promote ADCC on hepatoma cells, but activate human NK cells in the presence of soluble HBsAg. Introduction of MLNS mutation increases binding to FcRn at pH 6.0.

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Example 7: In Vitro Study of Drug-Drug Interaction between HBC34-V35-MLNS-GAALIE and a Pol/RT Inhibitor

An *in vitro* study was conducted to identify possible combination effects of HBC34-V35-MLNS-GAALIE with the HBV pol/RT inhibitor Entecavir (ETV). *In vitro* combination effects were determined using HBC34-V35-MLNS-GAALIE and ETV in HepG2.2.15 cells in a checkerboard format. HBsAg and HBV DNA levels were used as read-outs and data were analyzed for combination effects using MacSynergy II (uab.edu/medicine/peds/macsynergy). For normalization, values obtained from untreated HepG2.2.15 cells were used as positive controls, while tissue culture medium was used as negative control. Synergy plots at 99% confidence were used for reporting. Data are shown in Figure 16. The synergy plots for both readouts show an additive effect of HBC34-V35-MLNS-GAALIE with ETV *in vitro*. Notably, no antagonism was observed. These data support the use of nucleoside analogs in combination with HBC34-V35-MLNS-GAALIE in a clinical setting.

Example 8: Identification and characterization of human monoclonal antibody HBC24

An anti-HBV human monoclonal antibody was isolated in a similar manner as described in Tragglia E. et al., 2004, Nat Med 10(8): 871-5 from a human patient. The antibody was characterized by determining the nucleotide and amino acid sequences of its variable regions and the complementarity determining regions (CDRs) therein and termed "HBC24". Accordingly, HBC24 is an IgG1-type fully human monoclonal antibody having the CDR, V_H and V_L sequences as shown above in Table 3. Exemplary nucleotide sequences encoding the V_H and V_L of HBC24 are provided in Table 4.

Example 9: Generation of germlined variants of HBC24 and functional testing

HBC24 is analyzed for the presence of somatic mutations in the variable regions relative to germline sequence. Identified somatic mutations are reverted to germline

sequence to produce HBC24 variants. HBC24 and variants are tested for binding (*in vitro*) and neutralization (*in vitro*; *in vivo*) of HBV and HBD serotypes using assays as described herein.

5 **Example 10: Introduction of Fc modifications to HBC24 and variants**

Further HBC24 variants are produced that contain the MLNS and GAALIE mutations in both Fc monomers. The HC amino acid sequences of selected variants are provided in SEQ ID NOs: 121 and 122. Variants are examined for: (1) *in vitro* binding to antigen; (2) *in vitro* neutralization of HBV serotypes using assays as described herein.

TABLE OF SEQUENCES AND SEQ ID NUMBERS (SEQUENCE LISTING):

SEQ ID NO	Sequence	Remarks
1	X ₁ X ₂ X ₃ TC X ₄ X ₅ X ₆ A X ₇ G wherein X ₁ , X ₂ , X ₃ , X ₄ , X ₅ , X ₆ and X ₇ may be any amino	epitope
2	X ₁ X ₂ X ₃ TC X ₄ X ₅ X ₆ A X ₇ G wherein X₁ is P, T or S, X₂ is C or S, X₃ is R, K, D or I, X₄ is M or T, X₅ is T, A or I, X₆ is T, P or L, and X₇ is Q, H or L.	

3	MENITSGFLGPLLVLQAGFFLLTRILTIQSLDSWWT SLNFLGGTTVCLGQNSQSPTSNSHPTSCPPTCPGYR WMCLRRFIIFLFILLCLIFLLVLLDYQGMLPVCPLIP GSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNC TCIIPSSWAFGKFLWEWASARFSWLSLLVPFVQWF VGLSPTVWLSVIWMMWYWGPSLYSILSPFLPLLPIFF CLWVYI	S domain of HBsAg (GenBank acc. no. J02203)
4	MENVTSGLGPLLVLQAGFFLLTRILTIQSLDSWWT SLNFLGGTTVCLGQNSQSPTSNSHPTSCPPTCPGYR WMCLRRFIIFLFILLCLIFLLVLLDYQGMLPVCPLIP GSSTTGTGPCRTCCTTPAQGTSMYPSCCCTKPSDGNC TCIIPSSWAFGKFLWEWASARFSWLSLLVPFVQWF VGLSPTVWLSVIWMMWYWGPSLYSTLSPFLPLLPIF FCLWVYI	S domain of HBsAg (GenBank acc. no. FJ899792)
5	QGMLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPS CCCTKPSDGNCCTCIIPSSWAFGKFLWEWASARFSW	J02203 (D, ayw3)
6	QGMLPVCPLIPGSSTTGTGPCRTCCTTPAQGTSMYPSC CCTKPSDGNCCTCIIPSSWAFGKFLWEWASARFSW	FJ899792 (D, adw2)
7	QGMLPVCPLIPGTTTTSTGPCKTCTTPAQGNSMFPSC CCTKPSDGNCCTCIIPSSWAFAKYLWEWASVRFSW	AM282986 (A)
8	QGMLPVCPLIPGSSTTSTGPCKTCTTPAQGTSMFPSC CCTKPTDGNCTCIIPSSWAFAKYLWEWASVRFSW	D23678 (B1)
9	QGMLPVCPLIPGTTSTSTGPCKTCTTPAQGTSMFPSC CCTKPSDGNCCTCIIPSSWAFARFLWEWASVRFSW	AB117758 (C1)
10	QGMLPVCPLIPGSSTTSTGPCRTCCTTLAQGTSMFPSC CCSKPSDGNCCTCIIPSSWAFGKFLWEWASARFSW	AB205192 (E)
11	QGMLPVCPLIPGTTTTSTGPCKTCTTLAQGTSMFPS CCCSKPSDGNCCTCIIPSSWALGKYLWEWASARESW	X69798 (F4)
12	QGMLPVCPLIPGSSTTSTGPCKTCTTPAQGNSMYPSC CCTKPSDGNCCTCIIPSSWAFAKYLWEWASVRFSW	AF160501 (G)
13	QGMLPVCPLIPGTTTTSTGPCKTCTTLAQGTSMFPS CCCTKPSDGNCCTCIIPSSWAFGKYLWEWASARFSW	AY090454 (H)
14	QGMLPVCPLIPGSSTTSTGPCKTCTTPAQGNSMYPSC CCTKPSDGNCCTCIIPSSWAFAKYLWEWASARFSW	AF241409 (I)
15	QGMLPVCPLIPGTTTTSTGPCRTCCTTAQGTSMFPSC CCTKPSDGNCCTCIIPSSWAFAKFLWEWASVRFSW	AB486012 (J)
16	CQGMLPVCPLIPGSSTTGTGTCRTCTTPAQGTSMYPS CCCTKPSDGNCCTCIIPSSWAFGKFLWEWASARFSW	HBsAg Y100C/P120T
17	QGMLPVCPLIPGSSTTGTGTCRTCTTPAQGTSMYPSC CCTKPSDGNCCTCIIPSSWAFGKFLWEWASARFSW	HBsAg P120T
18	QGMLPVCPLIPGSSTTGTGTCRTCTTPAQGTSMYPSC CCTKPLDGNCTCIIPSSWAFGKFLWEWASARFSW	HBsAg P120T/S143L

19	QGMLPVCPLIPGSSTTGTGPSRTCTTPAQGTSMYPSC CCTKPSDGNCTCIPISSWAFGKFLWEWASARFSW	HBsAg C121S
20	QGMLPVCPLIPGSSTTGTGPCDTCTTPAQGTSMYPSC CCTKPSDGNCTCIPISSWAFGKFLWEWASARFSW	HBsAg R122D
21	QGMLPVCPLIPGSSTTGTGPCITCTTPAQGTSMYPSC CCTKPSDGNCTCIPISSWAFGKFLWEWASARFSW	HBsAg R122I
22	QGMLPVCPLIPGSSTTGTGPCRNCTTPAQGTSMYPSC CCCTKPSDGNCTCIPISSWAFGKFLWEWASARFSW	HBsAg T123N
23	QGMLPVCPLIPGSSTTGTGPCRTCTTPAHGTSMYPSC CCTKPSDGNCTCIPISSWAFGKFLWEWASARFSW	HBsAg Q129H
24	QGMLPVCPLIPGSSTTGTGPCRTCTTPALGTSMYPSC CCTKPSDGNCTCIPISSWAFGKFLWEWASARFSW	HBsAg Q129L
25	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTSHYPSC CCTKPSDGNCTCIPISSWAFGKFLWEWASARFSW	HBsAg M133H
26	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTSLYPSC CCTKPSDGNCTCIPISSWAFGKFLWEWASARFSW	HBsAg M133L
27	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTSTYPSC CCTKPSDGNCTCIPISSWAFGKFLWEWASARFSW	HBsAg M133T
28	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTSMYPSC CCTEPSDGNCTCIPISSWAFGKFLWEWASARFSW	HBsAg K141E
29	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTSMYPSC CCTKSSDGNCTCIPISSWAFGKFLWEWASARFSW	HBsAg P142S
30	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTSMYPSC CCTKPKDGNCTCIPISSWAFGKFLWEWASARFSW	HBsAg S143K
31	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTSMYPSC CCTKPSAGNCTCIPISSWAFGKFLWEWASARFSW	HBsAg D144A
32	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTSMYPSC CCTKPSDRNCTCIPISSWAFGKFLWEWASARFSW	HBsAg G145R
33	QGMLPVCPLIPGSSTTGTGPCRTCTTPAQGTSMYPSC CCTKPSDGACTCIPISSWAFGKFLWEWASARFSW	HBsAg N146A
34	GRIFRSFY	HBC34 CDRH1 aa
35	NQDGSEK	HBC34 CDRH2 aa
36	AAWSGNSGGMDV	HBC34 CDRH3 aa
37	KLGNKN	HBC34 CDRL1 aa
38	EVK	HBC34 CDRL2 aa
39	VIYEVKYRP	HBC34 CDRL2 long aa

40	QTWDSTTVV	HBC34 CDRL3 aa
41	ELQLVESGGGWVQPGGSQRLSCAASGRIFRSFYMS WVRQAPGKGLEWVATINQDGSEKLYVDSVKGRFTI SRDNAKNSLFLQMNNLRVEDTAVYYCAAWSGNSG GMDVWGOGTTVSVSS	HBC34, HBC34- V7, HBC34-V34, HBC34-V35 VH aa
42	SYELTQPPSVSVSPGQTVSIPCSGDKLGKNVCWFQ HKPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTI SGTQAMDEAAAYFCQTWDSTTVVFGGGTRLTVL	HBC34 VL aa
43	GGACGCATCTTTAGAAAGTTTTTAC	HBC34 CDRH1 nuc
44	ATAAACCAAGATGGAAGTGAGAAA	HBC34 CDRH2 nuc
45	GCGGCTTGGAGCGGCAATAGTGGGGGTATGGACG TC	HBC34 CDRH3 nuc
46	AAATTGGGGAATAAAAAT	HBC34 CDRL1 nuc
47	GAGGTAAA	HBC34 CDRL2 nuc
48	gtcatctatGAGGTAAAtaccgcccc	HBC34 CDRL2 long nuc
49	CAGACGTGGGACAGCACCACTGTGGTG	HBC34 CDRL3 nuc
50	GAACTGCAGCTGGTGGAGTCTGGGGGAGGCTGGG TCCAGCCGGGGGGTCCCAGAGACTGTCCTGTGC AGCCTCTGGACGCATCTTTAGAAAGTTTTTACATGA GCTGGGTCCGCCAGGCCCCAGGGAAGGGGCTGGA GTGGGTGGCCACTATAAACCAAGATGGAAGTGAG AAATTATATGTGGACTCTGTGAAGGGCCGATTCA CCATCTCCAGAGACAACGCCAAGAACTCACTATT TCTGCAAATGAACAACCTGAGAGTCGAGGACACG GCCGTTTATTACTGCGCGGCTTGAGCGGCAATA GTGGGGGTATGGACGTCTGGGGCCAGGGGACCAC GGTCTCCGTCTCCTCA	HBC34 VH nuc

51	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGT GTCCCCAGGACAGACAGTCAGCATCCCCTGCTCT GGAGATAAATTGGGGAATAAAAAATGTTTGCTGGT TTCAGCATAAGCCAGGCCAGTCCCCTGTGTTGGTC ATCTATGAGGTAAATACCGCCCCTCGGGGATTCC TGAGCGATTCTCTGGCTCCAACCTCTGGGAACACA GCCACTCTGACCATCAGCGGGACCCAGGCTATGG ATGAGGCTGCCTATTTCTGTCAGACGTGGGACAG CACCCTGTGGTGTTCGGCGGAGGGACCAGGCTG ACCGTCCTA	HBC34 VL nuc
52	<u>X</u> GSSTTSTGPCRTCMT <u>X</u> PSDGN <u>A</u> T <u>A</u> IPSSW <u>X</u> wherein the residues coded as <u>X</u> were substituted with Cysteines	peptide
53	TSTGPCRTCMTTAQG	peptide
54	GMLPVCPLIPGSSTTSTGPCRTCMTT	peptide
55	<u>X</u> SMYPS <u>A</u> S <u>A</u> TKPSDGN <u>X</u> TGPCRTCMTTAQGT <u>S</u> <u>X</u> wherein the residues coded as <u>X</u> were substituted with Cysteines	peptide
56	PCRTCMTTAQG	amino acids 120 – 130 of the S domain of HBsAg (HBV-D J02203)
57	PCX ₁ TCX ₂ X ₃ X ₄ AQG, wherein X ₁ is R or K, X ₂ is M or T, X ₃ is T or I, and X ₄ is T, P or L	epitope
58	QTFDSTTVV	HBC34-V7 CDRL3 and HBC34-V23 CDRL3 (aa)
59	SYELTQPPSVSVSPGQTVSIPCSGDKLGKNVCWFQH KPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTIS GTQAMDEAAYFCQTFDSTTVVFGGGTRLTVL	HBC34-V7 VL
60	AAGCTGGGGAACAAAAAT	HBC34-V7 CDRL1 and HBC-V23 CDRL1 (nuc)
61	GAGGTGAAA	HBC34-V7 CDRL2 and HBC34v23 CDRL2 nuc

62	GTCATCTACGAGGTGAAATATCGGCCT	HBC34-V7 CDRL2 long and CDRL2 HBC34-V23 long
63	CAGACATTCGATTCCACCACAGTGGTC	CDRL3 HBC34-V7 and CDRL3 HBC34-V23 nuc
64	TCTTACGAGCTGACACAGCCACCTAGCGTGTCGT CTCTCCAGGACAGACCGTGTCCATCCCTTGCTCTG GCGACAAGCTGGGGAACAAAAATGTCTGTTGGTTC CAGCACAAGCCAGGGCAGAGTCCCGTGCTGGTCAT CTACGAGGTGAAATATCGGCCTTCAGGAATTCCAG AACGGTTCAGCGGATCAAACAGCGGCAATACTGC AACCCTGACAATTAGCGGGACCCAGGCCATGGAC GAAGCCGCTTATTTCTGCCAGACATTCGATTCCAC CACAGTGGTCTTTGGCGGGGGAAGTAGGCTGACCG TGCTG	HBC34-V7, HBC34-V34, and HBC34-V35 VL nuc
65	SYELTQPPSVSVSPGQTASITCSGDKLGKNACWYQ QKPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTI SGTQAMDEADYYCQTFDSTTVVFGGGTKLTVL	HBC34-V23 VL aa
66	INQDGSEK	HBC34wt CDRH2
67	EVQLVESGGGLVQPGGSLRLSCAASGRIFRSFYMSW VRQAPGKGLEWVANINQDGSEKLYVDSVKGRFTISR DNAKNSLFLQMNNLRVEDTAVYYCAAWSGNSGGM DVWGQGTTTVTVSS	HBC34-V31, HBC34-V32 and HBC34-V33 VH
68	GAGGTGCAGCTGGTGGAATCCGGCGGGGGACTGG TGCAGCCTGGCGGCTCACTGAGACTGAGCTGTGCA GCTTCTGGAAGAATCTTCAGATCTTTTACATGAGT TGGGTGAGACAGGCTCCTGGGAAGGGACTGGAGT GGGTCGCAAACATCAATCAGGACGGATCAGAAAA GCTGTATGTGGATAGCGTCAAAGGCAGGTTCACTA TTTCCCGCGACAACGCCAAAAATTCTCTGTTTCTGC AGATGAACAATCTGCGGGTGGAGGATACCGCTGTC TACTATTGTGCAGCCTGGTCTGGCAACAGTGGAGG CATGGACGTGTGGGGACAGGGAACACAGTGACA GTCAGCTCC	HBC34-V31, HBC34-V32 and HBC34-V33 VH (nuc)

69	TCTTACGAGCTGACACAGCCCCCTAGCGTGTCCGT CTCTCCAGGCCAGACAGCATCCATCACTTGCTCTG GCGACAAGCTGGGGAACAAAAATGCCTGTTGGTA TCAGCAGAAGCCAGGGCAGAGTCCCGTGCTGGTC ATCTACGAGGTGAAATATCGGCCTTCAGGAATTCC AGAAAGATTCAAGTGGATCAAACAGCGGCAATACT GCTACCCTGACAATTAGCGGGACCCAGGCCATGGA CGAAGCTGATTACTATTGCCAGACATTCGATTCCA CCACAGTGGTCTTTGGCGGGGGAACCTAAGCTGACC GTGCTG	HBC34-V23 VL nuc
70	GAAGTGCAGCTGGTCTGAATCAGGAGGAGGGTGGG TCCAGCCCGGAGGGAGCCAGAGACTGTCTTGTGCC GCATCAGGGAGGATCTTCAGGAGCTTCTACATGTC CTGGGTGCGCCAGGCACCAGGCAAGGGACTGGAG TGGGTGCGCCACCATCAACCAGGACGGATCTGAAA AGCTGTATGTGGATAGTGTCAAAGGCCGGTTCACA ATTAGCAGAGACAACGCTAAAAATTCTCTGTTTCT GCAGATGAACAATCTGCGAGTGGAGGATACCGCC GTCTACTATTGCGCCGCTTGGTCTGGCAACAGCGG CGGGATGGATGTCTGGGGGCAGGGCACAACAGTG AGCGTCTCTTCC	HBC34 wt VH codon optimized
71	TCATACGAACTGACTCAGCCTCCCTCCGTCTCCGTC TCACCTGGACAGACCGTCTCAATCCCCTGCTCCGG CGATAAACTGGGCAACAAGAACGTGTGCTGGTTCC AGCACAAACCCGGACAGAGTCCTGTGCTGGTCATC TACGAGGTCAAGTATCGGCCAAGCGGCATTCCCGA AAGATTCAAGCGGCTCCAACCTCTGGGAATACCGCAA CACTGACTATCTCTGGAACCCAGGCAATGGACGAG GCAGCTTACTTTTGCCAGACTTGGGATTCAACTAC TGTCGTGTTTCGGCGGCGGAACTAGACTGACTGTCC TG	HBC34 wt VL codon optimized
72	GGGAGGATCTTCAGGAGCTTCTAC	HBC34 wt CDRH1 codon optimized
73	ATCAACCAGGACGGATCTGAAAAG	HBC34 wt CDRH2 codon optimized
74	GCCGCTTGGTCTGGCAACAGCGGCGGGATGGATGT C	HBC34 wt CDRH3 codon optimized
75	AAACTGGGCAACAAGAAC	HBC34 wt CDRL1 codon optimized
76	GAGGTCAAG	HBC34 wt CDRL2 codon optimized

77	GTCATCTACGAGGTCAAGTATCGGCCA	HBC34 wt CDRL2 long codon optimized
78	CAGACTTGGGATTCAACTACTGTCGTG	HBC34 wt CDRL3 codon optimized
79	GGSGG	linker
80	TGPCRTC	epitope
81	GNCTCIP	epitope
82	CCIPSSWAFGCSTTSTGPCRTCC wherein in particular thy cysteines at positions 2, 21, and 24 are coupled to acetamidomethyl.	discontinuous epitope mimic
83	CGNCTCIPSSWAF ~~C~~ STTSTGPCRTCC wherein in particular thy cysteines at positions 4, 6, 24, and 27 are coupled to acetamidomethyl.	discontinuous epitope mimic
84	CGGGCSTTSTGPCRTCC wherein in particular thy cysteines at positions 13 and 16 are coupled to acetamidomethyl.	looped epitope mimic
85	STTSTGPCRTC	epitope
86	GNCTCIPSSWAF ~~C~~	epitope
87	GNCTCIPSSWAF	epitope
88	PCRXC	epitope
89	SYELTQPPSVSVSPGQTVSIPCSGDKLGKNVAVWFQH KPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTIS GTQAMDEAAYFCQTFDSTTVVFGGGTRLTVL	HBC34-V35 VL
90	SYELTQPPSVSVSPGQTVSIPCSGDKLGKNVSWWFQH KPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTIS GTQAMDEAAYFCQTFDSTTVVFGGGTRLTVL	HBC34-V34 VL
91	ELQLVESGGGWVQPGGSQRLSCAASGRIFRSFYMSW VRQAPGKGLEWVATINQDGSEKLYVDSVKGRFTISR DNAKNSLFLQMNNLRVEDTAVYYCAAWSGNSGGM DVWGQGTTVSVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLAGPSVFLFPPKPKDTL MISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPLPEEKTIKAKGQPREPQVYTLPPSRDEL TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHE ALHSHYTQKSLSLSPGK	HC of HBC34-V35- MLNS-GAALIE and HBC34-V34- MLNS-GAALIE (g1M17, 1)

92	ELQLVESGGGWVQPGGSQRLSCAASGRIFRSFYMSW VRQAPGKGLEWVATINQDGSEKLYVDSVKGRFTISR DNAKNSLFLQMNNLRVEDTAVYYCAAWSGNSGGM DVWGQGTTVSVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSRDEL KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFCFVLSH LHSHYTKQKSLSPGK	HC of HBC34-V35- MLNS and HBC34- V34-MLNS (g1M17, 1)
93	SYELTQPPSVSVSPGQTVSIPCSGDKLGKKNVAFQH KPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTIS GTQAMDEAAAYFCQTFDSTTVVFGGGTRLTVLGQPK AAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVA WKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPE QWKSHRYSYSCQVTHEGSTVEKTVAPTECS	LC of HBC34-V35
94	SYELTQPPSVSVSPGQTVSIPCSGDKLGKKNVSWFQH KPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTIS GTQAMDEAAAYFCQTFDSTTVVFGGGTRLTVLGQPK AAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVA WKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPE QWKSHRYSYSCQVTHEGSTVEKTVAPTECS	LC of HBC34-V34
95	EVQLLESGGGLVQPGGSLRLSCAASGSTFTKYAMSW VRQAPGKGLEWVASISGSPGFIDITYYADSVKGRF TISRDTSKNTLYLQMNSLRAEDTALYYCAKDVGVI SYYYAMDVWGQGTAVTVSS	HBC24 VH
96	EIVLTQSPGTLSPGERATLSCRASQGLSSSYLAWY QQKPGQAPRLIYSASTRATGIPDRFSGSGSGTDFTLT ISRLEPEDFAVYYCQYAYSPPRWTFGGGTKVEIK	HBC24 VL
97	GSTFTKYA	CDRH1 of HBC24
98	ISGSPGF	CDRH2 of HBC24
99	LYYCAKDVGVISSYYYAMDV	CDRH3 of HBC24
100	QGLSSSY	CDRL1 of HBC24
101	SAS	CDRL2 of HBC24
102	QYAYSPPRWTF	CDRL3 of HBC24

103	gagctgcagctggtggagtcggcgccggctgggtgcagcctggcggtcccag aggctgagctgtgccgttctggcaggatctccggctctttacatgtcttgggtgcg gcaggctccaggcaaggcctggagtggtggctaccatcaaccaggacggctc cgagaagctgtatgtggatagcgtgaaggcgagattcacaatctctcgcgacaacg ccaagaactccctgtttctgcagatgaacaatctgagggtggaggataccgccgtgt actattgcgccgttggcttggaatagcggcgcatggacgtgtggggacaggg caccaccgtgtccgtgtccagc	VH of HBC34-V7, HBC34-V35, and HBC34-V34 (codon optimized)
104	agctacgagctgacacagccccctccgtgtccgtgtcccctggacagaccgtgtc catcccatgcagcggcgacaagctgggcaacaagaacgtgtcctggttcagcata agcctggccagtcccccgtgtggtcatctacgaggtgaagtataggcccagcgg catccctgagcgggttctgtggtccaacagcggcaatacagccaccctgacaatctc tggcacacaggctatggacgaggccgttatttctgccagaccttgattccaccac agtgggtgttcggcgccggcaccagactgacagtgtctg	HBC34-V34 VL (codon optimized)
105	agctacgagctgacacagccccctccgtgtccgtgtcccctggacagaccgtgtc catcccatgcagcggcgacaagctgggcaacaagaacgtggcctggttcagcat aagcctggccagtcccccgtgtggtcatctacgaggtgaagtataggcccagcgg gcatccctgagcgggttctgtggtccaacagcggcaatacagccaccctgacaatc tctggcacacaggctatggacgaggccgttatttctgccagaccttgattccacca cagtgggtgttcggcgccggcaccagactgacagtgtctg	HBC34-V35 VL (codon optimized)
106	gaggtgcagttgttgagctctgggggagggcttggtacagcctggggggtccctga gactctcctgtgcagcctctGGATCCACTTTTACCAAATATGC CatgagctgggtccgtcaggctccagggaaggggctggagtggtgcgaagtA TTAGTGGAAAGTgttctgtgtttGGTATTGACACAtactacgca gactccgttaagggccggttcaccatctccagagacactccaagaacaccctgtat ctgcaaatgaacagcctgagagccgaggacacggccttatattactgtGCGAA AGATGTCTGGGGTTATCGGGTCATACTATTACTACG CTATGGACGTCtgggggtcaa	HBC24 VH (wild type)
107	aaattgtgttgacgcagctctccaggcacctgtctttgtctccaggggaagagcca ccctctcctgcagggccagtCAGGGTCTTAGCAGCAGTTACtta gcctgtgaccagcagaaacctggccaggctcccaggctcctcatctatAGTGC GTCCaccagggccactggcatccagacaggttcagtggcagtggtctggga cagacttactctcaccatcagcagactggagcctgaagatttgcagtgattactgt CAACAGTATGCTTACTCACCTCGGTGGACGttcgcca agggaccaaggtggagatcaaac	HBC24 VL (wild type)

108	GAGGTGCAGCTGCTGGAAAGCGGCGGCGGCCTGG TGCAGCCCGGCGGCTCCCTGAGGCTGTCTTGCGCC GCCTCTGGCAGCACCTTCACAAAGTATGCAATGTC TTGGGTGCGCCAGGCACCAGGCAAGGGCCTGGAG TGGGTGGCCTCCATCTCTGGCAGCGTGCCTGGCTT CGGCATCGACACCTACTATGCCGATTCCGTGAAGG GCCGGTTTACAATCAGCAGAGACACCTCCAAGAAC ACACTGTATCTGCAGATGAATTCTCTGCGGGCCGA GGACACCGCCCTGTACTATTGTGCCAAGGATGTGG GCGTGATCGGCAGCTACTATTACTATGCAATGGAC GTGTGGGGACAGGGAACAGCAGTGACAGTGAGCT CC	HBC24 VH (codon optimized)
109	GAGATCGTGCTGACCCAGTCTCCTGGCACACTGTC CCTGTCCCCTGGAGAGAGAGCCACCCTGTCTTGA GAGCCTCTCAGGGCCTGAGCTCCTCTTACCTGGCC TGGTATCAGCAGAAGCCTGGACAGGCCCTCGGCT GCTGATCTACTCTGCCTCCACCAGAGCAACAGGCA TTCCTGACCGCTTCTCCGGATCTGGAAGCGGCACA GACTTCACCCTGACAATCAGCCGGCTGGAGCCTGA GGACTTCGCCGTGTACTATTGTGTCAGCAGTACGCCT ATTCCCCAAGGTGGACCTTTGGCCAGGGCACAAAG GTGGAGATCAAG	HBC24 VL (codon optimized)
110	agctacgagctgacacagcccccttccgtgtccgtgtccctggacagaccgtgtc catcccatgcagcggcgacaagctgggcaacaagaacgtgtgctgttcagcata agcctggccagtcctccgtgctgtcatctacgaggtgaagtataggccagcgg catcctgagcgggttctctggtccaacagcggcaatacagccaccctgacaatctc tggcacacaggctatggacgaggccgttatttctgccagaccttgattccaccac agtgtgttcggcggcgccagactgacagtgtg	HBC34-V7 VL (codon optimized)
111	SYELTQPPSVSVSPGQTASITCSGDKLGNKNASWYQ QKPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTI SGTQAMDEADYYCQTFDSTTVVFGGGTKLTVL	HBC34-V23- L_C40S
112	SYELTQPPSVSVSPGQTASITCSGDKLGNKNAAWYQ QKPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTI SGTQAMDEADYYCQTFDSTTVVFGGGTKLTVL	HBC34-V23- L_C40A
113	SYELTQPPSVSVSPGQTVSIPCSGDKLGNKNVSWFQH KPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTIS GTQAMDEAAYFCQTDSTTVVFGGGTRLTVL	HBC34-V31- L_C40S
114	SYELTQPPSVSVSPGQTVSIPCSGDKLGNKNVAWFQH KPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTIS GTQAMDEAAYFCQTDSTTVVFGGGTRLTVL	HBC34-V31- L_C40A

115	SYELTQPPSVSVSPGQTVSIPCSGDKLGKNVSWFQH KPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTIS GTQAMDEAAYFCQTFDSTTVVFGGGTRLTVL	HBC34-V32- L_C40S
116	SYELTQPPSVSVSPGQTVSIPCSGDKLGKNVAWFQH KPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTIS GTQAMDEAAYFCQTDSTTVVFGGGTRLTVL	HBC34-V32- L_C40A
117	SYELTQPPSVSVSPGQTASITCSGDKLGKNASWYQ QKPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTI SGTQAMDEADYYCQTFDSTTVVFGGGTKLTVL	HBC34-V33- L_C40S
118	SYELTQPPSVSVSPGQTASITCSGDKLGKNAAWYQ QKPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTI SGTQAMDEADYYCQTFDSTTVVFGGGTKLTVL	HBC34-V33- L_C40A
119	SYELTQPPSVSVSPGQTVSIPCSGDKLGKNVSWFQH KPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTIS GTQAMDEAAYFCQTDSTTVVFGGGTRLTVL	HBC34-L_C40S
120	SYELTQPPSVSVSPGQTVSIPCSGDKLGKNVAWFQH KPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTIS GTQAMDEAAYFCQTDSTTVVFGGGTRLTVL	HBC34-L_C40A
121	EVQLES GGGLVQPGGSLRLSCAASGSTFTKYAMSW VRQAPGKGLEWVASISGSVPFGIDTYADSVKGRF TISRDTSKNTLYLQMNSLRAEDTALYYCAKDVGVI SYYYAMDVWGQGTAVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFC SVLHEALHSHYTQKSLSLSPGK	HBC24-MLNS

122	EVQLLESGGGLVQPGGSLRLSCAASGSTFTKYAMSW VRQAPGKGLEWVASISGSVPFGIDTYYADSVKGRF TISRDTSKNTLYLQMNSLRAEDTALYYCAKDVGVI SYYYYAMDVWGQGTAVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLAGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPLPEEKISKAKGQPREPQVYTL PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFC SVLHEALHSHYTQKSLSLSPGK	HBC24-MLNS- GAALIE
123	ELQLVESGGGWVQPGGSQRLSCAASGRIFRSFYMSW VRQAPGKGLEWVATINQDGSEKLYVDSVKGRFTISR DNAKNSLFLQMNNLRVEDTAVYYCAAWSGNSGGM DVWGQGTTSVSSAKTTAPSVYPLAPVCGDTTGSSV TLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIE PRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVL MISLSPIVTCVVVDVSEDDPDVQISWVFNNEVHTAQ TQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKV NNKDLPAPIERTISKPKGSVRAPQVYVLPPEEEMTK KKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTE PVLDSGGSYFMYSKLRVEKKNWVERNSYSCSVVHE GLHNHHTTKSFSRTPGK	HBC34-V7-mu (IgG2a) HC
124	SYELTQPPSVSVSPGQTVSIPCSGDKLGKNKNCWFQ H KPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATL TISGTQAMDEAAYFCQTFDSTTVVFGGGTRLTVL GQPKSPSVTLFPPSSEETNKATLVCTITDFYPGVV TVDWKVDGTPVTQGMETTQPSKQSNNKYMSSYLTL TARAWERHSSYSCQVTHEGHTVEKSLSRADCS	HBC34-V7-mu (IgG2a) LC

125	ELQLVESGGGWVQPGGSQRLSCAASGRIFRSFYMSW VRQAPGKGLEWVATINQDGSEKLYVDSVKGRFTISR DNAKNSLFLQMNNLRVEDTAVYYCAAWSGNSGGM DVWGQGTTVSVSSAKTTAPSVYPLAPVCGDTTGSSV TLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKIE PRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMI LSPIVTCVVVDVSEDDPDVQISWVFNVEVHTAQTQ THREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNN KDLPAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQ VTLTCMVTDMPEDIYVEWTNNGKTELNYKNTEPV LSDSGSYFMYSKLRVEKKNWVERNSYSCSVVHEGL HNHHTTKSFSRTPGK	HBC34-V35-mu (IgG2a) HC
126	SYELTQPPSVSVSPGQTVSIPCSGDKLGKNVAVWFQH KPGQSPVLVIYEVKYRPSGIPERFSGSNSGNTATLTIS GTQAMDEAAYFCQTFDSTTVVFGGGTRLTVLGQPKS SPSVTLFPPSSEETNKATLVCTITDFYPGVVTVDW KVDGTPVTQGMETTQPSKQSNKYMSSYLTLTAR AWERHSSYSCQVTHEGHTVEKSLSRADCS	HBC34-V35-mu (IgG2a) LC
127	EVQLLESGGGLVQPGGSLRLSCAASGSTFTKYAMSW VRQAPGKGLEWVASISGSVPGFGIDTYADSVKGRF TISRDTSKNTLYLQMNSLRAEDTALYYCAKDVGVI SYYYAMDVWGQGTAVTVSSAKTTAPSVYPLAPVC GDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPAS STKVDKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPP KIKDVLMI LSPIVTCVVVDVSEDDPDVQISWVFNVEVHTAQTQ THREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNN KDLPAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQ VTLTCMVTDMPEDIYVEWTNNGKTELNYKNTEPV LSDSGSYFMYSKLRVEKKNWVERNSYSCSVVHEGL HNHHTTKSFSRTPGK	HBC24-mu (IgG2a) HC
128	EIVLTQSPGTLSPGERATLSCRASQGLSSSYLAWY QQKPGQAPRLLIYSASTRATGIPDRFSGSGSGTDFTLT ISRLEPEDFAVYYCQQYAYSPRWTFGQGTKVEIKAD AAPTVSIFPPSSEQLTSGGASVVCFLNFPYKDI NVKWKIDGSERQNGVLNSWTDQDSKDYSTYSMSSTLTLTK DEYERHNSYTCEATHKTSTSPIVKSFNRNEC	HBC24-mu (IgG2a) LC

129	ELQLVESGGGWVQPGGSQRLSCAASGRIFRSFYMSW VRQAPGKGLEWVATINQDGSEKLYVDSVKGRFTISR DNAKNSLFLQMNNLRVEDTAVYYCAAWSGNSGGM DVWGQGTTVSVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSRDEL KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	HBC34-V7, HBC34-V34, HBC34-V35 HC (wild-type)
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130	GCCTCCACAAAGGGCCCAAGCGTGTTTCCACTGGC TCCCTCTTCCAAGTCTACCTCCGGCGGCACAGCCG CTCTGGGATGTCTGGTGAAGGATTACTTCCCAGAG CCCGTGACCGTGTCTTGGAAGTCCGGCGCCCTGAC CAGCGGAGTGCATACATTTCCAGCTGTGCTGCAGA GCTCTGGCCTGTACTCTCTGTCCAGCGTGGTGACC GTGCCCTCTTCCAGCCTGGGCACCCAGACATATAT CTGCAACGTGAATCACAAGCCAAGCAATACAAAG GTGGACAAGAAGGTGGAGCCCAAGTCTTGTGATA AGACCCATACATGCCCTCCATGTCCAGCTCCAGAG CTGCTGGGCGGCCCAAGCGTGTTCTGTTTCCACC CAAGCCTAAGGATACCTGATGATCTCCAGAACCC CCGAGGTGACATGCGTGGTGGTGGACGTGAGCCA CGAGGATCCTGAGGTGAAGTTCAACTGGTACGTGG ACGGCGTGGAGGTGCATAATGCTAAGACCAAGCC CAGGGAGGAGCAGTACAACCTCTACCTATCGGGTG GTGTCCGTGCTGACAGTGCTGCACCAGGATTGGCT GAACGGCAAGGAGTATAAGTGCAAGGTGTCTAAT AAGGCCCTGCCCCTCTATCGAGAAGACCATCTC CAAGGCCAAGGGCCAGCCTAGAGAGCCACAGGTG TACACACTGCCTCCATCTCGCGATGAGCTGACCAA GAACCAGGTGTCCCTGACATGTCTGGTGAAGGGCT TCTATCCTTCCGACATCGCTGTGGAGTGGGAGAGC AATGGCCAGCCAGAGAACAATTACAAGACCACAC CCCCTGTGCTGGACAGCGATGGCTCTTTCTTTCTGT ATAGCAAGCTGACCGTGGACAAGTCTCGCTGGCAG CAGGGCAACGTGTTTAGCTGTTCTGTGATGCATGA GGCCCTGCACAATCATTATACACAGAAGTCCCTGA GCCTGTCTCCTGGCAAG	HBC34-V7, HBC34-V34, HBC34-V35 CH1- hinge-CH2-CH3 (codon-optimized)
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131	GAGCTGCAGCTGGTGGAGTCCGGCGGCGGCTGGG TGCAGCCTGGCGGCTCCCAGAGGCTGAGCTGTGCC GCTTCTGGCAGGATCTTCCGGTCCTTTTACATGTCT TGGGTGCGGCAGGCTCCAGGCAAGGGCCTGGAGT GGGTGGCTACCATCAACCAGGACGGCTCCGAGAA GCTGTATGTGGATAGCGTGAAGGGCAGATTCACAA TCTCTCGCGACAACGCCAAGAACTCCCTGTTTCTG CAGATGAACAATCTGAGGGTGGAGGATAACCGCCG TGTAATTGCGCCGCTTGGTCTGGCAATAGCGGC GGCATGGACGTGTGGGGACAGGGCACCAACCGTGT CCGTGTCCAGCGCCTCCACAAAGGGCCCAAGCGTG TTTCCACTGGCTCCCTCTTCCAAGTCTACCTCCGGC GGCACAGCCGCTCTGGGATGTCTGGTGAAGGATTA CTTCCCAGAGCCCGTGACCGTGTCTTGGAACCTCCG GCGCCCTGACCAGCGGAGTGCATACATTTCCAGCT GTGCTGCAGAGCTCTGGCCTGTACTCTCTGTCCAG CGTGGTGACCGTGCCCTCTTCCAGCCTGGGCACCC AGACATATATCTGCAACGTGAATCACAAGCCAAGC AATACAAAGGTGGACAAGAAGGTGGAGCCCAAGT CTTGTGATAAGACCCATACATGCCCTCCATGTCCA GCTCCAGAGCTGCTGGGCGGCCCAAGCGTGTTCT GTTTCCACCCAAGCCTAAGGATACCCTGATGATCT CCAGAACCCCCGAGGTGACATGCGTGGTGGTGG CGTGAGCCACGAGGATCCTGAGGTGAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGCATAATGCTAA GACCAAGCCCAGGGAGGAGCAGTACAACCTCTACC TATCGGGTGGTGTCCGTGCTGACAGTGCTGCACCA GGATTGGCTGAACGGCAAGGAGTATAAGTGCAAG GTGTCTAATAAGGCCCTGCCCCTCCTATCGAGAA GACCATCTCCAAGGCCAAGGGCCAGCCTAGAGAG CCACAGGTGTACACACTGCCTCCATCTCGCGATGA GCTGACCAAGAACCAGGTGTCCCTGACATGTCTGG TGAAGGGCTTCTATCCTTCCGACATCGCTGTGGAG TGGGAGAGCAATGGCCAGCCAGAGAACAATTACA AGACCACACCCCCTGTGCTGGACAGCGATGGCTCT TTCTTTCTGTATAGCAAGCTGACCGTGGACAAGTC TCGCTGGCAGCAGGGCAACGTGTTTAGCTGTTCTG TGATGCATGAGGCCCTGCACAATCATTATACACAG AAGTCCCTGAGCCTGTCTCCTGGCAAGTGATGAGG TACCGTGCGACGGCCGGCAAGCCCCCGCTCCCCGG GCTCTCGCGGTCTGACGAGGAAAGCTT	HBC34-V7, HBC34-V34, HBC34-V35 VH- CH1-hinge-CH2- CH3 (codon- optimized)
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132	GGACAGCCAAAGGCTGCTCCATCTGTGACCCTGTT TCCACCCTCTTCCGAGGAGCTGCAGGCCAACAAGG CCACCCTGGTGTGCCTGATCTCTGACTTCTACCCTG GAGCTGTGACAGTGGCTTGGAAGGCTGATAGCTCT CCCGTGAAGGCTGGCGTGGAGACAACAACCCCTA GCAAGCAGTCTAACAATAAGTACGCCGCTTCCAGC TATCTGTCTCTGACACCAGAGCAGTGGAAGTCCCA CCGCTCTTATTCCTGCCAGGTGACCCATGAGGGCA GCACCGTGGAGAAGACAGTGGCCCCCACCAGAGTG TTCT	HBC34-V7 CL (codon-optimized)
133	AGCTACGAGCTGACACAGCCCCCTTCCGTGTCCGT GTCCCCTGGACAGACCGTGTCCATCCCATGCAGCG GCGACAAGCTGGGCAACAAGAACGTGTGCTGGTTT CAGCATAAGCCTGGCCAGTCCCCCGTGCTGGTCAT CTACGAGGTGAAGTATAGGCCAGCGGCATCCCTG AGCGGTTCTCTGGCTCCAACAGCGGCAATACAGCC ACCCTGACAATCTCTGGCACACAGGCTATGGACGA GGCCGCTTATTTCTGCCAGACCTTTGATTCCACCAC AGTGGTGTTCGGCGGGCGGCACCAGACTGACAGTGC TGGGACAGCCAAAGGCTGCTCCATCTGTGACCCTG TTTCCACCCTCTTCCGAGGAGCTGCAGGCCAACA GGCCACCCTGGTGTGCCTGATCTCTGACTTCTACCC TGGAGCTGTGACAGTGGCTTGGAAGGCTGATAGCT CTCCCGTGAAGGCTGGCGTGGAGACAACAACCCCT AGCAAGCAGTCTAACAATAAGTACGCCGCTTCCAG CTATCTGTCTCTGACACCAGAGCAGTGGAAGTCCC ACCGCTCTTATTCCTGCCAGGTGACCCATGAGGGC AGCACCGTGGAGAAGACAGTGGCCCCCACCAGAGT GTTCT	HBC34-V7 LC (VL-CL) (codon- optimized)
134	GGACAGCCAAAGGCTGCTCCATCTGTGACCCTGTT TCCACCCTCTTCCGAGGAGCTGCAGGCCAACAAGG CCACCCTGGTGTGCCTGATCTCTGACTTCTACCCTG GAGCTGTGACAGTGGCTTGGAAGGCTGATAGCTCT CCCGTGAAGGCTGGCGTGGAGACAACAACCCCTA GCAAGCAGTCTAACAATAAGTACGCCGCTTCCAGC TATCTGTCTCTGACACCAGAGCAGTGGAAGTCCCA CCGCTCTTATTCCTGCCAGGTGACCCATGAGGGCA GCACCGTGGAGAAGACAGTGGCCCCCACCAGAGTG	HBC34-V34, HBC34-V35 CL (codon- optimized)

135	AGCTACGAGCTGACACAGCCCCCTTCCGTGTCCGT GTCCCCTGGACAGACCGTGTCCATCCCATGCAGCG GCGACAAGCTGGGCAACAAGAACGTGTCCTGGTTT CAGCATAAGCCTGGCCAGTCCCCCGTGCTGGTCAT CTACGAGGTGAAGTATAGGCCAGCGGCATCCCTG AGCGGTTCTCTGGCTCCAACAGCGGCAATACAGCC ACCTTGACAATCTCTGGCACACAGGCTATGGACGA GGCCGCTTATTTCTGCCAGACCTTTGATTCCACCAC AGTGGTGTTCGGCGGCGGCACCAGACTGACAGTGC TGGGACAGCCAAAGGCTGCTCCATCTGTGACCCTG TTTCCACCCTCTTCCGAGGAGCTGCAGGCCAACA GGCCACCCTGGTGTGCCTGATCTCTGACTTCTACCC TGGAGCTGTGACAGTGGCTTGGAAGGCTGATAGCT CTCCCGTGAAGGCTGGCGTGGAGACAACAACCCCT AGCAAGCAGTCTAACAATAAGTACGCCGCTTCCAG CTATCTGTCTCTGACACCAGAGCAGTGGAAGTCCC ACCGCTCTTATTCCTGCCAGGTGACCCATGAGGGC AGCACCGTGGAGAAGACAGTGGCCCCCACCAGT GTTCT	HBC34-V34 LC (VL-CL) (codon- optimized)
136	AGCTACGAGCTGACACAGCCCCCTTCCGTGTCCGT GTCCCCTGGACAGACCGTGTCCATCCCATGCAGCG GCGACAAGCTGGGCAACAAGAACGTGGCCTGGTT TCAGCATAAGCCTGGCCAGTCCCCCGTGCTGGTCA TCTACGAGGTGAAGTATAGGCCAGCGGCATCCCT GAGCGGTTCTCTGGCTCCAACAGCGGCAATACAGC CACCCTGACAATCTCTGGCACACAGGCTATGGACG AGGCCGCTTATTTCTGCCAGACCTTTGATTCCACCA CAGTGGTGTTCGGCGGCGGCACCAGACTGACAGTG CTGGGACAGCCAAAGGCTGCTCCATCTGTGACCCT GTTTCCACCCTCTTCCGAGGAGCTGCAGGCCAACA AGGCCACCCTGGTGTGCCTGATCTCTGACTTCTAC CCTGGAGCTGTGACAGTGGCTTGGAAGGCTGATAG CTCTCCCGTGAAGGCTGGCGTGGAGACAACAACCC CTAGCAAGCAGTCTAACAATAAGTACGCCGCTTCC AGCTATCTGTCTCTGACACCAGAGCAGTGGAAGTC CCACCGCTCTTATTCCTGCCAGGTGACCCATGAGG GCAGCACCGTGGAGAAGACAGTGGCCCCCACCAG GTGTTCT	HBC34-V35 LC (VL-CL) (codon- optimized)
137	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	WT hIgG1 Fc

138	ELQLVESGGGWVQPGGSQRLSCAASGRIFRSFYMSW VRQAPGKGLEWVATINQDGSEKLYVDSVKGRFTISR DNAKNSLFLQMNNLRVEDTAVYYCAAWSGNSGGM DVWGQGTTVSVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLAGPSVFLFPPKPKDTL MISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPLPEEKTIKAKGQPREPQVYTLPPSRDEL TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHE ALHNHYTQKSLSLSPGK	HBC34, HBC34-V7, HBC34-V23, HBC34-V34, HBC34-V35, HBC34_C40S, HBC34_C40A, HBC34-V23_C40S, HBC34-V23_C40A HC with GAALIE mutation in hIgG1 Fc
139	ESKYGPCCPPCPAPPVAGP	Chimeric hinge sequence

The various embodiments described above can be combined to provide further
 5 embodiments. All of the U.S. patents, U.S. patent application publications, U.S. patent
 applications, foreign patents, foreign patent applications and non-patent publications
 referred to in this specification and/or listed in the Application Data Sheet are
 incorporated herein by reference, in their entirety. Aspects of the embodiments can be
 modified, if necessary to employ concepts of the various patents, applications and
 10 publications to provide yet further embodiments.

U.S. Provisional Application 62/782,274, filed December 19, 2018 and U.S.
 Provisional Application 62/860,085, filed June 11, 2019 are incorporated herein by
 reference, in their entirety.

These and other changes can be made to the embodiments in light of the above-
 15 detailed description. In general, in the following claims, the terms used should not be
 construed to limit the claims to the specific embodiments disclosed in the specification
 and the claims, but should be construed to include all possible embodiments along with
 the full scope of equivalents to which such claims are entitled. Accordingly, the claims
 are not limited by the disclosure.

CLAIMS

1. An isolated antibody, or an antigen binding fragment thereof, comprising:
 - (i) a heavy chain variable region (V_H) comprising at least 90% identity to the amino acid sequence according to SEQ ID NO:41; and
 - (ii) a light chain variable region (V_L) comprising at least 90% identity to the amino acid sequence according to any one of SEQ ID NOs: 59, 89, or 90, provided that the amino acid at position 40 of the V_L according to IMGT numbering is not a cysteine,wherein the antibody or antigen binding fragment thereof binds to the antigenic loop region of HBsAg and neutralizes infection with hepatitis B virus and hepatitis delta virus.
2. The antibody or antigen binding fragment of claim 1, wherein:
 - (i) the V_H comprises at least 95% identity to the amino acid sequence according to SEQ ID NO:41; and/or
 - (ii) the V_L comprises at least 95% identity to the amino acid sequence according to any one of SEQ ID NOs: 59, 89, or 90.
3. The antibody or antigen binding fragment of claim 1 or 2, wherein the amino acid at position 40 of the V_L is alanine.
4. The antibody or antigen binding fragment of claim 1 or 2, wherein the amino acid at position 40 of the V_L is serine.
5. The antibody or antigen binding fragment of claim 1 or 2, wherein the amino acid at position 40 of the V_L is glycine.
6. The antibody or antigen binding fragment of any one of claims 1-5, comprising CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 sequences according to SEQ ID NOs:
 - (i) 34-36, 37, 38, and 40, respectively;

- (ii) 34, 66, 36, 37, 38, and 40, respectively;
 - (iii) 34-36, 37, 39, and 40, respectively;
 - (iv) 34, 66, 36, 37, 39, and 40, respectively;
 - (v) 34-36, 37, 38, and 58, respectively;
 - (vi) 34, 66, 36, 37, 38, and 58, respectively;
 - (vii) 34-36, 37, 39, and 58, respectively; or
 - (vii) 34, 66, 36, 37, 39, and 58, respectively.
7. The antibody or antigen binding fragment of any one of claims 1-3 or 6, wherein the V_L comprises or consists of the amino acid sequence according to SEQ ID NO:89.
8. The antibody or antigen binding fragment of any one of claims 1, 2, 4, or 6, wherein the V_L comprises or consists of the amino acid sequence according to SEQ ID NO:90.
9. The isolated antibody of any one of claims 1-8, wherein the V_H comprises or consists of the amino acid sequence according to SEQ ID NO:41.
10. The isolated antibody of any one of claims 1-3, 6, 7, or 9, wherein the V_H comprises or consists of the amino acid sequence according to SEQ ID NO:41 and V_L comprises or consists of the amino acid sequence according to SEQ ID NO:89.
11. The isolated antibody of any one of claims 1, 2, 4, 6, 8, or 9, wherein the V_H comprises or consists of the amino acid sequence according to SEQ ID NO:41 and V_L comprises or consists of the amino acid sequence according to SEQ ID NO:90.
12. An isolated antibody, or an antigen binding fragment thereof, comprising:
- (i) a heavy chain variable region (V_H) comprising at least 90% identity to the amino acid sequence according to SEQ ID NO:95; and

- (ii) a light chain variable region (V_L) comprising at least 90% identity to the amino acid sequence according to SEQ ID NO:96, wherein the antibody or antigen binding fragment thereof binds to the antigenic loop region of HBsAg and neutralizes infection with hepatitis B virus and hepatitis delta virus.
- 13. The antibody or antigen binding fragment of claim 12, wherein:
 - (i) the V_H comprises at least 95% identity to the amino acid sequence according to SEQ ID NO:95; and/or
 - (ii) the V_L comprises at least 95% identity to the amino acid sequence according to SEQ ID NO:96.
- 14. The antibody or antigen binding fragment of claim 12 or 13, comprising CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 sequences according to SEQ ID NOs:97-102, respectively.
- 15. The antibody or antigen binding fragment of any one of claims 1-14, wherein the antibody, or the antigen binding fragment thereof, comprises a human antibody, a monoclonal antibody, a purified antibody, a single chain antibody, a Fab, a Fab', a F(ab')₂, a Fv, or a scFv.
- 16. The antibody or antigen binding fragment of any one of claims 1-15, wherein the antibody or antigen binding fragment is a multi-specific antibody or antigen binding fragment.
- 17. The antibody or antigen binding fragment of any one of claim 16, wherein the antibody or antigen binding fragment is a bispecific antibody or antigen binding fragment.
- 18. The antibody of any one of claims 1-17, or an antigen binding fragment thereof, wherein the antibody or the antigen binding fragment comprises a Fc moiety.

19. The antibody or antigen binding fragment of claim 18, wherein the Fc moiety comprises a mutation that enhances binding to FcRn as compared to a reference Fc moiety that does not comprise the mutation.
20. The antibody or antigen binding fragment of claim 18 or 19, wherein the Fc moiety comprises a mutation that enhances binding to a Fc γ R, preferably a Fc γ RIIA or Fc γ RIIIA as compared to a reference Fc moiety that does not comprise the mutation.
21. The antibody or antigen binding fragment of any one of claims 18-20, wherein the Fc moiety is an IgG isotype or is derived from an IgG isotype.
22. The antibody or antigen binding fragment of any one of claims 19-21, wherein the mutation that enhances binding to FcRn comprises: M428L; N434S; N434H; N434A; N434S; M252Y; S254T; T256E; T250Q; P257I; Q311I; D376V; T307A; E380A; or any combination thereof.
23. The antibody or antigen binding fragment of claim 22, wherein the mutation that enhances binding to FcRn comprises:
 - (i) M428L/N434S;
 - (ii) M252Y/S254T/T256E;
 - (iii) T250Q/M428L;
 - (iv) P257I/Q311I;
 - (v) P257I/N434H;
 - (vi) D376V/N434H;
 - (vii) T307A/E380A/N434A; or
 - (viii) any combination of (i)-(vii).
24. The antibody or antigen binding fragment of claim 23, wherein the mutation that enhances binding to FcRn comprises M428L/N434S.

25. The antibody or antigen binding fragment of any one of claims 20-24, wherein the mutation that enhances binding to a Fc γ R comprises S239D; I332E; A330L; G236A; or any combination thereof.
26. The antibody or antigen binding fragment of claim 25, wherein the mutation that enhances binding to a Fc γ R comprises:
- (i) S239D/I332E;
 - (ii) S239D/A330L/I332E;
 - (iii) G236A/S239D/I332E; or
 - (iv) G236A/A330L/I332E.
27. The antibody or antigen binding fragment of claim 25 or 26, wherein the mutation that enhances binding to a Fc γ R comprises or consists of G236A/A330L/I332E, and optionally does not comprise S239D.
28. The antibody or antigen binding fragment of any one of claims 18-27, wherein the Fc moiety comprises the amino acid substitution mutations: M428L; N434S; G236A; A330L; and I332E, and optionally does not comprise S239D.
29. An isolated antibody, or an antigen binding fragment thereof, comprising:
- (i) a heavy chain variable region (V_H) comprising the amino acid sequence according to SEQ ID NO:41; and
 - (ii) a light chain variable region (V_L) comprising the amino acid sequence according to SEQ ID NO:89,
- wherein the antibody or antigen binding fragment thereof binds to the antigenic loop region of HBsAg and neutralizes infection with hepatitis B virus and hepatitis delta virus.
30. The isolated antibody or antigen binding fragment of claim 29, further comprising an Fc moiety.

31. The isolated antibody or antigen binding fragment of claim 30, wherein the Fc moiety is derived from an IgG isotype and comprises M428L and N434S substitution mutations.
32. The isolated antibody or antigen binding fragment of claim 30 or 31, wherein the Fc moiety is derived from an IgG isotype and comprises G236A, A330L, and I332E substitution mutations, and optionally does not comprise a S239D mutation.
33. The isolated antibody or antigen binding fragment of claim 32, wherein the Fc moiety comprises M428L, N434S, G236A, A330L, and I332E substitution mutations.
34. The antibody or antigen binding fragment of any one of claims 1-11 and 15-33, comprising the heavy chain (HC) amino acid sequence according to SEQ ID NO: 91 or 138.
35. The antibody or antigen binding fragment of any one of claims 1-11 and 15-31, comprising the heavy chain (HC) amino acid sequence according to SEQ ID NO: 92.
36. The antibody or antigen binding fragment of any one of claims 1-3, 6, 7, 9, 10, and 15-35, comprising the light chain (LC) amino acid sequence according to SEQ ID NO:93.
37. The antibody or antigen binding fragment of any one of claims 1, 2, 4, 6, 8, 11, and 15-28, comprising the light chain (LC) amino acid sequence according to SEQ ID NO:94.
38. The antibody or antigen binding fragment of claim 34 or 36, comprising the HC amino acid sequence according to SEQ ID NO:91 and the LC amino acid sequence according to SEQ ID NO:93.

39. The antibody or antigen binding fragment of claim 35 or 37, comprising the HC amino acid sequence according to SEQ ID NO:92 and the LC amino acid sequence according to SEQ ID NO:94.
40. The antibody or antigen binding fragment of claim 34 or 37, comprising the HC amino acid sequence according to SEQ ID NO:91 and the LC amino acid sequence according to SEQ ID NO:94.
41. The antibody or antigen binding fragment of claim 35 or 36, comprising the HC amino acid sequence according to SEQ ID NO:92 and the LC amino acid sequence according to SEQ ID NO:93.
42. An isolated antibody, or an antigen binding fragment thereof, comprising:
- (i) a heavy chain (HC) comprising the amino acid sequence according to SEQ ID NO:91; and
 - (ii) a light chain (LC) comprising the amino acid sequence according to SEQ ID NO:93,
- wherein the antibody or antigen binding fragment thereof binds to the antigenic loop region of HBsAg and neutralizes infection with hepatitis B virus and hepatitis delta virus.
43. The antibody or antigen binding fragment of any one of claims 1-42, wherein the antibody or the antigen binding fragment is capable of binding an HBsAg of a genotype selected from the HBsAg genotypes A, B, C, D, E, F, G, H, I, and J, or any combination thereof.
44. The antibody or antigen binding fragment of any one of claims 1-43, wherein the antibody or antigen binding fragment is capable of reducing a serum concentration of HBV DNA in a mammal having an HBV infection.

45. The antibody or antigen binding fragment of any one of claims 1-44, wherein the antibody or antigen binding fragment is capable of reducing a serum concentration of HBsAg in a mammal having an HBV infection.
46. The antibody or antigen binding fragment of any one of claims 1-45, wherein the antibody or antigen binding fragment is capable of reducing a serum concentration of HBeAg in a mammal having an HBV infection.
47. The antibody or antigen binding fragment of any one of claims 1-46, wherein the antibody or antigen binding fragment is capable of reducing a serum concentration of HBcrAg in a mammal having an HBV infection.
48. A fusion protein, comprising:
- (i) an extracellular component comprising the antigen binding fragment of any one of claims 1-47;
 - (ii) a transmembrane domain; and
 - (iii) an intracellular component comprising an effector domain or a functional variant or portion thereof, and optionally comprising a signaling domain from a co-stimulatory protein or a functional variant or portion thereof.
49. The fusion protein of claim 48, wherein the antigen binding fragment comprises a scFv comprising a variable heavy chain (V_H) domain and/or a variable light chain (V_L) domain.
50. The fusion protein of claim 49, wherein the scFv comprises a peptide linker.
51. The fusion protein of claim 50, wherein the scFv has a V_L -linker- V_H orientation.
52. The fusion protein of claim 50, wherein the scFv has a V_H -linker- V_L orientation.

53. The fusion protein of any one of claims 48-52, wherein the transmembrane domain comprises a transmembrane domain from a CD4, a CD8, a CD27, or a CD28.
54. The fusion protein of any one of claims 48-53, wherein the intracellular component comprises an effector domain from CD3 ζ .
55. The fusion protein of any one of claims 48-54, wherein the intracellular component further comprises a signaling domain from one or two of a 4-1BB (CD137), CD28, OX40, (CD134), ICOS (CD278), CD27, CD2, CD5, ICAM-1 (CD54), LFA-1 (CD11a/CD18), GITR, CD30, CD40, BAFF-R, HVEM, LIGHT, MKG2C, SLAMF7, Nkp80, CD160, B7-H3, and a ligand that specifically binds with CD83.
56. The fusion protein of any one of claims 48-55, wherein the fusion protein comprises a chimeric antigen receptor (CAR).
57. An isolated polynucleotide comprising a nucleotide sequence that encodes the antibody, the antigen binding fragment, or the fusion protein of any one of claims 1-56.
58. The polynucleotide of claim 57, wherein the nucleotide sequence that encodes the antibody, antigen binding fragment, or fusion protein is codon optimized for expression in a host cell.
59. The polynucleotide of claim 57 or 58, comprising a nucleotide sequence having at least 80% identity to the nucleotide sequence according to any one of SEQ ID NOs: 103-110 and 130-136.
60. The polynucleotide of claim 59, comprising a V_H-encoding nucleotide sequence according to SEQ ID NO:103, and a V_L-encoding nucleotide sequence according to SEQ ID NO:105.

61. The polynucleotide of claim 59, comprising a V_H-encoding nucleotide sequence according to SEQ ID NO:103, and a V_L-encoding nucleotide sequence according to SEQ ID NO:104.
62. The polynucleotide of claim 54, comprising a V_H-encoding nucleotide sequence according to SEQ ID NO: 108, and a V_L-encoding nucleotide sequence according to SEQ ID NO: 109.
63. A polynucleotide that encodes an antibody or an antigen binding fragment thereof, comprising a V_H-encoding nucleotide sequence according to SEQ ID NO: 103 and a V_L-encoding nucleotide sequence according to SEQ ID NO:110, wherein the encoded antibody or antigen binding fragment binds to the antigenic loop region of HBsAg and neutralizes infection with hepatitis B virus and hepatitis delta virus.
64. A vector comprising the polynucleotide of any one of claims 57-63.
65. The vector of claim 64, wherein the vector comprises a lentiviral vector or a retroviral vector.
66. A host cell comprising a heterologous polynucleotide of any one of claims 57-63.
67. A pharmaceutical composition comprising:
- (i) the antibody or antigen binding fragment of any one of claims 1-47;
 - (ii) the fusion protein according to any one of claims 48-56;
 - (iii) the polynucleotide according to any one of claims 57-63;
 - (iv) the vector according to claim 64 or 65;
 - (v) the host cell of claim 66; or
 - (vi) any combination of (i)-(v).

68. The pharmaceutical composition according to claim 67, further comprising a pharmaceutically acceptable excipient, diluent or carrier.
69. A kit comprising:
- (a) a component selected from:
 - (i) the antibody or antigen binding fragment of any one of claims 1-47;
 - (ii) the fusion protein according to claim 48-56;
 - (iii) the polynucleotide according to any one of claims 57-63;
 - (iv) the vector according to claim 64 or 65;
 - (v) the host cell of claim 66;
 - (vi) the pharmaceutical composition of claim 67 or 68; or
 - (vii) any combination of (i)-(vi); and
 - (b) instructions for using the component to prevent, treat, attenuate, and/or diagnose a hepatitis B infection and/or a hepatitis D infection.
70. The composition of claim 67 or 68, or the kit of claim 69, further comprising:
- (i) a polymerase inhibitor, wherein the polymerase inhibitor optionally comprises Lamivudine, Adefovir, Entecavir, Telbivudine, Tenofovir, or any combination thereof;
 - (ii) an interferon, wherein the interferon optionally comprises IFNbeta and/or IFNalpha; (iii) a checkpoint inhibitor, wherein the checkpoint inhibitor optionally comprises an anti-PD-1 antibody or antigen binding fragment thereof, an anti-PD-L1 antibody or antigen binding fragment thereof, and/or an anti-CTLA4 antibody or antigen binding fragment thereof;
 - (iv) an agonist of a stimulatory immune checkpoint molecule; or
 - (v) any combination of (i)-(iv).
71. The composition or kit of claim 70, wherein the polymerase inhibitor comprises lamivudine.

72. A method of producing the antibody or antigen binding fragment of any one of claims 1-47, or the fusion protein of any one of claims 48-56, comprising culturing the host cell of claim 66 under conditions and for a time sufficient to produce the antibody, antigen binding fragment, or fusion protein.
73. Use of: (i) the antibody or antigen binding fragment of any one of claims 1-47; (ii) the fusion protein of any one of claims 48-56; (iii) the polynucleotide of any one of claims 57-63; (iv) the vector of claim 64 or 65; (v) the host cell of claim 66; and/or (vi) the pharmaceutical composition of claim 67 or 68, in the manufacture of a medicament to prevent, treat, attenuate, and/or diagnose a hepatitis B infection and/or a hepatitis D infection in a subject.
74. A method of treating, preventing, and/or attenuating a hepatitis B and/or hepatitis D infection in a subject, comprising administering to the subject an effective amount of: (i) the antibody or antigen binding fragment of any one of claims 1-47; (ii) the fusion protein of any one of claims 48-56; (iii) the polynucleotide of any one of claims 57-63; (iv) the vector of claim 64 or 65; (v) the host cell of claim 66; and/or (vi) the pharmaceutical composition of claim 67 or 68.
75. The method of claim 74, further comprising administering to the subject one or more of: (vii) a polymerase inhibitor, wherein the polymerase inhibitor optionally comprises Lamivudine, Adefovir, Entecavir, Telbivudine, Tenofovir, or any combination thereof; (viii) an interferon, wherein the interferon optionally comprises IFNbeta and/or IFNalpha; (ix) a checkpoint inhibitor, wherein the checkpoint inhibitor optionally comprises an anti-PD-1 antibody or antigen binding fragment thereof, an anti-PD-L1 antibody or antigen binding fragment thereof, and/or an anti-CTLA4 antibody or antigen binding fragment thereof; (x) an agonist of a stimulatory immune checkpoint molecule; or (xi) any combination of (vii)-(x).

76. The method of claim 74 or 75, wherein the hepatitis B infection is a chronic hepatitis B infection.
77. The method of any one of claims 74-76, wherein the subject has received a liver transplant.
78. The method of any one of claims 74-77, wherein the subject is non-immunized against hepatitis B.
79. The method of any one of claims 74-78, wherein the subject is a newborn.
80. The method of any one of claims 74-79, wherein the subject is undergoing or has undergone hemodialysis.
81. A method for *in vitro* diagnosis of a hepatitis B and/or a hepatitis D infection, the method comprising:
- (i) contacting a sample from a subject with an antibody or antigen-binding fragment of any one of claims 1-47 or a fusion protein of any one of claims 48-56; and
 - (ii) detecting a complex comprising an antigen and the antibody, or comprising an antigen and the antigen binding fragment, or detecting a complex comprising an antigen and the fusion protein.
82. The method of claim 81, wherein the sample comprises blood isolated from the subject.
83. A method for detecting the presence or absence of an epitope in a correct conformation in an anti-hepatitis-B and/or an anti-hepatitis-D vaccine, the method comprising:
- (i) contacting the vaccine with
 - (a) an antibody or antigen-binding fragment of any one of claims 1-47 and/or

- (b) a fusion protein of any one of claims 48-56; and
 - (ii) determining whether a complex comprising an antigen and the antibody, or comprising an antigen and the antigen binding fragment, or comprising an antigen and the fusion protein, has been formed.
84. An isolated antibody, or an antigen binding fragment thereof, comprising:
- (i) a heavy chain variable region (V_H) comprising a CDRH1 amino acid sequence according to SEQ ID NO:34, a CDRH2 amino acid sequence according to SEQ ID NO:35 or 66, a CDRH3 amino acid sequence according to SEQ ID NO:36;
 - (ii) a light chain variable region (V_L) comprising a CDRL1 acid sequence according to SEQ ID NO:37, a CDRL2 acid sequence according to SEQ ID NO:38 or 39, and CDRL3 amino acid sequence according to SEQ ID NO:58 or 40; and
 - (iii) a Fc moiety, wherein the Fc moiety comprises G236A/A330L/I332E.
85. The antibody or antigen binding fragment of claim 84, wherein the Fc moiety does not comprise S239D.
86. The antibody or antigen binding fragment of claim 84 or 85, wherein the Fc moiety further comprises M428L/N434S.
87. The antibody or antigen binding fragment of any one of claims 84-86, wherein the V_H comprises or consists of the amino acid sequence according to any one of SEQ ID NOs:41 or 67 and wherein the V_L comprises or consists of the amino acid sequence according to any one of SEQ ID NOs:42, 59, 65, 89, 90, and 111-120.
88. An isolated antibody, or an antigen binding fragment thereof, comprising:
- (i) a heavy chain variable region (V_H) comprising a CDRH1 amino acid sequence according to SEQ ID NO:97, a CDRH2 amino acid sequence

- according to SEQ ID NO:98, a CDRH3 amino acid sequence according to SEQ ID NO:99;
- (ii) a light chain variable region (V_L) comprising a CDRL1 acid sequence according to SEQ ID NO:100, a CDRL2 acid sequence according to SEQ ID NO:100, and CDRL3 amino acid sequence according to SEQ ID NO:102; and
 - (iii) a Fc moiety, wherein the Fc moiety comprises G236A/A330L/I332E.

89. The antibody or antigen binding fragment of claim 88, wherein the Fc moiety does not comprise S239D.

90. The antibody or antigen binding fragment of claim 88 or 89, wherein the Fc moiety further comprises M428L/N434S.

91. The antibody or antigen binding fragment of any one of claims 88-90, wherein the V_H comprises or consists of the amino acid sequence according to SEQ ID NO:95, and wherein the V_L comprises or consists of the amino acid sequence according to SEQ ID NO:96.

92. The antibody or antigen binding fragment of any one of claims 1-47 and 84-91, wherein the antibody or antigen binding fragment:

- (i) has enhanced binding to a human $Fc\gamma RIIA$, a human $Fc\gamma RIIIA$, or both, as compared to a reference polypeptide that includes a Fc moiety that does not comprise G236A/A330L/I332E, wherein the human $Fc\gamma RIIA$ is optionally H131 or R131, and/or the human $Fc\gamma RIIIA$ is optionally F158 or V158;
- (ii) has reduced binding to a human $Fc\gamma RIIB$, as compared to a reference polypeptide that includes a Fc moiety that does not comprise G236A/A330L/I332E;
- (iii) does not bind to a human $Fc\gamma RIIB$;

- (iv) has reduced binding to a human C1q, as compared to a reference polypeptide that includes a Fc moiety that does not comprise G236A/A330L/I332E;
- (v) does not bind to a human C1q;
- (vi) activates a FcγRIIA, a human FcγRIIA, or both, to a greater degree than does a reference polypeptide that includes a Fc moiety that does not comprise G236A/A330L/I332E, wherein the human FcγRIIA is optionally H131 or R131, and/or the human FcγRIIA is optionally F158 or V158;
- (vii) does not activate a human FcγRIIB;
- (viii) activates a human natural killer (NK) cell in the presence of HBsAg to a greater degree than does a reference polypeptide that includes a Fc moiety that does not comprise G236A/A330L/I332E, wherein the reference polypeptide is optionally an antibody that binds to an HB Ag, optionally an HBsAg;
- (ix) has an HBsAg EC₅₀ of from about 12.75 ng/mL to about 19.9 ng/mL, or from about 12.75 ng/mL to about 12.84 ng/mL, or about 12.79 ng/mL, or from about 16.22 ng/mL to about 19.9 ng/mL, or about 17.97 ng/mL, and/or (b) has an HBeAg EC₅₀ about from about 10.78 ng/mL to about 13.72 ng/mL, or from about 10.78 ng/mL to about 10.93 ng/mL, or about 10.85 ng/mL, or from about 11.59 ng/mL to about 13.72 ng/mL, or about 12.61 ng/mL, wherein the HBV is optionally HBV Genotype D, and wherein the EC₅₀ is optionally determined *in vitro* by measuring HBsAg or HBeAg, respectively, secreted by HepG2 cells overexpressing NTCP and infected with the HBV, at day 7 following administration of the antibody or antigen binding fragment to the HepG2 cells;
- (x) has an HBsAg EC₅₀ of from about 10.43 ng/mL to about 22.41 ng/mL, or about 13.81 ng/mL to about 16.56 ng/mL, or about 15.12 ng/mL, or from about 12.24 ng/mL to about 22.41 ng/mL, or about 16.56 ng/mL, or from about 10.43 ng/mL to about 20.08 ng/mL, or about 14.47 ng/mL, and/or (b) has an HBeAg EC₅₀ about from about 10.39 ng/mL to about 13.99 ng/mL, or from about 10.63 ng/mL to about 10.66 ng/mL, or about 10.64

ng/mL, or from about 10.39 ng/mL to about 10.60 ng/mL, or about 10.49 ng/mL, or from about 13.25 ng/mL to about 13.99 ng/mL, or about 13.61 ng/mL, wherein the HBV is optionally HBV Genotype D, and wherein the EC₅₀ is optionally determined *in vitro* by measuring HBsAg or HBeAg, respectively, secreted by HepG2 cells overexpressing NTCP and infected with the HBV, at day 7 following administration of the antibody or antigen binding fragment to the HepG2 cells;

- (xi) is capable of binding to an HBsAg variant comprising HBsAg-Y100C/P120T, HBsAg-P120T, HBsAg-P120S/S143L, HBsAg-C121S, HBsAg-R122D, HBsAg-R122I, HBsAg-T123N, HBsAg-Q129H, HBsAg-Q129L, HBsAg-M133H, HBsAg-M133L, HBsAg-M133T, HBsAg-K141E, HBsAg-P142S, HBsAg-S143K, HBsAg-D144A, HBsAg-G145R, HBsAg-N146A, or any combination thereof;
- (xii) has improved binding to an HBsAg variant comprising HBsAg-Y100C/P120T, HBsAg-P120T, HBsAg-P120S/S143L, HBsAg-C121S, HBsAg-R122D, HBsAg-R122I, HBsAg-T123N, HBsAg-Q129H, HBsAg-Q129L, HBsAg-M133H, HBsAg-M133L, HBsAg-M133T, HBsAg-K141E, HBsAg-P142S, HBsAg-S143K, HBsAg-D144A, HBsAg-G145R, HBsAg-N146A, or any combination thereof, as compared to a reference antibody or antigen binding fragment that binds to HBsAg and that includes a Fc moiety that does not comprise G236A/A330L/I332E; and/or
- (xiii) is capable of neutralizing (a) an HBV of genotype A with an EC₅₀ of about 2.34 ng/mL; (b) an HBV of genotype B with an EC₅₀ of about 2.22 ng/mL; (c) an HBV of genotype C with an EC₅₀ of about 0.92 ng/mL; (d) an HBV of genotype D with an EC₅₀ of about 1.10 ng/mL; (e) an HBV of genotype E with an EC₅₀ of about 1.12 ng/mL; (f) an HBV of genotype F with an EC₅₀ of about 1.93 ng/mL; (g) an HBV of genotype G with an EC₅₀ of about 1.43 ng/mL; and/or (h) an HBV of genotype H with an EC₅₀ of about 1.93 ng/mL, wherein the EC₅₀ is optionally determined using a recombinant HDV engineered to express an HBsAg of the HBV genotype.