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- (71) **Applicant:** ISA PHARMACEUTICALS B.V. [NL/NL];
J.H. Oortweg 19, NL-2333 CH Leiden (NL).
- (72) **Inventors:** KREBBER, Wilhelmus Johannes Theodorus
Alexander; Roodborststraat 37, NL-2333 VN Leiden
(NL). KESSLER, Johan Herman; Oranjegracht 27, NL-
2312 ND Leiden (NL). MELIEF, Cornelis Joseph Maria;
Wilhelminapark 33, NL-2012 KC Haarlem (NL). KWAP-
PENBERG, Kitty Michelle Corinne; Marie Jungiusstraat
34, NL-2331 NZ Leiden (NL).
- (74) **Agent:** NEDERLANDSCH OCTROOIBUREAU; P.O.
Box 29720, 2502 LS The Hague (NL).

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(54) **Title:** SYNTHETIC LONG PEPTIDES (SLP) FOR THERAPEUTIC VACCINATION AGAINST HEPATITIS B VIRUS INFECTION

(57) **Abstract:** The present invention relates to the fields of medicine and immunology. In particular, it relates to novel peptides that may be used in the treatment and/or prevention of a Hepatitis B viral infection and/or an Hepatitis B related disease or condition.



Synthetic Long Peptides (SLP) for therapeutic vaccination against Hepatitis B virus infection

FIELD OF THE INVENTION

5 The present invention relates to the fields of medicine and immunology. In particular, it relates to novel peptides that may be used in the treatment and/or prevention of a Hepatitis B viral infection and/or an Hepatitis B related disease or condition.

10 BACKGROUND OF THE INVENTION

Chronic infection with the hepatitis B virus (HBV) is a major global health problem. HBV is the prototype member of the Hepadnaviridae family, which have a strong preference for infecting liver cells (Ganem et al, 2004).

15 Despite the availability since three decades of an efficacious preventive vaccine for the protection against hepatitis B, an estimated two billion people have nevertheless been infected with HBV and more than 240 million currently have chronic (long-term) hepatitis B infection, with a geographical predominance in regions outside Western Europe and North America (World Health Organization, July 2013).

20 Transmission of the virus between people occurs by direct blood-to-blood contact or via semen or vaginal fluid of an infected person. In endemic areas, the infection occurs characteristically by perinatal transmission from mother to child. Thus, although HBV is not transmitted casually, the virus - via similar modes of entry as human immunodeficiency virus (HIV) but being at least 50 times more infectious - can be easily transmitted by perinatal, percutaneous or sexual exposure. Frequent person-to-
25 person contact with infected individuals accordingly poses a serious risk to groups like health workers.

30 Infection with HBV can develop as an acute viral hepatitis, an illness that begins with general ill-health, loss of appetite, nausea, vomiting, body aches, mild fever, and dark urine, and then progresses to development of jaundice. The illness lasts for a few weeks and then gradually improves in most affected adults. A few people may have more severe liver disease (fulminant hepatic failure), and may die as a result. The infection may be entirely asymptomatic and may go unrecognized. Chronic infection with hepatitis B virus either may be asymptomatic or may be associated with a chronic

inflammation of the liver (chronic hepatitis), leading to cirrhosis over a period of many years. This type of infection dramatically increases the incidence of hepatocellular carcinoma (liver cancer), also with a latency of many years.

5 Treatment of chronically HBV-infected individuals with antiviral drugs such as nucleoside/nucleotide analogues (e.g. Entecavir and Tenofovir) or interferon (IFN) α efficiently decreases serum viral loads. However, antiviral therapy rarely leads to a sustained virological response and drug resistance occurs (Zoulim et al., 2012). Moreover, the great majority of HBV carriers remains untreated.

10 Approximately 15-40% of chronic HBV carriers will develop clinically significant liver diseases in their lifetime with a high risk of death from liver cirrhosis and associated liver failure or hepatocellular carcinoma (HCC) (Lok, 2002; and Huang et al., 2011). Yearly up to one million people die worldwide due to the acute or chronic consequences of hepatitis B (Michel et al, 2001; Grimm et al, 2013). Due to the failure of antiviral drugs to eradicate infection, and consequently the need for long-term if not
15 lifelong antiviral therapy with its drawbacks such as toxic side-effects and high costs, there is an urgent need for novel therapeutic approaches (Grimm et al., 2013).

The present invention is meant to enable efficacious therapeutic vaccination against chronic HBV infection. Therapeutic vaccination constitutes a promising strategy to treat chronic hepatitis B (Michel et al., 2011).

20 Next to the humoral immune response against HBV, which is predominantly involved in the protection against HBV infection by the current prophylactic vaccines (Lok, 2002), the cellular immune response is unequivocally involved in the natural resistance against HBV infection.

Perinatal transmission of HBV from mothers to neonates and infections during
25 the first years of life result in persistent infection in more than 90% of children. By contrast, infection during adulthood clears spontaneously in more than 90% of cases and results in lifelong protective immunity (Rehermann et al., 2005).

In acute, self-limited hepatitis B virus infection, vigorous polyclonal and multispecific CD8⁺ cytotoxic T cell (CTL) and CD4⁺ T-helper (Th) cell responses to
30 many HBV antigens are readily demonstrable in the peripheral blood (Michel et al., 2011).

These T cell responses are crucial in HBV clearance and control. Experiments in HBV-infected chimpanzees have shown the essential role of HBV-specific CD8⁺ T

cells as effector cells in this process (Thimme et al., 2003). In contrast to the response in patients with resolved HBV infections, in patients with chronic hepatitis B the T cell responses are usually very weak, focused on only a few epitopes and functionally impaired (Michel et al., 2011). The goal of therapeutic vaccination is to install vigorous and robust multivalent CTL and T-helper cell responses directed to many HBV antigens, thereby pursuing viral clearance, hepatitis control and cure.

Despite the fact that great progress has been made in understanding the etiology and epidemiology of the disease, there is still a need for an effective therapeutic HBV vaccine.

DETAILED DESCRIPTION OF THE INVENTION

The inventors identified a selection of HBV antigens to be used for efficacious therapeutic vaccination. Based on HLA class I and class II binding capacities of HBV protein-derived peptides and analysis of the generation of these HLA class I binding peptides by cleavages made by the proteasome, the most immunogenic regions, covering a very high percentage of all possible T cell epitopes in the global hepatitis B patient population, have been uncovered in the HBV polymerase protein, core protein, X protein and large surface protein. These regions contain high numbers of T cell epitopes and when administered to the hepatitis B patient - either as chemically synthesized long peptide or via genetic approaches - such a vaccination is envisioned to induce a vigorous T cell response, resolving the HBV infection.

The use of relatively short peptides is highly preferred for medical purposes as these can be efficiently synthesized *in vitro*, which is not possible or uneconomical for native proteins larger than approximately 100, i.e. 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105 amino acids. Chemical synthesis of peptides is routine practice and various suitable methods are known to the skilled person. Chemical synthesis of peptides also overcomes the problems associated with recombinant production of intact proteins, which is difficult to standardize and requires extensive purification and quality control measures. Peptides with a length that exceeds the length of human leukocyte antigen (HLA) class I and class II epitopes (e.g. having a length as indicated below herein) are particularly advantageous for use as vaccine component because they are large enough to be taken up by professional antigen presenting cells (APC), in particular Dendritic cell (DC), as explained in WO02/070006, and processed in the DC

before cell surface presentation of the contained HLA class I-presented and HLA class II-presented epitopes takes place. Therefore, the disadvantageous induction of T cell tolerance by the systemic presentation of minimal HLA class I-presented epitopes on non-antigen presenting cells (as shown in Toes et al., 1996a, and Toes et al., 1996b), is prevented by the application of peptides exceeding the length of human leukocyte antigen (HLA) class I and class II epitopes (as shown in Zwaveling et al., 2002).

The present invention relates to novel peptides of about 15 to about 100 amino acids in length, also denominated herein as long peptides, that each exceed the length of human leukocyte antigen (HLA) class I and class II presented epitopes and that induce a combined CD4⁺ and CD8⁺ T cell response that is therapeutically successful and inducing cure in a high percentage of patients. Preferably, the long peptides of the invention are synthetic peptides, denominated herein as synthetic long peptides (SLPs). As compared to vaccination with the peptides of the present invention, therapeutic vaccination with full length HBV proteins is likely to be less potent (Rosalia et al., 2013). From the viewpoint of manufacture and administration of peptides to patients, immunization with the complete set of overlapping long peptides or SLPs spanning the full length HBV polymerase, HBV core protein, HBV X protein and HBV large surface protein is not feasible. To narrow the number of peptides in a vaccine, it is needed to incorporate the most immunogenic SLPs that are recognized by the highest percentage of patients. The present invention provides for peptides and peptide vaccines to meet this need. Using a stepwise sophisticated selection procedure based on bioinformatics analyses that are experimentally underpinned, the long peptide and/or SLP sequences with the highest coverage of HLA class I-restricted cytotoxic T lymphocyte epitopes and HLA class II-restricted T helper epitopes were identified. The selections as described herein identify the long peptide and/or SLP sequences that incorporate HBV-derived T cell epitopes that are presented on all predominantly expressed HLA class I and class II alleles. By covering the vast majority of worldwide expressed HLA haplotypes (Bui et al., 2006), the long peptide and/or SLP vaccine composition can be used in all HBV infected individuals. The present invention describes the identification and selection of HBV-derived long peptides, preferably SLPs, that are highly immunogenic and capable of inducing a potent combined HBV-directed CD4⁺ T helper and CD8⁺ cytotoxic T cell response, when administered as a vaccine composition to patients. Such highly immunogenic long peptides from HBV have not been disclosed in

the prior art. The HBV-derived long peptides of the invention were identified based on a putative immunogenicity score developed and validated by the inventors and as disclosed herein. The putative immunogenicity is quantified herein using the T cell Regional Immunogenicity Assessment (TRIA) score. The TRIA score is based on the cumulative Class I-BCI score of said peptide, which is indicative for their immunogenic CTL activating capacity, and the cumulative Class II-B score of said peptide, which is indicative for their immunogenic Th-cell activating capacity. Calculation of the cumulative Class I-BCI score and the cumulative Class II-B score is described in detail herein in the Examples section. The TRIA score is calculated as the sum of the cumulative Class I-BCI score and the cumulative Class II-B score. A strong correlation was found between this TRIA score and the T cell responses found in PBMC of HBV-immune donors. Therefore, the TRIA score enables the selection of optimal immunogenic long peptides.

In a first aspect, the present invention provides a peptide derived from an HBV protein. Preferably the peptide of the invention comprises or consists of a peptide selected from the group consisting of SEQ ID NO: 51-79, 1142-1145 and 1468-1471, more preferably the peptide of the invention comprises or consist of a peptide selected from the group consisting of SEQ ID NO: 51, 55, 60, 63, 64, 68, 71, 74, 75, 76, 77, 1142 and 1469, more preferably selected from the group consisting of SEQ ID NO: 51, 55, 60, 63, 64, 68, 71, 74, 75, 77, 1142 and 1469, even more preferably selected from the group consisting of SEQ ID NO: 55, 60, 63, 64, 68, 71, 74, 75, 76, 77 and 1469, even more preferably selected from the group consisting of SEQ ID NO: 55, 60, 63, 64, 68, 71, 74, 75, 77 and 1469, even more preferably selected from the group consisting of SEQ ID NO: 60, 63, 71, 74, 75 and 1469, most preferably selected from the group of SEQ ID NO: 75, 1469 and 63. Further preferred is a peptide of the invention that comprises or consists of a peptide selected from the group consisting of SEQ ID NO: 51, 60, 63, 64, 68, 71, 74-77. Also preferred is a peptide of the invention that comprises or consists of a peptide selected from the group consisting of SEQ ID NO: 63, 71 and 75. Preferably, the peptide of the invention comprises at least about 70 predicted T-cell epitopes. More preferably, the peptide of the invention comprises at least about 70 predicted T-cell epitopes and at least about 3 proteasomal cleavage sites. Preferably, the peptide of the invention comprises at least about 70 predicted HLA class I-restricted

CD8⁺ cytotoxic T-cell epitopes, at least about 1 predicted HLA class II-restricted CD4⁺ T-helper epitope. More preferably, the peptide of the invention comprises at least about 70 predicted HLA class I-restricted CD8⁺ cytotoxic T-cell epitopes, at least about 1 predicted HLA class II-restricted CD4⁺ T-helper epitope and at least about 3 proteasomal cleavage sites. HLA class I-restricted CD8⁺ cytotoxic T-cell epitope is also denominated herein as CTL epitope and HLA class II-restricted CD4⁺ T-helper epitope is also denominated herein as Th-cell epitope. Preferably, the peptide of the invention comprises at least about 70 predicted CTL epitopes, at least about 15 predicted Th-cell epitopes. More preferably, the peptide of the invention comprises at least about 70 predicted CTL epitopes, at least about 15 predicted Th-cell epitopes and at least about 3 proteasomal cleavage sites. Preferably, the peptide of the invention comprises at least about 95 predicted CTL epitopes, at least about 25 predicted Th-cell epitopes. More preferably, the peptide of the invention comprises at least about 95 predicted CTL epitopes, at least about 25 predicted Th-cell epitopes and at least about 3 proteasomal cleavage sites. Preferably, the peptide of the invention comprises at least about 125 predicted CTL epitopes, at least about 50 predicted Th-cell epitopes. More preferably, a peptide of the invention comprises at least about 125 predicted CTL epitopes, at least about 50 predicted Th-cell epitopes and at least about 3 proteasomal cleavage sites. Preferably, a peptide of the invention has a TRIA score of at least about 6300, at least about 8000, at least about 9000, at least about 10000, or preferably at least about 14000.

A peptide of the invention can advantageously be used in the prevention and/or treatment of an HBV related disease or condition in a subject, preferably a mammal, more preferably a human. Preferably, the peptide of the invention comprises or consists of an amino acid sequence, preferably a contiguous amino acid sequence, of any of the proteins selected from the group consisting of HBV protein polymerase, HBV core protein, HBV X-protein and HBV large surface protein. Preferably, said peptide comprises or consists of a peptide selected from the group consisting of SEQ ID NO: 51-79, 1142-1145 and 1468-1471. A peptide of this group is characterized in that it has a TRIA score of at least 6300, indicating the high immunogenic capacity for CD4⁺ and CD8⁺ T cell activation. Furthermore, a peptide of this group is characterized in that it comprises at least 70 predicted HLA class I-restricted CD8⁺ cytotoxic T-cell epitopes,

at least 1 predicted HLA class II-restricted CD4⁺ T-helper epitope. . Preferably, a peptide of this group comprises at least 3 proteasomal cleavage sites.

More preferably, the peptide of the invention comprises or consists of a peptide selected from the group consisting of SEQ ID NO: 51-53, 55-57, 60-66, 68-78, 1142-
5 1145 and 1468-1471. A peptide of this group is characterized in that it has a TRIA score of at least 8000.

More preferably, the peptide of the invention comprises or consists of a peptide selected from the group consisting of SEQ ID NO: 51-53, 55-57, 60-66, 68, 69, 71-79, 1142-1145 and 1468-1471. A peptide of this group is characterized in that it comprises
10 at least 70 predicted CTL epitopes, at least 15 predicted Th-cell epitopes. Preferably, a peptide of this group comprises at least 3 proteasomal cleavage sites. Preferably, the peptide of the invention comprises or consists of a peptide selected from the group consisting of SEQ ID NO: 51-53, 55, 57, 60, 63, 64, 66, 68, 71, 72, 74-78, 1142, 1145, 1468-1471.

15 More preferably, the peptide of the invention comprises or consists of a peptide selected from the group consisting of SEQ ID NO: 53, 55-57, 60-66, 68, 69, 71, 73-78, 1142-1145, 1468-1471. A peptide of this group is characterized in that it has a TRIA score of at least 9000.

Even more preferably, the peptide of the invention is a peptide that comprises or
20 consists of a peptide selected from the group consisting of SEQ ID NO: 55-57, 60-65, 68, 69, 71, 74, 75, 77, 78, 1142-1145, 1468, 1469 and 1471. A peptide of this group is characterized in that it has a TRIA score of at least 10000.

Even more preferably, the peptide of the invention comprises or consists of a peptide selected from the group consisting of SEQ ID NO: 52, 53, 55, 57, 60, 61, 63,
25 64, 68, 69, 71, 72, 75, 77, 78, 1142-1145, 1468, 1469 and 1471. A peptide of this group is characterized in that it comprises at least 95 predicted CTL epitopes, at least 25 predicted Th-cell epitopes. Preferably, a peptide of this group comprises at least 3 proteasomal cleavage sites. Preferably, the peptide of the invention comprises or consists of a peptide selected from the group consisting of SEQ ID NO: 55, 60, 63, 64,
30 68, 71, 75, 77, 1142, 1469.

Most preferably, the peptide of the invention comprises or consists of a peptide selected from the group consisting of SEQ ID NO: 63, 75, 1143-1145, 1468 and 1469. A peptide of this group is characterized in that it has a TRIA score of at least 14000.

Furthermore, a peptide of this group is characterized in that it comprises at least 125 predicted CTL epitopes, at least 50 predicted Th-cell epitopes. Preferably, a peptide of this group comprises at least 3 proteasomal cleavage sites.

A “T-cell epitope” is defined herein as a linear fragment of a polypeptide antigen, which is recognized and bound by a T-cell receptor, preferably a human T-cell receptor, after being made accessible to a T-cell receptor by intracellular proteolytic processing of the polypeptide antigen and subsequent presentation by an HLA class I or HLA class II molecule on the cell surface of an antigen-presenting cell. A “predicted T-cell epitope” is to be understood herein as a linear fragment of a polypeptide antigen for which liberation from the source protein or peptide by proteolytic cleavage and T-cell receptor recognition and/or binding has been predicted using bioinformatics analyses based on algorithms that predict HLA class I and II peptide binding and C-terminal generation by the proteasome of all possible HLA class I binding peptides (with a length of a HLA class I ligand; 8 – 12 aa) contained in the HBV proteins. A “confirmed T-cell epitope” is to be understood herein as a linear fragment of a polypeptide antigen for which liberation from the source protein or source polypeptide by proteolytic cleavage and T-cell receptor recognition and/or binding, and more preferably CD4⁺ or CD8⁺ T cell activation capability, have been established experimentally as disclosed herein. A “linear fragment” is understood herein to be a contiguous amino acid sequence of a polypeptide antigen, said polypeptide antigen preferably being an HBV protein, more preferably a protein selected from the group consisting of HBV protein polymerase, HBV core protein, HBV X-protein and HBV large surface protein. An identical linear fragment of a polypeptide antigen showing binding affinity to a second or further type of HLA class I or HLA class II molecule is to be understood herein as a second or further T-cell epitope. In other words, a specific linear fragment of a polypeptide antigen being capable to bind to two types of HLA molecules is understood herein to be two separate or distinct T-cell epitopes, and is scored twice within the cumulative BCI Class I- and/or Class II-B score. A T-cell epitope typically comprises or consists of at least 8 amino acids and up to 20 or (exceptionally) even more amino acids. A T-cell epitope can be an HLA class I-restricted CD8⁺ cytotoxic T cell (CTL) epitope or an HLA class II-restricted CD4⁺ T-helper (Th-)cell epitope. HLA class I restricted epitopes (also referred to as CTL epitopes) are typically presented via the classical proteasome dependent HLA class I processing route, whereas HLA class-II

molecules are typically loaded with linear fragments in the late endosomal compartment. Preferably, a peptide according to the invention comprises T-cell epitopes that are selected from the group consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-1140, and 1146 - 1466 (see Tables 4-7). A preferred peptide according to the invention comprises at least 70, 71, 72, 73, 74, 75, 79, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 205, 210, 215, 220, 225 or from about 230 to about 233 predicted T-cell epitopes from HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein. A more preferred peptide according to the invention comprises at least 95, 96, 97, 98, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 205, 210, 215, 220, 225 or from about 230 to about 233 predicted T-cell epitopes from HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein. An even more preferred peptide according to the invention comprises at least 70, 71, 72, 73, 74, 75, 79, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 205, 210, 215, 220, 225 or from about 230 to about 233 predicted T-cell epitopes selected from the group consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-1140, and 1146 - 1466. An even more preferred peptide according to the invention comprises at least 95, 96, 97, 98, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 205, 210, 215, 220, 225 or from about 230 to about 233 predicted T-cell epitopes selected from the group consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-1140, and 1146 - 1466. Preferably, the predicted T-cell epitopes of the present invention are confirmed experimentally as disclosed herein. A preferred peptide according to the invention comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65 or 70 confirmed T-cell epitopes from HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein. A more preferred peptide according to the invention comprises at least 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90 or 95 confirmed T-cell epitopes from HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein. An even more preferred peptide according to the invention comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65 or 70 confirmed T-cell

epitopes selected from the group consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-1140, and 1146 - 1466. An even more preferred peptide according to the invention comprises at least 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90 or 95 confirmed T-cell epitopes
5 selected from the group consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-1140, and 1146 - 1466.

A “proteasomal cleavage site” is understood herein as a site in a protein or polypeptide that is cleaved by the proteasome, preferably a human proteasome/proteasome naturally present in a human cell. A specific proteasomal
10 cleavage site liberating the C-terminus of the epitope is preferably present exactly after the C-terminus of the epitope amino acid sequence, in order to allow the epitope’s C-terminal residue to be liberated from the larger peptide and to be presented by the HLA class I molecule. The first important event that defines an HLA class I-restricted CD8⁺ cytotoxic T-cell (CTL) epitope is the release of the epitope (or the epitope-precursor)
15 from its flanking protein regions through enzymatic cleavage by cytosolic peptidases. The multicatalytic proteasome is the primary enzyme complex required for the generation of the exact C-terminus of the vast majority of CTL epitopes (Rock et al., 2004). Proteasomes are multicatalytic enzyme complexes abundantly present intracellularly and are considered responsible for the generation of the C terminus of
20 the vast majority of CTL epitopes (Craiu et al, 1997; Stoltze et al., 1998; Mo et al., 1999). The generation of the amino-terminus of a CTL epitope, on the other hand, is much more flexible because several amino-terminal exo-peptidases (like ERAP1, puromycin sensitive aminopeptidase, bleomycin hydrolase and others) reside in the cytosol and endoplasmic reticulum and these trimming enzymes have the capacity to
25 shorten an N-terminal elongated epitope-precursor to its precise length. In contrast, C-terminal trimming has not been reported. Therefore the identification of the proteasome-mediated cleavage sites in a protein or in a polypeptide, like a peptide of the invention, can be used as an important identifier of almost every CTL epitope, because the proteasomal cleavages determine and enable C-terminal epitope generation
30 (Kessler et al., 2001; Kessler and Melief, 2007). The assessment of proteasomal cleavage sites in the HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein identifies the C-termini of intracellularly produced HBV peptide fragments, specifically for HLA class I presented peptide fragments. Length

requirements are much less strict for loading of HLA class II with peptide fragments. Therefore, precise enzymatic generation of the HLA class II binding peptide fragment is not needed. These T-cell epitope requirements have been used in the present invention to localize and design long peptides derived from the full length sequences of
5 an HBV protein which comprises preferred CD8⁺ cytotoxic T cell (CTL) and CD4⁺ T-helper (Th-)cell epitopes and/or combinations thereof and are thus highly immunogenic and therefore suitable peptides for synthesis and (therapeutic) vaccination purposes.

Proteasome mediated proteolytic cleavages can be predicted *in silico* using a prediction algorithm. Cleavage as performed by the proteasome can be verified in a
10 proteasome mediated cleavage assay as disclosed herein, which measures the C-terminal liberation of the epitope from its flanking regions (Kessler et al., 2001; Kessler and Melief, 2007). A cell free proteasome cleavage assay identifying and quantitatively measuring the amino acid (aa) positions and the abundance of cleavages by the proteasome in a polypeptide can be used to determine which peptides are generated
15 from the source protein (or source polypeptide), thereby establishing the peptide pool available for epitope generation. The cell free proteasome cleavage assay involves the co-incubation of a polypeptide (preferably having a length of 28-40 aa, more preferably having a length of 30-39 aa) with a preparation of purified proteasomes in an appropriate buffer solution. Two main forms of proteasomes exist, the
20 immunoproteasomes, which are mainly expressed in professional antigen presenting cells, like *e.g.* Dendritic Cells, and the constitutive proteasomes, which are expressed mainly in other cell types. These types contain variant catalytic subunits with slightly different catalytic activity. Although most epitopes are liberated by both types of proteasomes, sometimes differential epitope generation occurs dependent on
25 proteasome type (Morel et al., 2000; Chapiro et al., 2006). Accordingly, proteasome-mediated cleavage assays may be performed separately with these two proteasome types. Preferably, a constitutive 20S-proteasome or immune 20S-proteasome is used as disclosed herein. The reaction mixture comprising the peptides to be cleaved and either of the two proteasome types (purified proteasome preparations) is incubated at 37°C
30 and samples are drawn at 1 h, 3 h, 6 h and 24 h time points as detailed in the Examples herein. Subsequently, generated peptide cleavage fragments and the remaining source polypeptide are identified and quantified by mass spectrometry (Kessler et al., 2001). This assay reveals both the positions in the polypeptide (and thus in the source protein)

where the proteasome cleaves and the cleavage efficiency (abundance) at these positions. A cleavage site can be confirmed by detection of fragments containing as COOH terminus the residue NH₂-terminal from the cleavage site together with the (possible) complementary fragment(s), as calculated from the intensities of the fragment peaks in the mass spectra (preferably present for >1%, more preferably present for $\geq 7\%$, at 24 h incubation), in both the digestion with constitutive proteasomes and the digestion with immunoproteasomes. Preferably, a peptide of the invention comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more, preferably at least 3, proteasomal cleavage site as defined herein. More preferably, a peptide of the invention comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more, preferably at least 3, proteasomal cleavage site as assessed and verified in a proteasomal cleavage assay as described above.

As indicated above, examples of T-cell epitopes are HLA class I-restricted CD8⁺ cytotoxic T cell (CTL) epitopes and HLA class II-restricted CD4⁺ T-helper (Th-)cell epitopes. A “CTL epitope” is understood herein as a linear fragment of a polypeptide antigen that is liberated from the source protein by proteasome mediated proteolytic cleavage and subsequently presented by an HLA class I molecule on the cell surface of an antigen presenting cell (APC), preferably a human antigen presenting cell. A “predicted CTL epitope” is understood herein as a linear fragment of a polypeptide antigen for which liberation from its source protein by proteolytic cleavages and HLA class I molecule binding have been predicted using bioinformatics analyses based on algorithms that predict HLA class I peptide binding and C-terminal generation by the proteasome of all HLA class I binding short peptides (with a length of a CTL epitope; 8 – 12 aa) contained in the HBV proteins. Preferably, a predicted CTL epitope of the present invention is confirmed experimentally as disclosed herein. A CTL epitope of the invention is preferably capable of activating a CD8⁺ T cell response. A “confirmed CTL epitope” is understood herein as a linear fragment of a polypeptide antigen for which liberation by proteolytic cleavages and HLA class I molecule binding, more preferably CD8⁺ T cell activation, have been established experimentally as disclosed herein. A CTL epitope of the invention is preferably capable of activating a CD8⁺ T cell response. A CTL epitope typically comprises at least 8 up to 12, or exceptionally up to 13 or 14 amino acids. Preferably a CTL epitope consists of 8-14 amino acids, *i.e.* has a length of at least 8 up to 14 amino acids.

A CTL epitope is defined by two important intracellular events being (i) proteasome mediated proteolytic cleavage and (ii) binding to an HLA class I molecule, which takes place in the endoplasmic reticulum (ER). The stronger a linear peptide fragment binds and the slower the off-rate, the more likely that this linear peptide
5 fragment will become a cell surface presented immunogenic CTL epitope (Van der Burg et al., 1996). Analysis of proteasome mediated proteolytic cleavages can be performed as indicated above. Preferably, specific binding to an HLA class I molecule is predicted using an *in silico* prediction algorithm and established by using an HLA class I peptide binding assay as known by the person skilled in the art (Kessler and
10 Melief, 2007; Kessler et al., 2003). Preferably, the HLA class I-restricted epitope in a long peptide according to the invention is predicted to be generated at its C-terminus by the proteasome and preferably has a predicted high affinity binding capacity for the HLA class I molecule using an assay as described in van der Burg et al., 1995 and Kessler et al., 2003; e.g. $IC_{50} \leq$ about 5 μ M may be considered high affinity binding,
15 about 5 μ M $< IC_{50} \leq$ about 15 μ M may be considered intermediate affinity binding, about 15 μ M $< IC_{50} \leq$ 100 μ M may be considered low affinity binding and $IC_{50} >$ about 100 μ M may be considered as no binding. To measure class I binding affinity of a peptide or fragments thereof, various HLA class I binding assays are available. The assays can be divided into cell-free assays (using soluble HLA) versus cellular assays
20 (using HLA class I molecules on the cell surface), and competitive assays (resulting in semi-quantitative data) versus assays that do not use a labeled reference peptide and are therefore quantitative (Kessler and Melief, 2007; Viatte et al., 2006). The assays have in common that the HLA class I peptide binding affinity is reliably assessed.

The actual presentation of a CTL epitope on the cell surface, *i.e.* the net result of
25 both proteasomal cleavage, possible other proteolytic events like N-terminal trimming, and binding and presentation by an HLA class I molecule, which events together define a CTL epitope as indicated above, can be demonstrated by a biochemical approach or by a functional approach using cytotoxic T cells with a T-cell receptor specific for the epitope and HLA class I molecule (geno)type, as known by the person skilled in the art
30 (Kessler and Melief, 2007).

The biochemical approach involves the biochemical purification of HLA-epitope complexes from cells expressing the HBV antigen of the invention together with the presenting HLA class I molecule (geno)type, followed by the mass spectrometric

search for the epitope in the eluted HLA class I-bound CTL receptor ligands as known by the person skilled in the art (Schirle et al., 2000; Schirle et al., 2001).

The functional approach involves a CTL line or clone that is specifically recognizing the HLA-epitope, which is used as a tool to demonstrate the natural processing and actual presentation of the epitope by HLA class I molecules. In this methodology, using a CTL induction assay as known in the art, either the synthetically generated minimal (*i.e.* exact length) epitope or the peptide sequence of interest encompassing the epitope, for instance a peptide, long peptides and/or SLP as defined herein, is used to stimulate and select HLA-epitope-specific cytotoxic T cells. To that end, briefly, a multivalent CD8⁺ T cell population, or a multivalent mixed CD8⁺ and CD4⁺ T cell population, is stimulated with autologous target cells of which the HLA class I molecules on the cell surface are either exogenously loaded with the precise synthetic epitope or endogenously loaded with intracellularly generated CTL epitopes derived from the exogenously loaded long peptide of the invention after its uptake by the antigen presenting target cells. In case the autologous target cells are loaded with a peptide, *e.g.* the synthetic long peptide of the invention, or fragments thereof, encompassing the epitope, the epitope is generated after cellular uptake of the peptide and its intracellular processing by the proteasome together with other N-terminal trimming peptidases. Subsequently, using a T cell recognition assay, the HLA-epitope-specific CTL is used to demonstrate the intracellular generation and natural presentation of the epitope of the invention by HLA class I molecules on the surface of HBV-infected cells. Specific recognition of an HLA class I restricted epitope by a CTL demonstrates the cell surface expression of the epitope and reveals its immunogenicity, *i.e.* the presence of epitope-specific T cells in the (T-cell receptor) repertoire of a selected donor. Preferably, the CD8⁺ T cell activating capability has been demonstrated *ex vivo* and/or *in vivo*, in T cells from human healthy control individuals or even more preferably in T cells from a human patient with an HBV related disease or condition and/or from a healthy control. The activation is preferably assessed *ex vivo* or *in vivo*, more preferably in a human patient with an HBV related disease. A CTL epitope for which liberation by proteolytic cleavage and HLA class I molecules presentation, or preferably CD8⁺ T cell activating capability, has been demonstrated experimentally is denominated herein as a confirmed CTL epitope.

A peptide of the invention preferably comprises at least 70, 71, 72, 73, 74, 75, 79, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 205, 210, 215, 220, 225, 230 and to up to 233 predicted CTL epitopes as defined herein. Preferably, a peptide of the invention

5 comprises at least 70, 71, 72, 73, 74, 75, 79, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 205, 210, 215, 220, 225, 230 and to up to 233 predicted CTL epitopes as defined herein. Preferably, a peptide according to the invention comprises at least 70, 71, 72, 73, 74, 75, 79, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160,

10 165, 170, 175, 180, 185, 190, 195, 200, 205, 210, 215, 220, 225, 230 and to up to 233 predicted CTL epitopes from the HBV core protein, HBV polymerase, HBV X protein

23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90 or 95 confirmed CTL epitopes as defined herein and verified using a functional assay as described above. Preferably, a peptide of the invention comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65 or 70 or preferably at least 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90 or 95 confirmed CTL epitopes selected from the group consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-685; 846-923, 959-1090, and 1146-1395.

A “Th-cell epitope” is understood herein to be a linear peptide fragment that is recognized by an HLA class II molecule. A “predicted Th-cell epitope” is understood herein as a linear fragment of a polypeptide antigen for which HLA class II molecule recognition has been predicted using sophisticated bioinformatics analyses that are experimentally underpinned. Preferably, a predicted Th-cell epitope of the present invention is confirmed experimentally as disclosed herein. A Th-cell epitope of the invention is preferably capable of inducing a CD4⁺ T cell response. A “confirmed Th-cell epitope” is understood herein as a linear fragment of a polypeptide antigen for which HLA class II molecule recognition has been established experimentally as known by the person skilled in the art and further detailed herein.

An HLA class II-restricted CD4⁺ T-helper cell (Th-cell) epitope typically comprises 15 up to 20, or exceptionally even more, amino acids. Preferably, an HLA class II-restricted T-helper cell epitope comprises or 10 – 20 or 10 – 15 amino acids. Specific recognition of a predicted HBV-derived Th-cell epitope can be tested and/or verified in a Th-cell induction assay. To this end the peptide or fragment thereof, long peptide and/or SLP sequence of interest comprising the predicted Th-cell epitope is exogenously loaded on the surface of target cells and subsequently these peptide-loaded target cells are co-incubated with a multivalent autologous T helper cell population. After several rounds of stimulation, epitope-specific T helper cells can be selected and can be back-tested for the recognition of the T helper cell epitope contained in the peptide or SLP thereby proving its natural cell surface presentation. Preferably, an HLA class II-restricted CD4⁺ T-helper cell epitope comprised in a peptide according to the invention is capable of inducing or activating a CD4⁺ T-helper cell in a human patient with an HBV related disease or condition. The induction or activation is preferably assessed *ex vivo* or *in vivo*, more preferably in a human patient with an HBV

related disease. Most preferably, the HLA class II-restricted epitope is capable of activating a CD4⁺ T-helper memory and/or CD4⁺ T-helper effector response, i.e. activation of a CD45RO-positive CD4⁺ T-helper cell. This will lead, by virtue of the 'license to kill' signal through CD40-triggering of DC (Lanzavecchia, 1998) to a more robust CD8⁺ effector and memory cytotoxic T cell response. In another setting the activated CD4⁺ T-helper cells may activate non-HLA restricted killer cells of the immune system. A Th-cell epitope for which recognition by an HLA class II molecule, or preferably CD4⁺ activating capability, has been demonstrated experimentally is denominated herein as a confirmed Th-cell epitope.

10 Preferably, a peptide according to the invention comprises at least one predicted Th-cell epitope from HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein. Preferably, a peptide of the invention comprises at least 1, 2, 3, 4, 5, 6, 8, 7, 8, 9, 10 or preferably at least 15 predicted Th-cell epitope(s) as defined herein. Preferably, a peptide according to the invention comprises at least 1, 2, 3, 4, 5, 15 6, 8, 7, 8, 9, 10, or preferably at least 15 predicted Th-cell epitope(s) from the HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein. Even more preferably, a peptide according to the invention comprises or consists of a contiguous amino acid sequence of any of the proteins selected from the group consisting of HBV core protein, HBV polymerase, HBV X protein and HBV large surface protein, wherein said contiguous amino acid sequence comprises at least 1, 2, 3, 20 4, 5, 6, 8, 7, 8, 9, 10, or preferably at least 15 predicted Th-cell epitope(s). Preferably, a peptide according to the invention comprises at least 1, 2, 3, 4, 5, 6, 8, 7, 8, 9, 10, or preferably at least 15 predicted Th-cell epitope(s) selected from the group consisting of SEQ ID NO: 686-845; 924-958, 1091-1140, and 1396 – 1466 (see Tables 4b, 5b, 6b, 25 and 7b). More preferably, a peptide of the invention comprises at least 1, 2, 3, 4, 5, 6, 8, 7, 8, 9, 10, or preferably at least 15 confirmed Th-cell epitope(s) as defined herein. Even more preferably, a peptide of the invention comprises at least 1, 2, 3, 4, 5, 6, 8, 7, 8, 9, 10, or preferably at least 15 confirmed Th-cell epitope(s) as defined herein and verified using an T helper cell induction assay as described above. Preferably, a peptide 30 of the invention comprises at least 1, 2, 3, 4, 5, 6, 8, 7, 8, 9, 10, or preferably at least 15 confirmed Th-cell epitope selected from the group consisting of SEQ ID NO: 686-845; 924-958, 1091-1140, and 1396 - 1466.

Preferably, a peptide according to the invention comprises both at least 70 predicted CTL epitopes and at least one predicted Th-cell epitope from the HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein. More preferably, a peptide according to the invention is a peptide derived from the HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein, preferably is a fragment of the HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein, that comprises at least 70 predicted CTL epitopes, at least one predicted Th-cell epitope and at least 3 proteasomal cleavage sites. The presence of at least 3 proteasomal cleavage sites, at least 70 predicted CTL epitopes and at least 1 Th epitope within a single peptide according to the invention, being a continuous amino acids fragment of an antigen protein of interest, has been observed to be particularly advantageous due to synergy between the Th response and the CTL response in mounting and maintaining an effective CD8⁺ cytotoxic T cell response. Several published studies have demonstrated that CD4⁺ T-helper cells upon interaction with HLA class II epitope presenting dendritic cells (DC) upregulate CD40 ligand. The interaction of the Th-cell by its CD40 ligand with the CD40 molecule on the DC leads to activation of the DC. Activated DCs display upregulated costimulatory molecules and secrete CTL-promoting cytokines. This allows both a more robust CD8⁺ CTL response induced by such an activated DC that presents HLA class I restricted epitopes and a much more robust CTL memory response (Ridge et al., 1998; Schoenberger et al., 1998; Sun et al., 2004). The need for CD40 expression on DC for robust CD8⁺ CTL responses following vaccination with synthetic long peptides (length of 35 aa.) has been demonstrated in Zwaveling et al. (2002).

Accordingly, a preferred peptide according to the invention comprises at least 70 predicted CTL epitopes and at least one predicted Th-cell epitope; preferably at least 70 predicted CTL epitopes selected from the group consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-685; 846-923, 959-1090, and 1146-1395 and at least one predicted Th-cell epitope selected from the group consisting of SEQ ID NO: 686-845; 924-958, 1091-1140, and 1396 - 1466. A more preferred peptide according to the invention comprises at least 70 predicted CTL epitopes and at least 15 predicted Th-cell epitopes; preferably at least 70 predicted CTL epitopes selected from the group consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-685; 846-923, 959-1090, and 1146-1395 and at least 15

predicted Th-cell epitopes selected from the group consisting of SEQ ID NO: 686-845; 924-95, 1091-1140, and 1396-1466. More preferably, a peptide according to the invention comprises at least 71, 72, 73, 74, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170 up to 175 predicted CTL epitopes
5 selected from the group consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-685; 846-923, 959-1090, and 1146-1395 and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
10 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95 up to 96 predicted Th-cell epitopes selected from the group consisting of SEQ ID NO: 686-845; 924-958, 1091-1140, and 1396-1466. Even more preferably, a peptide according to the invention comprises at least 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170 up to 175 predicted CTL epitopes selected from the group
15 consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-685; 846-923, 959-1090, and 1146-1395 and at least 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95 up to 96 predicted Th-
20 cell epitopes selected from the group consisting of SEQ ID NO: 686-845; 924-958, 1091-1140, and 1396-1466. Preferably, a peptide according to the invention comprises at least 95 predicted CTL epitopes as defined herein and at least 25 predicted Th-cell epitopes as defined herein.

More preferably, a preferred peptide according to the invention comprises at least
25 5 confirmed CTL epitopes and at least one confirmed Th-cell epitope; preferably at least 5 confirmed CTL epitopes selected from the group consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-685; 846-923, 959-1090, and 1146 - 1395 and at least one confirmed Th-cell epitope selected from the group consisting of SEQ ID NO: 686-845; 924-958, 1091-1140, and 1396-1466. A more
30 preferred peptide according to the invention comprises at least 15 confirmed CTL epitopes and at least one confirmed Th-cell epitope; preferably at least 15 confirmed CTL epitopes selected from the group consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-685; 846-923, 959-1090, and 1146-1395 and

at least one confirmed Th-cell epitope selected from the group consisting of SEQ ID NO: 686-845; 924-95, 1091-1140, and 1396-1466. More preferably, a peptide according to the invention comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65 or 70 confirmed CTL epitopes selected from the group consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-685; 846-923, 959-1090, and 1146 - 1395 and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 confirmed Th-cell epitopes selected from the group consisting of SEQ ID NO: 686-845; 924-958, 1091-1140, and 1396-1466. Even more preferably, a peptide according to the invention comprises at least 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90 or 95 confirmed CTL epitopes selected from the group consisting of SEQ ID NO: 80-276, 278-314, 316-429, 432-483, 486-545, 548-636, 638-685; 846-923, 959-1090, and 1146 - 1395 and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 confirmed Th-cell epitopes selected from the group consisting of SEQ ID NO: 686-845; 924-958, 1091-1140, and 1396 - 1466. Preferably, a peptide according to the invention comprises at least 15 confirmed CTL epitopes as defined herein and at least 5 confirmed Th-cell epitopes as defined herein.

The HLA class I epitopes in the peptides according to the invention are preferably capable of being presented on HLA molecules being encoded by HLA alleles that are predominant in the population of human subjects to be treated. Preferred HLA class I epitopes in peptides according to the invention are epitopes capable of binding to: HLA-A0101; HLA-A0201; HLA-A0206; HLA-A0301; HLA-A1101; HLA-A2301; HLA-A2402; HLA-A2501; HLA-A2601; HLA-A2902; HLA-A3001; HLA-A3002; HLA-A3101; HLA-A3201; HLA-A3303; HLA-A6801; HLA-A6802; HLA-A7401; HLA-B0702; HLA-B0801; HLA-B1301; HLA-B1302; HLA-B1402; HLA-B1501; HLA-B1502; HLA-B1525; HLA-B1801; HLA-B2702; HLA-B2705; HLA-B3501; HLA-B3503; HLA-B3701; HLA-B3801; HLA-B3901; HLA-B4001; HLA-B4002; HLA-B4402; HLA-B4403; HLA-B4601; HLA-B4801; HLA-B4901; HLA-B5001; HLA-B5101; HLA-B5201; HLA-B5301; HLA-B5501; HLA-B5601; HLA-B5701; HLA-B5801 and HLA-B5802. In a preferred embodiment, a peptide of the invention, covers at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% of the HLA class I molecules that are encoded by HLA alleles predominant in the population of human subjects to be treated, wherein "Cover an HLA class I molecule"

is understood herein as comprising a CTL epitope that shows binding affinity, preferably intermediate binding affinity, more preferably high binding affinity to said HLA class I molecule. Preferably, a peptide of the invention covers at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% of group of HLA class I molecules consisting of: HLA-A0101; HLA-A0201; HLA-A0206; HLA-A0301; HLA-A1101; HLA-A2301; HLA-A2402; HLA-A2501; HLA-A2601; HLA-A2902; HLA-A3001; HLA-A3002; HLA-A3101; HLA-A3201; HLA-A3303; HLA-A6801; HLA-A6802; HLA-A7401; HLA-B0702; HLA-B0801; HLA-B1301; HLA-B1302; HLA-B1402; HLA-B1501; HLA-B1502; HLA-B1525; HLA-B1801; HLA-B2702; HLA-B2705; HLA-B3501; HLA-B3503; HLA-B3701; HLA-B3801; HLA-B3901; HLA-B4001; HLA-B4002; HLA-B4402; HLA-B4403; HLA-B4601; HLA-B4801; HLA-B4901; HLA-B5001; HLA-B5101; HLA-B5201; HLA-B5301; HLA-B5501; HLA-B5601; HLA-B5701; HLA-B5801 and HLA-B5802.

The HBV genome (SEQ ID NO: 3; see Table 1) consists of a partially double-stranded circular DNA molecule having four overlapping open reading frames (ORFs) that are responsible for the transcription and expression of seven different hepatitis B proteins through the use of multiple in-frame start codons. The HBV proteins are the core protein and the e antigen (HBeAg) encoded by the C gene, the HBV polymerase encoded by the P gene, the viral surface proteins (small (S), middle (M), and large (L)) encoded by the S gene, and X protein encoded by the X gene. There is an outer shell (or envelope) composed of several proteins known collectively as HBs or surface Proteins. This outer shell is frequently referred to as the surface coat. The outer surface coat surrounds an inner protein shell, composed of HBc protein. This inner shell is referred to as the core particle or capsid. Finally the core particle surrounds the viral DNA and the enzyme DNA polymerase.

The HBV core protein is the major component of the viral nucleocapsid. The amino acid sequences of the HBV polymerase, HBV core protein, HBV X protein and HBV large surface protein are represented by SEQ ID NO: 1, 4, 45 and 1141 respectively (see Table 1).

A preferred amino acid sequence of a human HBV polymerase protein is a sequence having at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 100% identity with the sequence depicted in SEQ ID NO: 1; a preferred coding sequence is a sequence having at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 100% identity with the sequence depicted in SEQ ID NO: 2. A preferred amino acid sequence of an HBV core protein is a sequence having at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 100% identity with the sequence depicted in

5 SEQ ID NO: 4; a preferred coding sequence is a sequence having at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 100% identity with the sequence depicted in SEQ ID NO: 5. A preferred amino acid sequence of an HBV large surface protein is a sequence having at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 100% identity with the

10 sequence depicted in SEQ ID NO: 1141, a preferred coding sequence is a sequence having at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 100% identity with the sequence depicted in SEQ ID NO: 1467.

The full length consensus amino acid sequence of the X protein was obtained by deducing the optimal sequence from the 39 published and reviewed full length (154 amino acid) HBV X protein amino acid sequences in the UniProt database (at: www.uniprot.org). These 39 sequences were first aligned and subsequently for each aa position the most frequently occurring aa was selected for that position in the consensus sequence. The 39 sequences with the following entries were included in the analysis:

15 P69713; P03165; P0C686; P69714; Q8JMY5; Q69604; Q05499; O91531; Q9PX75; P20976; P20975; P20977; P24026; Q9PXA2; Q67923; P0C685; P0C678; O93195; Q9E6S8; P12936; Q91C38; Q913A9; Q8JMY3; Q8JN06; Q8JNZ5; Q69607; Q9IBI5; Q80IU5; Q4R1S9; Q4R1S1; Q9YZR6; P0C687; Q9QMI3; P0C681; Q80IU8; Q99HR6; P17102; Q67877; and Q69027 (see Table 2). A preferred consensus amino acid sequence of a human HBV X protein is a sequence having at least about 70%,

25 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 100% identity with the sequence depicted in SEQ ID NO: 45. The consensus amino acid sequence may be encoded by any coding sequence known or designed; the person skilled in the art knows how to design a coding sequence from a known amino acid sequence; such coding sequence may be a codon-optimized sequence. The terms “HBV

30 X protein” and “consensus HBV X protein” are used interchangeably herein.

Percentage of identity is herein determined by calculating the ratio of the number of identical nucleotides/amino acids in the sequence divided by the length of the total nucleotides/amino acids of said sequence, minus the lengths of any gaps. Identity with

a given SEQ ID NO means identity based on the full length of said sequence (*i.e.* over its whole length or as a whole).

Within the context of the present invention, “a peptide derived from an HBV protein” means that the peptide comprises at least 15 and at most 100 consecutive amino acids originating from the HBV core protein, HBV polymerase, HBV X consensus protein and/or HBV large surface protein. In other words, “a peptide derived from the HBV polymerase protein” comprises at most 100 consecutive amino acids of SEQ ID NO: 1, “a peptide derived from the HBV core protein” comprises at most 100 consecutive amino acids of SEQ ID NO: 4, “a peptide derived from the HBV X consensus protein” comprises at most 100 consecutive amino acids of SEQ ID NO: 45, and “a peptide derived from the HBV large surface protein” comprises at most 100 consecutive amino acids of SEQ ID NO: 1141. Preferably, “a peptide derived from the HBV polymerase protein” consists of at most 100 consecutive amino acids of SEQ ID NO: 1, “a peptide derived from the HBV core protein” consists of at most 100 consecutive amino acids of SEQ ID NO: 4, “a peptide derived from the HBV X consensus protein” consists of at most 100 consecutive amino acids of SEQ ID NO: 45, and “a peptide derived from the HBV large surface protein” consists of at most 100 consecutive amino acids of SEQ ID NO: 1141. Therefore, by definition, a peptide according to the invention is distinct from a full length HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein, as these full length proteins are all longer than 100 amino acids. Preferably, the peptide of the present invention is from about 15 to about 100 amino acids in length. More preferably the length of the peptide is from 15 up to 100 length indicated herein as the length of the peptide is 15-100 amino acids, or preferably the length of the peptide is 15-95 amino acids, or 15-90 amino acids, or 15-85 amino acids, or 15-70 amino acids, or 15-65 amino acids, or 15-60 amino acids, or 15-55 amino acids, or 15-50 amino acids, even more preferably 15-45 amino acids, even more preferably, 15-40 amino acids, even more preferably 17-39, even more preferably 19-43 amino acids, even more preferably 22-40 amino acids, even more preferably 28-40 and even more preferably 30-39 amino acids. Within the context of the present invention “a peptide which comprises at most 100 amino acids derived from an HBV protein” preferably means that the number of consecutive amino acids originating from an HBV protein, preferably being a protein selected from the group consisting of HBV core protein, HBV polymerase, HBV X

consensus protein and HBV large surface protein and present in a peptide as defined herein, is 100, 99, 98, 97, 96, 95, 94, 93, 92, 91, 90, 89, 88, 87, 86, 85, 84, 83, 82, 81, 80, 79, 78, 77, 76, 75, 74, 73, 72, 71, 70, 69, 68, 67, 66, 65, 64, 63, 62, 61, 60, 59, 58, 57, 56, 55, 54, 53, 52, 51, 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, or 30 amino acids or less. Within the context of the present invention "a peptide which comprises at least 15 amino acids derived from an HBV protein" preferably means that the number of consecutive amino acids originating from a protein selected from the group consisting of HBV core protein, HBV polymerase, HBV X consensus protein and HBV large surface protein and present in a peptide as defined herein, is at least 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44 or 45 amino acids. Within the context of the present invention "a peptide which comprises 15-100 amino acids derived from an HBV protein" preferably means that the number of consecutive amino acids originating from a protein selected from the group consisting of HBV core protein, HBV polymerase, HBV X consensus protein and HBV large surface protein and present in a peptide as defined herein, is at least 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44 or 45 amino acids and no more than 100, 99, 98, 97, 96, 95, 94, 93, 92, 91, 90, 89, 88, 87, 86, 85, 84, 83, 82, 81, 80, 79, 78, 77, 76, 75, 74, 73, 72, 71, 70, 69, 68, 67, 66, 65, 64, 63, 62, 61, 60, 59, 58, 57, 56, 55, 54, 53, 52, 51, 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, or 30 amino acids. Within the context of the present invention "a peptide which comprises 15-100 amino acids derived from an HBV protein" preferably means that the number of consecutive amino acids originating from a protein selected from the group consisting of SEQ ID NO: 1, 4, 45 and 1141 and present in a peptide as defined herein, is at least 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44 or 45 amino acids and no more than about 100, 99, 98, 97, 96, 95, 94, 93, 92, 91, 90, 89, 88, 87, 86, 85, 84, 83, 82, 81, 80, 79, 78, 77, 76, 75, 74, 73, 72, 71, 70, 69, 68, 67, 66, 65, 64, 63, 62, 61, 60, 59, 58, 57, 56, 55, 54, 53, 52, 51, 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, or 30 amino acids. More preferably, the length of the contiguous amino acid sequence from HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein comprised within the peptide is 15-100 amino acids, or preferably 15-95 amino acids, or 15-90 amino acids, or 15-85 amino acids, or 15-70 amino acids, or 15-

65 amino acids, or 15-60 amino acids, or 15-55 amino acids, or 15-50 amino acids, even more preferably 15-45 amino acids, even more preferably, 15-40 amino acids, even more preferably 17-39, even more preferably 19-43 amino acids, even more preferably 22-40 amino acids, even more preferably 28-40 and even more preferably 30-39 amino acids. Even more preferably, the length of the contiguous amino acid sequence from the sequences selected from the group consisting of SEQ ID NO: 1, 4, 45 and 1141 comprised within the peptide is 15-100 amino acids, or preferably 15-95 amino acids, or 15-90 amino acids, or 15-85 amino acids, or 15-70 amino acids, or 15-65 amino acids, or 15-60 amino acids, or 15-55 amino acids, or 15-50 amino acids, even more preferably 15-45 amino acids, even more preferably, 15-40 amino acids, even more preferably 17-39, even more preferably 19-43 amino acids, even more preferably 22-40 amino acids, even more preferably 28-40 and even more preferably 30-39 amino acids. A peptide according to the invention may comprise additional amino acids than the ones originating from an HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein or may entirely be made of or consist of an amino acid sequence originating from a protein selected from the group consisting of HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein. A peptide according to the invention may comprise several parts of non-contiguous amino acid sequences from an HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein, wherein it is to be understood that said peptide has a length, a TRIA score and/or amount and type of T cell epitopes as defined herein.

According to one embodiment, a peptide according to the invention consists of any of the contiguous amino acid sequence from HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein as defined herein and indicated by its representing SEQ ID NO, whereby it is understood that no amino acids are appended to either end of the said peptide.

According to another embodiment, the peptide according to the invention comprises any of the contiguous amino acid sequences from HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein as defined herein and indicated by its representing SEQ ID NO and further may comprise a modified amino acid and/or a covalently linked functional group such as a fluorinated group, a human toll-like receptor ligand and/or agonist, an oligonucleotide conjugate, PSA, a sugar

chains or glycan, a pam3cys and/or derivative thereof, preferably a pam3cys lipopeptide or variant or derivative thereof, preferably such as described in WO2013051936A1, CpG oligodeoxynucleotides (CpG-ODNs), Cyclic dinucleotides (CDNs), 2-aminoisobutyric acid (Abu), Muramyl dipeptide (MDP), a DC pulse cassette, a tetanus toxin derived peptide.

In an embodiment, the peptide of the invention comprises or consists of a non-naturally occurring sequence as a result of the synthesis of non-natural lengths or as a result of comprising additional amino acids not originating from an HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein or as a result of comprising non-contiguous amino acid sequences from an HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein, and/or as a result of comprising a modified amino acid and/or a non-naturally occurring amino acid and/or a covalently linked functional group such as a fluorinated group, a fluorocarbon group, a human toll-like receptor ligand and/or agonist, an oligonucleotide conjugate, PSA, a sugar chains or glycan, a pam3cys and/or derivative thereof preferably such as described in WO2013051936A1, CpG oligodeoxynucleotides (CpG-ODNs), Cyclic dinucleotides (CDNs), a DC pulse cassette, a tetanus toxin derived peptide, a human HMGB1 derived peptide; either within the peptide or appended to the peptide, as indicated above. The peptide of the invention may comprise 2-aminoisobutyric acid (Abu, an isostereomer of cysteine). A cysteine of the peptide of the invention may be replaced by Abu. Encompassed within the present invention is a peptide of SEQ ID NO: 77, wherein the N-terminal cysteine has been replaced by Abu.

Preferably, a peptide of the invention is an isolated peptide, wherein "isolated" does not reflect the extent to which the peptide is purified, but indicates that the peptide has been removed from its natural milieu (i.e., that has been subject to human manipulation), and may be a recombinantly produced peptide or a synthetically produced peptide.

Preferably, the invention relates to a peptide that can be effectively used in the prevention, partial clearance and/or treatment or full clearance of a HBV related disease or condition in a subject, preferably as detectable by:

- an activation or an induction of the immune system and/or an increase in HBV specific activated CD4⁺ and/or CD8⁺ T-cells in peripheral blood or an increase of the cytokines produced by these T-cells after at least one week of treatment; and/or

- an inhibition of proliferation of HBV infection or a detectable decrease of HBV infected cells or a decrease in cell viability of HBV infected cells; and/or
- an induction or increased induction of HBV infected cell death; and/or
- an inhibition or prevention of the increase of HBV infected cells.

5 In all embodiments of the present invention, a subject is preferably a mammal, more preferably a human. A subject may be an animal model, preferably a non-human mammalian model with humanized HLA class I and class II molecules, or a mammalian, preferably human, organ, such as a liver.

10 In all embodiments of the present invention, the term “HBV related disease or condition” is preferably defined as acute HBV infection, chronic HBV infection and other conditions where the hepatitis virus is found in the blood or body fluids containing blood of a subject, such as liver cirrhosis and liver cancer, or optionally of an asymptomatic subject that is characterized by the presence of the virus in the body of said subject.

15 In the context of the invention, a patient may survive and may be considered as being disease free as a consequence of treatment according to the invention. Alternatively, the disease or condition may have been stopped or regressed (*i.e.* cleared or partially cleared infection). A significant increase of HBV-specific activated CD4⁺ or CD8⁺ cells in peripheral blood at least one week after vaccination is preferably at
20 least a 5%, 10%, 20%, 30% increase or more. An inhibition of the proliferation of HBV infected cells is preferably at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75% inhibition or more. An induction of HBV infected cell death may be at least 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, or more. HBV infection may be inhibited at least 5%, 10%, 20%, 30%, 40%,
25 50%, 55%, 60%, 65%, 70% or 75% induction, or more. HBV infected cells may be reduced by at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 100%.

In each embodiment, within this or further aspects disclosed herein, wherein the effect of a peptide according to the invention, a composition according to the invention,
30 a polynucleotide according to the invention, a viral vector comprising a polynucleotide according to the invention and/or a cell according to the invention and/or a cell obtained or obtainable by a method according to the invention, is quantified, the assay

may be carried out by comparison to a subject not treated or to the same subject before treatment.

Acute and chronic HBV infection can be treated using the present invention. A peptide according to the invention comprising epitopes which are to be presented to T-cell receptors of CD8⁺ cytotoxic T cells and/or CD4⁺ T-helper cells preferably fulfill a number of structural requirements as defined herein. *In vitro* and *ex vivo* T cell experiments are preferably used to confirm the capability of peptides according to the invention to induce substantial CD4⁺ T-helper and CD8⁺ cytotoxic T cell responses. The peptides of the present invention thereby provide a marked improvement in the selection of relatively short peptides that may be chemically synthesized, comprising the most potent and most widely applicable HLA class I and/or class II presented T cell epitopes derived from HBV.

In an embodiment, a peptide is distinct from a contiguous sequence of amino acids of HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein.

A peptide according to the invention comprising a T-cell epitope from HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein, may be modified by deletion or substitution of one or more amino acids, by extension at the N- and/or C-terminus with additional amino acids or functional groups, which may improve bio-availability, targeting to T-cells, or comprise or release immune modulating substances that provide adjuvant or (co) stimulatory functions. The optional additional amino acids at the N- and/or C-terminus are preferably not present in the corresponding positions in the native amino acid sequence of HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein.

A peptide according to the invention comprising a T-cell epitope is obtainable by chemical synthesis and subsequent purification according to methods well-known in the art. (see e.g. Atherton et al., 1989; Barany et al., 1979; Fields et al., 1997). A peptide according to the invention is preferably soluble in physiologically acceptable watery solutions (e.g. PBS) comprising no more than 35, 20, 10, 5 or 0% DMSO. In such a solution the peptide according to the invention is preferably soluble at a concentration of at least 0.5, 1, 2, 4, or 8 mg peptide per ml. More preferably, a mixture of more than one different peptide according to the invention is soluble at a concentration of at least 0.5, 1, 2, 4, or 8 mg peptide per ml in such solutions.

The peptides according to the invention may be easily synthesized and are large enough to be taken up by professional antigen presenting cells, in particular dendritic cells (DC), processed by the proteasome and/or the endosomal/lysosomal degradation and antigen processing system and preferably have sufficient length to contain at least 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 73, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170 to preferably up to 175 CTL epitopes and/or at least 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 to preferably up to 96 Th-cell epitopes as defined herein. Optionally, a peptide according to the invention may comprise N- or C-terminal extensions, which may be amino acids, modified amino acids or other functional groups that may for instance enhance bio-availability, cellular uptake, processing and/or solubility.

Preferably, a peptide according to the invention is a peptide comprising a peptide with an amino acid sequence selected from the group consisting of:

- a fragment of 15 to 30 amino acids of SEQ ID NO: 51, preferably contiguous amino acids,
- a fragment of 15 to 35 amino acids of SEQ ID NO: 52, preferably contiguous amino acids,
- a fragment of 15 to 33 amino acids of SEQ ID NO: 53, preferably contiguous amino acids,
- a fragment of 15 to 33 amino acids of SEQ ID NO: 54, preferably contiguous amino acids,
- a fragment of 15 to 39 amino acids of SEQ ID NO: 55, preferably contiguous amino acids,
- a fragment of 15 to 35 amino acids of SEQ ID NO: 56, preferably contiguous amino acids,
- a fragment of 15 to 34 amino acids of SEQ ID NO: 57, preferably contiguous amino acids,
- a fragment of 15 to 32 amino acids of SEQ ID NO: 58, preferably contiguous amino acids,
- a fragment of 15 to 33 amino acids of SEQ ID NO: 59, preferably contiguous amino acids,
- a fragment of 15 to 38 amino acids of SEQ ID NO: 60, preferably contiguous amino acids,

- a fragment of 15 to 38 amino acids of SEQ ID NO: 61, preferably contiguous amino acids,
- a fragment of 15 to 33 amino acids of SEQ ID NO: 62, preferably contiguous amino acids,
- 5 - a fragment of 15 to 34 amino acids of SEQ ID NO: 63, preferably contiguous amino acids,
- a fragment of 15 to 36 amino acids of SEQ ID NO: 64, preferably contiguous amino acids,
- a fragment of 15 to 34 amino acids of SEQ ID NO: 65, preferably contiguous
- 10 amino acids,
- a fragment of 15 to 34 amino acids of SEQ ID NO: 66, preferably contiguous amino acids,
- a fragment of 15 to 34 amino acids of SEQ ID NO: 67, preferably contiguous amino acids,
- 15 - a fragment of 15 to 39 amino acids of SEQ ID NO: 68, preferably contiguous amino acids,
- a fragment of 15 to 35 amino acids of SEQ ID NO: 69, preferably contiguous amino acids,
- a fragment of 15 to 32 amino acids of SEQ ID NO: 70, preferably contiguous
- 20 amino acids,
- a fragment of 15 to 38 amino acids of SEQ ID NO: 71, preferably contiguous amino acids,
- a fragment of 15 to 36 amino acids of SEQ ID NO: 72, preferably contiguous amino acids,
- 25 - a fragment of 15 to 36 amino acids of SEQ ID NO: 73, preferably contiguous amino acids,
- a fragment of 15 to 35 amino acids of SEQ ID NO: 74, preferably contiguous amino acids,
- a fragment of 15 to 34 amino acids of SEQ ID NO: 75, preferably contiguous
- 30 amino acids,
- a fragment of 15 to 33 amino acids of SEQ ID NO: 76, preferably contiguous amino acids,

- a fragment of 15 to 35 amino acids of SEQ ID NO: 77, preferably contiguous amino acids,
- a fragment of 15 to 35 amino acids of SEQ ID NO: 78, preferably contiguous amino acids,
- 5 - a fragment of 15 to 34 amino acids of SEQ ID NO: 79, preferably contiguous amino acids,
- a fragment of 15 to 34 amino acids of SEQ ID NO: 1142, preferably contiguous amino acids,
- a fragment of 15 to 34 amino acids of SEQ ID NO: 1143, preferably contiguous
- 10 amino acids,
- a fragment of 15 to 34 amino acids of SEQ ID NO: 1144, preferably contiguous amino acids,
- a fragment of 15 to 36 amino acids of SEQ ID NO: 1145, preferably contiguous amino acids,
- 15 - a fragment of 15 to 32 amino acids of SEQ ID NO: 1468, preferably contiguous amino acids,
- a fragment of 15 to 31 amino acids of SEQ ID NO: 1469, preferably contiguous amino acids,
- a fragment of 15 to 30 amino acids of SEQ ID NO: 1470, preferably contiguous
- 20 amino acids,
- a fragment of 15 to 31 amino acids of SEQ ID NO: 1471, preferably contiguous amino acids, and;
- wherein the length of the preferably contiguous amino acid sequence is preferably at least 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32 or
- 25 33 amino acids and/or preferably no more than 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15 amino acids, most preferably a length of 30-39 amino acids.

In a second aspect, the invention provides a polynucleotide encoding a peptide

30 according to the invention, preferably a peptide as defined herein above. A polynucleotide may be any polynucleotide comprising e.g. RNA, DNA, and/or cDNA; a polynucleotide may be single stranded or double stranded and may comprise nucleotide analogues and/or nucleotide equivalents such as a peptide nucleic acid

(PNA) and a morpholino nucleotide analogue. A polynucleotide may be codon optimized for a host of choice to facilitate expression of the encoded subject matter.

The polynucleotide according to the invention does not encode a wild-type full length HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein, but rather encode a peptide according to the invention as such, or flanked by amino acid sequence that are not contiguous with a wild-type HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein. Such flanking amino acids may be from proteins other than a wild-type HBV and/or they may be from other locations within a wild-type HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein that are not contiguous with the peptide they flank. Preferably, the polynucleotide encodes two or more peptides according to the invention arranged as beads-on-string, whereby the peptides according to the invention (the beads) are linked directly together and/or are linked through linker sequences that are from proteins other than a wild-type HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein, and/or from other locations within a wild-type HBV core protein, HBV polymerase, HBV X protein and/or HBV large surface protein, that are not contiguous with the peptide they flank. The amino acid sequences flanking or linking the peptides may comprise proteolytic cleavage sites. A polynucleotide according to the invention may be applied to deliver a peptide according to the invention in various ways. A polynucleotide according to the invention may e.g. be used in the production of recombinant protein or peptide in a suitable host cell (e.g. a bacterial host cell such as *E. coli*, a suitable yeast host cell such as *S. cerevisiae*, a suitable filamentous fungal such as an *Aspergillus* or mammalian host cell) from which the recombinant protein or peptide may be purified. Alternatively the polynucleotide may be operably linked to expression regulatory sequences (promoters and the like) and incorporated in an expression construct for human cells. Such (autologous) cells may be transfected or transduced *ex vivo* to be (re)-administered to a subject in need thereof. Alternatively such expression construct according to the invention may be incorporated into a suitable gene therapy vector. Viral vectors (based on a defective virus) are more efficient agents for gene transfer as compared to non-viral agents. Suitable viral expression constructs include e.g. vectors that are based on adenovirus, adeno-associated virus (AAV), retroviruses or modified vaccinia Ankara (MVA). The polynucleotide according to the invention may also be operably linked to a sequence

encoding and adjuvant such as a Toll-like receptor (TLR) ligand, a NOD ligand, or a RIG-I ligand.

In a third aspect, the present invention provides a cell comprising the polynucleotide according to the second aspect of the invention. Such cell can be used for e.g. production of a peptide according to the invention or for medical purposes such as prevention and/or treatment of an HBV related disease as defined elsewhere herein. Said cell may be any host cell. For the specific applications such as described here above, the selection of the host cell may be made according to such use. The host cell may be a prokaryote or may be a eukaryote. A preferred prokaryote cell is *E. coli*. When the cell is a eukaryote, the cell preferably is a mammalian, insect, plant, fungal, or algal cell. Preferred mammalian cells include e.g. Chinese hamster ovary (CHO) cells, COS cells, 293 cells, PerC6 cells, and antigen presenting cells such as dendritic cells. Preferred insect cells include e.g. Sf9 and Sf21 cells and derivatives thereof. Preferred fungal cells include *Candida*, *Hansenula*, *Kluyveromyces*, *Pichia*, *Saccharomyces*, *Schizosaccharomyces*, *Yarrowia* and filamentous fungal cells. Most preferably, the eukaryotic cell is a human antigen presenting cell, preferably a dendritic cell.

Methods to introduce a polynucleotide into a cell are known to the person skilled in the art. When expression of the polynucleotide is desired, the person skilled in the art knows how to achieve such; the polynucleotide may e.g. be provided with proper control sequences such as a promoter and terminator sequence and may be inserted into a proper vector such as a plasmid or a method described in the second aspect of the invention may be used.

The present invention also provides for an antigen presenting cell such as a dendritic cell as defined earlier herein that has been contacted and/or loaded with a peptide according to the invention, preferably a peptide according to the first aspect of the present invention. Such preferably autologous dendritic cell may be used for immune therapeutic treatment of a subject in need thereof. Such dendritic cell can be isolated from the subject, loaded with at least one peptide according to the invention and used for treatment.

In a fourth aspect, the present invention provides a method for the preparation of an HBV specific T-cell, said method comprising contacting a T-cell with an antigen presenting cell expressing a polynucleotide according to the invention and/or contacting a T-cell with an antigen presenting cell loaded with a peptide according to the invention; and, optionally, culturing said T-cell. The T-cell is preferably a CD8⁺ cytotoxic T-cell or a CD4⁺ T-helper cell.

Contacting a cell with a polynucleotide may be performed using any method known to the person skilled in the art, preferably a polynucleotide according to the invention is introduced into the antigen presenting cell (APC), preferably a dendritic cell, using transfection. Before contacting, the polynucleotide according to the invention may be provided with proper control sequences, or be comprised into a proper vector such as described elsewhere herein.

Contacting a T-cell with a peptide according to the invention can be performed by any method known to the person skilled in the art. Preferably, a peptide or an epitope comprised in a peptide is presented to the CD8⁺ cytotoxic T-cell or CD4⁺ T-helper cell by an HLA class I or an HLA class II molecule on the surface of an antigen presenting cell, preferably a dendritic cell. The person skilled in the art knows how to load an antigen presenting cell with a peptide.

Culturing said T-cell may be performed using any method known by the person skilled in the art. Maintaining a T-cell under conditions to keep the cell alive is herein also to be construed to be culturing.

Preferably, the T-cell according to this aspect of the invention is contacted with a peptide according to the invention as defined in the first aspect of the invention.

In a fifth aspect, the present invention provides a T-cell obtainable by the method depicted in the fourth aspect of the present invention. Preferably, such T-cell is a T-cell that is obtained by the method according to the fourth aspect of the invention. The T-cell is preferably a CD8⁺ cytotoxic T-cell or a CD4⁺ T-helper cell.

Preferably, the T-cell according to this aspect of the invention has been contacted with a peptide according to the invention as defined in the first aspect of the invention.

In a sixth aspect, the present invention provides a composition useful for the prevention and/or treatment of an HBV related disease or related condition, comprising a peptide according to the invention and/or a polynucleotide according to the invention and/or a cell, preferably a T-cell, according to the invention and/or a cell, preferably a T-cell, obtained by the method according to the fourth aspect of the invention and a pharmaceutically acceptable carrier.

When comprising a peptide according to the invention, the composition according to the invention preferably comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32 and up to 33 different peptides according to the invention. Preferably, a composition according to the invention comprises a peptide according to the invention as defined in the first aspect of the invention. In a preferred embodiment, a composition of the invention comprises a combination of peptides wherein said combination of peptides covers at least 70%, 80%, 90%, 92%, 94%, 95%, 96%, 97%, 98%, 99% or 100% of the HLA class I molecules that are encoded by HLA alleles predominant in the population of human subjects to be treated as defined herein above.

When comprising a polynucleotide according to the present invention, the composition according to the invention preferably comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32 and up to 33 different polynucleotides according to the invention. Preferably, a composition according to the invention comprises a polynucleotide according to the invention as defined in the second aspect of the invention.

When comprising a cell according to the invention, the composition according to the invention preferably comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32 and up to 33 different cells, preferably T-cells that have been contacted with a peptide according to the invention. Preferably, said T-cells have been contacted with a peptide according to the invention as defined in the first aspect of the invention. The T-cell is preferably a CD8⁺ cytotoxic T-cell or a CD4⁺ T-helper cell.

In a preferred embodiment, the composition of the invention comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32 and up to 33 different peptides of the peptides consisting of or comprising of a peptide selected from the group consisting of SEQ ID NO: 51-79,

1142-1145 and 1468-1471, more preferably selected from the group consisting of SEQ ID NO: 51, 55, 60, 63, 64, 68, 71, 74, 75, 76, 77, 1142 and 1469, more preferably selected from the group consisting of SEQ ID NO: 51, 55, 60, 63, 64, 68, 71, 74, 75, 77, 1142 and 1469, even more preferably selected from the group consisting of SEQ ID NO: 55, 60, 63, 64, 68, 71, 74, 75, 76, 77 and 1469, even more preferably selected from the group consisting of SEQ ID NO: 55, 60, 63, 64, 68, 71, 74, 75, 77 and 1469, even more preferably selected from the group consisting of SEQ ID NO: 60, 63, 71, 74, 75 and 1469, most preferably selected from the group of SEQ ID NO: 75, 1469 and 63. Further preferred is a composition that comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32 and up to 33 different peptides of the peptides consisting of or comprising of a peptide selected from the group consisting of SEQ ID NO: 51, 60, 63, 64, 68, 71, 74-77, more preferably selected from the group consisting of SEQ ID NO: 63, 71 and 75.

In a preferred embodiment, the composition of the invention comprises at least a peptide that comprises or consists of a peptide of SEQ ID NO: 63 and peptide that comprises or consists of a peptide of SEQ ID NO: 1143.

Also preferred is a composition that comprises at least a peptide that comprises or consists of a peptide of SEQ ID NO: 63 and peptide that comprises or consists of a peptide of SEQ ID NO: 75.

Also preferred is a composition that comprises at least a peptide that comprises or consists of a peptide of SEQ ID NO: 1143 and peptide that comprises or consists of a peptide of SEQ ID NO: 75.

Also preferred is a composition that comprises at least a peptide that comprises or consists of a peptide of SEQ ID NO: 71 and peptide that comprises or consists of a peptide of SEQ ID NO: 75.

Also preferred is a composition that comprises at least a peptide that comprises or consists of a peptide of SEQ ID NO: 71 and peptide that comprises or consists of a peptide of SEQ ID NO: 63.

Also preferred is a composition that comprises at least a peptide that comprises or consists of a peptide of SEQ ID NO: 1144 and peptide that comprises or consists of a peptide of SEQ ID NO: 63.

Also preferred is a composition that comprises at least a peptide that comprises or consists of a peptide of SEQ ID NO: 1144 and peptide that comprises or consists of a peptide of SEQ ID NO: 75.

Also preferred is a composition that comprises at least a peptide that comprises
5 or consists of a peptide of SEQ ID NO: 1144 and peptide that comprises or consists of a peptide of SEQ ID NO: 1143.

Also preferred is a composition that comprises at least a peptide that comprises or consists of a peptide of SEQ ID NO: 63, a peptide that comprises or consists of a peptide of SEQ ID NO: 1143, and a peptide that comprises or consists of a peptide of
10 SEQ ID NO: 75.

Also preferred is a composition that comprises at least a peptide that comprises or consists of a peptide of SEQ ID NO: 63, a peptide that comprises or consists of a peptide of SEQ ID NO: 1143, a peptide that comprises or consists of a peptide of SEQ ID NO: 75, and a peptide that comprises or consists of a peptide of SEQ ID NO: 1144.

Also preferred is a composition that comprises at least a peptide that comprises
15 or consists of a peptide of SEQ ID NO: 75, and a peptide that comprises or consists of a peptide of SEQ ID NO: 1469. Also preferred is a composition that comprises at least a peptide that comprises or consists of a peptide of SEQ ID NO: 63, and a peptide that comprises or consists of a peptide of SEQ ID NO: 1469.

Also preferred is a composition that comprises at least a peptide that comprises
20 or consists of a peptide of SEQ ID NO: 75, a peptide that comprises or consists of a peptide of SEQ ID NO: 1469, and a peptide that comprises or consists of a peptide of SEQ ID NO: 63. Preferably, said composition further comprising a peptide that comprises or consists of a peptide of SEQ ID NO: 60 and/or that comprises or consists
25 of a peptide of SEQ ID NO: 71, and/or that comprises or consists of a peptide of SEQ ID NO: 74.

A preferred composition of the invention comprises a peptide that consists of or comprises a peptide of SEQ ID NO: 75, a peptide that consists of or comprises a peptide of SEQ ID NO: 63, and a peptide that consists of or comprises a peptide of
30 SEQ ID NO: 1469

A preferred composition of the invention comprises a peptide that consists of or comprises a peptide of SEQ ID NO: 75, a peptide that consists of or comprises a

peptide of SEQ ID NO: 63, and a peptide that consists of or comprises a peptide of SEQ ID NO: 71.

A pharmaceutically acceptable carrier can be any such carrier known to the person skilled in the art, e.g. buffered aqueous solutions at physiological ionic strength
5 and/or osmolarity (such as e.g. PBS).

Preferably, a composition according to the present invention further comprises at least one adjuvant. Such adjuvant may be any adjuvant known to the person skilled in the art. Preferred adjuvants are defined later herein.

A preferred use of a peptide, polynucleotide, composition, cell and/or T-cell
10 according to the invention or a T-cell obtainable or obtained by a method according to the invention is the use as a medicament. A specific preferred use of a peptide, polynucleotide, composition, cell and/or T-cell according to the invention or a T-cell obtainable or obtained by a method according to the invention is for the treatment and/or prevention of an HBV related disease or condition. Accordingly, the invention
15 provides for the use of a peptide, polynucleotide, composition, cell and/or T-cell according to the invention or a T-cell obtainable or obtained by a method according to the invention for the manufacturing of a medicament for the treatment and/or prevention of an HBV related disease.

The invention further provides a method for the prevention and/or treatment of
20 an HBV related disease or condition comprising administering to a subject an effective amount of a peptide, polynucleotide, composition, cell or T-cell according to the invention and/or a T-cell obtainable or obtained by a method according to the invention.

Formulation of medicaments, ways of administration and the use of
25 pharmaceutically acceptable excipients are known and customary in the art and for instance described in Remington; The Science and Practice of Pharmacy, 21st Edition 2005, University of Sciences in Philadelphia. Pharmaceutical compositions and medicaments according to the invention are preferably formulated to be suitable for intravenous or subcutaneous, or intramuscular administration, although other
30 administration routes can be envisaged, such as mucosal administration or intradermal and/or intracutaneous administration, e.g. by injection. Intradermal administration is preferred herein. Advantages and/or preferred embodiments that are specifically

associated with intradermal administration are later on defined in a separate section entitled "intradermal administration".

It is furthermore encompassed by the present invention that the administration of a peptide, a polynucleotide, a composition and/or a cell according to the invention and/or a cell obtainable or obtained by a method according to the invention with an appropriate pharmaceutical excipient such as an adjuvant and/or a carrier may be carried out as a single administration. Alternatively, the administration may be repeated if needed and/or distinct peptides, polynucleotides, compositions and/or cells according to the invention and/or cells obtainable or obtained by a method according to the invention with appropriate pharmaceutical excipients such as adjuvants and/or carriers, may be sequentially administered.

The peptide, polynucleotide, composition and/or cell according to the invention and/or cell obtainable or obtained by a method according to the invention (also referred to as medicaments according to the invention) may preferably comprise at least one immune response stimulating compound or adjuvant. Advantageously the medicaments according to the invention may additionally comprise one or more synthetic adjuvants. Such adjuvant may be admixed to the medicament according to the invention or may be administered separately to the subject, mammal or human, to be treated. Particularly preferred are those adjuvants that are known to act via the Toll-like receptors and/or via a RIG-I (Retinoic acid- Inducible Gene-1) protein and/or via an endothelin receptor. Immune modifying compounds that are capable of activation of the innate immune system can be activated particularly well via Toll like receptors (TLRs), including TLRs 1 - 10. Compounds capable of activating TLR receptors and modifications and derivatives thereof are well documented in the art. TLR1 may be activated by bacterial lipoproteins and acetylated forms thereof, TLR2 may in addition be activated by Gram positive bacterial glycolipids, LPS, LPA, LTA, fimbriae, outer membrane proteins, heat shock proteins from bacteria or from the host, and Mycobacterial lipoarabinomannans. TLR3 may be activated by dsRNA, in particular of viral origin, or by the chemical compound poly(I:C). TLR4 may be activated by Gram negative LPS, LTA, Heat shock proteins from the host or from bacterial origin, viral coat or envelope proteins, taxol or derivatives thereof, hyaluronan containing oligosaccharides and fibronectins. TLR5 may be activated with bacterial flagellae or flagellin. TLR6 may be activated by mycobacterial lipoproteins and group B Streptococcus heat labile soluble factor (GBS-

F) or Staphylococcus modulins. TLR7 may be activated by imidazoquinolines, such as imiquimod, resiquimod and derivatives imiquimod or resiquimod. TLR9 may be activated by unmethylated CpG DNA or chromatin - IgG complexes. In particular TLR3, TLR7 and TLR9 play an important role in mediating an innate immune response against viral infections, and compounds capable of activating these receptors are particularly preferred for use in the methods of treatment and in the compositions or medicaments according to the invention. Particularly preferred adjuvants comprise, but are not limited to, synthetically produced compounds comprising dsRNA, poly(I:C), unmethylated CpG DNA which trigger TLR3 and TLR9 receptors, IC31, a TLR 9 agonist, IMSAVAC, a TLR 4 agonist, Montanide ISA-51, Montanide ISA 720 (an adjuvant produced by Seppic 7, France). RIG-I protein is known to be activated by ds-RNA just like TLR3 (Kato et al, 2005). A particularly preferred TLR ligand is a pam3cys and/or derivative thereof, preferably a pam3cys lipopeptide or variant or derivative thereof, preferably such as described in WO2013051936A1. Further preferred adjuvants are Cyclic dinucleotides (CDNs), Muramyl dipeptide (MDP) and poly-ICLC. In a preferred embodiment, the adjuvants of the invention are non-naturally occurring adjuvants such as the pam3cys lipopeptide derivative as described in WO2013051936A1, Poly-ICLC, imidazoquinoline such as imiquimod, resiquimod or derivatives thereof, CpG oligodeoxynucleotides (CpG-ODNs) having a non-naturally occurring sequence, and peptide-based adjuvants, such as muramyl dipeptide (MDP) or tetanus toxoid peptide, comprising non-naturally occurring amino acids.

In another preferred embodiment, the synthetic adjuvant compounds are physically linked to the peptides of the invention. Physical linkage of adjuvants and costimulatory compounds or functional groups to the HLA class I and HLA class II epitope comprising peptides provides an enhanced immune response by improved targeting to antigen-presenting cells, in particular dendritic cells, that internalize, metabolize and display antigen and by simultaneously stimulating such cells to up-regulate expression of a variety of co-stimulatory molecules, thereby becoming efficient T cell response inducing and enhancing cells. Another preferred immune modifying compound is an inhibitor of an endothelin receptor such as BQ-788 (Buckanovich RJ et al., 2008; Ishikawa K, 1994). BQ-788 is N-cis-2,6-dimethylpiperidinocarbonyl-L-gamma-methylleucyl-D - 1 - methoxycarbonyltryptophanyl-D-norleucine. However any derivative of BQ-788 or

modified BQ-788 compound is also encompassed within the scope of this invention. Another preferred immune response stimulating compound or adjuvant is Interferon alpha (IFN α), more preferably pegylated Interferon alpha, which may be admixed to the medicament according to the invention, or may be administered separately to the subject as an immuno-modulatory agent. It is to be construed herein that when an immune response stimulating compound is admixed to the medicament according to the invention, it is depicted as an adjuvant; when administered separately, it is depicted as an immuno-modulatory agent, or an immuno-modulator, which terms are used herein interchangeably. Furthermore, the use of antigen presenting cell (co)stimulatory molecules, as set out in WO99/61065 and in WO03/084999, in combination with the peptides and compositions of the invention is preferred. In particular the use of 4-1BB and/or CD40 ligands, agonistic antibodies, OX40 ligands, CD27 ligands or functional fragments and derivatives thereof, as well as synthetic compounds with similar agonistic activity are preferably administered separately or combined with the peptides of the invention to subjects to be treated in order to further stimulate the mounting of an optimal immune response in the subject.

In addition, a preferred embodiment comprises delivery of the medicaments according to the invention, with or without additional immune stimulants such as TLR ligands and/or anti CD40/anti-4-1BB/ anti-OX-40 or anti-CD27 antibodies in a slow release vehicle such as mineral oil (e.g. Montanide ISA 51) or PLGA. Alternatively, the medicament according to the invention may be delivered intradermally, e.g. by injection, with or without immune stimulants (adjuvants and/or immuno-modulators). Preferably, for intradermal delivery the medicaments according to the invention are administered in a composition consisting of the medicaments and one or more immunologically inert pharmaceutically acceptable carriers, e.g. buffered aqueous solutions at physiological ionic strength and/or osmolarity (such as e.g. PBS).

In a preferred embodiment, a medicament according to the invention as defined herein is formulated to be suitable for intradermal administration or application. Intradermal is known to the skilled person. In the context of the invention, intradermal is synonymous with intradermal and is distinct from subcutaneous. A most superficial application of a substance is epicutaneous (on the skin), then would come an intradermal application (in or into the skin), then a subcutaneous application (in the tissues just under the skin), then an intramuscular application (into the body of the

muscle). An intradermal application is usually given by injection. An intradermal injection of a substance can be done to test a possible reaction, allergy and/or cellular immunity to it, but can also be performed to elicit a specific antibody or T cell immune response. A subcutaneous application is usually also given by injection: a needle is
5 injected in the tissues under the skin.

The advantage of intradermal administration is that the formulation procedure can be simplified and be made more robust. Furthermore, intradermal vaccine delivery has been repeatedly shown to allow significant dose sparing for eliciting vaccine-induced antibody or T cell responses when compared to conventional administration methods
10 such as intramuscular and subcutaneous administration. This effect is attributed to the relatively dense network of immune cells present in the skin. This was also shown with the HPV16 synthetic long peptides in a human study published by Van der Burg et al. (2007). In this study it was shown that intradermal injection of pools of HPV16 synthetic long peptides is safe and results in the migration of HPV16-specific T cells
15 into the skin as well as in an increase in the number of HPV16-specific T cells circulating in the blood.

In an embodiment, a medicament according to the invention does not comprise any adjuvant such as Montanide ISA-51, and specifically Montanide ISA-51. This means that the formulation of the medicament is more simple: an oil-water based
20 emulsion is preferably also not present in a medicament according to the invention. Accordingly, a medicament according to the invention preferably does not comprise an adjuvant such as Montanide ISA-51 and specifically Montanide ISA-51 and/or does not comprise an oil-in-water based emulsion; more preferably a medicament according to the invention comprises neither of these to adjuvant and even more preferably
25 comprises no adjuvant at all. Therefore, in an embodiment, the medicament according to the invention is a, preferably buffered, aqueous solution, preferably at physiological ionic strength and/or osmolality, such as e.g. PBS (Phosphate Buffer Saline) or water for injection (WFI), comprising or consisting of one or more medicaments as defined earlier herein. The skilled person knows how to prepare such a solution.

30 A medicament according to the invention has another advantage, which is that by intradermally administering low amounts of a medicament, preferably a peptide as earlier herein defined, an immunogenic effect may still be achieved. The amount of

each peptide used is preferably ranged from 1 and 1000 µg, more preferably from 5 and 500 µg, even more preferably from 10 and 100 µg.

In an embodiment, the medicament according to the invention comprises a peptide as earlier defined herein and at least one adjuvant, said adjuvant being not formulated in an oil-in water based emulsion and/or not being of an oil-in-water emulsion type as earlier defined herein. This type of medicament according to the invention may be administered as a single administration. Alternatively, the administration of a peptide as earlier herein defined and/or an adjuvant may be repeated if needed and/or distinct peptides and/or distinct adjuvants may be sequentially administered. It is further encompassed by the present invention that a peptide according to the invention is administered intradermally whereas an adjuvant as defined herein is sequentially administered. The adjuvant may be intradermally administered. However any other way of administration may be used for the adjuvant. Intradermal administration of a peptide may be attractive since typically and depending on the disease, the injection of the vaccine is realized at or as close by as possible to the site of the disease resulting in the local activation of the disease draining lymph node, resulting in a stronger local activation of the immune system. A preferred immune response stimulating compound (immuno-modulator) or adjuvant for intradermal administration is Interferon alpha (IFN α), more preferably pegylated Interferon alpha, which may be admixed to the medicament according to the invention, or may be administered separately, for example by subcutaneous injection to the subject. When administered separately the Interferon alpha is preferably also administered subcutaneously and is preferably administered at a dose of 1 microgram/kilogram of body weight within 10 cm proximity to the site where the medicament according to the invention is administered, such described in Zeestraten et al, 2013.

Another typical advantage of the medicaments according to the invention is that relatively low amounts of peptides may be used, in one single shot, in a simple formulation and without any adjuvant known to give undesired side-effects as Montanide ISA-51.

The medicament for intradermal administration may be any medicament according to the invention as defined herein. A medicament according to the invention used for subcutaneous administration may be the same as the one used for intradermal administration and may thus be any medicament according to the invention as defined

herein. The skilled person knows how to formulate a medicament suited for subcutaneous administration.

Preferably, a medicament according to the invention for subcutaneous administration comprises a peptide as already herein defined in combination with an
5 adjuvant. Preferred adjuvants or immune modulators have already been mentioned herein. Other preferred adjuvants are of the type of an oil-in water emulsions such as incomplete Freund's adjuvant or IFA, Montanide ISA-51 or Montanide ISA 720 (Seppic France). In a further preferred embodiment, a medicament according to the invention suited for subcutaneous administration comprises one or more peptides
10 according to the invention, an adjuvant or immune modulator as earlier defined herein and an inert pharmaceutically acceptable carrier and/or excipients all as earlier defined herein. Formulation of medicaments, and the use of pharmaceutically acceptable excipients are known and customary in the art and for instance described in Remington; The Science and Practice of Pharmacy, 21st Edition 2005, University of Sciences in
15 Philadelphia. A preferred immune response stimulating compound or adjuvant for subcutaneous administration is Interferon alpha (IFN α), more preferably pegylated Interferon alpha, which may be admixed to the medicament according to the invention, or may be administered separately to the subject. When administered separately, the Interferon alpha is preferably also administered subcutaneously and is preferably
20 administered at a dose of 1 microgram/kilogram of body weight within 10 cm proximity to the site where the medicament according to the invention is administered, such described in Zeestraten et al., 2013.

In an embodiment, the medicament according to the invention suited for intradermal administration may be simultaneously administered with a medicament
25 according to the invention suited for subcutaneous administration. Alternatively, both medicaments may be sequentially intradermally and subsequently subcutaneously administered or *vice versa* (first subcutaneous administration followed by intradermal administration). In this embodiment as in the earlier described embodiment dedicated to the intradermal administration, the intradermal and/or subcutaneous administration
30 of a medicament according to the invention, preferably a peptide according to the invention, and/or of an adjuvant may be repeated if needed and/or of distinct medicament, preferably peptides and/or of distinct adjuvants may be sequentially intradermally and/or subcutaneously administered. It is further encompassed by the

present invention that a medicament according to the invention, preferably a peptide is administered intradermally and/or subcutaneously whereas an adjuvant as defined herein is sequentially administered as immune-modulator. The adjuvant or immune-modulator may be intradermally and/or subcutaneously administered. However any
5 other way of administration may be used for the adjuvant or immune-modulator.

We expect the combination of an intradermal and a subcutaneous administration of a medicament according to the invention is advantageous. DC in the epidermis are clearly different from DC in the dermis and in the subcutis. The intracutaneous (intradermal) immunization will cause antigen processing and activation of epidermal
10 DC (Langerin-positive Langerhans cells) that through their dendritic network are in close contact with the keratinocytes. This will also optimally activate inflammatory pathways in the interactions between Langerhans cell and keratinocytes, followed by trafficking of antigen loaded and activated Langerhans cell to the skin-draining lymph nodes. The subcutaneous administration will activate other DC subsets, that will also
15 become loaded with antigen and travel independently to the skin- draining lymph nodes. Conceivably, the use of a medicament which may be administered both intradermally and subcutaneously may lead to a synergistic stimulation of T-cells in these draining nodes by the different DC subsets.

A medicament according to the present invention and the methods of treatment
20 described herein using a medicament according to the invention may advantageously be combined with other medicaments and methods of treatment. As such, a medicament according to the invention or a method of treatment according to the invention may be combined with e.g. therapy, and/or antibody therapy against an HBV related disease or may be combined with e.g. immunotherapy and/or antibody therapy against another
25 than HBV related disease, or may be combined with immunotherapy against another antigen than HBV to treat an HBV related disease.

In this document and in its claims, the verb "to comprise" and its conjugations is used in its non-limiting sense to mean that items following the word are included, but
30 items not specifically mentioned are not excluded. In addition, reference to an element by the indefinite article "a" or "an" does not exclude the possibility that more than one of the element is present, unless the context clearly requires that there be one and only one of the elements. The indefinite article "a" or "an" thus usually means "at least one".

The word “about” or “approximately” when used in association with a numerical value (e.g. about 10) preferably means that the value may be the given value (of 10) more or less 0.1% of the value.

The sequence information as provided herein should not be so narrowly construed as to require inclusion of erroneously identified bases. The skilled person is capable of identifying such erroneously identified bases and knows how to correct for such errors. In case of sequence errors, the sequence of the HBV core, HBV polymerase and HBV large surface protein polypeptides obtainable by expression of the gene present in SEQ ID NO: 5, 2 and 1467 containing the respective nucleic acid sequence coding for the polypeptides should prevail.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

Unless stated otherwise, the practice of the invention will employ standard conventional methods of molecular biology, virology, microbiology or biochemistry. Such techniques are described in Sambrook *et al.* (1989) *Molecular Cloning, A Laboratory Manual* (2nd edition), Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press; in Sambrook and Russell (2001) *Molecular Cloning: A Laboratory Manual*, Third Edition, Cold Spring Harbor Laboratory Press, NY; in Volumes 1 and 2 of Ausubel *et al.* (1994) *Current Protocols in Molecular Biology, Current Protocols*, USA; and in Volumes I and II of Brown (1998) *Molecular Biology LabFax*, Second Edition, Academic Press (UK); *Oligonucleotide Synthesis* (N. Gait editor); *Nucleic Acid Hybridization* (Hames and Higgins, eds.).

LEGENDS TO THE FIGURES

Figure 1: Proteasome-mediated cleavage pattern of long vaccine peptides as predicted *in silico* and observed in experimental *in vitro* digestions. For each SLP, the observed cleavage sites are indicated by arrows (major and minor cleavage sites are indicated by bold and thin arrows, respectively, as further detailed herein). Further, for each of the ten SLPs tested in the digestion experiments (SLP1, SLP10 and SLP21 in Figure 1A; SLP14, SLP18 and SLP21 in Figure 1B; SLP24, SLP25 and SLP26 in Figure 1C; and SLP 27 in Figure 1D), the predicted C-score is indicated in the first row, the confirmed predicted cleavage sites are indicated in the second row (indicated as ‘+’), the amino

acid position within the source protein is indicated in the third row, the respective amino acids in the sequence are indicated in the fourth row, and the amino acid number within the SLP is indicated in the fifth row. For SLP27, C* indicates the cysteine replacement by Abu.

5

Figure 2: Overview of responding naïve donors after T cell induction with HBV-derived long peptides. Combined data of IFN γ production as measured by ELISA ('ELISA'); hatched box SI (Stimulation Index) > 1.5, and T cell proliferation ('Prolif') as measured by 3H thymidine incorporation; hatched box SI > 1.5. N.t.: not tested

10

Figure 3: Overview of responding HBV-immune donors after stimulation with HBV-derived long peptides. Data represent IFN γ -ELISpot results, with hatched boxes indicating a positive response with SI (Stimulation Index) > 3, white boxes SI < 3.

15 **Figure 4:** The average Stimulation Index (SI) for each peptide, as measured in an IFN γ ELISpot assay, plotted against the predicted TRIA score of the corresponding peptide. Abu-SLP27 is indicated (ϕ).

20 The invention is further explained in the following examples. These examples do not limit the scope of the invention, but merely serve to clarify the invention.

EXAMPLES

Introduction

25 In the current invention, we developed an optimal T cell inducing vaccine composition consisting of synthetic long peptides to treat chronically HBV-infected patients. A selection of 37 long peptides (Table 3; sequences ranging from 30 to 39 amino acids) was made encompassing the regions of the HBV Polymerase, Core protein, Surface Antigen and X-protein with the highest putative T cell immunity inducing capacity. To this end first putative HLA class I restricted cytotoxic T cell
30 (CTL) epitopes and putative HLA class II restricted T helper epitopes were identified in these proteins using algorithms that predict HLA class I and II peptide binding and C-terminal generation by the proteasome of all HLA class I binding short peptides (with a length of a CTL epitope; 8 – 12 aa) contained in the HBV proteins. Numerical values were assigned to all putative CTL epitopes and T helper epitopes reflecting their

immunogenicity quality. The quality of any CTL epitope was assessed using the so-called Class I-BCI score (Class I-Binding-Cleavage-Immunogenicity score), incorporating the combination of the HLA class I binding capacity of the epitope in conjunction with the likelihood of its C-terminal liberation from the source protein by the proteasome. Putative T helper epitopes were assessed using the so-called Class II-B score (Class II-Binding score) reflecting their binding capacity and thus predicted immunogenic quality. The combined cumulative value, *i.e.* the sum of the cumulative Class I-BCI score and the cumulative Class II-B score, was calculated for all possible long peptides, reflecting the cumulative quantity and quality of all CTL epitopes and T helper epitopes, and is expressed in the T cell Regional Immunogenicity Assessment (TRIA) score. Accordingly, the TRIA score enabled the assessment of the total T cell immunogenicity of any possible long peptide (length 30 – 39 aa) in the HBV proteins. The 37 HBV-derived long peptides with the highest TRIA scores were selected.

Next, we assessed whether naïve donors and donors that have cleared an HBV infection in the past are able to respond to one or more of a subset of 13 long peptides with varying TRIA scores selected from the broad set of 37 long peptides.

PBMC were obtained from buffy coats of twelve healthy donors, six of which were HBV-naïve and six others had cleared an HBV-infection in the past. Using long-term T cell induction assays, we found responses against 12 out of 13 peptides in naïve donors (eleven of which induced responses in multiple donors), confirming the ability of these SLPs to induce T cell responses in a great majority of individuals that had not encountered the antigens before. The strength of T cell responses found in PBMC of HBV-immune donors against these 13 long vaccine peptides correlated with their predicted strength of overall T cell immunogenicity, as expressed in their TRIA scores, validating the predictive value of the TRIA score for selecting immunogenic peptides. Thus the TRIA score is a reliable criterion for the selection of optimal immunogenic long peptides, invigorating us to select the long peptides with the highest TRIA scores into our HBV SLP-based vaccine.

Material and methods

Peptide synthesis

Peptides were synthesized using solid phase Fmoc/tBu chemistry on a PTI Prelude peptide synthesizer and purified on a Gilson preparative HPLC system to >

95% purity. The identity and purity of the peptides were confirmed with UPLC-MS on a Waters Acquity UPLC/TQD system.

5 *Prediction of CTL and T helper cell immunity inducing capacity in selected HBV-derived SLPs by net-based algorithm*

The putative CTL immunity inducing capacity per SLP was predicted by calculating the cumulative Class I-BCI score per SLP. As detailed below, the cumulative BCI score is based on the Class I-B score, which is a measure for HLA class I peptide binding, and the C-score, which is a measure for proteosomal epitope
10 liberation.

The putative T helper cell immunity inducing capacity per SLP was predicted by calculating the cumulative Class II-B score per SLP. As detailed below, the cumulative Class II-B score is based on the Class II-B score, which is a measure for HLA class II peptide binding.

15 The total putative immunity inducing capacity per SLP was predicted by summation of the cumulative Class I-BCI score and the cumulative Class II-B score, which value is denominated herein as the TRIA score.

Class I-B score

20 Peptide binding to 50 HLA class I molecules (see text) of HBV polymerase-derived peptides, HBV Core protein-derived peptides, HBV Surface Antigen-derived peptides and HBV X protein-derived peptides was assessed *in silico* using a proprietary algorithm. The upper 1.5th percentile of the predicted binding peptides to each HLA class I molecule was selected. The 'Class I-Binding score (Class I-B score)' is derived
25 from the ranking of the predicted binding affinity of the peptides. Briefly, the ranking was first reversed and subsequently normalized to 100, so that the peptide predicted to bind best has a score of 100. Example: five peptides were selected (5 within the 1.5th percentile). Peptides were first assigned the 'reverse ranking score' 5 to 1 (5 for the best binding peptide). Subsequently, each reverse ranking score is normalized to the
30 number of peptides within the upper 1.5th percentile, so that the best binder scores 100. To that end, the ranking score for each peptide is multiplied with 100/5 (=20). The best binder then obtains a Class I-B score: 5 x 20 = 100, the second best binder has a Class I-B score of 4 x 20 = 80, etc. In general, the ranking score is multiplied with 100/n (n=

number of peptide within the 1,5th percentile). As a consequence, the best predicted binder (to a certain HLA class I molecule) always scores 100, irrespective of the precise number of peptides within the 1,5th percentile that are selected.

5 C-score

C-terminal generation by the proteasome of the upper 1.5th percentile of predicted high affinity binding peptides of HBV polymerase, HBV Core protein, HBV Surface Antigen and HBV X-protein (for each HLA class I molecule) was assessed using two proprietary algorithms, which predict the likelihood of a proteasomal cleavage after a certain amino acid position in HBV polymerase, HBV Core protein, HBV Surface Antigen and HBV X-protein, respectively, and can score between 0 and 1, where a higher value represents a higher likelihood of cleavage after the amino acid. The value 0.5 may be used as an arbitrary threshold value: > 0.5 the cleavage is likely to occur, and < 0.5 the cleavage is likely to not occur. Accordingly, a value close to 1 indicates a high likelihood of cleavage after the specific residue. Because great differences between the predictions by both different algorithms occur, we developed the Cleavage score (C-score) that takes into account the prediction results of both proprietary algorithms. The C-score is the summation of the separate scores by both methods. Therefore, the C-score for each position in HBV polymerase is maximally (close to) 2, and minimally (close to) 0, where close to 2 reflects a very high likelihood by BOTH methods that the cleavage after the residue will be produced by the proteasome, and a C-score close to 1 is considered as an indifferent tendency for cleavage by the proteasome (as predicted on average by both network methods).

25 Class I-BCI score

To incorporate in one quantitative measure both the Class I-B score and the C-score, which are the measures indicative for the likelihood that a peptide will bind with high affinity to HLA class I molecules and will be C-terminally produced, the Class I-Binding-Cleavage-Immunogenicity (Class I-BCI) score was developed. The Class I-BCI score is the Class I-B score multiplied by the C-score. As such the Class I-BCI can attain a maximal value of 200 (100 x 2) (arbitrary units).

Cumulative Class I-BCI score

The cumulative Class I-BCI score for each long peptide according to the invention was used as (one of two) selection criterion to identify the peptides of the invention. The cumulative Class I-BCI score is a quantitative reflection of both the total number of CD8⁺ cytotoxic T cell epitopes that are contained in a long peptide according to the invention and their predicted quality, in terms of binding capacity and likelihood of intracellular generation by the proteasome, and is as such indicative for the CD8⁺ cytotoxic T cell-inducing power of each peptide according to the invention (its CD8⁺ T cell immunogenicity). A relatively high cumulative Class I-BCI score of a peptide according to the invention indicates a high CD8⁺ T cell immunogenicity.

Class II-B score

Peptide binding to 13 prevalent HLA class II molecules of HBV polymerase-derived peptides, HBV Core protein-derived peptides, HBV Surface Antigen-derived peptides and HBV X protein-derived peptides was assessed *in silico* using a proprietary algorithm. The 'Class II-Binding score' (Class II-B score) is derived from the ranking of the predicted binding affinity of the peptides. Briefly, the ranking was first reversed and subsequently normalized to 100, so that the peptide predicted to bind best has a score of 100. To reduce the number of peptides in the list, all length variants of peptides predicted to bind to a particular HLA class II molecule with a lower predicted binding (lower Class II-B score) are discarded in the list.

Cumulative Class II-B score

The cumulative Class II-B score for each long peptide according to the invention was used as the second selection criterion to identify the peptides of the invention. The cumulative Class II-B score is a quantitative reflection of both the total number of CD4⁺ T-helper cell epitopes that are contained in a long peptide according to the invention and their predicted quality, in terms of binding capacity, and is as such indicative for the CD4⁺ T cell-inducing power of each peptide according to the invention (its CD4⁺ T cell immunogenicity). A relatively high cumulative Class II-B score of a peptide according to the invention indicates a high CD4⁺ T cell immunogenicity

T cell Regional Immunogenicity Assessment (TRIA) score

The TRIA score for a particular peptide of the invention (SLP) is the sum of cumulative Class I-BCI score and the cumulative Class II-B score of that particular long peptide of the invention (SLP).

5 *Proteasomal digestion*

Dithiotreitol (DTT; Sigma-Aldrich) was freshly dissolved in UPLC-grade water and added to a 2X concentrated proteasome digestion buffer (60 mM Trizma-base; pH 7.5; Sigma-Aldrich, 20 mM KCl; Sigma-Aldrich, 10 mM MgCl₂; Sigma-Aldrich, 10 mM NaCl; Sigma-Aldrich) to an end concentration DTT of 2 mM. Then, 130 µl UPLC-
10 grade water was added to 3 reaction vials, along with 150 µl of the 2X concentrated proteasome digestion buffer containing 2 mM DTT, and 10 µl of the peptide to be tested (stock concentration 300 nmol/ml). After vortexing the vials, 10 µl of water was added to vial 1 (mock control digest), 1 µg (10 µl) of constitutive 20S-proteasome (stock 0.1 mg/ml; Enzo Life Sciences) to vial 2, and 1 µg (10 µl) of immune 20S-
15 proteasome (stock 0.1 mg/ml; Enzo Life Sciences) to vial 3. A 50 µl sample for T=0 was taken directly after vortexing and 4 µl of Formic acid (Sigma-Aldrich) was added to stop the reaction. The reaction vials were vortexed and incubated at 37°C. Samples of 50 µl were collected after 1h, 3h, 6h and 24h incubation. The reactions were stopped with 4 µl Formic acid, and all samples were stored at 20°C.

20 *Mass spectrometry analysis of digested fragments*

A Q-TOF1 mass spectrometer (Waters) equipped with an online nanoelectrospray interface with an approximate flow rate of 250 nl/min was used for electrospray ionization–mass spectrometry. Peptide-digestion samples were trapped on a precolumn (MCA-300-05-C18; Dionex) and were eluted with a steep gradient of 70–90% buffer B
25 over 10 min (buffer A, water, acetonitrile and formic acid, 95:3:1 (vol/vol/vol); buffer B, water, acetonitrile and formic acid, 10:90:1 (vol/vol/vol)). Mass spectra were recorded from a mass of 50–2000 daltons. In tandem mass spectrometry mode, ions were selected with a window of 3 daltons. The collision gas was argon (4×10^{-5} mbar), and the collision voltage was ~30 V. For peptide digestion by purified constitutive
30 proteasome and immunoproteasome, peaks in the mass spectra were searched in source substrate peptides with BioLynx software (Waters) and the abundance of a specific digestion fragment was assessed quantitatively as its percentage of the total summed intensities, including undigested substrate.

Cells

Peripheral blood mononuclear cells (PBMC) from healthy donors were isolated by centrifugation over a Ficoll gradient. To generate dendritic cells (DCs), approximately 50×10^6 PBMC were brought to a concentration of 3×10^6 cells/ml complete medium (IMDM, Lonza, supplemented with 8% HS, Seralab; penicillin/streptomycin, Lonza; L-glutamin, Lonza) and seeded 3 ml/well in a 6-wells plate (Corning). After incubation for 1.5 hours at 37°C, non-adherent cells were washed away in three washing steps using complete medium (day 0). The adherent cells were cultured for three days at 37°C in 2 ml/well of complete medium containing 800 U/ml GM-CSF and 500 U/ml IL-4 (Peprotech). On day 3, 1 ml of complete medium containing 2400 U/ml GM-CSF and 1500 U/ml IL-4 was added to each well and cultured for another three days at 37°C.

Induction of T cells

On day 6, long peptides distributed over 3 pools were added to monocyte-derived DCs of naïve donors at a 3 nmol/ml concentration and incubated overnight at 37°C. Pool 1 comprises SLP 26 (SEQ ID NO: 76), SLP 24 (SEQ ID NO: 74), SLP 1 (SEQ ID NO: 51) and SLP 30 (SEQ ID NO: 1142); Pool 2 comprises Abu-SLP 27 (SEQ ID NO: 77, wherein the cysteine on amino acid position 1 is replaced by Abu), SLP 25 (SEQ ID NO: 75), SLP 10 (SEQ ID NO: 60) and SLP 34 (SEQ ID NO: 1469); and Pool 3 comprises SLP 5 (SEQ ID NO: 55), SLP 13 (SEQ ID NO: 63), SLP 14 (SEQ ID NO: 64) and SLP 21 (SEQ ID NO: 21). On day 7, the cells were washed twice with complete medium to remove peptides. DC and autologous PBMC were co-cultured in a 1:10 ratio for 10 days at 37°C in the presence of 10 ng/ml IL-7 and 100 pg/ml IL-12p70. The T cell lines generated by this process were checked every 2-3 days and split when necessary.

Restimulation of T cell lines

Three days after T cell induction (day 10), a second batch of autologous DC was differentiated and loaded with peptide pools as described above. On day 10 after initiation of the T cell line (day 17), the peptide-loaded DC were washed twice with complete medium and added to the T cells in a 1:10 (DC:T cell) ratio in the presence of 10 ng/ml IL-7 and 100 pg/ml IL-12p70. The cells were co-cultured for 7 days. On day

17, also a new batch of DC was differentiated and loaded with peptide pools as described above. For this second restimulation, starting on day 24, DC and T cells were co-cultured in a 1:10 ratio. Two days after restimulation, 30 IU/ml IL-2 (Peprotech) and 5 ng/ml IL-15 (Peprotech) were added to the culture medium. A third restimulation, starting on day 31, was performed identically to the second restimulation.

T cell proliferation and IFN γ production

To measure T cell activation and proliferation, autologous DC were loaded for 6 hours with each of the 13 HBV-derived peptides separately on day 23, 30 and 37 of the T cell induction protocol described above. The DCs were washed and 5,000 peptide-loaded DC were co-cultured with 50,000 T cells for 48 hours. Then, supernatant was collected for ELISA (IFN γ ELISA, Diaclone) and culture medium containing ^3H thymidine was added to all wells. Radioactive ^3H thymidine is incorporated in the DNA of newly formed (proliferated) cells, which is measured after 16 hours of incubation on a MicroBeta liquid scintillation counter (Wallac/Perkin Elmer).

IFN γ -ELISpot

To detect antigen-specific IFN γ -producing human T cells, the PBMC were first pre-stimulated with 3 nmol/ml of the indicated peptide for 72 hours at 37°C. During this stimulation, ELISpot PVDF plates (Mabtech) were coated with 5 $\mu\text{g/ml}$ anti-human IFN γ mAb 1-D1K coating antibody (Mabtech) in PBS and incubated overnight at 4°C. After stimulation of the PBMC, the coating antibody was aspirated from the plate, and washed 4 times with PBS. To block aspecific binding, 100 μl of IMDM containing 8% FCS was added to all wells and incubated at 37°C for 1 hour. In the meantime, stimulated PBMC were harvested, centrifuged, resuspended in X-vivo 15 medium (Lonza) and counted. All PBMC samples were brought to a concentration of 1.5×10^6 cells/ml in X-vivo 15 medium. The medium in the wells of the PVDF plate was aspirated and 100 μl of each PBMC sample was added to the plate in quadruplicates. The plates were incubated at 37°C overnight. The next day, the supernatant was discarded and plates are washed 6 times with PBS/Tween20 0.05%. The biotinylated anti-human IFN γ mAb 7-B6-1 (Mabtech) was added to all wells (100 $\mu\text{l/well}$) at a 0.3 $\mu\text{g/ml}$ concentration in PBS with 1% FBS, and incubated for 2 hours at RT. Next, plates were washed 6 times using PBS/Tween20 0.05% and 1 $\mu\text{g/ml}$ Extravidin-Alkaline phosphatase (ALP) (Sigma-Aldrich) was added to all wells (100 $\mu\text{l/well}$) in

PBS with 1% FBS. The plates were incubated for 1 hour at RT. ALP substrate solution BCIP/NBT-plus (Mabtech) was prepared and 100 µl/well was added to all wells after the plates were washed 4 times with PBS/Tween20 0.05%. To terminate the colorimetric reaction (after 1-20 minutes), tap water was used to wash the plates extensively. After drying, the formed spots were measured on a Biosys Bioreader 5000.

Results

Selection of long peptides based on HLA class I peptide binding prediction and predicted C-terminal generation of all possible CD8⁺ T cell epitopes contained in the long peptides

A high quality CD8⁺ T cell epitope is defined as a peptide that possesses both a predicted high affinity for the HLA class I molecule to which it binds and is also predicted to be generated at its C-terminus by a proteolytic cleavage of the proteasome. Peptides according to the present invention were selected in HBV protein regions that contain optimally high numbers of high quality CD8⁺ and CD4⁺ T cell epitopes. To this end, first the HLA class I binding and C-terminal generation of all possible CD8⁺ T cell epitopes was assessed using a proprietary HLA class I peptide binding algorithm and two proprietary algorithms predicting the cleavages by the proteasome. Subsequently, we devised a single quantitative measure, the so-called binding-cleavage-immunogenicity (BCI) Class I-score, that for each short peptide (8 – 13 amino acids) incorporates both its predicted binding affinity for the HLA class I molecule to which it binds and the likelihood that the peptide is generated by the proteasome in the cells. The Class I-BCI score is calculated from (1) the binding Class I-score (Class I-B score), which is derived from the results of the *in silico* prediction of HLA class I peptide binding using the aforementioned algorithm, and (2) the cleavage score (C-score), which is derived from the results of the *in silico* prediction of the proteasome-mediated C-terminal generation of the peptide by the proteasome using the aforementioned algorithms. Tables 4a, 5a, 6a, and 7a present the Class I-BCI score for all possible CD8⁺ T cell epitopes of these Polymerase, Core protein, Surface Antigen or X-protein derived SLPs, respectively, together with the cumulative BCI Class I score. Tables 4b, 5b, 6b and 7b present the Class II-B score for all possible CD4⁺ T cell epitopes of these Polymerase, Core protein, Surface Antigen or X-protein derived SLPs, respectively, together with the cumulative Class II-B score. Together the

cumulative Class I-BCI score (for CTL epitopes) and the cumulative B Class II-score (for T helper epitopes) resulted in one quantitative value, the so-called Total Regional Immunogenicity Assessment (TRIA) score, reflecting the overall T cell immunogenicity of a long vaccine peptide (Table 3). Based on the highest TRIA scores, 37 SLPs derived from HBV Polymerase, Core protein, Surface Antigen or X-protein were selected for further evaluation (Table 3). From these, to validate the predictive power of the TRIA score, we chose a representative set of 13 SLPs, which included SLP with relatively low and high TRIA scores, for *in vitro* immunogenicity assessment. These 13 peptides were divided over three peptide pools for T cell induction assays, as described (see below).

Peptide fragment analysis after proteasomal digestion of SLPs reveals high accuracy of in silico predictions

An important component of the identification of putative CTL epitopes is the prediction of their C-terminal generation by a proteasome-mediated cleavage. To validate the reliability of this prediction, proteasomal digestion patterns were experimentally assessed for all but 3 of the 13 functionally tested long vaccine peptides (three long peptides were not being cleaved due to technical reasons).

Digestion experiments were performed separately with 20S constitutive proteasomes and 20S immuno proteasome preparations. The combined analysis of cleavages produced by both types of proteasomes allows the assessment of the C-terminal generation of CTL epitopes that are expressed both on the surface of antigen presenting cells (mainly dendritic cells), containing immunoproteasomes, and on the surface of cancer cells, especially from solid tumors, which mainly express constitutive proteasomes. For vaccination purposes these epitopes are preferred because vaccination with such epitopes will allow the induction of CTL by vaccination and the subsequent eradication of cancer cells by these CTL after recognition of the epitopes on the surface of cancer cells.

As indicated in Figure 1, 10 long peptides of the invention (length 30 - 39 aa) were co-incubated in an appropriate buffer with the proteasome preparations at 37°C for 0, 1, 3, 6 and 24 h. After incubation for the indicated interval reactions were stopped and digestion mixtures, containing the digestion fragments, were measured by mass spectrometry as described herein. The mass spectra were (semi-quantitatively)

analyzed to assess the position and abundance of the cleavage sites. The results of 24 h digestion are shown in Figure 1.

The observed cleavage sites observed after 24 h incubation are indicated with arrows. Only cleavage sites that were observed in both the digestion with constitutive proteasomes and the digestion with immunoproteasomes are shown. Major cleavage sites and minor cleavages sites at 24 h digestion are depicted with bold and thin arrows, respectively, according to the following classification:

Major cleavage site: fragments containing as COOH terminus the residue NH₂-terminal from the cleavage site together with the (possible) complementary fragment(s) are present for $\geq 7\%$ at 24 h incubation, as calculated from the intensities of the fragment peaks in the mass spectra.

Minor cleavage site: fragments containing as COOH terminus the residue NH₂-terminal from the cleavage site together with the (possible) complementary fragment(s) are present for $< 7\%$ at 24 h incubation. Cleavage sites with a cumulative fragment abundance of $< 1\%$ are not shown.

Figure 1 also indicates the C-score of proteasomal cleavage prediction. This score indicates the likelihood of cleavage C-terminal of the residue directly under the C-score. If the C-score > 1 the cleavage site is considered predicted to be cleaved by both the constitutive proteasome and the immunoproteasome. As described herein, the C-score is a summation of the predictions by two in silico algorithms separately predicting the proteasome-mediated cleavages by constitutive proteasomes and the cleavages by immunoproteasomes. Each separate prediction can attain a maximal value of 1. Accordingly, the maximal value of the C-score is 2. C-scores > 1 are together counted as the total number of predicted cleavage sites (the C-terminus of the long substrate peptide is not taken into account, because cleavage after this residue cannot be tested).

Figure 1 further indicates the confirmed cleavages (indicated by '+'), which are those predicted cleavage sites (C-score > 1) that are confirmed to be cleaved after 24 h in the proteasome-mediated digestion assay.

As indicated by Figure 1, for SLP1 36% (4/11), for SLP10 71% (10/14), for SLP13 62% (10/ 16), for SLP14 100% (13/13), for SLP18 65% (13/20), for SLP21 87% (14/16), for SLP24 62% (10/16), for SLP25 57% (8/14), for SLP26 72% (8/11), and for SLP27 75% (9/12) of the predicted cleavage sites have been confirmed here.

Induction of T cell responses against 12 out of 13 selected peptides in a naïve population

To assess whether the 13 selected peptides are able to induce a T cell response in naïve donors, PBMC were isolated from buffy coats derived from six healthy donors that had not experienced an HBV-infection. These PBMC were restimulated with either of the 3 peptide pools to obtain T cell lines, that were subsequently stimulated with the selected 13 peptides. The production of IFN γ and T cell proliferation (^{3} H thymidine incorporation) were measured as a read-out for T cell activation. Results are shown in Figure 2, indicating the percentage of donors showing a positive T cell response with a stimulation index (SI) of 1.5 or higher. The SI is calculated by dividing the measured sample value by the value of non-stimulated control cells. Induced responses in naïve donors were detected against 12 of the 13 pre-selected peptides, while 11 pre-selected peptides induced a response in multiple naïve donors.

Strength of pre-existing T cell responses in HBV-immune donors correlates with TRIA score

Subjects that have gone through an HBV infection and successfully cleared it, possess circulating memory T cells specific for HBV. To assess the relevance of the selected vaccine peptides for the clearance of a naturally occurring HBV infection, we tested the presence of T cell responses against the 13 selected HBV peptides in PBMC derived from six HBV-immune donors. After isolation of the PBMC, cells were stimulated with each of the 13 peptides and an IFN γ -ELISpot was performed to detect T cell responses. PBMC samples from 3 out of 6 tested donors showed a positive IFN γ response against one or more of the 13 peptides (SI > 3). Responses were observed against 11 (SLP 5, 10, 13, 14, 18, 21, 24, 25, 26, 27 and 34, represented by SEQ ID NO: 55, 60, 63, 64, 68, 71, 74, 75, 76, 77 and 1469, respectively) out of the 13 peptides, 6 of which induced responses in multiple donors (SLP 10, 13, 21, 24, 25 and 34, represented by SEQ ID NO: 60, 63, 71, 74, 75 and 1469, respectively). The results are summarized in Figure 3, indicating the donors showing a positive IFN γ^+ T cell response against a peptide. For each SLP tested, the average SI of the IFN γ -responses was calculated; 1.21 for SLP1, 2.11 for SLP5, 2.40 for SLP10, 2.44 for SLP13, 1.97 for SLP14, 1.86 for SLP18, 2.87 for SLP21, 2.54 for SLP24, 2.66 for SLP25, 1.56 for SLP26, 1.66 for Abu-SLP27, 1.49 for SLP30 and 3.02 for SLP34. Importantly, when

the average SI of the IFN γ -responses to each peptide is plotted against the corresponding TRIA score, we see a significant correlation (Figure 4), both while including ($R^2=0.37$, $p=0.028$; see Figure 4) the results of Abu-SLP27 and while excluding ($R^2=0.34$, $p=0.048$; not shown) the results of Abu-SLP27. This validates the use of the TRIA score for the selection of immunogenic peptides.

Discussion

The experimental results presented herein validate, and therefore support, the selection and underscore the immunological relevance of the HBV-derived long vaccine peptides of the present invention. These long vaccine peptides encompass the HBV protein regions with the highest number of high quality HLA class I and HLA class II binding epitopes in an outbred population. A preferred combination of the vaccine peptides will be incorporated in a novel HBV SLP vaccine composition to treat chronically HBV-infected patients. Using algorithms to predict the peptide binding affinity of short peptides (8 – 12 aa) for all prevalent HLA class I molecules and the likelihood of the C-terminal generation of these short peptides by cleavage by the proteasome, in combination with the identification of the putative T helper epitopes, we identified highly immunogenic regions from which the optimal 37 long vaccine peptides were selected.

To enable proper selection of long vaccine peptides in the present invention, a quantitative measure was developed, the TRIA score. Without such a quantitative measure attributed to all possible long HBV peptides, a proper selection of the optimal long peptides is not possible. The TRIA score is a quantitative representation of the quality and quantity of all putative HLA class I restricted CD8⁺ cytotoxic T cell epitopes and HLA class II restricted CD4⁺ T helper epitopes contained in a long peptide. The TRIA score was calculated for all possible HBV peptides with a length of 30 – 39 aa, which is the optimal peptide length for vaccination purposes, enabling the rational selection of a set of highly immunogenic long vaccine peptides.

For further testing and validation of the immunological relevance, we selected a set of 13 SLP with varying TRIA scores. First, we experimentally digested these SLP using either constitutive proteasome or immunoproteasome. The generated fragments showed a clear overlap with the predicted C-terminal cleavage sites, expressed in the BCI score.

Thereafter, T cell assays were performed using PBMC from both naïve and HBV-immune donors. Nearly all 13 selected SLPs were able to induce T cell responses in PBMC derived from naïve healthy donors, which proves that the selected SLP set has the potential to induce responses by the T cell repertoire that had not been stimulated before. Within the same set of vaccine peptides, a strong correlation was observed between the TRIA score of a certain vaccine peptide and the strength of the IFN γ -response in HBV-immune donors, indicating that the TRIA score is a predictive value for *in vivo* immunogenicity and thus functionality of the vaccine peptides.

Table 1. Protein and DNA sequences of HBV polymerase, HBV core and HBV large surface proteins.

SEQ ID NO:	SEQ type	Gene / Gene product	Sequence
1	Protein	HBV Polymerase	MPLSYQHFRKLLLLDDGTEAGPLEEELPRLADADLHRRVAE DLNLGNLNVSI PWTHKVG NFTGLYSSTVPIFNPEWQTPSFP KIH LQEDI INRCQQFVGPLTVNEKRRLKLIMPARFYPTHK YLPLDKGIKPYYPDQVVNH YFQTRHYLHTLWKAGILYKRET TRSASFCGSPYSWEQELQHGR LVIKTSQRHGDESFCSSSG ILSRSSVGPCIRSQLKQSR LGLQPRQGR LASSQPSRSGSIR AKAHPSTRRYFGVEPSGSGHIDHSVNNSSSCLHQSAVRKAA YSHLSTSKRQSSSGHAVEFHC LPPNSAGSQSQGSVSSCWWL QFRNSKPCSEYCLSHLVNLREDWGPCDEHGEHHIRIPRTPA RVTGGVFLVDKNPHNTAESRLVVD FSQFSRGISRVS WPKFA VPNLQSLTNLLSSNLSWLSLDVSAAFYH IPLHPAAMP HLLI GSSGLSRYVARLSSNSRINNNQYGT MQNLHDSCSRQLYVSL MLLYKTYGWLHLHYSHPIVLGFRKIPMGVGLSPFLLAQFTS AICSVVRRAFP HCLAFSYMDDVVLGAKSVQHRESLYTAVTN FLLSLGIHLNPNKTKRWGYS LNFMGYIIGSWGTL PQDHIVQ KIKHCFRKLFPVNRPIDWKVCQ RIVGLLGFAAPFTQCGYPAL MPYACIQAKQAF TFSPTYKAFLSKQYMNLYPVARQRPGLC QVFADATPTGWGLAIGHQRM RGT FVAPLP IHTAELLAACFA RSRSGAKLIGT DNSVVL SRKYTSFPWLLGCTANWILRGTSF VYVPSALNPADDPSRGR LGLSRPLLR LFPQPTTGRTSLYAV SPSVPSHLPVRVHFASPLHVAWRPP
2	CDS	HBV Polymerase	See sequence listing
3	Genomic	HBV genome	See sequence listing
4	Protein	HBV Core	MQLFHLCLIISCTCPTVQASKLC LGWLWGM DIDPYKEFGAT VELLSFLPSDFFP SVRDLLDTASALYREALESPEHCS PHHT ALRQAILCWGELMTLATWVGNNLED PASRD LVVNYVNTNVG LKIRQLLWFHISCLTFGRET VLEYLV SFGVWIRT PPAYRPP NAPILSTLPETT VVRRDRGRSPRRRT PSPRRRRSPSPRRR RSQSRESQC
5	CDS	HBV Core	See sequence listing
1141	Protein	HBV large surface protein	MGGWSSKPRKMGMTNLSVPNPLGFFPDHQLDPAFGANSNNP DWDFNPVKDDWPAANQVG VGA FGPRLT PPHGGILGWSPQAQ GILTTVSTIPPPASTNRQSGRQPTPI SPPLRDSHPQAMQWN STAFHQTLQDPRVRGLYLPAGGSSSGTVNPAPNIASHISSI SARTGDPVTNMENITSGFLGPLLV LQAGFFLLTRILTIPQS LDSWWTSLNFLGGSPVCLGQNSQSPTS NHSPTSCPPICPGY RWMCLRRFII FLFILLCLIFLLVLLDYQGMLPVCPLIPGS TTTSTGPCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIS SWAFAKYLWEWASVRFSWLSLLVPFVQWFVGLSPTVWLSAI WMMWYWGPSLYSIVSPFIPLLP IFFCLWVYI

Table 2. Different HBV X protein variants and the deduced consensus protein sequence.

SEQ ID NO.	UniProt ENTRY	HBV genotype source	Number of mismatches as compared to consensus sequence	X protein sequence
6	Q91C38	Hepatitis B virus genotype A1 subtype adw2 (isolate South Africa/84/2001) (HBV-A)	12	see sequence listing
7	O91531	Hepatitis B virus genotype A2 (isolate Japan/1 ID11HCCW/1998) (HBV-A)	9	see sequence listing
8	P69714	Hepatitis B virus genotype A2 subtype adw (isolate Japan/Nishioka/1983) (HBV-A)	8	see sequence listing
9	P17102	Hepatitis B virus genotype A2 subtype adw2 (isolate Germany/991/1990) (HBV-A)	7	see sequence listing
10	P69713	Hepatitis B virus genotype A2 subtype adw2 (strain Rutter 1979) (HBV-A)	7	see sequence listing
11	Q4R1S1	Hepatitis B virus genotype A3 (isolate Cameroon/CMR711/1994) (HBV-A)	16	see sequence listing
12	Q4R1S9	Hepatitis B virus genotype A3 (isolate Cameroon/CMR983/1994) (HBV-A)	15	see sequence listing
13	P0C678	Hepatitis B virus genotype B1 (isolate Japan/Ry 30/2002) (HBV-B)	11	see sequence listing
14	Q9PX75	Hepatitis B virus genotype B1 (isolate Japan/Yamagata-2/1998) (HBV-B)	12	see sequence listing
15	P20976	Hepatitis B virus genotype B1 subtype adw (isolate Japan/pJDW233/1988) (HBV-B)	8	see sequence listing
16	P20975	Hepatitis B virus genotype B2 (isolate Indonesia/pJDW420/1988) (HBV-B)	10	see sequence listing
17	Q9PXA2	Hepatitis B virus genotype B2 (isolate Vietnam/16091/1992) (HBV-B)	15	see sequence listing
18	P0C685	Hepatitis B virus genotype B2 (isolate Vietnam/9873/1997) (HBV-B)	11	see sequence listing
19	Q67923	Hepatitis B virus genotype B2 subtype adw (isolate China/patient4/1996) (HBV-B)	11	see sequence listing
20	P20977	Hepatitis B virus genotype B/C subtype adw (isolate Okinawa/pODW282/1998) (HBV-B)	12	see sequence listing
21	Q9E6S8	Hepatitis B virus genotype C (isolate Vietnam/3270/2000) (HBV-C)	6	see sequence listing
22	P0C686	Hepatitis B virus genotype C subtype adr (isolate Japan/Nishioka/1983) (HBV-C)	9	see sequence listing
23	P12936	Hepatitis B virus genotype C subtype adr (strain Japan/adr4/1983) (HBV-C)	8	see sequence listing
24	Q9YZR6	Hepatitis B virus genotype C subtype ar (isolate Japan/S-207/1988) (HBV-C)	10	see sequence listing
25	Q69027	Hepatitis B virus genotype C subtype ayr (isolate Human/Japan/Okamoto/-) (HBV-C)	8	see sequence listing
26	P0C687	Hepatitis B virus genotype C subtype ayw (isolate Australia/AustrC/1992) (HBV-C)	14	see sequence listing
27	Q913A9	Hepatitis B virus genotype C subtype ayw (isolate China/Tibet127/2002) (HBV-C)	5	see sequence listing
28	P24026	Hepatitis B virus genotype D (isolate France/alpha1/1989) (HBV-D)	12	see sequence listing

SEQ ID NO.	UniProt ENTRY	HBV genotype source	Number of mismatches as compared to consensus sequence	X protein sequence
29	O93195	Hepatitis B virus genotype D (isolate Germany/1-9/1991) (HBV-D)	14	see sequence listing
30	P0C681	Hepatitis B virus genotype D subtype ayw (isolate Australia/AustKW/1991) (HBV-D)	9	see sequence listing
31	P03165	Hepatitis B virus genotype D subtype ayw (isolate France/Tiollais/1979) (HBV-D)	7	see sequence listing
32	Q67877	Hepatitis B virus genotype D subtype ayw (isolate Italy/CI/1992) (HBV-D)	8	see sequence listing
33	Q9QMI3	Hepatitis B virus genotype D subtype ayw (isolate Japan/JYW796/1988) (HBV-D)	9	see sequence listing
34	Q80IU8	Hepatitis B virus genotype E (isolate Cote d'Ivoire/ABI-129/2003) (HBV-E)	11	see sequence listing
35	Q80IU5	Hepatitis B virus genotype E (isolate Cote d'Ivoire/ABI-212/2003) (HBV-E)	7	see sequence listing
36	Q69604	Hepatitis B virus genotype E subtype ayw4 (isolate Kou) (HBV-E)	8	see sequence listing
37	Q8JMY3	Hepatitis B virus genotype F1 subtype adw4 (isolate El Salvador/1116Sal/1997) (HBV-F)	20	see sequence listing
38	Q99HR6	Hepatitis B virus genotype F2 (isolate Argentina/sa16/2000) (HBV-F)	19	see sequence listing
39	Q05499	Hepatitis B virus genotype F2 (isolate Brazil/w4B) (HBV-F)	21	see sequence listing
40	Q69607	Hepatitis B virus genotype F2 subtype adw4q (isolate Senegal/9203) (HBV-F)	21	see sequence listing
41	Q9IBI5	Hepatitis B virus genotype G (isolate United States/LAS2523/2002) (HBV-G)	31	see sequence listing
42	Q8JMY5	Hepatitis B virus genotype H (isolate United States/LAS2523/2002) (HBV-H)	22	see sequence listing
43	Q8JN06	Hepatitis B virus genotype H subtype adw4 (isolate Nicaragua/1853Nic/1997) (HBV-H)	22	see sequence listing
44	Q8JMZ5	Hepatitis B virus genotype H subtype adw4 (isolate Nicaragua/2928Nic/1997) (HBV-H)	22	see sequence listing
45	-	Consensus aa sequence	-	MAARLCCQIDPARDVLCIRPV GAESRGRPLSGPLGALPSPSP SAVPADHGAHLSLRGLPVCAF SSAGPCALRFTSARRMETTVN AHQILPKVLHKRTLGLSAMST TDLEAYFKDCVFKDWEELGEE IRLKVFLGGCRHKLVCSAP CNFTSA

Table 3. Synthetic long peptide (SLP) sequences.

SEQ ID NO:	SLP #	Cumulative Class I-BCI ⁴	Cumulative Class II-B score ^B	TRIA score ^C	Source	Sequence
51	SLP1	7264	780	8044	HBV Polymerase aa 1 - 30	MPLSYQHFRKLLLLDDGTEAGPLEEELPRL
52	SLP2	6943	1323	8266	HBV Polymerase aa 52 - 86	I P W T H K V G N F T G L Y S S T V P I E N P E W Q T P S F P K I H L
53	SLP3	6469	3070	9539	HBV Polymerase aa 103 - 135	V N E K R R L K L I M P A R F Y P T H T K Y L P L D K G I K P Y Y
54	SLP4	6169	143	6312	HBV Polymerase aa 118 - 150	Y P T H T K Y L P L D K G I K P Y Y P D Q V V N H Y F Q T R H Y L
55	SLP5	11815	1519	13334	HBV Polymerase aa 139 - 177	V V N H Y F Q T R H Y L H T L W K A G I L Y K R E T T R S A S F C G S P Y S W
56	SLP6	10432	928	11360	HBV Polymerase aa 143 - 177	Y F Q P R H Y L H T L W K A G I L Y K R E T T R S A S F C G S P Y S W
57	SLP7	10325	1817	12142	HBV Polymerase aa 137 - 170	D Q V V N H Y F Q T R H Y L H T L W K A G I L Y K R E T T R S A S F
58	SLP8	7246	3	7249	HBV Polymerase aa 316 - 347	S Q S G S V S S C W W L O F R N S K P C S E Y C L S H L V N L
59	SLP9	6722	527	7249	HBV Polymerase aa 385 - 417	T A E S R L V V D F S Q F S R G I S R V S W P K F A V P N L Q S L
60	SLP10	11926	943	12869	HBV Polymerase aa 419 - 456	N L L S N L S W L S L D V S A A F Y H I P L H P A A M P H L L I G S S G L
61	SLP11	12384	1058	13442	HBV Polymerase aa 422 - 459	S S N L S W L S L D V S A A F Y H I P L H P A A M P H L L I G S S G L S R Y
62	SLP12	12198	426	12624	HBV Polymerase aa 427 - 459	W L S L D V S A A F Y H I P L H P A A M P H L L I G S S G L S R Y
63	SLP13	15733	3046	18779	HBV Polymerase aa 481 - 514	H D S C S R Q L Y V S L M L L Y K T Y G W K L H L Y S H P I V L G F
64	SLP14	12015	1042	13057	HBV Polymerase aa 524 - 559	S P F L L A Q F T S A I C S V V R R A F P H C L A F S Y M D D V V L G A
65	SLP15	11658	783	12441	HBV Polymerase aa 526 - 559	F L L A Q F T S A I C S V V R R A F P H C L A F S Y M D D V V L G A
66	SLP16	8255	1482	9737	HBV Polymerase aa 565 - 598	R E S L Y T A V T N F L L S L G I H L N P N K T R P W G Y S L N E M
67	SLP17	6396	223	6619	HBV Polymerase aa 584 - 617	N P N K T R W G Y S L N E M G Y I I G S W G T L P Q D H I V Q K I
68	SLP18	12576	1365	13941	HBV Polymerase aa 653 - 691	Y P A L M P L Y A C I Q A K Q A F T S P T Y K A F L S K Q Y M N L Y P V A R
69	SLP19	10420	1181	11601	HBV Polymerase aa 657 - 691	M P L Y A C I Q A K Q A F T S P T Y K A F L S K Q Y M N L Y P V A R
70	SLP20	7869	244	8113	HBV Polymerase aa 715 - 746	Q R M R G T F V A P L P I H T A E L L A A C F A P S R S G A K L
71	SLP21	8555	1591	10146	HBV Polymerase aa 754 - 791	V L S R K Y T S F P W L L G C T A N W I L R G T S F V Y V P S A L N P A D D
72	SLP22	6817	1709	8526	HBV Polymerase aa 757 - 792	R K Y T S F P W L L G C T A N W I L R G T S F V Y V P S A L N P A D D P

73	SLP23	8553	903	9456	HBV Polymerase aa 754 - 789	VLSRKYSFEWLLGCTANWILRGTSFVYVPSALNPA
74	SLP24	7277	4649	11926	HBV Core aa 107 - 141	DPASRDLVNVVNTNVGLKTRQLLWFHISCLTFGR
75	SLP25	11331	5493	16824	HBV Core aa 136 - 169	CLTFGRETVLEYLVSGVWIRTPPAYRPPNAPIL
76	SLP26	5422	4414	9836	HBV consensus seq X protein aa 36 - 68	ALPSPSPSAVPADHGAHLSLRGLPVCASFSSAGP
77	SLP27	6468	3788	10256	HBV consensus seq X protein aa 61 - 95	CAFSSAGPCALRFTSARRMETTVNAHQILPKVLHK
78	SLP28	7354	3170	10524	HBV consensus seq X protein aa 86 - 120	HQILPKVLHRTILGLSAMSTTDLEAYFKDCVFKDW
79	SLP29	5862	1024	6886	HBV consensus seq X protein aa 108 - 141	LEAYFKDCVFKDWEELGEEIPLKVFLVGGCRHKL
1142	SLP30	6882	4798	11680	HBV large surface protein aa 175 - 210	MENITSGFLGFLVLVQAGFFLLTRILTIPOSLDSWW
1143	SLP31	10214	7238	17452	HBV large surface protein aa 239 - 274	CPPICPGYRWMLRRFIIFLFILLCLIFLLVLDDY
1144	SLP32	14976	1815	16791	HBV large surface protein aa 323 - 358	CIPIPSSWAFKYLWEWASVRFWSWLSLLVPFVQWVFV
1468	SLP33	13107	1815	14922	HBV large surface protein aa 327 - 358	PSSWAFKYLWEWASVRFWSWLSLLVPFVQWVFV
1469	SLP34	12851	1815	14666	HBV large surface protein aa 328 - 358	SSWAFKYLWEWASVRFWSWLSLLVPFVQWVFV
1145	SLP35	9736	4425	14161	HBV large surface protein aa 365 - 400	WLSAIWMWYWGSPSLYSIVSPFIPILLPIFFCLWVYI
1470	SLP36	5389	4035	9424	HBV large surface protein aa 371 - 400	MMWYWGSPSLYSIVSPFIPILLPIFFCLWVYI
1471	SLP37	6880	4160	11040	HBV large surface protein aa 370 - 400	WMWYWGSPSLYSIVSPFIPILLPIFFCLWVYI

^A Cumulative Class I-BCI score: See *Material and Methods* (Examples section).

^B Cumulative Class II-B score: See *Material and Methods* (Examples section).

^C TRIA score is the sum of the Cumulative Class I-BCI score and the Cumulative Class II-B score.

Table 4a. Predicted HLA class I-restricted CD8⁺ cytotoxic T cell epitopes contained in SLP sequences from HBV polymerase protein.

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
1	8	8	MPLSYQH ^F	80	A*6802	9	1,42	13	1	1	30	
1	8	8	MPLSYQH ^F	81	B*0801	20	88	29	1	88	88	
1	8	8	MPLSYQH ^F	82	B*1402	62	88	88	1	88	88	
1	8	8	MPLSYQH ^F	83	B*1502	13	88	18	1	88	88	
1	8	8	MPLSYQH ^F	84	B*1801	57	88	81	1	88	88	
1	8	8	MPLSYQH ^F	85	B*3503	96	88	136	1	88	88	
1	8	8	MPLSYQH ^F	86	B*5101	77	88	109	1	88	88	
1	8	8	MPLSYQH ^F	87	B*5301	92	88	130	1	88	88	
1	8	8	MPLSYQH ^F	88	B*5501	26	88	36	1	88	88	
1	8	8	MPLSYQH ^F	89	B*5601	23	88	33	1	88	88	
1	9	9	MPLSYQH ^F	81	A*3101	77	1,83	142	1	88	88	
1	9	9	MPLSYQH ^F	82	A*3303	77	88	142	1	88	88	
1	9	9	MPLSYQH ^F	83	A*6801	78	88	143	1	88	88	
1	9	9	MPLSYQH ^F	84	B*5101	22	88	40	1	88	88	
2	9	8	PLSYQH ^F	82	A*3101	22	88	39	1	88	88	
2	9	8	PLSYQH ^F	83	A*3303	45	88	83	1	88	88	
2	9	8	PLSYQH ^F	84	A*7401	28	88	51	1	88	88	
1	10	10	MPLSYQH ^F	83	B*3501	41	1,21	50	1	88	88	
3	10	8	LSYQH ^F	84	A*0301	90	88	110	1	88	88	
3	10	8	LSYQH ^F	85	A*1101	89	88	108	1	88	88	
3	10	8	LSYQH ^F	86	A*3001	43	88	53	1	88	88	
3	10	8	LSYQH ^F	87	A*7401	45	88	55	1	88	88	
1	11	11	MPLSYQH ^F	85	B*0702	87	1,89	165	1	88	88	
1	11	11	MPLSYQH ^F	86	B*0801	97	88	183	1	88	88	
1	11	11	MPLSYQH ^F	87	B*1402	96	88	182	1	88	88	
1	11	11	MPLSYQH ^F	88	B*3501	45	88	86	1	88	88	
1	11	11	MPLSYQH ^F	89	B*3503	86	88	164	1	88	88	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
1	11	11	MPLSYQHFRKL	88	B*3901	58	22	111	1	22	22	
1	11	11	MPLSYQHFRKL	88	B*5101	90	22	170	1	22	22	
1	11	11	MPLSYQHFRKL	88	B*5301	66	22	124	1	22	22	
1	11	11	MPLSYQHFRKL	88	B*5501	79	22	150	1	22	22	
1	11	11	MPLSYQHFRKL	88	B*5601	62	22	117	1	22	22	
3	11	9	LSYQHFRKL	86	B*5201	45	22	85	1	22	22	
4	11	8	SYQHFRKL	87	A*2301	57	22	108	1	22	22	
4	11	8	SYQHFRKL	88	A*2402	65	22	123	1	22	22	
3	12	10	LSYQHFRKLL	88	B*5201	37	1,82	68	1	22	22	
4	12	9	SYQHFRKLL	89	A*2402	26	22	48	1	22	22	
5	12	8	YQHFRKLL	90	B*0801	66	22	120	1	22	22	
5	12	8	YQHFRKLL	88	B*1402	54	22	98	1	22	22	
5	12	8	YQHFRKLL	88	B*3901	78	22	142	1	22	22	
5	12	8	YQHFRKLL	88	B*4801	71	22	130	1	22	22	
3	13	11	LSYQHFRKLLL	91	B*0801	59	1,71	101	1	22	22	
3	13	11	LSYQHFRKLLL	88	B*5201	65	22	111	1	22	22	
3	13	11	LSYQHFRKLLL	88	B*5701	11	22	18	1	22	22	
4	13	10	SYQHFRKLLL	92	A*2301	28	22	47	1	22	22	
4	13	10	SYQHFRKLLL	88	A*2402	33	22	57	1	22	22	
5	13	9	YQHFRKLLL	93	B*0801	31	22	52	1	22	22	
5	13	9	YQHFRKLLL	88	B*1402	61	22	104	1	22	22	
5	13	9	YQHFRKLLL	88	B*3901	64	22	109	1	22	22	
5	13	9	YQHFRKLLL	88	B*4801	98	22	168	1	22	22	
6	13	8	QHFRKLLL	94	B*1402	80	22	136	1	22	22	
6	13	8	QHFRKLLL	88	B*3801	55	22	94	1	22	22	
6	13	8	QHFRKLLL	88	B*3901	77	22	131	1	22	22	
4	14	11	SYQHFRKLLLL	95	A*2301	76	1,85	140	1	22	22	
4	14	11	SYQHFRKLLLL	88	A*2402	82	22	152	1	22	22	
5	14	10	YQHFRKLLLL	96	A*0201	36	22	67	1	22	22	
5	14	10	YQHFRKLLLL	88	B*1402	53	22	97	1	22	22	
5	14	10	YQHFRKLLLL	88	B*3901	70	22	130	1	22	22	
5	14	10	YQHFRKLLLL	88	B*4801	85	22	156	1	22	22	
6	14	9	QHFRKLLLL	97	B*1402	60	22	110	1	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
6	14	9	QHFRKLLLL	98	B*3801	84	98	155	1	98	98	
7	14	8	HFRLKLLLL	99	B*0801	75	99	138	1	99	99	
5	15	11	YQHFRLKLLLL	100	B*2705	94	100	75	1	94	94	
6	16	11	QHFRKLLLLDD	101	B*2705	18	101	10	1	94	94	
8	18	11	FRKLLLLDDGT	102	B*2705	51	102	6	1	94	94	
12	20	9	LLDDDGTEA	103	A*0201	24	103	34	1	94	94	
13	23	11	LLDDDGTEAGPL	104	A*0206	33	104	26	1	94	94	
18	27	10	TEAGPLEEEL	105	B*1301	70	105	96	1	94	94	
18	27	10	TEAGPLEEEL	106	B*3701	10	106	13	1	94	94	
18	27	10	TEAGPLEEEL	107	B*3801	35	107	47	1	94	94	
18	27	10	TEAGPLEEEL	108	B*4002	60	108	82	1	94	94	
23	30	8	LEELPRL	109	B*0702	75	109	133	1	94	94	
23	30	8	LEELPRL	110	B*1301	69	110	122	1	94	94	
23	30	8	LEELPRL	111	B*3701	52	111	93	1	94	94	
23	30	8	LEELPRL	112	B*3801	33	112	58	1	94	94	
23	30	8	LEELPRL	113	B*4001	74	113	131	1	94	94	
Cumulative BCI Class I score ^E :									7264			
52	61	10	IPWTHKVGNF	106	B*1402	43	1,19	52	2	52	86	
52	61	10	IPWTHKVGNF	107	B*3501	47	98	55	2	52	98	
52	61	10	IPWTHKVGNF	108	B*3503	64	98	76	2	52	98	
52	61	10	IPWTHKVGNF	109	B*5301	41	98	49	2	52	98	
52	61	10	IPWTHKVGNF	110	B*5501	41	98	48	2	52	98	
54	61	8	WTHKVGNF	107	A*2501	84	98	100	2	52	98	
54	61	8	WTHKVGNF	108	A*2601	82	98	98	2	52	98	
54	61	8	WTHKVGNF	109	B*4601	44	98	53	2	52	98	
54	61	8	WTHKVGNF	110	B*5802	10	98	12	2	52	98	
52	62	11	IPWTHKVGNFT	108	B*5501	50	0,50	25	2	52	98	
52	62	11	IPWTHKVGNFT	109	B*5601	60	98	30	2	52	98	
54	64	11	WTHKVGNFTGL	109	A*2501	80	1,66	132	2	52	98	
54	64	11	WTHKVGNFTGL	110	A*2601	64	98	107	2	52	98	
56	64	9	HKVGNFTGL	110	B*1402	23	98	39	2	52	98	
56	64	9	HKVGNFTGL	111	B*3901	35	98	58	2	52	98	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
57	64	8	KVGNFTGL	111	A*3201	32	22	53	2	22	22	
55	65	11	THKVGNTGLY	112	A*3002	28	1,39	39	2	22	22	
56	65	10	HKVGNTGLY	113	A*2601	23	22	32	2	22	22	
56	65	10	HKVGNTGLY	22	A*2902	21	22	29	2	22	22	
56	65	10	HKVGNTGLY	22	A*3002	80	22	111	2	22	22	
57	65	9	KVGNFTGLY	114	A*0101	34	22	47	2	22	22	
57	65	9	KVGNFTGLY	22	A*0301	39	22	55	2	22	22	
57	65	9	KVGNFTGLY	22	A*2902	79	22	110	2	22	22	
57	65	9	KVGNFTGLY	22	A*3002	100	22	139	2	22	22	
58	65	8	VGNFTGLY	115	A*0101	49	22	68	2	22	22	
58	65	8	VGNFTGLY	22	A*2902	62	22	86	2	22	22	
58	65	8	VGNFTGLY	22	A*3002	93	22	129	2	22	22	
61	71	11	FTGLYSSTVPI	116	A*2501	24	1,12	27	2	22	22	
61	71	11	FTGLYSSTVPI	22	A*3201	30	22	34	2	22	22	
61	71	11	FTGLYSSTVPI	22	A*6802	31	22	35	2	22	22	
61	71	11	FTGLYSSTVPI	22	B*5101	15	22	17	2	22	22	
61	71	11	FTGLYSSTVPI	22	B*5201	24	22	26	2	22	22	
62	71	10	TGLYSSTVPI	117	B*5201	33	22	37	2	22	22	
63	71	9	GLYSSTVPI	118	A*0201	69	22	77	2	22	22	
63	71	9	GLYSSTVPI	22	A*3201	88	22	99	2	22	22	
63	71	9	GLYSSTVPI	22	B*1525	42	22	48	2	22	22	
63	71	9	GLYSSTVPI	22	B*5201	35	22	40	2	22	22	
64	71	8	LYSSTVPI	119	A*2301	66	22	73	2	22	22	
64	71	8	LYSSTVPI	22	A*2402	81	22	91	2	22	22	
63	72	10	GLYSSTVPIF	120	A*2402	44	1,40	61	2	22	22	
63	72	10	GLYSSTVPIF	22	A*3001	74	22	104	2	22	22	
63	72	10	GLYSSTVPIF	22	B*1501	95	22	133	2	22	22	
63	72	10	GLYSSTVPIF	22	B*1502	80	22	112	2	22	22	
63	72	10	GLYSSTVPIF	22	B*1525	92	22	128	2	22	22	
64	72	9	LYSSTVPIF	121	A*2301	79	22	111	2	22	22	
64	72	9	LYSSTVPIF	22	A*2402	98	22	138	2	22	22	
65	72	8	YSSTVPIF	122	A*0101	26	22	37	2	22	22	
65	72	8	YSSTVPIF	22	B*4601	85	22	119	2	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
65	72	8	YSSTVPIF	123	B*5301	59	1.22	83	2	123	123	
65	72	8	YSSTVPIF	124	B*5701	56	1.22	79	2	124	124	
65	72	8	YSSTVPIF	125	B*5801	80	1.22	112	2	125	125	
65	72	8	YSSTVPIF	126	B*5802	77	1.22	108	2	126	126	
65	74	10	YSSTVPIFNP	127	B*5701	98	0.65	64	2	127	127	
65	74	10	YSSTVPIFNP	128	B*5801	85	1.22	55	2	128	128	
66	76	11	SSTVPIFNPEW	129	B*5701	100	1.48	148	2	129	129	
66	76	11	SSTVPIFNPEW	130	B*5801	97	1.22	143	2	130	130	
66	76	11	SSTVPIFNPEW	131	B*5802	93	1.22	137	2	131	131	
67	76	10	STVPIFNPEW	132	B*4402	19	1.22	28	2	132	132	
67	76	10	STVPIFNPEW	133	B*4403	64	1.22	95	2	133	133	
67	76	10	STVPIFNPEW	134	B*5802	91	1.22	135	2	134	134	
69	76	8	VPIFNPEW	135	B*3503	5	1.22	8	2	135	135	
69	76	8	VPIFNPEW	136	B*5101	32	1.22	47	2	136	136	
69	76	8	VPIFNPEW	137	B*5301	90	1.22	133	2	137	137	
70	79	10	PIFNPEWQTP	138	A*3201	36	0.51	19	2	138	138	
71	81	11	IFNPEWQTPSF	139	A*2301	95	1.19	112	2	139	139	
71	81	11	IFNPEWQTPSF	140	A*2402	79	1.22	94	2	140	140	
73	81	9	NPEWQTPSF	141	B*0702	55	1.22	65	2	141	141	
73	81	9	NPEWQTPSF	142	B*3501	92	1.22	109	2	142	142	
73	81	9	NPEWQTPSF	143	B*3503	62	1.22	74	2	143	143	
73	81	9	NPEWQTPSF	144	B*5301	84	1.22	99	2	144	144	
74	81	8	PEWQTPSF	145	B*1801	71	1.22	85	2	145	145	
74	81	8	PEWQTPSF	146	B*4402	62	1.22	73	2	146	146	
74	81	8	PEWQTPSF	147	B*4403	72	1.22	85	2	147	147	
76	83	8	WQTPSFPK	148	A*1101	7	0.81	5	2	148	148	
74	84	11	PEWQTPSFPKI	149	B*1301	82	1.32	108	2	149	149	
74	84	11	PEWQTPSFPKI	150	B*1302	15	1.22	20	2	150	150	
74	84	11	PEWQTPSFPKI	151	B*4001	4	1.22	6	2	151	151	
74	84	11	PEWQTPSFPKI	152	B*4402	31	1.22	41	2	152	152	
74	84	11	PEWQTPSFPKI	153	B*4403	36	1.22	48	2	153	153	
74	84	11	PEWQTPSFPKI	154	B*4901	78	1.22	103	2	154	154	
76	84	9	WQTPSFPKI	155	A*0206	67	1.22	88	2	155	155	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
76	84	9	WQTPSFPKI	33	B*1301	99	33	130	2	33	33	
76	84	9	WQTPSFPKI	33	B*1302	51	33	67	2	33	33	
76	84	9	WQTPSFPKI	33	B*3701	38	33	50	2	33	33	
76	84	9	WQTPSFPKI	33	B*4801	10	33	13	2	33	33	
76	84	9	WQTPSFPKI	33	B*4901	17	33	23	2	33	33	
76	84	9	WQTPSFPKI	33	B*5201	100	33	132	2	33	33	
76	86	11	WQTPSFPKIHL	134	B*1301	86	1,51	130	2	33	33	
76	86	11	WQTPSFPKIHL	33	B*1302	14	33	21	2	33	33	
76	86	11	WQTPSFPKIHL	33	B*3701	33	33	50	2	33	33	
76	86	11	WQTPSFPKIHL	33	B*3801	59	33	89	2	33	33	
76	86	11	WQTPSFPKIHL	33	B*3901	44	33	67	2	33	33	
76	86	11	WQTPSFPKIHL	33	B*4001	30	33	46	2	33	33	
76	86	11	WQTPSFPKIHL	33	B*4801	83	33	125	2	33	33	
78	86	9	TPSFPKIHL	135	B*0702	10	33	15	2	33	33	
Cumulative BCI Class I score:										6943		
104	111	8	NEKRLRLKL	136	B*0801	83	1,27	105	3	103	135	
104	112	9	NEKRLRLKLI	137	B*4402	42	0,71	30	3	33	33	
104	112	9	NEKRLRLKLI	33	B*4901	4	33	3	3	33	33	
106	113	8	KRLRLKLIM	138	B*2702	69	0,90	62	3	33	33	
106	113	8	KRLRLKLIM	33	B*2705	49	33	44	3	33	33	
107	114	8	RRLKLIMP	139	B*2702	39	0,23	9	3	33	33	
107	114	8	RRLKLIMP	33	B*2705	100	33	23	3	33	33	
106	115	10	KRLRLKLIMPA	140	B*2705	16	1,60	26	3	33	33	
107	115	9	RRLKLIMPA	141	B*2702	93	33	148	3	33	33	
107	115	9	RRLKLIMPA	33	B*2705	99	33	157	3	33	33	
108	115	8	RLKLIMPA	142	A*3001	52	33	83	3	33	33	
108	115	8	RLKLIMPA	33	B*0801	46	33	73	3	33	33	
106	116	11	KRLRLKLIMPAR	143	B*2705	42	0,86	36	3	33	33	
107	116	10	RRLKLIMPAR	144	A*3101	49	33	42	3	33	33	
107	116	10	RRLKLIMPAR	33	B*2702	63	33	54	3	33	33	
107	116	10	RRLKLIMPAR	33	B*2705	97	33	83	3	33	33	
108	116	9	RLKLIMPAR	145	A*3101	96	33	83	3	33	33	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
108	116	9	RLKLIMPAR	55	A*3303	61	55	52	3	55	55	
108	116	9	RLKLIMPAR	55	A*7401	91	55	78	3	55	55	
107	117	11	RRLKLIMPARF	146	B*2705	78	1,18	91	3	55	55	
108	117	10	RLKLIMPARF	147	B*1501	16	55	18	3	55	55	
110	117	8	KLIMPARF	148	A*2301	9	55	10	3	55	55	
110	117	8	KLIMPARF	55	A*3201	95	55	112	3	55	55	
110	117	8	KLIMPARF	55	B*1501	55	55	64	3	55	55	
110	117	8	KLIMPARF	55	B*1525	58	55	68	3	55	55	
108	118	11	RLKLIMPARFY	149	A*0301	34	1,43	49	3	55	55	
108	118	11	RLKLIMPARFY	55	A*3001	32	55	45	3	55	55	
108	118	11	RLKLIMPARFY	55	A*3002	92	55	131	3	55	55	
108	118	11	RLKLIMPARFY	55	B*1501	14	55	20	3	55	55	
109	118	10	LKLIMPARFY	150	A*2902	35	55	50	3	55	55	
110	118	9	KLIMPARFY	151	A*0301	38	55	54	3	55	55	
110	118	9	KLIMPARFY	55	A*3002	75	55	107	3	55	55	
111	118	8	LIMPARFY	152	A*2902	71	55	102	3	55	55	
111	118	8	LIMPARFY	55	A*3002	68	55	97	3	55	55	
111	118	8	LIMPARFY	55	B*1501	45	55	65	3	55	55	
111	118	8	LIMPARFY	55	B*1502	50	55	71	3	55	55	
111	118	8	LIMPARFY	55	B*1525	27	55	39	3	55	55	
111	118	8	LIMPARFY	55	B*3501	24	55	34	3	55	55	
111	120	10	LIMPARFYPT	153	A*0206	77	0,18	13	3	55	55	
113	120	8	MPARFYPT	154	A*6802	21	55	4	3	55	55	
113	120	8	MPARFYPT	55	B*0801	58	55	10	3	55	55	
113	120	8	MPARFYPT	55	B*1402	35	55	6	3	55	55	
113	120	8	MPARFYPT	55	B*3503	80	55	14	3	55	55	
113	120	8	MPARFYPT	55	B*5101	75	55	13	3	55	55	
113	120	8	MPARFYPT	55	B*5301	23	55	4	3	55	55	
113	120	8	MPARFYPT	55	B*5501	100	55	18	3	55	55	
113	121	9	MPARFYPTH	155	B*3501	84	1,01	85	3	55	55	
113	121	9	MPARFYPTH	55	B*3503	23	55	23	3	55	55	
113	121	9	MPARFYPTH	55	B*5301	62	55	63	3	55	55	
113	121	9	MPARFYPTH	55	B*5501	57	55	58	3	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
113	121	9	MPARFYPTH	156	B*5601	45	1,38	45	3	156	156	
113	122	10	MPARFYPTHT	157	B*3501	23	0,98	22	3	157	157	
113	122	10	MPARFYPTHT	158	B*3503	19	1,38	19	3	158	158	
113	122	10	MPARFYPTHT	159	B*5301	10	1,38	10	3	159	159	
113	122	10	MPARFYPTHT	160	B*5501	73	1,38	72	3	160	160	
113	122	10	MPARFYPTHT	161	B*5601	81	1,38	79	3	161	161	
115	122	8	ARFYPTHT	162	B*2705	15	1,38	15	3	162	162	
113	123	11	MPARFYPTHTK	163	B*5501	49	1,38	67	3	163	163	
113	123	11	MPARFYPTHTK	164	B*5601	54	1,38	74	3	164	164	
115	123	9	ARFYPTHTK	165	B*2705	87	1,38	119	3	165	165	
116	123	8	RFYPTHTK	166	A*0301	84	1,38	115	3	166	166	
116	123	8	RFYPTHTK	167	A*3001	79	1,38	109	3	167	167	
116	123	8	RFYPTHTK	168	A*3101	76	1,38	105	3	168	168	
116	123	8	RFYPTHTK	169	A*7401	57	1,38	79	3	169	169	
115	124	10	ARFYPTHTKY	170	A*2902	6	1,50	10	3	170	170	
115	124	10	ARFYPTHTKY	171	B*2702	61	1,50	92	3	171	171	
115	124	10	ARFYPTHTKY	172	B*2705	55	1,50	83	3	172	172	
116	124	9	RFYPTHTKY	173	A*2902	92	1,50	138	3	173	173	
116	124	9	RFYPTHTKY	174	A*3002	1	1,50	2	3	174	174	
117	124	8	FYPHTTKY	175	B*3501	51	1,50	76	3	175	175	
115	125	11	ARFYPTHTKYL	176	B*2702	67	1,93	130	3	176	176	
115	125	11	ARFYPTHTKYL	177	B*2705	34	1,93	66	3	177	177	
116	125	10	RFYPTHTKYL	178	B*4801	4	1,93	7	3	178	178	
117	125	9	FYPHTTKYL	179	A*2402	39	1,93	74	3	179	179	
118	125	8	YPHTTKYL	180	B*1402	42	1,93	82	3	180	180	
118	125	8	YPHTTKYL	181	B*3501	17	1,93	33	3	181	181	
118	125	8	YPHTTKYL	182	B*3503	78	1,93	151	3	182	182	
118	125	8	YPHTTKYL	183	B*5101	43	1,93	83	3	183	183	
118	125	8	YPHTTKYL	184	B*5301	51	1,93	98	3	184	184	
118	125	8	YPHTTKYL	185	B*5501	31	1,93	60	3	185	185	
117	126	10	FYPHTTKYLP	186	A*2402	54	0,14	7	3	186	186	
118	126	9	YPHTTKYLP	187	B*5301	2	1,93	0	3	187	187	
117	127	11	FYPHTTKYLPL	188	A*2301	52	0,94	49	3	188	188	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein									Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
117	127	11	FYPHTTKYLPL	..	A*2402	56	..	53	3	..	..
118	127	10	YPHTTKYLPL	171	B*0702	65	..	61	3	..	..
118	127	10	YPHTTKYLPL	..	B*1402	100	..	94	3	..	..
118	127	10	YPHTTKYLPL	..	B*3501	75	..	70	3	..	..
118	127	10	YPHTTKYLPL	..	B*3503	100	..	94	3	..	..
118	127	10	YPHTTKYLPL	..	B*3901	96	..	90	3	..	..
118	127	10	YPHTTKYLPL	..	B*5101	83	..	78	3	..	..
118	127	10	YPHTTKYLPL	..	B*5301	82	..	77	3	..	..
118	127	10	YPHTTKYLPL	..	B*5501	87	..	82	3	..	..
118	127	10	YPHTTKYLPL	..	B*5601	67	..	63	3	..	..
120	127	8	THTKYLPL	172	B*1402	95	..	89	3	..	..
120	127	8	THTKYLPL	..	B*3801	80	..	75	3	..	..
119	128	10	PHTTKYLPD	173	A*3001	46	0,71	33	3	..	..
121	129	9	HTKYLPD	174	A*0301	18	0,41	7	3	..	..
121	129	9	HTKYLPD	..	A*3001	90	..	37	3	..	..
123	131	9	KYLPD	175	A*2301	34	1,23	43	3	..	..
123	131	9	KYLPD	..	A*2402	21	..	26	3	..	..
125	132	8	LPLDKGK	176	B*3501	56	0,80	45	3	..	..
125	134	10	LPLDKGKPY	177	B*3501	87	1,08	94	3	..	..
125	134	10	LPLDKGKPY	..	B*3503	36	..	39	3	..	..
125	134	10	LPLDKGKPY	..	B*5301	39	..	43	3	..	..
125	134	10	LPLDKGKPY	..	B*5501	13	..	14	3	..	..
126	134	9	PLDKGKPY	178	A*0101	25	..	27	3	..	..
127	134	8	LDKGKPY	179	B*3501	9	..	10	3	..	..
125	135	11	LPLDKGKPY	180	B*3501	77	1,16	90	3	..	..
125	135	11	LPLDKGKPY	..	B*5301	57	..	67	3	..	..
126	135	10	PLDKGKPY	181	A*0101	55	..	64	3	..	..
126	135	10	PLDKGKPY	..	A*2902	3	..	4	3	..	..
					Cumulative Class I-BCI score:			6469			
118	127	10	YPHTTKYLPL	171	B*0702	65	0,94	61	4	118	150
118	127	10	YPHTTKYLPL	..	B*1402	100	..	94	4	..	..
118	127	10	YPHTTKYLPL	..	B*3501	75	..	70	4	..	..

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
118	127	10	YPTHTKYLPL	„	B*3503	100	„	94	4	„	„	
118	127	10	YPTHTKYLPL	„	B*3901	96	„	90	4	„	„	
118	127	10	YPTHTKYLPL	„	B*5101	83	„	78	4	„	„	
118	127	10	YPTHTKYLPL	„	B*5301	82	„	77	4	„	„	
118	127	10	YPTHTKYLPL	„	B*5501	87	„	82	4	„	„	
118	127	10	YPTHTKYLPL	„	B*5601	67	„	63	4	„	„	
120	127	8	THTKYLPL	172	B*1402	95	„	89	4	„	„	
120	127	8	THTKYLPL	„	B*3801	80	„	75	4	„	„	
119	128	10	P THTKYLPLD	173	A*3001	46	0,71	33	4	„	„	
121	129	9	HTKYLPLDK	174	A*0301	18	0,41	7	4	„	„	
121	129	9	HTKYLPLDK	„	A*3001	90	„	37	4	„	„	
123	131	9	KYLPLDKGI	175	A*2301	34	1,23	43	4	„	„	
123	131	9	KYLPLDKGI	„	A*2402	21	„	26	4	„	„	
125	132	8	LPLDKGIK	176	B*3501	56	0,80	45	4	„	„	
125	134	10	LPLDKGIKPY	177	B*3501	87	1,08	94	4	„	„	
125	134	10	LPLDKGIKPY	„	B*3503	36	„	39	4	„	„	
125	134	10	LPLDKGIKPY	„	B*5301	39	„	43	4	„	„	
125	134	10	LPLDKGIKPY	„	B*5501	13	„	14	4	„	„	
126	134	9	PLDKGIKPY	178	A*0101	25	„	27	4	„	„	
127	134	8	LDKGIKPY	179	B*3501	9	„	10	4	„	„	
125	135	11	LPLDKGIKPY	180	B*3501	77	1,16	90	4	„	„	
125	135	11	LPLDKGIKPY	„	B*5301	57	„	67	4	„	„	
126	135	10	PLDKGIKPY	181	A*0101	55	„	64	4	„	„	
126	135	10	PLDKGIKPY	„	A*2902	3	„	4	4	„	„	
132	139	8	KPYYPDQV	182	B*5101	65	1,05	68	4	„	„	
132	139	8	KPYYPDQV	„	B*5501	64	„	67	4	„	„	
132	139	8	KPYYPDQV	„	B*5601	59	„	62	4	„	„	
132	140	9	KPYYPDQVV	183	B*0702	36	1,80	65	4	„	„	
132	140	9	KPYYPDQVV	„	B*5101	70	„	126	4	„	„	
132	140	9	KPYYPDQVV	„	B*5501	86	„	155	4	„	„	
132	140	9	KPYYPDQVV	„	B*5601	65	„	118	4	„	„	
135	142	8	YPDQVVNH	184	B*3501	89	1,63	146	4	„	„	
134	143	10	YYPDQVVNH	185	A*0101	23	1,33	30	4	„	„	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
134	143	10	YYPDQVVNHY	187	A*2402	25	1.77	33	4	134	143	
134	143	10	YYPDQVVNHY	188	A*2902	65	1.77	87	4	134	143	
134	143	10	YYPDQVVNHY	189	A*3002	25	1.77	34	4	134	143	
135	143	9	YYPDQVVNHY	190	A*0101	62	1.77	83	4	135	143	
135	143	9	YYPDQVVNHY	191	B*3501	83	1.77	110	4	135	143	
135	143	9	YYPDQVVNHY	192	B*3503	55	1.77	74	4	135	143	
135	143	9	YYPDQVVNHY	193	B*5301	44	1.77	59	4	135	143	
136	143	8	PDQVVNHY	194	B*3501	4	1.77	5	4	136	143	
134	144	11	YYPDQVVNHYF	195	A*2301	100	1.77	177	4	134	144	
135	144	10	YYPDQVVNHYF	196	B*3501	100	1.77	177	4	135	144	
135	144	10	YYPDQVVNHYF	197	B*3503	95	1.77	168	4	135	144	
135	144	10	YYPDQVVNHYF	198	B*5301	100	1.77	177	4	135	144	
137	144	8	DQVVNHYF	199	B*1801	52	1.77	93	4	137	144	
137	147	11	DQVVNHYFQTR	200	A*3303	21	1.63	34	4	137	147	
138	147	10	QVVNHYFQTR	201	A*3101	1	1.77	2	4	138	147	
138	147	10	QVVNHYFQTR	202	A*3303	86	1.77	140	4	138	147	
138	147	10	QVVNHYFQTR	203	A*6801	68	1.77	110	4	138	147	
138	147	10	QVVNHYFQTR	204	A*7401	17	1.77	28	4	138	147	
139	147	9	VVNHYFQTR	205	A*3101	87	1.77	143	4	139	147	
139	147	9	VVNHYFQTR	206	A*3303	73	1.77	120	4	139	147	
139	147	9	VVNHYFQTR	207	A*7401	72	1.77	117	4	139	147	
139	149	11	VVNHYFQTRHY	208	A*0101	42	1.90	79	4	139	149	
139	149	11	VVNHYFQTRHY	209	A*2902	70	1.77	133	4	139	149	
139	149	11	VVNHYFQTRHY	210	A*3002	90	1.77	172	4	139	149	
139	149	11	VVNHYFQTRHY	211	B*1501	50	1.77	95	4	139	149	
139	149	11	VVNHYFQTRHY	212	B*1502	44	1.77	85	4	139	149	
141	149	9	NHYFQTRHY	213	B*3801	16	1.77	31	4	141	149	
142	149	8	HYFQTRHY	214	A*2902	25	1.77	48	4	142	149	
142	149	8	HYFQTRHY	215	A*3002	44	1.77	83	4	142	149	
141	150	10	NHYFQTRHYL	216	B*1402	94	1.93	181	4	141	150	
141	150	10	NHYFQTRHYL	217	B*3801	53	1.77	102	4	141	150	
141	150	10	NHYFQTRHYL	218	B*3901	88	1.77	170	4	141	150	
142	150	9	HYFQTRHYL	219	A*2301	69	1.77	133	4	142	150	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
142	150	9	HYFQTRHYL	199	B*1402	34	199	66	4	139	177	
142	150	9	HYFQTRHYL	199	B*3901	3	199	5	4	139	177	
143	150	8	YFQTRHYL	199	A*2301	74	199	143	4	139	177	
143	150	8	YFQTRHYL	199	A*2402	74	199	142	4	139	177	
143	150	8	YFQTRHYL	199	B*0801	93	199	180	4	139	177	
Cumulative Class I-BCI score:									6169			
139	149	11	VNHYFQTRHY	194	A*0101	42	1,90	79	5	139	177	
139	149	11	VNHYFQTRHY	199	A*2902	70	199	133	5	139	177	
139	149	11	VNHYFQTRHY	199	A*3002	90	199	172	5	139	177	
139	149	11	VNHYFQTRHY	199	B*1501	50	199	95	5	139	177	
139	149	11	VNHYFQTRHY	199	B*1502	44	199	85	5	139	177	
141	149	9	NHYFQTRHY	195	B*3801	16	199	31	5	139	177	
142	149	8	HYFQTRHY	196	A*2902	25	199	48	5	139	177	
142	149	8	HYFQTRHY	199	A*3002	44	199	83	5	139	177	
141	150	10	NHYFQTRHYL	197	B*1402	94	1,93	181	5	139	177	
141	150	10	NHYFQTRHYL	199	B*3801	53	199	102	5	139	177	
141	150	10	NHYFQTRHYL	199	B*3901	88	199	170	5	139	177	
142	150	9	HYFQTRHYL	198	A*2301	69	199	133	5	139	177	
142	150	9	HYFQTRHYL	199	B*1402	34	199	66	5	139	177	
142	150	9	HYFQTRHYL	199	B*3901	3	199	5	5	139	177	
143	150	8	YFQTRHYL	199	A*2301	74	199	143	5	139	177	
143	150	8	YFQTRHYL	199	A*2402	74	199	142	5	139	177	
143	150	8	YFQTRHYL	199	B*0801	93	199	180	5	139	177	
142	151	10	HYFQTRHYLH	200	A*2301	33	0,39	13	5	139	177	
142	151	10	HYFQTRHYLH	199	A*2402	49	199	19	5	139	177	
142	151	10	HYFQTRHYLH	199	A*2902	16	199	6	5	139	177	
143	151	9	YFQTRHYLH	201	A*2902	57	199	22	5	139	177	
143	153	11	YFQTRHYLHTL	202	A*2301	98	1,22	120	5	139	177	
143	153	11	YFQTRHYLHTL	199	A*2402	100	199	122	5	139	177	
143	153	11	YFQTRHYLHTL	199	B*0801	100	199	122	5	139	177	
144	153	10	FQTRHYLHTL	203	A*0201	27	199	33	5	139	177	
144	153	10	FQTRHYLHTL	199	B*1301	63	199	77	5	139	177	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
144	153	10	FQTRHYLHTL	22	B*1402	52	22	63	5	22	22	
144	153	10	FQTRHYLHTL	22	B*3701	62	22	75	5	22	22	
144	153	10	FQTRHYLHTL	22	B*3801	71	22	87	5	22	22	
144	153	10	FQTRHYLHTL	22	B*3901	94	22	114	5	22	22	
144	153	10	FQTRHYLHTL	22	B*4801	81	22	98	5	22	22	
145	153	9	QTRHYLHTL	204	A*2501	65	22	79	5	22	22	
146	153	8	TRHYLHTL	205	B*1402	72	22	87	5	22	22	
146	153	8	TRHYLHTL	22	B*2702	60	22	73	5	22	22	
146	153	8	TRHYLHTL	22	B*2705	70	22	85	5	22	22	
144	154	11	FQTRHYLHTLW	206	B*1301	68	1,50	101	5	22	22	
144	154	11	FQTRHYLHTLW	22	B*2702	37	22	56	5	22	22	
145	154	10	QTRHYLHTLW	207	B*4402	35	22	52	5	22	22	
145	154	10	QTRHYLHTLW	22	B*5802	70	22	104	5	22	22	
146	154	9	TRHYLHTLW	208	B*2702	76	22	114	5	22	22	
147	154	8	RHYLHTLW	209	A*2301	47	22	70	5	22	22	
147	154	8	RHYLHTLW	22	A*2402	35	22	52	5	22	22	
147	154	8	RHYLHTLW	22	B*2702	99	22	148	5	22	22	
147	154	8	RHYLHTLW	22	B*3801	98	22	147	5	22	22	
147	154	8	RHYLHTLW	22	B*5701	35	22	52	5	22	22	
147	154	8	RHYLHTLW	22	B*5801	22	22	33	5	22	22	
147	154	8	RHYLHTLW	22	B*5802	26	22	39	5	22	22	
145	155	11	QTRHYLHTLWK	210	A*0301	54	0,72	39	5	22	22	
145	155	11	QTRHYLHTLWK	22	A*1101	35	22	25	5	22	22	
145	155	11	QTRHYLHTLWK	22	A*3001	96	22	69	5	22	22	
146	155	10	TRHYLHTLWK	211	B*2705	36	22	26	5	22	22	
147	155	9	RHYLHTLWK	212	A*0301	70	22	51	5	22	22	
147	155	9	RHYLHTLWK	22	B*2702	7	22	5	5	22	22	
148	155	8	HYLHTLWK	213	A*3101	29	22	21	5	22	22	
146	156	11	TRHYLHTLWKA	214	B*2705	58	1,23	72	5	22	22	
148	156	9	HYLHTLWKA	215	A*2301	31	22	38	5	22	22	
147	157	11	RHYLHTLWKAG	216	B*2705	6	0,73	4	5	22	22	
148	157	10	HYLHTLWKAG	217	A*3201	74	22	54	5	22	22	
148	158	11	HYLHTLWKAGI	218	A*2301	93	0,63	59	5	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
148	158	11	HYLHTLWKAGI	22	A*2402	95	22	60	5	22	22	
149	158	10	YLHTLWKAGI	219	A*0201	7	22	4	5	22	22	
151	158	8	HTLWKAGI	220	A*3201	62	22	39	5	22	22	
149	159	11	YLHTLWKAGIL	221	B*0801	88	0,85	75	5	22	22	
149	159	11	YLHTLWKAGIL	22	B*3901	22	22	19	5	22	22	
150	159	10	LHTLWKAGIL	222	B*0801	69	22	59	5	22	22	
150	159	10	LHTLWKAGIL	22	B*3801	51	22	43	5	22	22	
150	159	10	LHTLWKAGIL	22	B*3901	34	22	29	5	22	22	
151	159	9	HTLWKAGIL	223	B*5802	1	22	1	5	22	22	
151	160	10	HTLWKAGILY	224	A*0101	72	1,87	134	5	22	22	
151	160	10	HTLWKAGILY	22	A*0301	7	22	12	5	22	22	
151	160	10	HTLWKAGILY	22	A*2501	47	22	88	5	22	22	
151	160	10	HTLWKAGILY	22	A*2601	67	22	125	5	22	22	
151	160	10	HTLWKAGILY	22	A*2902	2	22	3	5	22	22	
151	160	10	HTLWKAGILY	22	A*3002	49	22	92	5	22	22	
152	160	9	TLWKAGILY	225	A*0301	36	22	67	5	22	22	
152	160	9	TLWKAGILY	22	A*2902	78	22	145	5	22	22	
152	160	9	TLWKAGILY	22	A*3002	4	22	8	5	22	22	
153	160	8	LWKAGILY	226	A*2902	56	22	104	5	22	22	
153	160	8	LWKAGILY	22	A*3002	85	22	158	5	22	22	
153	160	8	LWKAGILY	22	B*3501	8	22	15	5	22	22	
151	161	11	HTLWKAGILYK	227	A*0301	89	1,41	125	5	22	22	
151	161	11	HTLWKAGILYK	22	A*1101	100	22	141	5	22	22	
151	161	11	HTLWKAGILYK	22	A*3001	78	22	110	5	22	22	
151	161	11	HTLWKAGILYK	22	A*3101	46	22	64	5	22	22	
151	161	11	HTLWKAGILYK	22	A*3303	25	22	36	5	22	22	
151	161	11	HTLWKAGILYK	22	A*6801	75	22	106	5	22	22	
151	161	11	HTLWKAGILYK	22	A*7401	83	22	117	5	22	22	
152	161	10	TLWKAGILYK	228	A*0301	87	22	122	5	22	22	
152	161	10	TLWKAGILYK	22	A*1101	59	22	83	5	22	22	
152	161	10	TLWKAGILYK	22	A*7401	71	22	100	5	22	22	
153	161	9	LWKAGILYK	229	A*3001	57	22	80	5	22	22	
152	162	11	TLWKAGILYKR	230	A*3101	61	1,49	91	5	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
152	162	11	TLWKAGILYKR	22	A*3303	72	22	107	5	22	22	
152	162	11	TLWKAGILYKR	22	A*7401	82	22	122	5	22	22	
153	162	10	LWKAGILYKR	231	A*3101	86	22	128	5	22	22	
153	162	10	LWKAGILYKR	22	A*3303	59	22	88	5	22	22	
155	162	8	KAGILYKR	232	A*3101	67	22	100	5	22	22	
155	162	8	KAGILYKR	22	A*7401	27	22	40	5	22	22	
158	166	9	ILYKRETTTR	233	A*0301	66	1,75	115	5	22	22	
158	166	9	ILYKRETTTR	22	A*3101	23	22	40	5	22	22	
158	166	9	ILYKRETTTR	22	A*3303	51	22	89	5	22	22	
158	166	9	ILYKRETTTR	22	A*7401	90	22	158	5	22	22	
158	168	11	ILYKRETTRSA	234	B*0801	56	1,80	100	5	22	22	
160	170	11	YKRETTTRSASF	235	B*0702	17	1,82	32	5	22	22	
160	170	11	YKRETTTRSASF	22	B*0801	81	22	148	5	22	22	
160	170	11	YKRETTTRSASF	22	B*1402	68	22	123	5	22	22	
160	170	11	YKRETTTRSASF	22	B*1501	53	22	97	5	22	22	
160	170	11	YKRETTTRSASF	22	B*1502	65	22	118	5	22	22	
160	170	11	YKRETTTRSASF	22	B*1525	46	22	83	5	22	22	
161	170	10	KRETTTRSASF	236	B*2702	53	22	97	5	22	22	
162	170	9	RETTTRSASF	237	B*4001	57	22	103	5	22	22	
162	170	9	RETTTRSASF	22	B*4402	88	22	161	5	22	22	
162	170	9	RETTTRSASF	22	B*4403	60	22	109	5	22	22	
162	170	9	RETTTRSASF	22	B*5001	44	22	80	5	22	22	
163	170	8	ETTTRSASF	238	A*2501	100	22	182	5	22	22	
163	170	8	ETTTRSASF	22	A*2601	100	22	182	5	22	22	
166	175	10	RSASFCGSPY	239	A*0101	79	1,16	92	5	22	22	
166	175	10	RSASFCGSPY	22	A*2501	45	22	52	5	22	22	
166	175	10	RSASFCGSPY	22	B*1501	94	22	108	5	22	22	
166	175	10	RSASFCGSPY	22	B*1502	78	22	90	5	22	22	
166	175	10	RSASFCGSPY	22	B*1525	80	22	92	5	22	22	
166	175	10	RSASFCGSPY	22	B*4403	32	22	37	5	22	22	
166	175	10	RSASFCGSPY	22	B*4601	84	22	97	5	22	22	
166	175	10	RSASFCGSPY	22	B*5802	68	22	79	5	22	22	
167	175	9	SASFCGSPY	240	A*3002	79	22	91	5	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein									Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
167	175	9	SASFCGSPY	22	B*3501	81	22	94	5	22	22
168	175	8	ASFCGSPY	241	A*1101	70	22	80	5	22	22
168	175	8	ASFCGSPY	22	A*2902	54	22	62	5	22	22
168	175	8	ASFCGSPY	22	B*5701	44	22	51	5	22	22
167	176	10	SASFCGSPYS	242	A*3001	8	0,16	1	5	22	22
167	176	10	SASFCGSPYS	22	B*5701	76	22	12	5	22	22
167	176	10	SASFCGSPYS	22	B*5801	76	22	12	5	22	22
168	176	9	ASFCGSPYS	243	B*5802	19	22	3	5	22	22
167	177	11	SASFCGSPYSW	244	B*5301	79	1,90	150	5	22	22
167	177	11	SASFCGSPYSW	22	B*5701	94	22	179	5	22	22
167	177	11	SASFCGSPYSW	22	B*5801	100	22	190	5	22	22
167	177	11	SASFCGSPYSW	22	B*5802	100	22	190	5	22	22
168	177	10	ASFCGSPYSW	245	B*4402	69	22	132	5	22	22
168	177	10	ASFCGSPYSW	22	B*4403	28	22	53	5	22	22
168	177	10	ASFCGSPYSW	22	B*5802	99	22	188	5	22	22
169	177	9	SFCGSPYSW	246	A*2301	26	22	49	5	22	22
					Cumulative BCI Class Iscore:			11815			
143	150	8	YFQTRHYL	199	A*2301	74	1,93	143	6	143	177
143	150	8	YFQTRHYL	22	A*2402	74	22	142	6	22	22
143	150	8	YFQTRHYL	22	B*0801	93	22	180	6	22	22
142	151	10	HYFQTRHYLH	200	A*2301	33	0,39	13	6	22	22
142	151	10	HYFQTRHYLH	22	A*2402	49	22	19	6	22	22
142	151	10	HYFQTRHYLH	22	A*2902	16	22	6	6	22	22
143	151	9	YFQTRHYLH	201	A*2902	57	22	22	6	22	22
143	153	11	YFQTRHYLHTL	202	A*2301	98	1,22	120	6	22	22
143	153	11	YFQTRHYLHTL	22	A*2402	100	22	122	6	22	22
143	153	11	YFQTRHYLHTL	22	B*0801	100	22	122	6	22	22
144	153	10	FQTRhYLHTL	203	A*0201	27	22	33	6	22	22
144	153	10	FQTRHYLHTL	22	B*1301	63	22	77	6	22	22
144	153	10	FQTRHYLHTL	22	B*1402	52	22	63	6	22	22
144	153	10	FQTRHYLHTL	22	B*3701	62	22	75	6	22	22
144	153	10	FQTRHYLHTL	22	B*3801	71	22	87	6	22	22

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
144	153	10	FQTRHYLHTL	22	B*3901	94	22	114	6	22	22	
144	153	10	FQTRHYLHTL	22	B*4801	81	22	98	6	22	22	
145	153	9	QTRHYLHTL	204	A*2501	65	22	79	6	22	22	
146	153	8	TRHYLHTL	205	B*1402	72	22	87	6	22	22	
146	153	8	TRHYLHTL	22	B*2702	60	22	73	6	22	22	
146	153	8	TRHYLHTL	22	B*2705	70	22	85	6	22	22	
144	154	11	FQTRHYLHTLW	206	B*1301	68	1,50	101	6	22	22	
144	154	11	FQTRHYLHTLW	22	B*2702	37	22	56	6	22	22	
145	154	10	QTRHYLHTLW	207	B*4402	35	22	52	6	22	22	
145	154	10	QTRHYLHTLW	22	B*5802	70	22	104	6	22	22	
146	154	9	TRHYLHTLW	208	B*2702	76	22	114	6	22	22	
147	154	8	RHYLHTLW	209	A*2301	47	22	70	6	22	22	
147	154	8	RHYLHTLW	22	A*2402	35	22	52	6	22	22	
147	154	8	RHYLHTLW	22	B*2702	99	22	148	6	22	22	
147	154	8	RHYLHTLW	22	B*3801	98	22	147	6	22	22	
147	154	8	RHYLHTLW	22	B*5701	35	22	52	6	22	22	
147	154	8	RHYLHTLW	22	B*5801	22	22	33	6	22	22	
147	154	8	RHYLHTLW	22	B*5802	26	22	39	6	22	22	
145	155	11	QTRHYLHTLWK	210	A*0301	54	0,72	39	6	22	22	
145	155	11	QTRHYLHTLWK	22	A*1101	35	22	25	6	22	22	
145	155	11	QTRHYLHTLWK	22	A*3001	96	22	69	6	22	22	
146	155	10	TRHYLHTLWK	211	B*2705	36	22	26	6	22	22	
147	155	9	RHYLHTLWK	212	A*0301	70	22	51	6	22	22	
147	155	9	RHYLHTLWK	22	B*2702	7	22	5	6	22	22	
148	155	8	HYLHTLWK	213	A*3101	29	22	21	6	22	22	
146	156	11	TRHYLHTLWKA	214	B*2705	58	1,23	72	6	22	22	
148	156	9	HYLHTLWKA	215	A*2301	31	22	38	6	22	22	
147	157	11	RHYLHTLWKAG	216	B*2705	6	0,73	4	6	22	22	
148	157	10	HYLHTLWKAG	217	A*3201	74	22	54	6	22	22	
148	158	11	HYLHTLWKAGI	218	A*2301	93	0,63	59	6	22	22	
148	158	11	HYLHTLWKAGI	22	A*2402	95	22	60	6	22	22	
149	158	10	YLHTLWKAGI	219	A*0201	7	22	4	6	22	22	
151	158	8	HTLWKAGI	220	A*3201	62	22	39	6	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
149	159	11	YLHTLWKAGIL	221	B*0801	88	0,85	75	6	55	55	
149	159	11	YLHTLWKAGIL	22	B*3901	22	22	19	6	55	55	
150	159	10	LHTLWKAGIL	222	B*0801	69	22	59	6	55	55	
150	159	10	LHTLWKAGIL	22	B*3801	51	22	43	6	55	55	
150	159	10	LHTLWKAGIL	22	B*3901	34	22	29	6	55	55	
151	159	9	HTLWKAGIL	223	B*5802	1	22	1	6	55	55	
151	160	10	HTLWKAGILY	224	A*0101	72	1,87	134	6	55	55	
151	160	10	HTLWKAGILY	22	A*0301	7	22	12	6	55	55	
151	160	10	HTLWKAGILY	22	A*2501	47	22	88	6	55	55	
151	160	10	HTLWKAGILY	22	A*2601	67	22	125	6	55	55	
151	160	10	HTLWKAGILY	22	A*2902	2	22	3	6	55	55	
151	160	10	HTLWKAGILY	22	A*3002	49	22	92	6	55	55	
152	160	9	TLWKAGILY	225	A*0301	36	22	67	6	55	55	
152	160	9	TLWKAGILY	22	A*2902	78	22	145	6	55	55	
152	160	9	TLWKAGILY	22	A*3002	4	22	8	6	55	55	
153	160	8	LWKAGILY	226	A*2902	56	22	104	6	55	55	
153	160	8	LWKAGILY	22	A*3002	85	22	158	6	55	55	
153	160	8	LWKAGILY	22	B*3501	8	22	15	6	55	55	
151	161	11	HTLWKAGILYK	227	A*0301	89	1,41	125	6	55	55	
151	161	11	HTLWKAGILYK	22	A*1101	100	22	141	6	55	55	
151	161	11	HTLWKAGILYK	22	A*3001	78	22	110	6	55	55	
151	161	11	HTLWKAGILYK	22	A*3101	46	22	64	6	55	55	
151	161	11	HTLWKAGILYK	22	A*3303	25	22	36	6	55	55	
151	161	11	HTLWKAGILYK	22	A*6801	75	22	106	6	55	55	
151	161	11	HTLWKAGILYK	22	A*7401	83	22	117	6	55	55	
152	161	10	TLWKAGILYK	228	A*0301	87	22	122	6	55	55	
152	161	10	TLWKAGILYK	22	A*1101	59	22	83	6	55	55	
152	161	10	TLWKAGILYK	22	A*7401	71	22	100	6	55	55	
153	161	9	LWKAGILYK	229	A*3001	57	22	80	6	55	55	
152	162	11	TLWKAGILYKR	230	A*3101	61	1,49	91	6	55	55	
152	162	11	TLWKAGILYKR	22	A*3303	72	22	107	6	55	55	
152	162	11	TLWKAGILYKR	22	A*7401	82	22	122	6	55	55	
153	162	10	LWKAGILYKR	231	A*3101	86	22	128	6	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
153	162	10	LWKAGILYKR	232	A*3303	59	22	88	6	22	22	
155	162	8	KAGILYKR	232	A*3101	67	22	100	6	22	22	
155	162	8	KAGILYKR	233	A*7401	27	22	40	6	22	22	
158	166	9	ILYKRETTTR	233	A*0301	66	1,75	115	6	22	22	
158	166	9	ILYKRETTTR	233	A*3101	23	22	40	6	22	22	
158	166	9	ILYKRETTTR	233	A*3303	51	22	89	6	22	22	
158	166	9	ILYKRETTTR	233	A*7401	90	22	158	6	22	22	
158	168	11	ILYKRETTTRSA	234	B*0801	56	1,80	100	6	22	22	
160	170	11	YKRETTTRSASF	235	B*0702	17	1,82	32	6	22	22	
160	170	11	YKRETTTRSASF	235	B*0801	81	22	148	6	22	22	
160	170	11	YKRETTTRSASF	235	B*1402	68	22	123	6	22	22	
160	170	11	YKRETTTRSASF	235	B*1501	53	22	97	6	22	22	
160	170	11	YKRETTTRSASF	235	B*1502	65	22	118	6	22	22	
160	170	11	YKRETTTRSASF	235	B*1525	46	22	83	6	22	22	
161	170	10	KRETTTRSASF	236	B*2702	53	22	97	6	22	22	
162	170	9	RETTTRSASF	237	B*4001	57	22	103	6	22	22	
162	170	9	RETTTRSASF	237	B*4402	88	22	161	6	22	22	
162	170	9	RETTTRSASF	237	B*4403	60	22	109	6	22	22	
162	170	9	RETTTRSASF	237	B*5001	44	22	80	6	22	22	
163	170	8	ETTTTRSASF	238	A*2501	100	22	182	6	22	22	
163	170	8	ETTTTRSASF	238	A*2601	100	22	182	6	22	22	
166	175	10	RSASFCGSPY	239	A*0101	79	1,16	92	6	22	22	
166	175	10	RSASFCGSPY	239	A*2501	45	22	52	6	22	22	
166	175	10	RSASFCGSPY	239	B*1501	94	22	108	6	22	22	
166	175	10	RSASFCGSPY	239	B*1502	78	22	90	6	22	22	
166	175	10	RSASFCGSPY	239	B*1525	80	22	92	6	22	22	
166	175	10	RSASFCGSPY	239	B*4403	32	22	37	6	22	22	
166	175	10	RSASFCGSPY	239	B*4601	84	22	97	6	22	22	
166	175	10	RSASFCGSPY	239	B*5802	68	22	79	6	22	22	
167	175	9	SASFCGSPY	240	A*3002	79	22	91	6	22	22	
167	175	9	SASFCGSPY	241	B*3501	81	22	94	6	22	22	
168	175	8	ASFCGSPY	241	A*1101	70	22	80	6	22	22	
168	175	8	ASFCGSPY	241	A*2902	54	22	62	6	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
168	175	8	ASFCGSPY	22	B*5701	44	22	51	6	22	22
167	176	10	SASFCGSPYS	242	A*3001	8	0,16	1	6	22	22
167	176	10	SASFCGSPYS	22	B*5701	76	22	12	6	22	22
167	176	10	SASFCGSPYS	22	B*5801	76	22	12	6	22	22
168	176	9	ASFCGSPYS	243	B*5802	19	22	3	6	22	22
167	177	11	SASFCGSPYSW	244	B*5301	79	1,90	150	6	22	22
167	177	11	SASFCGSPYSW	22	B*5701	94	22	179	6	22	22
167	177	11	SASFCGSPYSW	22	B*5801	100	22	190	6	22	22
167	177	11	SASFCGSPYSW	22	B*5802	100	22	190	6	22	22
168	177	10	ASFCGSPYSW	245	B*4402	69	22	132	6	22	22
168	177	10	ASFCGSPYSW	22	B*4403	28	22	53	6	22	22
168	177	10	ASFCGSPYSW	22	B*5802	99	22	188	6	22	22
169	177	9	SFCGSPYSW	246	A*2301	26	22	49	6	22	22
Cumulative Class I-BCI score:									10432		
137	147	11	DQVNHYFQTR	191	A*3303	21	1,63	34	7	137	170
138	147	10	QVNHYFQTR	192	A*3101	1	22	2	7	22	22
138	147	10	QVNHYFQTR	22	A*3303	86	22	140	7	22	22
138	147	10	QVNHYFQTR	22	A*6801	68	22	110	7	22	22
138	147	10	QVNHYFQTR	22	A*7401	17	22	28	7	22	22
139	147	9	VVNHYFQTR	193	A*3101	87	22	143	7	22	22
139	147	9	VVNHYFQTR	22	A*3303	73	22	120	7	22	22
139	147	9	VVNHYFQTR	22	A*7401	72	22	117	7	22	22
139	149	11	VVNHYFQTRHY	194	A*0101	42	1,90	79	7	22	22
139	149	11	VVNHYFQTRHY	22	A*2902	70	22	133	7	22	22
139	149	11	VVNHYFQTRHY	22	A*3002	90	22	172	7	22	22
139	149	11	VVNHYFQTRHY	22	B*1501	50	22	95	7	22	22
139	149	11	VVNHYFQTRHY	22	B*1502	44	22	85	7	22	22
141	149	9	NHYFQTRHY	195	B*3801	16	22	31	7	22	22
142	149	8	HYFQTRHY	196	A*2902	25	22	48	7	22	22
142	149	8	HYFQTRHY	22	A*3002	44	22	83	7	22	22
141	150	10	NHYFQTRHYL	197	B*1402	94	1,93	181	7	22	22
141	150	10	NHYFQTRHYL	22	B*3801	53	22	102	7	22	22

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
141	150	10	NHYFQTRHYL	198	B*3901	88	170	133	7	170	133	
142	150	9	HYFQTRHYL	198	A*2301	69	133	66	7	133	66	
142	150	9	HYFQTRHYL	198	B*1402	34	66	5	7	66	5	
142	150	9	HYFQTRHYL	198	B*3901	3	5	22	7	5	22	
143	150	8	YFQTRHYL	199	A*2301	74	143	120	7	143	120	
143	150	8	YFQTRHYL	199	A*2402	74	142	122	7	142	122	
143	150	8	YFQTRHYL	199	B*0801	93	180	33	7	180	33	
142	151	10	HYFQTRHYLH	200	A*2301	33	0,39	13	7	13	39	
142	151	10	HYFQTRHYLH	200	A*2402	49	19	19	7	19	19	
142	151	10	HYFQTRHYLH	200	A*2902	16	6	6	7	6	6	
143	151	9	YFQTRHYLH	201	A*2902	57	22	22	7	22	22	
143	153	11	YFQTRHYLHTL	202	A*2301	98	1,22	120	7	120	120	
143	153	11	YFQTRHYLHTL	202	A*2402	100	122	122	7	122	122	
143	153	11	YFQTRHYLHTL	202	B*0801	100	122	122	7	122	122	
144	153	10	FQTRHYLHTL	203	A*0201	27	33	33	7	33	33	
144	153	10	FQTRHYLHTL	203	B*1301	63	77	77	7	77	77	
144	153	10	FQTRHYLHTL	203	B*1402	52	63	63	7	63	63	
144	153	10	FQTRHYLHTL	203	B*3701	62	75	75	7	75	75	
144	153	10	FQTRHYLHTL	203	B*3801	71	87	87	7	87	87	
144	153	10	FQTRHYLHTL	203	B*3901	94	114	114	7	114	114	
144	153	10	FQTRHYLHTL	203	B*4801	81	98	98	7	98	98	
145	153	9	QTRHYLHTL	204	A*2501	65	79	79	7	79	79	
146	153	8	TRHYLHTL	205	B*1402	72	87	87	7	87	87	
146	153	8	TRHYLHTL	205	B*2702	60	73	73	7	73	73	
146	153	8	TRHYLHTL	205	B*2705	70	85	85	7	85	85	
144	154	11	FQTRHYLHTLW	206	B*1301	68	1,50	101	7	101	101	
144	154	11	FQTRHYLHTLW	206	B*2702	37	56	56	7	56	56	
145	154	10	QTRHYLHTLW	207	B*4402	35	52	52	7	52	52	
145	154	10	QTRHYLHTLW	207	B*5802	70	104	104	7	104	104	
146	154	9	TRHYLHTLW	208	B*2702	76	114	114	7	114	114	
147	154	8	RHYLHTLW	209	A*2301	47	70	70	7	70	70	
147	154	8	RHYLHTLW	209	A*2402	35	52	52	7	52	52	
147	154	8	RHYLHTLW	209	B*2702	99	148	148	7	148	148	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
147	154	8	RHYLHTLW	22	B*3801	98	22	147	7	22	22	
147	154	8	RHYLHTLW	22	B*5701	35	22	52	7	22	22	
147	154	8	RHYLHTLW	22	B*5801	22	22	33	7	22	22	
147	154	8	RHYLHTLW	22	B*5802	26	22	39	7	22	22	
145	155	11	QTRHYLHTLWK	210	A*0301	54	0,72	39	7	22	22	
145	155	11	QTRHYLHTLWK	22	A*1101	35	22	25	7	22	22	
145	155	11	QTRHYLHTLWK	22	A*3001	96	22	69	7	22	22	
146	155	10	TRHYLHTLWK	211	B*2705	36	22	26	7	22	22	
147	155	9	RHYLHTLWK	212	A*0301	70	22	51	7	22	22	
147	155	9	RHYLHTLWK	22	B*2702	7	22	5	7	22	22	
148	155	8	HYLHTLWK	213	A*3101	29	22	21	7	22	22	
146	156	11	TRHYLHTLWKA	214	B*2705	58	1,23	72	7	22	22	
148	156	9	HYLHTLWKA	215	A*2301	31	22	38	7	22	22	
147	157	11	RHYLHTLWKAG	216	B*2705	6	0,73	4	7	22	22	
148	157	10	HYLHTLWKAG	217	A*3201	74	22	54	7	22	22	
148	158	11	HYLHTLWKAGI	218	A*2301	93	0,63	59	7	22	22	
148	158	11	HYLHTLWKAGI	22	A*2402	95	22	60	7	22	22	
149	158	10	YLHTLWKAGI	219	A*0201	7	22	4	7	22	22	
151	158	8	HTLWKAGI	220	A*3201	62	22	39	7	22	22	
149	159	11	YLHTLWKAGIL	221	B*0801	88	0,85	75	7	22	22	
149	159	11	YLHTLWKAGIL	22	B*3901	22	22	19	7	22	22	
150	159	10	LHTLWKAGIL	222	B*0801	69	22	59	7	22	22	
150	159	10	LHTLWKAGIL	22	B*3801	51	22	43	7	22	22	
150	159	10	LHTLWKAGIL	22	B*3901	34	22	29	7	22	22	
151	159	9	HTLWKAGIL	223	B*5802	1	22	1	7	22	22	
151	160	10	HTLWKAGILY	224	A*0101	72	1,87	134	7	22	22	
151	160	10	HTLWKAGILY	22	A*0301	7	22	12	7	22	22	
151	160	10	HTLWKAGILY	22	A*2501	47	22	88	7	22	22	
151	160	10	HTLWKAGILY	22	A*2601	67	22	125	7	22	22	
151	160	10	HTLWKAGILY	22	A*2902	2	22	3	7	22	22	
151	160	10	HTLWKAGILY	22	A*3002	49	22	92	7	22	22	
152	160	9	TLWKAGILY	225	A*0301	36	22	67	7	22	22	
152	160	9	TLWKAGILY	22	A*2902	78	22	145	7	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
152	160	9	TLWKAGILY	22	A*3002	4	22	8	7	22	22	
153	160	8	LWKAGILY	226	A*2902	56	22	104	7	22	22	
153	160	8	LWKAGILY	22	A*3002	85	22	158	7	22	22	
153	160	8	LWKAGILY	22	B*3501	8	22	15	7	22	22	
151	161	11	HTLWKAGILYK	227	A*0301	89	1,41	125	7	22	22	
151	161	11	HTLWKAGILYK	22	A*1101	100	22	141	7	22	22	
151	161	11	HTLWKAGILYK	22	A*3001	78	22	110	7	22	22	
151	161	11	HTLWKAGILYK	22	A*3101	46	22	64	7	22	22	
151	161	11	HTLWKAGILYK	22	A*3303	25	22	36	7	22	22	
151	161	11	HTLWKAGILYK	22	A*6801	75	22	106	7	22	22	
151	161	11	HTLWKAGILYK	22	A*7401	83	22	117	7	22	22	
152	161	10	TLWKAGILYK	228	A*0301	87	22	122	7	22	22	
152	161	10	TLWKAGILYK	22	A*1101	59	22	83	7	22	22	
152	161	10	TLWKAGILYK	22	A*7401	71	22	100	7	22	22	
153	161	9	LWKAGILYK	229	A*3001	57	22	80	7	22	22	
152	162	11	TLWKAGILYKR	230	A*3101	61	1,49	91	7	22	22	
152	162	11	TLWKAGILYKR	22	A*3303	72	22	107	7	22	22	
152	162	11	TLWKAGILYKR	22	A*7401	82	22	122	7	22	22	
153	162	10	LWKAGILYKR	231	A*3101	86	22	128	7	22	22	
153	162	10	LWKAGILYKR	22	A*3303	59	22	88	7	22	22	
155	162	8	KAGILYKR	232	A*3101	67	22	100	7	22	22	
155	162	8	KAGILYKR	22	A*7401	27	22	40	7	22	22	
158	166	9	ILYKRETTTR	233	A*0301	66	1,75	115	7	22	22	
158	166	9	ILYKRETTTR	22	A*3101	23	22	40	7	22	22	
158	166	9	ILYKRETTTR	22	A*3303	51	22	89	7	22	22	
158	166	9	ILYKRETTTR	22	A*7401	90	22	158	7	22	22	
158	168	11	ILYKRETTTRSA	234	B*0801	56	1,80	100	7	22	22	
160	170	11	YKRETTTRSASF	235	B*0702	17	1,82	32	7	22	22	
160	170	11	YKRETTTRSASF	22	B*0801	81	22	148	7	22	22	
160	170	11	YKRETTTRSASF	22	B*1402	68	22	123	7	22	22	
160	170	11	YKRETTTRSASF	22	B*1501	53	22	97	7	22	22	
160	170	11	YKRETTTRSASF	22	B*1502	65	22	118	7	22	22	
160	170	11	YKRETTTRSASF	22	B*1525	46	22	83	7	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
161	170	10	KRETRRSASF	236	B*2702	53	22	97	7	22	22	
162	170	9	RETRRSASF	237	B*4001	57	22	103	7	22	22	
162	170	9	RETRRSASF	22	B*4402	88	22	161	7	22	22	
162	170	9	RETRRSASF	22	B*4403	60	22	109	7	22	22	
162	170	9	RETRRSASF	22	B*5001	44	22	80	7	22	22	
163	170	8	ETTRRSASF	238	A*2501	100	22	182	7	22	22	
163	170	8	ETTRRSASF	22	A*2601	100	22	182	7	22	22	
					Cumulative Class I-BCI score:			10325				
316	326	11	SQSQGSVSSCW	247	B*4402	46	1,49	69	8	316	347	
316	326	11	SQSQGSVSSCW	22	B*4403	24	22	36	8	22	22	
317	326	10	QSQGSVSSCW	248	B*4402	54	22	80	8	22	22	
317	326	10	QSQGSVSSCW	22	B*5802	64	22	95	8	22	22	
319	326	8	QGSVSSCW	249	B*5801	15	22	23	8	22	22	
317	327	11	QSQGSVSSCWW	250	B*5701	79	1,02	80	8	22	22	
317	327	11	QSQGSVSSCWW	22	B*5801	88	22	90	8	22	22	
317	327	11	QSQGSVSSCWW	22	B*5802	75	22	77	8	22	22	
319	327	9	QGSVSSCWW	251	B*5701	38	22	39	8	22	22	
319	327	9	QGSVSSCWW	22	B*5801	10	22	10	8	22	22	
320	327	8	GSVSSCWW	252	B*5701	92	22	94	8	22	22	
320	327	8	GSVSSCWW	22	B*5801	95	22	97	8	22	22	
320	327	8	GSVSSCWW	22	B*5802	84	22	86	8	22	22	
318	328	11	SQGSVSSCWWL	253	B*4801	37	1,77	65	8	22	22	
320	329	10	GSVSSCWWLQ	254	A*3201	21	0,81	17	8	22	22	
320	330	11	GSVSSCWWLQF	255	B*1525	22	1,91	42	8	22	22	
320	330	11	GSVSSCWWLQF	22	B*5701	74	22	142	8	22	22	
320	330	11	GSVSSCWWLQF	22	B*5802	65	22	125	8	22	22	
321	330	10	SVSSCWWLQF	256	A*2601	31	22	59	8	22	22	
321	330	10	SVSSCWWLQF	22	A*3201	58	22	110	8	22	22	
322	330	9	VSSCWWLQF	257	A*0101	53	22	101	8	22	22	
322	330	9	VSSCWWLQF	22	A*2402	23	22	44	8	22	22	
322	330	9	VSSCWWLQF	22	B*4601	21	22	41	8	22	22	
322	330	9	VSSCWWLQF	22	B*5701	58	22	110	8	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
322	330	9	VSSCWWLQF	22	B*5801	73	22	139	8	22	22	
323	330	8	SSCWWLQF	258	A*2301	21	22	40	8	22	22	
323	330	8	SSCWWLQF	22	A*3201	42	22	81	8	22	22	
323	330	8	SSCWWLQF	22	B*5801	59	22	113	8	22	22	
321	331	11	SVSSCWWLQFR	259	A*1101	65	0,81	53	8	22	22	
321	331	11	SVSSCWWLQFR	22	A*3303	100	22	81	8	22	22	
321	331	11	SVSSCWWLQFR	22	A*6801	96	22	78	8	22	22	
321	331	11	SVSSCWWLQFR	22	A*7401	98	22	79	8	22	22	
322	331	10	VSSCWWLQFR	260	A*3101	95	22	77	8	22	22	
322	331	10	VSSCWWLQFR	22	A*3303	56	22	46	8	22	22	
322	331	10	VSSCWWLQFR	22	B*5701	30	22	25	8	22	22	
322	331	10	VSSCWWLQFR	22	B*5801	42	22	34	8	22	22	
323	331	9	SSCWWLQFR	261	A*1101	41	22	34	8	22	22	
323	331	9	SSCWWLQFR	22	A*3101	94	22	76	8	22	22	
323	331	9	SSCWWLQFR	22	A*3303	85	22	69	8	22	22	
323	331	9	SSCWWLQFR	22	A*7401	87	22	70	8	22	22	
324	331	8	SCWWLQFR	262	A*3303	44	22	36	8	22	22	
327	334	8	WLQFRNSK	263	A*0301	20	0,52	10	8	22	22	
328	335	8	LQFRNSKP	264	A*0206	21	0,10	2	8	22	22	
327	336	10	WLQFrNSKPC	265	A*0201	18	0,14	3	8	22	22	
328	337	10	LQFRNSKPCS	266	A*3001	99	0,26	26	8	22	22	
329	339	11	QFRNSKPCSEY	267	A*3002	10	1,63	16	8	22	22	
331	339	9	RNSKPCSEY	268	A*3002	8	22	14	8	22	22	
332	339	8	NSKPCSEY	269	A*3002	20	22	32	8	22	22	
336	343	8	CSEYCLSH	270	A*0101	40	0,58	23	8	22	22	
337	344	8	SEYCLSHL	271	B*1301	97	1,01	98	8	22	22	
337	344	8	SEYCLSHL	22	B*1302	37	22	37	8	22	22	
337	344	8	SEYCLSHL	22	B*1801	67	22	67	8	22	22	
337	344	8	SEYCLSHL	22	B*3701	100	22	101	8	22	22	
337	344	8	SEYCLSHL	22	B*3801	96	22	97	8	22	22	
337	344	8	SEYCLSHL	22	B*4001	100	22	101	8	22	22	
337	344	8	SEYCLSHL	22	B*4002	100	22	101	8	22	22	
337	344	8	SEYCLSHL	22	B*4402	85	22	85	8	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
337	344	8	SEYCLSHL	22	B*4403	88	22	89	8	22	22	
337	344	8	SEYCLSHL	22	B*4801	46	22	47	8	22	22	
337	344	8	SEYCLSHL	22	B*4901	96	22	97	8	22	22	
337	344	8	SEYCLSHL	22	B*5001	96	22	97	8	22	22	
337	344	8	SEYCLSHL	22	B*5201	57	22	57	8	22	22	
335	345	11	PCSEYCLSHLV	272	A*0201	40	1,78	71	8	22	22	
337	345	9	SEYCLSHLV	273	B*1301	94	22	168	8	22	22	
337	345	9	SEYCLSHLV	22	B*1302	48	22	85	8	22	22	
337	345	9	SEYCLSHLV	22	B*1801	29	22	51	8	22	22	
337	345	9	SEYCLSHLV	22	B*4001	65	22	116	8	22	22	
337	345	9	SEYCLSHLV	22	B*4002	70	22	125	8	22	22	
337	345	9	SEYCLSHLV	22	B*4402	77	22	137	8	22	22	
337	345	9	SEYCLSHLV	22	B*4403	80	22	142	8	22	22	
337	345	9	SEYCLSHLV	22	B*4901	100	22	178	8	22	22	
337	345	9	SEYCLSHLV	22	B*5001	100	22	178	8	22	22	
337	345	9	SEYCLSHLV	22	B*5201	71	22	126	8	22	22	
337	346	10	SEYCLSHLVN	274	B*4001	39	0,24	10	8	22	22	
337	346	10	SEYCLSHLVN	22	B*4403	76	22	18	8	22	22	
337	346	10	SEYCLSHLVN	22	B*5001	24	22	6	8	22	22	
337	347	11	SEYCLSHLVNL	275	B*1301	100	1,66	166	8	22	22	
337	347	11	SEYCLSHLVNL	22	B*1302	45	22	75	8	22	22	
337	347	11	SEYCLSHLVNL	22	B*1801	86	22	142	8	22	22	
337	347	11	SEYCLSHLVNL	22	B*3701	95	22	158	8	22	22	
337	347	11	SEYCLSHLVNL	22	B*3801	94	22	156	8	22	22	
337	347	11	SEYCLSHLVNL	22	B*4001	96	22	158	8	22	22	
337	347	11	SEYCLSHLVNL	22	B*4002	95	22	157	8	22	22	
337	347	11	SEYCLSHLVNL	22	B*4402	81	22	134	8	22	22	
337	347	11	SEYCLSHLVNL	22	B*4403	84	22	139	8	22	22	
337	347	11	SEYCLSHLVNL	22	B*4901	91	22	151	8	22	22	
337	347	11	SEYCLSHLVNL	22	B*5001	92	22	152	8	22	22	
337	347	11	SEYCLSHLVNL	22	B*5201	63	22	104	8	22	22	
338	347	10	EYCLSHLVNL	276	A*2301	48	22	80	8	22	22	
				Cumulative Class I-BCI score:						7246		

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
386	394	9	AESRLVVDF	278	B*1801	10	1,80	17	9	385	417	
386	394	9	AESRLVVDF	279	B*4001	48	22	86	9	22	22	
386	394	9	AESRLVVDF	280	B*4002	50	22	90	9	22	22	
386	394	9	AESRLVVDF	281	B*4402	100	22	180	9	22	22	
386	394	9	AESRLVVDF	282	B*4403	100	22	180	9	22	22	
386	394	9	AESRLVVDF	283	B*4901	43	22	78	9	22	22	
386	394	9	AESRLVVDF	284	B*5001	36	22	65	9	22	22	
386	396	11	AESRLVDFSQ	279	B*4402	15	0,65	10	9	22	22	
386	396	11	AESRLVDFSQ	280	B*4403	8	22	5	9	22	22	
387	397	11	ESRLVDFSQF	280	A*2501	49	1,86	91	9	22	22	
387	397	11	ESRLVDFSQF	281	A*2601	5	22	10	9	22	22	
388	397	10	SRLVDFSQF	281	B*2702	92	22	170	9	22	22	
389	397	9	RLVDFSQF	282	A*2301	43	22	80	9	22	22	
389	397	9	RLVDFSQF	283	B*1501	70	22	131	9	22	22	
389	397	9	RLVDFSQF	284	B*1525	78	22	145	9	22	22	
390	397	8	LVDFSQF	283	A*2501	59	22	110	9	22	22	
390	397	8	LVDFSQF	285	A*2601	79	22	148	9	22	22	
390	397	8	LVDFSQF	286	B*1501	59	22	110	9	22	22	
390	397	8	LVDFSQF	287	B*1502	72	22	134	9	22	22	
390	397	8	LVDFSQF	288	B*1525	56	22	104	9	22	22	
390	397	8	LVDFSQF	289	B*4601	57	22	107	9	22	22	
389	399	11	RLVDFSQFSR	284	A*0301	15	1,78	26	9	22	22	
389	399	11	RLVDFSQFSR	290	A*3101	81	22	144	9	22	22	
389	399	11	RLVDFSQFSR	291	A*7401	96	22	172	9	22	22	
390	399	10	LVDFSQFSR	285	A*3101	89	22	158	9	22	22	
390	399	10	LVDFSQFSR	292	A*3201	6	22	11	9	22	22	
390	399	10	LVDFSQFSR	293	A*3303	83	22	148	9	22	22	
390	399	10	LVDFSQFSR	294	A*6801	88	22	157	9	22	22	
390	399	10	LVDFSQFSR	295	A*7401	70	22	124	9	22	22	
391	399	9	VDFSQFSR	286	A*1101	11	22	19	9	22	22	
391	399	9	VDFSQFSR	296	A*3303	18	22	33	9	22	22	
391	399	9	VDFSQFSR	297	A*7401	79	22	141	9	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
390	400	11	LVVDFSQFSRG	287	A*6802	6	0,16	1	9	55	55	
392	401	10	VDFSQFSRGI	288	B*1301	76	1,23	93	9	55	55	
392	401	10	VDFSQFSRGI	55	B*1302	44	55	54	9	55	55	
392	401	10	VDFSQFSRGI	55	B*5201	88	55	108	9	55	55	
393	403	11	DFSQFSRGISR	289	A*3303	55	0,77	42	9	55	55	
394	403	10	FSQFSRGISR	290	A*3101	14	55	11	9	55	55	
394	403	10	FSQFSRGISR	55	A*3303	11	55	9	9	55	55	
394	403	10	FSQFSRGISR	55	A*6801	60	55	46	9	55	55	
395	403	9	SQFSRGISR	291	A*1101	13	55	10	9	55	55	
395	403	9	SQFSRGISR	55	A*3101	62	55	48	9	55	55	
395	403	9	SQFSRGISR	55	A*3303	70	55	54	9	55	55	
395	403	9	SQFSRGISR	55	A*7401	95	55	73	9	55	55	
396	403	8	QFSRGISR	292	A*3303	48	55	37	9	55	55	
395	404	10	SQFSrGISRV	293	A*0201	45	1,90	85	9	55	55	
395	404	10	SQFSRGISRV	55	B*1302	23	55	43	9	55	55	
395	404	10	SQFSRGISRV	55	B*1402	4	55	8	9	55	55	
395	404	10	SQFSRGISRV	55	B*3901	27	55	52	9	55	55	
395	404	10	SQFSRGISRV	55	B*4801	35	55	66	9	55	55	
395	404	10	SQFSRGISRV	55	B*5201	69	55	130	9	55	55	
398	405	8	SRGISRVs	294	B*2705	12	0,22	3	9	55	55	
397	406	10	FSRGISRVsW	295	B*4601	38	1,40	53	9	55	55	
397	406	10	FSRGISRVsW	55	B*5301	15	55	21	9	55	55	
397	406	10	FSRGISRVsW	55	B*5802	87	55	122	9	55	55	
398	406	9	SRGISRVsW	296	B*2702	65	55	91	9	55	55	
399	406	8	RGISRVsW	297	B*2702	28	55	39	9	55	55	
399	406	8	RGISRVsW	55	B*5701	73	55	102	9	55	55	
399	406	8	RGISRVsW	55	B*5801	68	55	95	9	55	55	
399	406	8	RGISRVsW	55	B*5802	74	55	103	9	55	55	
400	408	9	GISRVsWPK	298	A*0301	62	0,98	61	9	55	55	
400	408	9	GISRVsWPK	55	A*1101	93	55	91	9	55	55	
400	408	9	GISRVsWPK	55	A*7401	40	55	39	9	55	55	
401	408	8	ISRVsWPK	299	A*0301	13	55	13	9	55	55	
401	408	8	ISRVsWPK	55	A*1101	30	55	30	9	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
401	408	8	ISRVSWPK	..	A*3001	95	..	92	9	..	..	
399	409	11	RGISRVSWPKF	300	A*2301	7	1,38	10	9	..	..	
399	409	11	RGISRVSWPKF	..	B*5802	7	..	10	9	..	..	
400	409	10	GISRVSWPKF	301	A*3001	55	..	77	9	..	..	
400	409	10	GISRVSWPKF	..	A*3201	98	..	136	9	..	..	
401	409	9	ISRVSWPKF	302	B*5701	88	..	122	9	..	..	
402	409	8	SRVSWPKF	303	B*2702	90	..	125	9	..	..	
402	409	8	SRVSWPKF	..	B*2705	57	..	78	9	..	..	
403	410	8	RVSWPKEFA	304	A*3001	16	0,84	14	9	..	..	
401	411	11	ISRVSWPKFAV	305	A*3001	70	1,60	111	9	..	..	
402	411	10	SRVSWPKFAV	306	B*3901	6	..	10	9	..	..	
403	411	9	RVSWPKEFAV	307	A*6802	4	..	7	9	..	..	
403	411	9	RVSWPKEFAV	..	B*0702	6	..	9	9	..	..	
404	411	8	VSWPKFAV	308	B*5201	41	..	66	9	..	..	
405	412	8	SWPKFAVP	309	A*0206	100	0,48	48	9	..	..	
404	414	11	VSWPKFAVPNL	310	B*5201	16	1,63	26	9	..	..	
404	414	11	VSWPKFAVPNL	..	B*5701	18	..	30	9	..	..	
405	414	10	SWPKFAVPNL	311	A*2301	78	..	127	9	..	..	
405	414	10	SWPKFAVPNL	..	A*2402	75	..	123	9	..	..	
406	414	9	WPKFAVPNL	312	B*1402	21	..	35	9	..	..	
406	414	9	WPKFAVPNL	..	B*3503	18	..	29	9	..	..	
409	417	9	FAVPNLQSL	313	A*0206	54	1,89	102	9	..	..	
409	417	9	FAVPNLQSL	..	B*3503	46	..	87	9	..	..	
409	417	9	FAVPNLQSL	..	B*4601	95	..	180	9	..	..	
410	417	8	AVPNLQSL	314	B*0702	29	..	55	9	..	..	
				Cumulative BCI Class Score:				6722				
420	427	8	LLSSNLWS	316	B*5301	20	1,77	35	10	419	456	
420	427	8	LLSSNLWS	..	B*5701	48	..	86	10	..	..	
420	427	8	LLSSNLWS	..	B*5801	66	..	117	10	..	..	
420	427	8	LLSSNLWS	..	B*5802	30	..	54	10	..	..	
419	428	10	NLLSSNLWSL	317	A*0201	100	1,54	154	10	..	..	
420	428	9	LLSSNLWSL	318	A*0201	86	..	133	10	..	..	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
421	428	8	LSSNLSWL	319	B*0702	78	..	121	10	..	..	
421	429	9	LSSNLSWLS	320	A*0101	30	0,55	16	10	..	..	
420	430	11	LLSSNLSWLSL	321	B*0801	8	1,74	15	10	..	..	
421	430	10	LSSNLSWLSL	322	A*3201	47	..	82	10	..	..	
421	430	10	LSSNLSWLSL	..	B*5701	27	..	48	10	..	..	
421	430	10	LSSNLSWLSL	..	B*5801	3	..	6	10	..	..	
421	430	10	LSSNLSWLSL	..	B*5802	29	..	50	10	..	..	
422	431	10	SSNLSWLSLD	323	A*3001	22	0,11	2	10	..	..	
422	432	11	SSNLSWLSLDV	324	A*0201	38	1,41	53	10	..	..	
424	432	9	NLSWLSLDV	325	A*0201	29	..	41	10	..	..	
425	432	8	LSWLSLDV	326	A*0206	4	..	6	10	..	..	
425	432	8	LSWLSLDV	..	B*1302	1	..	2	10	..	..	
425	432	8	LSWLSLDV	..	B*5201	55	..	77	10	..	..	
425	435	11	LSWLSLDVSA	327	B*5601	9	0,74	7	10	..	..	
427	435	9	WLSLDVSA	328	A*0201	14	..	10	10	..	..	
426	436	11	SWLSLDVSAAF	329	A*2301	91	1,90	174	10	..	..	
426	436	11	SWLSLDVSAAF	..	A*2402	93	..	177	10	..	..	
426	436	11	SWLSLDVSAAF	..	A*2902	32	..	60	10	..	..	
426	436	11	SWLSLDVSAAF	..	B*1801	38	..	72	10	..	..	
427	436	10	WLSLDVSAAF	330	B*1501	72	..	137	10	..	..	
427	436	10	WLSLDVSAAF	..	B*1502	89	..	169	10	..	..	
427	436	10	WLSLDVSAAF	..	B*1525	54	..	103	10	..	..	
428	436	9	LSLDVSAAF	331	B*1501	73	..	140	10	..	..	
428	436	9	LSLDVSAAF	..	B*1525	76	..	145	10	..	..	
428	436	9	LSLDVSAAF	..	B*3501	69	..	132	10	..	..	
428	436	9	LSLDVSAAF	..	B*3503	51	..	98	10	..	..	
428	436	9	LSLDVSAAF	..	B*4601	75	..	144	10	..	..	
428	436	9	LSLDVSAAF	..	B*5801	63	..	119	10	..	..	
427	437	11	WLSLDVSAAFY	332	A*0101	74	1,81	133	10	..	..	
427	437	11	WLSLDVSAAFY	..	A*2601	38	..	69	10	..	..	
427	437	11	WLSLDVSAAFY	..	A*2902	75	..	135	10	..	..	
427	437	11	WLSLDVSAAFY	..	B*1502	22	..	40	10	..	..	
428	437	10	LSLDVSAAFY	333	A*0101	100	..	181	10	..	..	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
428	437	10	LSLDVSAAFY	33	A*2902	83	33	149	10	33	33	
428	437	10	LSLDVSAAFY	33	A*3002	99	33	178	10	33	33	
428	437	10	LSLDVSAAFY	33	B*1501	22	33	40	10	33	33	
428	437	10	LSLDVSAAFY	33	B*4601	69	33	124	10	33	33	
428	437	10	LSLDVSAAFY	33	B*5802	57	33	102	10	33	33	
429	437	9	SLDVSAAFY	334	A*0101	85	33	153	10	33	33	
429	437	9	SLDVSAAFY	33	A*3002	59	33	107	10	33	33	
430	437	8	LDVSAAFY	335	B*3501	31	33	55	10	33	33	
430	439	10	LDVSAAFYHI	336	B*1301	96	1,79	171	10	33	33	
430	439	10	LDVSAAFYHI	33	B*1302	49	33	88	10	33	33	
430	439	10	LDVSAAFYHI	33	B*3701	57	33	102	10	33	33	
430	439	10	LDVSAAFYHI	33	B*4901	57	33	101	10	33	33	
430	439	10	LDVSAAFYHI	33	B*5201	98	33	175	10	33	33	
431	439	9	DVSAAFYHI	337	A*6802	46	33	81	10	33	33	
432	439	8	VSAAFYHI	338	A*3201	18	33	32	10	33	33	
432	439	8	VSAAFYHI	33	B*1302	28	33	50	10	33	33	
432	439	8	VSAAFYHI	33	B*5101	8	33	15	10	33	33	
432	439	8	VSAAFYHI	33	B*5201	96	33	172	10	33	33	
432	439	8	VSAAFYHI	33	B*5701	65	33	116	10	33	33	
432	439	8	VSAAFYHI	33	B*5801	64	33	115	10	33	33	
432	439	8	VSAAFYHI	33	B*5802	49	33	88	10	33	33	
431	441	11	DVSAAFYHIPL	339	A*2501	33	1,00	33	10	33	33	
431	441	11	DVSAAFYHIPL	33	A*2601	51	33	51	10	33	33	
432	441	10	VSAAFYHIPL	340	A*6802	35	33	35	10	33	33	
432	441	10	VSAAFYHIPL	33	B*5802	14	33	15	10	33	33	
433	441	9	SAAFYHIPL	341	B*1402	79	33	79	10	33	33	
433	441	9	SAAFYHIPL	33	B*3503	34	33	34	10	33	33	
434	441	8	AAFYHIPL	342	B*0801	64	33	65	10	33	33	
434	441	8	AAFYHIPL	33	B*1402	57	33	57	10	33	33	
434	441	8	AAFYHIPL	33	B*3801	6	33	6	10	33	33	
434	441	8	AAFYHIPL	33	B*3901	32	33	33	10	33	33	
434	441	8	AAFYHIPL	33	B*4801	63	33	64	10	33	33	
433	442	10	SAAFYHIPLH	343	A*3001	83	0,25	20	10	33	33	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
434	444	11	AAFYHIPLHPA	344	A*3001	11	0,89	10	10	55	55
434	444	11	AAFYHIPLHPA	55	B*5501	20	55	18	10	55	55
434	444	11	AAFYHIPLHPA	55	B*5601	21	55	18	10	55	55
437	444	8	YHIPLHPA	345	B*1402	19	55	17	10	55	55
437	444	8	YHIPLHPA	55	B*3901	87	55	78	10	55	55
437	445	9	YHIPLHPAA	346	B*1402	18	0,62	11	10	55	55
436	446	11	FYHIPLHPAAM	347	A*2402	19	1,63	31	10	55	55
437	446	10	YHIPLHPAAM	348	B*1402	99	55	161	10	55	55
437	446	10	YHIPLHPAAM	55	B*3503	74	55	121	10	55	55
437	446	10	YHIPLHPAAM	55	B*3801	86	55	140	10	55	55
437	446	10	YHIPLHPAAM	55	B*3901	100	55	163	10	55	55
438	446	9	HIPLHPAAM	349	A*2501	73	55	120	10	55	55
438	446	9	HIPLHPAAM	55	B*1402	3	55	5	10	55	55
439	446	8	IPLHPAAM	350	B*1402	86	55	140	10	55	55
439	446	8	IPLHPAAM	55	B*3503	93	55	152	10	55	55
439	446	8	IPLHPAAM	55	B*5101	55	55	90	10	55	55
439	446	8	IPLHPAAM	55	B*5301	64	55	104	10	55	55
439	446	8	IPLHPAAM	55	B*5501	85	55	138	10	55	55
439	446	8	IPLHPAAM	55	B*5601	73	55	119	10	55	55
439	449	11	IPLHPAAMPHL	351	B*0702	58	1,61	93	10	55	55
439	449	11	IPLHPAAMPHL	55	B*1402	31	55	50	10	55	55
439	449	11	IPLHPAAMPHL	55	B*3503	32	55	52	10	55	55
439	449	11	IPLHPAAMPHL	55	B*5101	53	55	86	10	55	55
439	449	11	IPLHPAAMPHL	55	B*5501	38	55	62	10	55	55
441	449	9	LHPAAMPHL	352	B*3801	76	55	121	10	55	55
442	449	8	HPAAMPHL	353	B*1402	85	55	136	10	55	55
442	449	8	HPAAMPHL	55	B*3503	73	55	117	10	55	55
442	449	8	HPAAMPHL	55	B*3901	53	55	85	10	55	55
442	449	8	HPAAMPHL	55	B*5101	48	55	78	10	55	55
442	449	8	HPAAMPHL	55	B*5301	38	55	61	10	55	55
442	449	8	HPAAMPHL	55	B*5501	55	55	88	10	55	55
442	449	8	HPAAMPHL	55	B*5601	29	55	47	10	55	55
441	450	10	LHPAAMPHLL	354	B*3801	67	1,81	122	10	55	55

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
442	450	9	HPAAMPHLL	355	B*0702	70	22	126	10	22	22
442	450	9	HPAAMPHLL	22	B*1402	93	22	168	10	22	22
442	450	9	HPAAMPHLL	22	B*3501	29	22	53	10	22	22
442	450	9	HPAAMPHLL	22	B*3503	85	22	154	10	22	22
442	450	9	HPAAMPHLL	22	B*3901	97	22	176	10	22	22
442	450	9	HPAAMPHLL	22	B*5301	33	22	59	10	22	22
442	450	9	HPAAMPHLL	22	B*5501	72	22	130	10	22	22
442	450	9	HPAAMPHLL	22	B*5601	58	22	104	10	22	22
441	451	11	LHPAAMPHLLI	356	B*3801	61	0,84	51	10	22	22
442	451	10	HPAAMPHLLI	357	B*1402	71	22	59	10	22	22
442	451	10	HPAAMPHLLI	22	B*3503	72	22	60	10	22	22
442	451	10	HPAAMPHLLI	22	B*3901	38	22	31	10	22	22
442	451	10	HPAAMPHLLI	22	B*5201	61	22	51	10	22	22
442	451	10	HPAAMPHLLI	22	B*5301	36	22	30	10	22	22
442	451	10	HPAAMPHLLI	22	B*5501	84	22	70	10	22	22
442	451	10	HPAAMPHLLI	22	B*5601	90	22	75	10	22	22
444	451	8	AAMPHLLI	358	A*3201	59	22	49	10	22	22
444	451	8	AAMPHLLI	22	B*1302	35	22	29	10	22	22
444	451	8	AAMPHLLI	22	B*5101	47	22	39	10	22	22
444	451	8	AAMPHLLI	22	B*5201	94	22	79	10	22	22
444	451	8	AAMPHLLI	22	B*5801	37	22	31	10	22	22
442	452	11	HPAAMPHLLIG	359	A*0201	51	0,32	16	10	22	22
442	452	11	HPAAMPHLLIG	22	A*0206	38	22	12	10	22	22
446	453	8	MPHLLIGS	360	A*6802	16	0,77	12	10	22	22
446	453	8	MPHLLIGS	22	B*5601	28	22	22	10	22	22
446	454	9	MPHLLIGSS	361	B*5501	37	0,26	10	10	22	22
446	454	9	MPHLLIGSS	22	B*5601	41	22	11	10	22	22
446	455	10	MPHLLIGSSG	362	B*0702	35	0,11	4	10	22	22
446	455	10	MPHLLIGSSG	22	B*3501	40	22	4	10	22	22
446	455	10	MPHLLIGSSG	22	B*5501	3	22	0	10	22	22
446	455	10	MPHLLIGSSG	22	B*5601	18	22	2	10	22	22
446	456	11	MPHLLIGSSGL	363	B*0702	93	1,81	168	10	22	22
446	456	11	MPHLLIGSSGL	22	B*0801	44	22	80	10	22	22

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
446	456	11	MPHLLIGSSGL	33	B*1402	92	33	167	10	33	33
446	456	11	MPHLLIGSSGL	33	B*3501	27	33	48	10	33	33
446	456	11	MPHLLIGSSGL	33	B*3503	70	33	127	10	33	33
446	456	11	MPHLLIGSSGL	33	B*3901	62	33	113	10	33	33
446	456	11	MPHLLIGSSGL	33	B*5101	40	33	73	10	33	33
446	456	11	MPHLLIGSSGL	33	B*5301	18	33	33	10	33	33
446	456	11	MPHLLIGSSGL	33	B*5501	71	33	129	10	33	33
446	456	11	MPHLLIGSSGL	33	B*5601	53	33	95	10	33	33
448	456	9	HLIGSSGL	364	B*1502	83	33	151	10	33	33
449	456	8	LLIGSSGL	365	B*0702	77	33	139	10	33	33
Cumulative BCI Class I Score:									11926		
422	432	11	SSNLSWLSLDV	324	A*0201	38	1,41	53	11	422	459
424	432	9	NLSWLSLDV	325	A*0201	29	33	41	11	33	33
425	432	8	LSWLSLDV	326	A*0206	4	33	6	11	33	33
425	432	8	LSWLSLDV	33	B*1302	1	33	2	11	33	33
425	432	8	LSWLSLDV	33	B*5201	55	33	77	11	33	33
425	435	11	LSWLSLDVSAA	327	B*5601	9	0,74	7	11	33	33
427	435	9	WLSLDVSAA	328	A*0201	14	33	10	11	33	33
426	436	11	SWLSLDVSAAF	329	A*2301	91	1,90	174	11	33	33
426	436	11	SWLSLDVSAAF	33	A*2402	93	33	177	11	33	33
426	436	11	SWLSLDVSAAF	33	A*2902	32	33	60	11	33	33
426	436	11	SWLSLDVSAAF	33	B*1801	38	33	72	11	33	33
427	436	10	WLSLDVSAAF	330	B*1501	72	33	137	11	33	33
427	436	10	WLSLDVSAAF	33	B*1502	89	33	169	11	33	33
427	436	10	WLSLDVSAAF	33	B*1525	54	33	103	11	33	33
428	436	9	LSLDVSAAF	331	B*1501	73	33	140	11	33	33
428	436	9	LSLDVSAAF	33	B*1525	76	33	145	11	33	33
428	436	9	LSLDVSAAF	33	B*3501	69	33	132	11	33	33
428	436	9	LSLDVSAAF	33	B*3503	51	33	98	11	33	33
428	436	9	LSLDVSAAF	33	B*4601	75	33	144	11	33	33
428	436	9	LSLDVSAAF	33	B*5801	63	33	119	11	33	33
427	437	11	WLSLDVSAAFY	332	A*0101	74	1,81	133	11	33	33

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
427	437	11	WLSLDVSAAFY	33	A*2601	38	33	69	11	33	33
427	437	11	WLSLDVSAAFY	33	A*2902	75	33	135	11	33	33
427	437	11	WLSLDVSAAFY	33	B*1502	22	33	40	11	33	33
428	437	10	LSLDVSAAFY	333	A*0101	100	33	181	11	33	33
428	437	10	LSLDVSAAFY	33	A*2902	83	33	149	11	33	33
428	437	10	LSLDVSAAFY	33	A*3002	99	33	178	11	33	33
428	437	10	LSLDVSAAFY	33	B*1501	22	33	40	11	33	33
428	437	10	LSLDVSAAFY	33	B*4601	69	33	124	11	33	33
428	437	10	LSLDVSAAFY	33	B*5802	57	33	102	11	33	33
429	437	9	SLDVSAAFY	334	A*0101	85	33	153	11	33	33
429	437	9	SLDVSAAFY	33	A*3002	59	33	107	11	33	33
430	437	8	LDVSAAFY	335	B*3501	31	33	55	11	33	33
430	439	10	LDVSAAFYHI	336	B*1301	96	1,79	171	11	33	33
430	439	10	LDVSAAFYHI	33	B*1302	49	33	88	11	33	33
430	439	10	LDVSAAFYHI	33	B*3701	57	33	102	11	33	33
430	439	10	LDVSAAFYHI	33	B*4901	57	33	101	11	33	33
430	439	10	LDVSAAFYHI	33	B*5201	98	33	175	11	33	33
431	439	9	DVSAAFYHI	337	A*6802	46	33	81	11	33	33
432	439	8	VSAAFYHI	338	A*3201	18	33	32	11	33	33
432	439	8	VSAAFYHI	33	B*1302	28	33	50	11	33	33
432	439	8	VSAAFYHI	33	B*5101	8	33	15	11	33	33
432	439	8	VSAAFYHI	33	B*5201	96	33	172	11	33	33
432	439	8	VSAAFYHI	33	B*5701	65	33	116	11	33	33
432	439	8	VSAAFYHI	33	B*5801	64	33	115	11	33	33
432	439	8	VSAAFYHI	33	B*5802	49	33	88	11	33	33
431	441	11	DVSAAFYHIPL	339	A*2501	33	1,00	33	11	33	33
431	441	11	DVSAAFYHIPL	33	A*2601	51	33	51	11	33	33
432	441	10	VSAAFYHIPL	340	A*6802	35	33	35	11	33	33
432	441	10	VSAAFYHIPL	33	B*5802	14	33	15	11	33	33
433	441	9	SAAFYHIPL	341	B*1402	79	33	79	11	33	33
433	441	9	SAAFYHIPL	33	B*3503	34	33	34	11	33	33
434	441	8	AAFYHIPL	342	B*0801	64	33	65	11	33	33
434	441	8	AAFYHIPL	33	B*1402	57	33	57	11	33	33

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
434	441	8	AAFYHIPL	33	B*3801	6	33	6	11	33	33
434	441	8	AAFYHIPL	33	B*3901	32	33	33	11	33	33
434	441	8	AAFYHIPL	33	B*4801	63	33	64	11	33	33
433	442	10	SAAFYHIPLH	343	A*3001	83	0,25	20	11	33	33
434	444	11	AAFYHIPLHPA	344	A*3001	11	0,89	10	11	33	33
434	444	11	AAFYHIPLHPA	33	B*5501	20	33	18	11	33	33
434	444	11	AAFYHIPLHPA	33	B*5601	21	33	18	11	33	33
437	444	8	YHIPLHPA	345	B*1402	19	33	17	11	33	33
437	444	8	YHIPLHPA	33	B*3901	87	33	78	11	33	33
437	445	9	YHIPLHPAA	346	B*1402	18	0,62	11	11	33	33
436	446	11	FYHIPLHPAAM	347	A*2402	19	1,63	31	11	33	33
437	446	10	YHIPLHPAAM	348	B*1402	99	33	161	11	33	33
437	446	10	YHIPLHPAAM	33	B*3503	74	33	121	11	33	33
437	446	10	YHIPLHPAAM	33	B*3801	86	33	140	11	33	33
437	446	10	YHIPLHPAAM	33	B*3901	100	33	163	11	33	33
438	446	9	HIPLHPAAM	349	A*2501	73	33	120	11	33	33
438	446	9	HIPLHPAAM	33	B*1402	3	33	5	11	33	33
439	446	8	IPLHPAAM	350	B*1402	86	33	140	11	33	33
439	446	8	IPLHPAAM	33	B*3503	93	33	152	11	33	33
439	446	8	IPLHPAAM	33	B*5101	55	33	90	11	33	33
439	446	8	IPLHPAAM	33	B*5301	64	33	104	11	33	33
439	446	8	IPLHPAAM	33	B*5501	85	33	138	11	33	33
439	446	8	IPLHPAAM	33	B*5601	73	33	119	11	33	33
439	449	11	IPLHPAAMP HL	351	B*0702	58	1,61	93	11	33	33
439	449	11	IPLHPAAMP HL	33	B*1402	31	33	50	11	33	33
439	449	11	IPLHPAAMP HL	33	B*3503	32	33	52	11	33	33
439	449	11	IPLHPAAMP HL	33	B*5101	53	33	86	11	33	33
439	449	11	IPLHPAAMP HL	33	B*5501	38	33	62	11	33	33
441	449	9	LHPAAMP HL	352	B*3801	76	33	121	11	33	33
442	449	8	HPAAMP HL	353	B*1402	85	33	136	11	33	33
442	449	8	HPAAMP HL	33	B*3503	73	33	117	11	33	33
442	449	8	HPAAMP HL	33	B*3901	53	33	85	11	33	33
442	449	8	HPAAMP HL	33	B*5101	48	33	78	11	33	33

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
442	449	8	HPAAMPHL	33	B*5301	38	33	61	11	33	33
442	449	8	HPAAMPHL	33	B*5501	55	33	88	11	33	33
442	449	8	HPAAMPHL	33	B*5601	29	33	47	11	33	33
441	450	10	LHPAAMPHLL	354	B*3801	67	1,81	122	11	33	33
442	450	9	HPAAMPHLL	355	B*0702	70	33	126	11	33	33
442	450	9	HPAAMPHLL	33	B*1402	93	33	168	11	33	33
442	450	9	HPAAMPHLL	33	B*3501	29	33	53	11	33	33
442	450	9	HPAAMPHLL	33	B*3503	85	33	154	11	33	33
442	450	9	HPAAMPHLL	33	B*3901	97	33	176	11	33	33
442	450	9	HPAAMPHLL	33	B*5301	33	33	59	11	33	33
442	450	9	HPAAMPHLL	33	B*5501	72	33	130	11	33	33
442	450	9	HPAAMPHLL	33	B*5601	58	33	104	11	33	33
441	451	11	LHPAAMPHLLI	356	B*3801	61	0,84	51	11	33	33
442	451	10	HPAAMPHLLI	357	B*1402	71	33	59	11	33	33
442	451	10	HPAAMPHLLI	33	B*3503	72	33	60	11	33	33
442	451	10	HPAAMPHLLI	33	B*3901	38	33	31	11	33	33
442	451	10	HPAAMPHLLI	33	B*5201	61	33	51	11	33	33
442	451	10	HPAAMPHLLI	33	B*5301	36	33	30	11	33	33
442	451	10	HPAAMPHLLI	33	B*5501	84	33	70	11	33	33
442	451	10	HPAAMPHLLI	33	B*5601	90	33	75	11	33	33
444	451	8	AAMPHLLI	358	A*3201	59	33	49	11	33	33
444	451	8	AAMPHLLI	33	B*1302	35	33	29	11	33	33
444	451	8	AAMPHLLI	33	B*5101	47	33	39	11	33	33
444	451	8	AAMPHLLI	33	B*5201	94	33	79	11	33	33
444	451	8	AAMPHLLI	33	B*5801	37	33	31	11	33	33
442	452	11	HPAAMPHLLIG	359	A*0201	51	0,32	16	11	33	33
442	452	11	HPAAMPHLLIG	33	A*0206	38	33	12	11	33	33
446	453	8	MPHLLIGS	360	A*6802	16	0,77	12	11	33	33
446	453	8	MPHLLIGS	33	B*5601	28	33	22	11	33	33
446	454	9	MPHLLIGSS	361	B*5501	37	0,26	10	11	33	33
446	454	9	MPHLLIGSS	33	B*5601	41	33	11	11	33	33
446	455	10	MPHLLIGSSG	362	B*0702	35	0,11	4	11	33	33
446	455	10	MPHLLIGSSG	33	B*3501	40	33	4	11	33	33

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
446	455	10	MPHLLIGSSG	33	B*5501	3	33	0	11	33	33	
446	455	10	MPHLLIGSSG	33	B*5601	18	33	2	11	33	33	
446	456	11	MPHLLIGSSGL	363	B*0702	93	1,81	168	11	33	33	
446	456	11	MPHLLIGSSGL	33	B*0801	44	33	80	11	33	33	
446	456	11	MPHLLIGSSGL	33	B*1402	92	33	167	11	33	33	
446	456	11	MPHLLIGSSGL	33	B*3501	27	33	48	11	33	33	
446	456	11	MPHLLIGSSGL	33	B*3503	70	33	127	11	33	33	
446	456	11	MPHLLIGSSGL	33	B*3901	62	33	113	11	33	33	
446	456	11	MPHLLIGSSGL	33	B*5101	40	33	73	11	33	33	
446	456	11	MPHLLIGSSGL	33	B*5301	18	33	33	11	33	33	
446	456	11	MPHLLIGSSGL	33	B*5501	71	33	129	11	33	33	
446	456	11	MPHLLIGSSGL	33	B*5601	53	33	95	11	33	33	
448	456	9	HLIGSSGL	364	B*1502	83	33	151	11	33	33	
449	456	8	LLIGSSGL	365	B*0702	77	33	139	11	33	33	
448	458	11	HLIGSSGLSR	366	A*0301	11	1,14	13	11	33	33	
448	458	11	HLIGSSGLSR	33	A*3101	19	33	22	11	33	33	
448	458	11	HLIGSSGLSR	33	A*3303	17	33	19	11	33	33	
448	458	11	HLIGSSGLSR	33	A*7401	62	33	71	11	33	33	
449	458	10	LLIGSSGLSR	367	A*7401	6	33	7	11	33	33	
449	459	11	LLIGSSGLSRY	368	A*2501	57	1,50	85	11	33	33	
449	459	11	LLIGSSGLSRY	33	A*2601	77	33	115	11	33	33	
449	459	11	LLIGSSGLSRY	33	A*2902	89	33	133	11	33	33	
449	459	11	LLIGSSGLSRY	33	A*3002	66	33	99	11	33	33	
449	459	11	LLIGSSGLSRY	33	B*1501	81	33	122	11	33	33	
449	459	11	LLIGSSGLSRY	33	B*1502	57	33	86	11	33	33	
449	459	11	LLIGSSGLSRY	33	B*1525	41	33	61	11	33	33	
449	459	11	LLIGSSGLSRY	33	B*4601	28	33	42	11	33	33	
450	459	10	LIGSSGLSRY	369	A*0101	45	33	68	11	33	33	
450	459	10	LIGSSGLSRY	33	A*3002	35	33	53	11	33	33	
451	459	9	IGSSGLSRY	370	A*3002	94	33	141	11	33	33	
452	459	8	GSSGLSRY	371	A*0101	83	33	124	11	33	33	
452	459	8	GSSGLSRY	33	A*3002	77	33	116	11	33	33	
					Cumulative Class I-BCI score:					12384		

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
427	435	9	WLSLDVSAA	328	A*0201	14	0,74	10	12	427	459	
426	436	11	SWLSLDVSAAF	329	A*2301	91	1,90	174	12	55	55	
426	436	11	SWLSLDVSAAF	33	A*2402	93	32	177	12	55	55	
426	436	11	SWLSLDVSAAF	33	A*2902	32	32	60	12	55	55	
426	436	11	SWLSLDVSAAF	33	B*1801	38	32	72	12	55	55	
427	436	10	WLSLDVSAAF	330	B*1501	72	32	137	12	55	55	
427	436	10	WLSLDVSAAF	33	B*1502	89	32	169	12	55	55	
427	436	10	WLSLDVSAAF	33	B*1525	54	32	103	12	55	55	
428	436	9	LSLDVSAAF	331	B*1501	73	32	140	12	55	55	
428	436	9	LSLDVSAAF	33	B*1525	76	32	145	12	55	55	
428	436	9	LSLDVSAAF	33	B*3501	69	32	132	12	55	55	
428	436	9	LSLDVSAAF	33	B*3503	51	32	98	12	55	55	
428	436	9	LSLDVSAAF	33	B*4601	75	32	144	12	55	55	
428	436	9	LSLDVSAAF	33	B*5801	63	32	119	12	55	55	
427	437	11	WLSLDVSAAFY	332	A*0101	74	1,81	133	12	55	55	
427	437	11	WLSLDVSAAFY	33	A*2601	38	32	69	12	55	55	
427	437	11	WLSLDVSAAFY	33	A*2902	75	32	135	12	55	55	
427	437	11	WLSLDVSAAFY	33	B*1502	22	32	40	12	55	55	
428	437	10	LSLDVSAAFY	333	A*0101	100	32	181	12	55	55	
428	437	10	LSLDVSAAFY	33	A*2902	83	32	149	12	55	55	
428	437	10	LSLDVSAAFY	33	A*3002	99	32	178	12	55	55	
428	437	10	LSLDVSAAFY	33	B*1501	22	32	40	12	55	55	
428	437	10	LSLDVSAAFY	33	B*4601	69	32	124	12	55	55	
428	437	10	LSLDVSAAFY	33	B*5802	57	32	102	12	55	55	
429	437	9	SLDVSAAFY	334	A*0101	85	32	153	12	55	55	
429	437	9	SLDVSAAFY	33	A*3002	59	32	107	12	55	55	
430	437	8	LDVSAAFY	335	B*3501	31	32	55	12	55	55	
430	439	10	LDVSAAFYHI	336	B*1301	96	1,79	171	12	55	55	
430	439	10	LDVSAAFYHI	33	B*1302	49	32	88	12	55	55	
430	439	10	LDVSAAFYHI	33	B*3701	57	32	102	12	55	55	
430	439	10	LDVSAAFYHI	33	B*4901	57	32	101	12	55	55	
430	439	10	LDVSAAFYHI	33	B*5201	98	32	175	12	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
431	439	9	DVSAAFYHI	337	A*6802	46	22	81	12	22	22
432	439	8	VSAAFYHI	338	A*3201	18	22	32	12	22	22
432	439	8	VSAAFYHI	22	B*1302	28	22	50	12	22	22
432	439	8	VSAAFYHI	22	B*5101	8	22	15	12	22	22
432	439	8	VSAAFYHI	22	B*5201	96	22	172	12	22	22
432	439	8	VSAAFYHI	22	B*5701	65	22	116	12	22	22
432	439	8	VSAAFYHI	22	B*5801	64	22	115	12	22	22
432	439	8	VSAAFYHI	22	B*5802	49	22	88	12	22	22
431	441	11	DVSAAFYHIPL	339	A*2501	33	1,00	33	12	22	22
431	441	11	DVSAAFYHIPL	22	A*2601	51	22	51	12	22	22
432	441	10	VSAAFYHIPL	340	A*6802	35	22	35	12	22	22
432	441	10	VSAAFYHIPL	22	B*5802	14	22	15	12	22	22
433	441	9	SAAFYHIPL	341	B*1402	79	22	79	12	22	22
433	441	9	SAFYHIPL	22	B*3503	34	22	34	12	22	22
434	441	8	AFYHIPL	342	B*0801	64	22	65	12	22	22
434	441	8	AFYHIPL	22	B*1402	57	22	57	12	22	22
434	441	8	AFYHIPL	22	B*3801	6	22	6	12	22	22
434	441	8	AFYHIPL	22	B*3901	32	22	33	12	22	22
434	441	8	AFYHIPL	22	B*4801	63	22	64	12	22	22
433	442	10	SAFYHIPLH	343	A*3001	83	0,25	20	12	22	22
434	444	11	AFYHIPLHPA	344	A*3001	11	0,89	10	12	22	22
434	444	11	AFYHIPLHPA	22	B*5501	20	22	18	12	22	22
434	444	11	AFYHIPLHPA	22	B*5601	21	22	18	12	22	22
437	444	8	YHIPLHPA	345	B*1402	19	22	17	12	22	22
437	444	8	YHIPLHPA	22	B*3901	87	22	78	12	22	22
437	445	9	YHIPLHPAA	346	B*1402	18	0,62	11	12	22	22
436	446	11	FYHIPLHPAAM	347	A*2402	19	1,63	31	12	22	22
437	446	10	YHIPLHPAAM	348	B*1402	99	22	161	12	22	22
437	446	10	YHIPLHPAAM	22	B*3503	74	22	121	12	22	22
437	446	10	YHIPLHPAAM	22	B*3801	86	22	140	12	22	22
437	446	10	YHIPLHPAAM	22	B*3901	100	22	163	12	22	22
438	446	9	HIPLHPAAM	349	A*2501	73	22	120	12	22	22
438	446	9	HIPLHPAAM	22	B*1402	3	22	5	12	22	22

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
439	446	8	IPLHPAAM	350	B*1402	86	22	140	12	22	22
439	446	8	IPLHPAAM	22	B*3503	93	22	152	12	22	22
439	446	8	IPLHPAAM	22	B*5101	55	22	90	12	22	22
439	446	8	IPLHPAAM	22	B*5301	64	22	104	12	22	22
439	446	8	IPLHPAAM	22	B*5501	85	22	138	12	22	22
439	446	8	IPLHPAAM	22	B*5601	73	22	119	12	22	22
439	449	11	IPLHPAAMP HL	351	B*0702	58	1,61	93	12	22	22
439	449	11	IPLHPAAMP HL	22	B*1402	31	22	50	12	22	22
439	449	11	IPLHPAAMP HL	22	B*3503	32	22	52	12	22	22
439	449	11	IPLHPAAMP HL	22	B*5101	53	22	86	12	22	22
439	449	11	IPLHPAAMP HL	22	B*5501	38	22	62	12	22	22
441	449	9	LHPAAMP HL	352	B*3801	76	22	121	12	22	22
442	449	8	HPAAMP HL	353	B*1402	85	22	136	12	22	22
442	449	8	HPAAMP HL	22	B*3503	73	22	117	12	22	22
442	449	8	HPAAMP HL	22	B*3901	53	22	85	12	22	22
442	449	8	HPAAMP HL	22	B*5101	48	22	78	12	22	22
442	449	8	HPAAMP HL	22	B*5301	38	22	61	12	22	22
442	449	8	HPAAMP HL	22	B*5501	55	22	88	12	22	22
442	449	8	HPAAMP HL	22	B*5601	29	22	47	12	22	22
441	450	10	LHPAAMP HLL	354	B*3801	67	1,81	122	12	22	22
442	450	9	HPAAMP HLL	355	B*0702	70	22	126	12	22	22
442	450	9	HPAAMP HLL	22	B*1402	93	22	168	12	22	22
442	450	9	HPAAMP HLL	22	B*3501	29	22	53	12	22	22
442	450	9	HPAAMP HLL	22	B*3503	85	22	154	12	22	22
442	450	9	HPAAMP HLL	22	B*3901	97	22	176	12	22	22
442	450	9	HPAAMP HLL	22	B*5301	33	22	59	12	22	22
442	450	9	HPAAMP HLL	22	B*5501	72	22	130	12	22	22
442	450	9	HPAAMP HLL	22	B*5601	58	22	104	12	22	22
441	451	11	LHPAAMP HLLI	356	B*3801	61	0,84	51	12	22	22
442	451	10	HPAAMP HLLI	357	B*1402	71	22	59	12	22	22
442	451	10	HPAAMP HLLI	22	B*3503	72	22	60	12	22	22
442	451	10	HPAAMP HLLI	22	B*3901	38	22	31	12	22	22
442	451	10	HPAAMP HLLI	22	B*5201	61	22	51	12	22	22

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
442	451	10	HPAAMPHELLI	33	B*5301	36	33	30	12	33	33	
442	451	10	HPAAMPHELLI	33	B*5501	84	33	70	12	33	33	
442	451	10	HPAAMPHELLI	33	B*5601	90	33	75	12	33	33	
444	451	8	AAMPHELLI	358	A*3201	59	33	49	12	33	33	
444	451	8	AAMPHELLI	33	B*1302	35	33	29	12	33	33	
444	451	8	AAMPHELLI	33	B*5101	47	33	39	12	33	33	
444	451	8	AAMPHELLI	33	B*5201	94	33	79	12	33	33	
444	451	8	AAMPHELLI	33	B*5801	37	33	31	12	33	33	
442	452	11	HPAAMPHELLIG	359	A*0201	51	0,32	16	12	33	33	
442	452	11	HPAAMPHELLIG	33	A*0206	38	33	12	12	33	33	
446	453	8	MPHELLIGS	360	A*6802	16	0,77	12	12	33	33	
446	453	8	MPHELLIGS	33	B*5601	28	33	22	12	33	33	
446	454	9	MPHELLIGSS	361	B*5501	37	0,26	10	12	33	33	
446	454	9	MPHELLIGSS	33	B*5601	41	33	11	12	33	33	
446	455	10	MPHELLIGSSG	362	B*0702	35	0,11	4	12	33	33	
446	455	10	MPHELLIGSSG	33	B*3501	40	33	4	12	33	33	
446	455	10	MPHELLIGSSG	33	B*5501	3	33	0	12	33	33	
446	455	10	MPHELLIGSSG	33	B*5601	18	33	2	12	33	33	
446	456	11	MPHELLIGSSGL	363	B*0702	93	1,81	168	12	33	33	
446	456	11	MPHELLIGSSGL	33	B*0801	44	33	80	12	33	33	
446	456	11	MPHELLIGSSGL	33	B*1402	92	33	167	12	33	33	
446	456	11	MPHELLIGSSGL	33	B*3501	27	33	48	12	33	33	
446	456	11	MPHELLIGSSGL	33	B*3503	70	33	127	12	33	33	
446	456	11	MPHELLIGSSGL	33	B*3901	62	33	113	12	33	33	
446	456	11	MPHELLIGSSGL	33	B*5101	40	33	73	12	33	33	
446	456	11	MPHELLIGSSGL	33	B*5301	18	33	33	12	33	33	
446	456	11	MPHELLIGSSGL	33	B*5501	71	33	129	12	33	33	
446	456	11	MPHELLIGSSGL	33	B*5601	53	33	95	12	33	33	
448	456	9	HELLIGSSGL	364	B*1502	83	33	151	12	33	33	
449	456	8	LLIGSSGL	365	B*0702	77	33	139	12	33	33	
448	458	11	HELLIGSSGLSR	366	A*0301	11	1,14	13	12	33	33	
448	458	11	HELLIGSSGLSR	33	A*3101	19	33	22	12	33	33	
448	458	11	HELLIGSSGLSR	33	A*3303	17	33	19	12	33	33	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
448	458	11	HLIGSSGLSR	367	A*7401	62	32	71	12	32	32
449	458	10	LLIGSSGLSR	367	A*7401	6	32	7	12	32	32
449	459	11	LLIGSSGLSRY	368	A*2501	57	1,50	85	12	32	32
449	459	11	LLIGSSGLSRY	368	A*2601	77	32	115	12	32	32
449	459	11	LLIGSSGLSRY	368	A*2902	89	32	133	12	32	32
449	459	11	LLIGSSGLSRY	368	A*3002	66	32	99	12	32	32
449	459	11	LLIGSSGLSRY	368	B*1501	81	32	122	12	32	32
449	459	11	LLIGSSGLSRY	368	B*1502	57	32	86	12	32	32
449	459	11	LLIGSSGLSRY	368	B*1525	41	32	61	12	32	32
449	459	11	LLIGSSGLSRY	368	B*4601	28	32	42	12	32	32
450	459	10	LIGSSGLSRY	369	A*0101	45	32	68	12	32	32
450	459	10	LIGSSGLSRY	369	A*3002	35	32	53	12	32	32
451	459	9	IGSSGLSRY	370	A*3002	94	32	141	12	32	32
452	459	8	GSSGLSRY	371	A*0101	83	32	124	12	32	32
452	459	8	GSSGLSRY	371	A*3002	77	32	116	12	32	32
					Cumulative Class I-BCI score:			12198			
485	492	8	SRQLYVSL	372	B*1402	84	1,59	134	13	481	514
485	492	8	SRQLYVSL	372	B*2702	89	32	142	13	32	32
485	492	8	SRQLYVSL	372	B*3901	86	32	137	13	32	32
485	492	8	SRQLYVSL	372	B*4801	2	32	3	13	32	32
484	493	10	CSRQLYVSLM	373	B*4601	43	1,55	66	13	32	32
485	493	9	SRQLYVSLM	374	B*2702	88	32	137	13	32	32
485	493	9	SRQLYVSLM	374	B*2705	85	32	132	13	32	32
486	493	8	RQLYVSLM	375	A*3201	53	32	82	13	32	32
486	493	8	RQLYVSLM	375	B*1301	85	32	131	13	32	32
486	493	8	RQLYVSLM	375	B*1302	13	32	20	13	32	32
486	493	8	RQLYVSLM	375	B*1402	15	32	24	13	32	32
486	493	8	RQLYVSLM	375	B*1501	48	32	75	13	32	32
486	493	8	RQLYVSLM	375	B*1525	75	32	116	13	32	32
486	493	8	RQLYVSLM	375	B*2702	73	32	114	13	32	32
486	493	8	RQLYVSLM	375	B*3901	51	32	79	13	32	32
486	493	8	RQLYVSLM	375	B*4801	94	32	146	13	32	32

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
485	494	10	SRQLYVSLML	376	B*1402	49	1,55	77	13	55	55	
485	494	10	SRQLYVSLML	55	B*2702	87	55	135	13	55	55	
485	494	10	SRQLYVSLML	55	B*2705	88	55	137	13	55	55	
485	494	10	SRQLYVSLML	55	B*3901	52	55	81	13	55	55	
486	494	9	RQLYVSLML	377	A*0206	19	55	29	13	55	55	
486	494	9	RQLYVSLML	55	A*3201	79	55	122	13	55	55	
486	494	9	RQLYVSLML	55	B*1301	80	55	125	13	55	55	
486	494	9	RQLYVSLML	55	B*1302	21	55	33	13	55	55	
486	494	9	RQLYVSLML	55	B*2702	72	55	112	13	55	55	
486	494	9	RQLYVSLML	55	B*2705	52	55	81	13	55	55	
486	494	9	RQLYVSLML	55	B*4001	52	55	81	13	55	55	
486	494	9	RQLYVSLML	55	B*4801	96	55	149	13	55	55	
487	494	8	QLYVSLML	378	A*0201	58	55	90	13	55	55	
485	495	11	SRQLYVSLMLL	379	B*1402	16	1,34	22	13	55	55	
485	495	11	SRQLYVSLMLL	55	B*2702	98	55	131	13	55	55	
485	495	11	SRQLYVSLMLL	55	B*2705	25	55	34	13	55	55	
486	495	10	RQLYVSLMLL	380	A*0206	48	55	64	13	55	55	
486	495	10	RQLYVSLMLL	55	B*1301	87	55	117	13	55	55	
486	495	10	RQLYVSLMLL	55	B*1302	34	55	45	13	55	55	
486	495	10	RQLYVSLMLL	55	B*2702	86	55	115	13	55	55	
486	495	10	RQLYVSLMLL	55	B*3801	10	55	14	13	55	55	
486	495	10	RQLYVSLMLL	55	B*3901	43	55	57	13	55	55	
486	495	10	RQLYVSLMLL	55	B*4801	100	55	134	13	55	55	
488	495	8	LYVSLMLL	381	A*2301	72	55	97	13	55	55	
488	495	8	LYVSLMLL	55	A*2402	72	55	96	13	55	55	
488	495	8	LYVSLMLL	55	B*0702	91	55	122	13	55	55	
486	496	11	RQLYVSLMLLY	382	A*0301	61	1,80	109	13	55	55	
486	496	11	RQLYVSLMLLY	55	B*1501	47	55	84	13	55	55	
486	496	11	RQLYVSLMLLY	55	B*1525	68	55	122	13	55	55	
486	496	11	RQLYVSLMLLY	55	B*2702	84	55	152	13	55	55	
486	496	11	RQLYVSLMLLY	55	B*2705	76	55	137	13	55	55	
487	496	10	QLYVSLMLLY	383	B*4403	44	55	79	13	55	55	
488	496	9	LYVSLMLLY	384	A*2902	98	55	177	13	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
489	496	8	YVSLMLLY	385	A*0101	94	22	170	13	22	22	
489	496	8	YVSLMLLY	22	A*2501	90	22	162	13	22	22	
489	496	8	YVSLMLLY	22	A*2601	97	22	176	13	22	22	
489	496	8	YVSLMLLY	22	A*3002	87	22	157	13	22	22	
489	496	8	YVSLMLLY	22	B*3501	88	22	159	13	22	22	
489	496	8	YVSLMLLY	22	B*4601	56	22	100	13	22	22	
487	497	11	QLYVSLMLLYK	386	A*1101	85	1,07	91	13	22	22	
487	497	11	QLYVSLMLLYK	22	A*7401	61	22	65	13	22	22	
488	497	10	LYVSLMLLYK	387	A*0301	25	22	26	13	22	22	
489	497	9	YVSLMLLYK	388	A*0301	67	22	72	13	22	22	
489	497	9	YVSLMLLYK	22	A*1101	91	22	98	13	22	22	
489	497	9	YVSLMLLYK	22	A*6801	66	22	71	13	22	22	
489	497	9	YVSLMLLYK	22	A*7401	12	22	13	13	22	22	
490	497	8	VSLMLLYK	389	A*0301	80	22	86	13	22	22	
490	497	8	VSLMLLYK	22	A*1101	98	22	105	13	22	22	
490	497	8	VSLMLLYK	22	A*7401	35	22	38	13	22	22	
489	499	11	YVSLMLLYKTY	390	A*0101	81	1,86	151	13	22	22	
489	499	11	YVSLMLLYKTY	22	A*2501	55	22	102	13	22	22	
489	499	11	YVSLMLLYKTY	22	A*2601	74	22	138	13	22	22	
489	499	11	YVSLMLLYKTY	22	A*2902	86	22	159	13	22	22	
489	499	11	YVSLMLLYKTY	22	A*3002	42	22	78	13	22	22	
489	499	11	YVSLMLLYKTY	22	B*1502	31	22	58	13	22	22	
489	499	11	YVSLMLLYKTY	22	B*4601	13	22	24	13	22	22	
490	499	10	VSLMLLYKTY	391	A*0101	75	22	140	13	22	22	
490	499	10	VSLMLLYKTY	22	A*3002	48	22	89	13	22	22	
490	499	10	VSLMLLYKTY	22	B*5802	38	22	70	13	22	22	
492	499	8	LMLLYKTY	392	A*2902	52	22	97	13	22	22	
492	499	8	LMLLYKTY	22	B*1525	19	22	35	13	22	22	
492	499	8	LMLLYKTY	22	B*3501	57	22	106	13	22	22	
491	500	10	SLMLLYKTYG	393	A*0201	9	0,13	1	13	22	22	
491	501	11	SLMLLYKTYGW	394	A*3201	68	1,93	132	13	22	22	
492	501	10	LMLLYKTYGW	395	A*2301	17	22	33	13	22	22	
492	501	10	LMLLYKTYGW	22	B*5301	28	22	54	13	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
492	501	10	LMLLYKTYGW	396	B*5802	36	32	70	13	32	32	
493	501	9	MLLYKTYGW	396	A*3201	92	32	179	13	32	32	
493	501	9	MLLYKTYGW	397	B*5701	36	32	70	13	32	32	
493	501	9	MLLYKTYGW	397	B*5801	31	32	59	13	32	32	
494	501	8	LLYKTYGW	397	A*3201	50	32	97	13	32	32	
494	501	8	LLYKTYGW	397	B*5701	47	32	91	13	32	32	
494	501	8	LLYKTYGW	397	B*5801	53	32	102	13	32	32	
494	501	8	LLYKTYGW	398	B*5802	6	32	11	13	32	32	
492	502	11	LMLLYKTYGWK	398	A*0206	15	0,71	10	13	32	32	
492	502	11	LMLLYKTYGWK	399	A*0301	79	32	56	13	32	32	
492	502	11	LMLLYKTYGWK	399	A*1101	20	32	14	13	32	32	
492	502	11	LMLLYKTYGWK	399	A*7401	34	32	24	13	32	32	
493	502	10	MLLYKTYGWK	399	A*0301	97	32	69	13	32	32	
493	502	10	MLLYKTYGWK	399	A*1101	26	32	19	13	32	32	
493	502	10	MLLYKTYGWK	399	A*7401	48	32	34	13	32	32	
494	502	9	LLYKTYGWK	400	A*0301	95	32	68	13	32	32	
495	502	8	LYKTYGWK	401	A*3001	24	32	17	13	32	32	
493	503	11	MLLYKTYGWKL	402	A*3201	52	32	100	13	32	32	
493	503	11	MLLYKTYGWKL	402	B*0801	98	32	192	13	32	32	
493	503	11	MLLYKTYGWKL	402	B*1402	9	32	18	13	32	32	
494	503	10	LLYKTYGWKL	403	A*0201	82	32	58	13	32	32	
495	503	9	LYKTYGWKL	404	A*2301	24	1,95	47	13	32	32	
495	503	9	LYKTYGWKL	404	A*2402	60	32	116	13	32	32	
496	503	8	YKTYGWKL	405	B*3901	84	32	165	13	32	32	
495	504	10	LYKTYGWKLH	406	A*3201	35	0,88	31	13	32	32	
497	504	8	KTYGWKLH	407	A*0301	59	32	52	13	32	32	
497	504	8	KTYGWKLH	407	A*7401	5	32	4	13	32	32	
495	505	11	LYKTYGWKLHL	408	A*2301	45	1,71	77	13	32	32	
495	505	11	LYKTYGWKLHL	408	A*2402	51	32	87	13	32	32	
496	505	10	YKTYGWKLHL	409	B*3901	12	32	20	13	32	32	
497	505	9	KTYGWKLHL	410	A*3201	86	32	148	13	32	32	
497	505	9	KTYGWKLHL	410	A*7401	4	32	6	13	32	32	
497	505	9	KTYGWKLHL	410	B*5701	68	32	117	13	32	32	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
497	505	9	KTYGWLHL	33	B*5801	47	33	81	13	33	33	
497	505	9	KTYGWLHL	33	B*5802	28	33	47	13	33	33	
498	505	8	TYGWLHL	411	A*2301	64	33	109	13	33	33	
498	505	8	TYGWLHL	33	A*2402	63	33	108	13	33	33	
496	506	11	YKTYGWLHLY	412	A*2902	30	1,90	57	13	33	33	
497	506	10	KTYGWLHLY	413	A*0101	77	33	147	13	33	33	
497	506	10	KTYGWLHLY	33	A*0301	92	33	175	13	33	33	
497	506	10	KTYGWLHLY	33	A*2501	78	33	148	13	33	33	
497	506	10	KTYGWLHLY	33	A*3002	97	33	185	13	33	33	
497	506	10	KTYGWLHLY	33	A*7401	85	33	162	13	33	33	
497	506	10	KTYGWLHLY	33	B*5802	83	33	157	13	33	33	
498	506	9	TYGWLHLY	414	A*2402	37	33	70	13	33	33	
498	506	9	TYGWLHLY	33	A*2902	90	33	172	13	33	33	
498	506	9	TYGWLHLY	33	A*3002	70	33	134	13	33	33	
499	506	8	YGWLHLY	415	A*2902	97	33	184	13	33	33	
499	506	8	YGWLHLY	33	A*3002	76	33	145	13	33	33	
499	506	8	YGWLHLY	33	B*3501	55	33	104	13	33	33	
500	510	11	GWKLHLYSHPI	416	B*0801	32	0,99	32	13	33	33	
501	510	10	WKLHLYSHPI	417	B*1301	54	33	53	13	33	33	
501	510	10	WKLHLYSHPI	33	B*1302	27	33	27	13	33	33	
501	510	10	WKLHLYSHPI	33	B*3701	43	33	42	13	33	33	
501	510	10	WKLHLYSHPI	33	B*3901	69	33	68	13	33	33	
501	510	10	WKLHLYSHPI	33	B*5201	78	33	78	13	33	33	
502	510	9	KLHLYSHPI	418	A*0201	49	33	48	13	33	33	
502	510	9	KLHLYSHPI	33	A*3201	77	33	77	13	33	33	
503	510	8	LHLYSHPI	419	B*1402	78	33	77	13	33	33	
503	510	8	LHLYSHPI	33	B*2702	10	33	10	13	33	33	
503	510	8	LHLYSHPI	33	B*3801	92	33	91	13	33	33	
503	510	8	LHLYSHPI	33	B*5101	52	33	51	13	33	33	
503	510	8	LHLYSHPI	33	B*5201	84	33	84	13	33	33	
502	511	10	KLHLYSHPIV	420	A*0201	13	0,55	7	13	33	33	
502	511	10	KLHLYSHPIV	33	A*3001	98	33	54	13	33	33	
503	511	9	LHLYSHPIV	421	B*5101	3	33	2	13	33	33	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
504	511	8	HLYSHPIV	422	A*0201	56	22	30	13	22	22	
504	511	8	HLYSHPIV	22	B*0801	25	22	14	13	22	22	
502	512	11	KLHLYSHPIVL	423	A*3201	41	1,95	80	13	22	22	
502	512	11	KLHLYSHPIVL	22	B*0801	27	22	53	13	22	22	
502	512	11	KLHLYSHPIVL	22	B*4801	56	22	109	13	22	22	
503	512	10	LHLYSHPIVL	424	B*1402	91	22	177	13	22	22	
503	512	10	LHLYSHPIVL	22	B*3801	78	22	151	13	22	22	
503	512	10	LHLYSHPIVL	22	B*3901	83	22	162	13	22	22	
504	512	9	HLYSHPIVL	425	A*0201	18	22	35	13	22	22	
504	512	9	HLYSHPIVL	22	B*1402	83	22	162	13	22	22	
504	512	9	HLYSHPIVL	22	B*1502	24	22	47	13	22	22	
504	512	9	HLYSHPIVL	22	B*3901	91	22	177	13	22	22	
505	512	8	LYSHPIVL	426	A*2301	22	22	44	13	22	22	
505	512	8	LYSHPIVL	22	A*2402	46	22	89	13	22	22	
504	514	11	HLYSHPIVLGF	427	A*2501	43	1,62	69	13	22	22	
504	514	11	HLYSHPIVLGF	22	A*2601	10	22	17	13	22	22	
504	514	11	HLYSHPIVLGF	22	A*3201	100	22	162	13	22	22	
504	514	11	HLYSHPIVLGF	22	B*1402	30	22	49	13	22	22	
504	514	11	HLYSHPIVLGF	22	B*1501	80	22	129	13	22	22	
504	514	11	HLYSHPIVLGF	22	B*1502	96	22	156	13	22	22	
504	514	11	HLYSHPIVLGF	22	B*1525	90	22	145	13	22	22	
505	514	10	LYSHPIVLGF	428	A*2301	84	22	136	13	22	22	
505	514	10	LYSHPIVLGF	22	A*2402	86	22	139	13	22	22	
505	514	10	LYSHPIVLGF	22	A*2902	76	22	123	13	22	22	
506	514	9	YSHPIVLGF	429	B*4601	64	22	103	13	22	22	
506	514	9	YSHPIVLGF	22	B*5801	71	22	115	13	22	22	
506	514	9	YSHPIVLGF	22	B*5802	59	22	96	13	22	22	
					Cumulative BCI Class Iscore:				15733			
524	531	8	SPFLLAQF	432	B*1402	67	1,59	106	14	524	559	
524	531	8	SPFLLAQF	22	B*1502	6	22	9	14	22	22	
524	531	8	SPFLLAQF	22	B*3503	61	22	97	14	22	22	
524	531	8	SPFLLAQF	22	B*5301	72	22	115	14	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
524	532	9	SPFLLAQFT	433	B*5601	17	0,30	5	14	55	55	
524	533	10	SPFLLAQFTS	434	A*3201	5	0,76	3	14	55	55	
524	533	10	SPFLLAQFTS	55	B*3501	1	55	1	14	55	55	
524	533	10	SPFLLAQFTS	55	B*5601	27	55	21	14	55	55	
526	533	8	FLLAQFTS	435	A*0201	42	55	32	14	55	55	
524	534	11	SPFLLAQFTSA	436	B*0702	46	0,92	43	14	55	55	
524	534	11	SPFLLAQFTSA	55	B*3503	3	55	2	14	55	55	
524	534	11	SPFLLAQFTSA	55	B*5101	25	55	23	14	55	55	
524	534	11	SPFLLAQFTSA	55	B*5501	98	55	90	14	55	55	
524	534	11	SPFLLAQFTSA	55	B*5601	95	55	88	14	55	55	
526	534	9	FLLAQFTSA	437	A*0201	84	55	78	14	55	55	
526	534	9	FLLAQFTSA	55	A*0206	98	55	91	14	55	55	
526	534	9	FLLAQFTSA	55	B*0801	78	55	72	14	55	55	
526	535	10	FLLAQFTSAI	438	A*0201	76	0,94	71	14	55	55	
526	535	10	FLLAQFTSAI	55	A*0206	79	55	75	14	55	55	
526	535	10	FLLAQFTSAI	55	B*1302	11	55	11	14	55	55	
526	535	10	FLLAQFTSAI	55	B*3801	47	55	44	14	55	55	
526	535	10	FLLAQFTSAI	55	B*4601	11	55	11	14	55	55	
526	535	10	FLLAQFTSAI	55	B*5201	14	55	13	14	55	55	
527	535	9	LLAQFTSAI	439	A*3201	3	55	3	14	55	55	
527	535	9	LLAQFTSAI	55	B*1525	17	55	16	14	55	55	
527	535	9	LLAQFTSAI	55	B*5501	19	55	18	14	55	55	
528	535	8	LAQFTSAI	440	B*5101	62	55	58	14	55	55	
528	535	8	LAQFTSAI	55	B*5201	76	55	72	14	55	55	
528	535	8	LAQFTSAI	55	B*5301	5	55	5	14	55	55	
527	537	11	LLAQFTSAICS	441	A*6802	22	0,41	9	14	55	55	
528	538	11	LAQFTSAICSV	442	B*5101	13	1,40	19	14	55	55	
528	538	11	LAQFTSAICSV	55	B*5201	12	55	16	14	55	55	
529	538	10	AQFTSAICSV	443	A*0201	55	55	77	14	55	55	
529	538	10	AQFTSAICSV	55	A*0206	85	55	119	14	55	55	
529	538	10	AQFTSAICSV	55	B*1301	83	55	116	14	55	55	
529	538	10	AQFTSAICSV	55	B*1302	46	55	65	14	55	55	
529	538	10	AQFTSAICSV	55	B*3701	14	55	20	14	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
529	538	10	AQFTSAICSV	55	B*3901	10	55	15	14	55	55	
529	538	10	AQFTSAICSV	55	B*4801	77	55	108	14	55	55	
529	538	10	AQFTSAICSV	55	B*4901	30	55	43	14	55	55	
529	538	10	AQFTSAICSV	55	B*5001	64	55	90	14	55	55	
529	538	10	AQFTSAICSV	55	B*5201	82	55	115	14	55	55	
531	538	8	FTSAICSV	444	A*2501	82	55	114	14	55	55	
531	538	8	FTSAICSV	55	A*2601	49	55	68	14	55	55	
529	539	11	AQFTSAICSVV	445	B*1301	75	1,34	100	14	55	55	
529	539	11	AQFTSAICSVV	55	B*1302	41	55	55	14	55	55	
529	539	11	AQFTSAICSVV	55	B*4002	20	55	27	14	55	55	
529	539	11	AQFTSAICSVV	55	B*4801	62	55	83	14	55	55	
529	539	11	AQFTSAICSVV	55	B*4901	26	55	35	14	55	55	
529	539	11	AQFTSAICSVV	55	B*5001	60	55	81	14	55	55	
529	539	11	AQFTSAICSVV	55	B*5201	53	55	71	14	55	55	
531	539	9	FTSAICSVV	446	A*6802	49	55	65	14	55	55	
531	539	9	FTSAICSVV	55	B*4601	31	55	42	14	55	55	
531	539	9	FTSAICSVV	55	B*5201	2	55	3	14	55	55	
531	539	9	FTSAICSVV	55	B*5601	4	55	5	14	55	55	
530	540	11	QFTSAICSVVR	447	A*3303	30	1,19	35	14	55	55	
531	540	10	FTSAICSVVR	448	A*3101	38	55	45	14	55	55	
531	540	10	FTSAICSVVR	55	A*3303	92	55	109	14	55	55	
531	540	10	FTSAICSVVR	55	A*6801	100	55	119	14	55	55	
531	540	10	FTSAICSVVR	55	A*7401	68	55	81	14	55	55	
531	540	10	FTSAICSVVR	55	B*5701	23	55	27	14	55	55	
532	540	9	TSAICSVVR	449	A*6801	82	55	98	14	55	55	
533	540	8	SAICSVVR	450	A*3101	11	55	14	14	55	55	
533	540	8	SAICSVVR	55	A*3303	39	55	47	14	55	55	
533	540	8	SAICSVVR	55	A*6801	81	55	96	14	55	55	
531	541	11	FTSAICSVVRR	451	A*1101	2	1,69	4	14	55	55	
531	541	11	FTSAICSVVRR	55	A*3101	32	55	54	14	55	55	
531	541	11	FTSAICSVVRR	55	A*3303	96	55	162	14	55	55	
531	541	11	FTSAICSVVRR	55	A*7401	77	55	130	14	55	55	
532	541	10	TSAICSVVRR	452	A*3101	37	55	62	14	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
532	541	10	TSAICSVVRR	32	A*6801	99	32	167	14	32	32	
533	541	9	SAICSVVRR	453	A*3101	6	32	11	14	32	32	
533	541	9	SAICSVVRR	32	A*3303	63	32	107	14	32	32	
533	541	9	SAICSVVRR	32	A*6801	85	32	144	14	32	32	
533	541	9	SAICSVVRR	32	A*7401	46	32	78	14	32	32	
534	541	8	AICSVVRR	454	A*3101	56	32	94	14	32	32	
534	541	8	AICSVVRR	32	A*7401	84	32	142	14	32	32	
533	543	11	SAICSVVRRAF	455	A*2501	10	1,06	11	14	32	32	
533	543	11	SAICSVVRRAF	32	B*0702	12	32	12	14	32	32	
533	543	11	SAICSVVRRAF	32	B*1501	78	32	83	14	32	32	
533	543	11	SAICSVVRRAF	32	B*1502	94	32	100	14	32	32	
533	543	11	SAICSVVRRAF	32	B*1525	88	32	94	14	32	32	
533	543	11	SAICSVVRRAF	32	B*3501	71	32	75	14	32	32	
533	543	11	SAICSVVRRAF	32	B*3503	31	32	33	14	32	32	
533	543	11	SAICSVVRRAF	32	B*4601	90	32	96	14	32	32	
536	543	8	CSVVRRAF	456	B*1502	30	32	31	14	32	32	
536	543	8	CSVVRRAF	32	B*1525	3	32	4	14	32	32	
536	543	8	CSVVRRAF	32	B*4601	36	32	38	14	32	32	
536	545	10	CSVVRRAFPH	457	B*5801	8	0,14	1	14	32	32	
538	545	8	VVRRAFPH	458	A*3001	10	32	1	14	32	32	
537	546	10	SVVRRAFPHC	459	A*3001	28	0,21	6	14	32	32	
537	547	11	SVVRRAFPHCL	460	B*0801	71	1,96	140	14	32	32	
539	547	9	VVRAFPCHL	461	B*1402	28	32	56	14	32	32	
539	547	9	VVRAFPCHL	32	B*2702	51	32	99	14	32	32	
539	547	9	VVRAFPCHL	32	B*2705	3	32	6	14	32	32	
540	547	8	RRAFPHCL	462	B*1402	47	32	93	14	32	32	
540	547	8	RRAFPHCL	32	B*2702	96	32	189	14	32	32	
540	547	8	RRAFPHCL	32	B*2705	93	32	182	14	32	32	
540	547	8	RRAFPHCL	32	B*3901	9	32	18	14	32	32	
540	547	8	RRAFPHCL	32	B*4801	6	32	11	14	32	32	
538	548	11	VVRRAFPHCLA	463	A*3001	86	1,06	91	14	32	32	
540	548	9	RRAFPHCLA	464	B*2702	45	32	47	14	32	32	
540	548	9	RRAFPHCLA	32	B*2705	39	32	41	14	32	32	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
541	548	8	RAFPHCIA	465	A*3001	68	22	72	14	22	22	
540	549	10	RRAFPHCIAF	466	B*2702	95	1,82	173	14	22	22	
540	549	10	RRAFPHCIAF	22	B*2705	91	22	165	14	22	22	
541	549	9	RAFPHCIAF	467	A*3201	73	22	132	14	22	22	
541	549	9	RAFPHCIAF	22	B*1301	79	22	143	14	22	22	
541	549	9	RAFPHCIAF	22	B*1402	66	22	119	14	22	22	
541	549	9	RAFPHCIAF	22	B*1501	84	22	153	14	22	22	
541	549	9	RAFPHCIAF	22	B*3501	68	22	124	14	22	22	
541	549	9	RAFPHCIAF	22	B*4601	97	22	176	14	22	22	
541	549	9	RAFPHCIAF	22	B*5201	75	22	135	14	22	22	
541	549	9	RAFPHCIAF	22	B*5701	59	22	107	14	22	22	
541	549	9	RAFPHCIAF	22	B*5801	81	22	148	14	22	22	
542	549	8	AFPHCIAF	468	A*2301	71	22	128	14	22	22	
542	549	8	AFPHCIAF	22	A*2402	70	22	128	14	22	22	
543	550	8	FPHCIAFS	469	B*3501	67	0,25	17	14	22	22	
543	550	8	FPHCIAFS	22	B*5501	17	22	4	14	22	22	
543	550	8	FPHCIAFS	22	B*5601	56	22	14	14	22	22	
541	551	11	RAFPHCIAFSY	470	A*0301	77	1,93	149	14	22	22	
541	551	11	RAFPHCIAFSY	22	A*3201	94	22	182	14	22	22	
541	551	11	RAFPHCIAFSY	22	B*1301	66	22	128	14	22	22	
541	551	11	RAFPHCIAFSY	22	B*1501	91	22	175	14	22	22	
541	551	11	RAFPHCIAFSY	22	B*1502	93	22	179	14	22	22	
541	551	11	RAFPHCIAFSY	22	B*1525	95	22	183	14	22	22	
541	551	11	RAFPHCIAFSY	22	B*5701	89	22	173	14	22	22	
541	551	11	RAFPHCIAFSY	22	B*5802	86	22	165	14	22	22	
542	551	10	AFPHCIAFSY	471	A*2902	94	22	181	14	22	22	
543	551	9	FPHCIAFSY	472	B*3501	97	22	188	14	22	22	
543	551	9	FPHCIAFSY	22	B*3503	91	22	175	14	22	22	
543	551	9	FPHCIAFSY	22	B*5301	98	22	190	14	22	22	
543	551	9	FPHCIAFSY	22	B*5501	83	22	160	14	22	22	
542	552	11	AFPHCIAFSYM	473	A*2402	4	1,02	4	14	22	22	
543	552	10	FPHCIAFSYM	474	B*0702	64	22	65	14	22	22	
543	552	10	FPHCIAFSYM	22	B*1402	90	22	92	14	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
543	552	10	FPHCLAFSYM	55	B*3501	96	55	98	14	55	55
543	552	10	FPHCLAFSYM	55	B*3503	99	55	100	14	55	55
543	552	10	FPHCLAFSYM	55	B*3901	68	55	69	14	55	55
543	552	10	FPHCLAFSYM	55	B*5101	98	55	100	14	55	55
543	552	10	FPHCLAFSYM	55	B*5301	97	55	98	14	55	55
543	552	10	FPHCLAFSYM	55	B*5501	97	55	98	14	55	55
543	552	10	FPHCLAFSYM	55	B*5601	87	55	89	14	55	55
545	555	11	HCLAFSYMDDV	475	A*0201	73	0,60	44	14	55	55
547	555	9	LAFSYMDDV	476	B*5101	20	55	12	14	55	55
547	556	10	LAFSYMDDVV	477	B*5201	51	0,34	17	14	55	55
549	556	8	FSYMDDVV	478	B*4601	34	55	12	14	55	55
549	556	8	FSYMDDVV	55	B*5101	23	55	8	14	55	55
549	556	8	FSYMDDVV	55	B*5201	39	55	13	14	55	55
547	557	11	LAFSYMDDVVVL	479	B*3503	11	1,21	13	14	55	55
547	557	11	LAFSYMDDVVVL	55	B*3801	29	55	35	14	55	55
547	557	11	LAFSYMDDVVVL	55	B*3901	19	55	24	14	55	55
547	557	11	LAFSYMDDVVVL	55	B*4801	23	55	28	14	55	55
549	557	9	FSYMDDVVVL	480	B*3901	25	55	30	14	55	55
549	557	9	FSYMDDVVVL	55	B*4601	62	55	76	14	55	55
550	557	8	SYMDDVVVL	481	A*2301	38	55	46	14	55	55
550	557	8	SYMDDVVVL	55	A*2402	47	55	57	14	55	55
551	559	9	YMDDVVVLGA	482	A*0101	66	1,49	98	14	55	55
551	559	9	YMDDVVVLGA	55	A*0201	100	55	149	14	55	55
551	559	9	YMDDVVVLGA	55	A*0206	71	55	105	14	55	55
552	559	8	MDDVVVLGA	483	A*6802	34	55	50	14	55	55
				Cumulative Class I-BCI score:				12015			
526	533	8	FLLAQFTS	435	A*0201	42	0,76	32	15	526	559
524	534	11	SPFLLAQFTSA	436	B*0702	46	0,92	43	15	55	55
524	534	11	SPFLLAQFTSA	55	B*3503	3	55	2	15	55	55
524	534	11	SPFLLAQFTSA	55	B*5101	25	55	23	15	55	55
524	534	11	SPFLLAQFTSA	55	B*5501	98	55	90	15	55	55
524	534	11	SPFLLAQFTSA	55	B*5601	95	55	88	15	55	55

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
526	534	9	FLLAQFTSA	437	A*0201	84	22	78	15	22	22
526	534	9	FLLAQFTSA	22	A*0206	98	22	91	15	22	22
526	534	9	FLLAQFTSA	22	B*0801	78	22	72	15	22	22
526	535	10	FLLAQFTSAI	438	A*0201	76	0,94	71	15	22	22
526	535	10	FLLAQFTSAI	22	A*0206	79	22	75	15	22	22
526	535	10	FLLAQFTSAI	22	B*1302	11	22	11	15	22	22
526	535	10	FLLAQFTSAI	22	B*3801	47	22	44	15	22	22
526	535	10	FLLAQFTSAI	22	B*4601	11	22	11	15	22	22
526	535	10	FLLAQFTSAI	22	B*5201	14	22	13	15	22	22
527	535	9	LLAQFTSAI	439	A*3201	3	22	3	15	22	22
527	535	9	LLAQFTSAI	22	B*1525	17	22	16	15	22	22
527	535	9	LLAQFTSAI	22	B*5501	19	22	18	15	22	22
528	535	8	LAQFTSAI	440	B*5101	62	22	58	15	22	22
528	535	8	LAQFTSAI	22	B*5201	76	22	72	15	22	22
528	535	8	LAQFTSAI	22	B*5301	5	22	5	15	22	22
527	537	11	LLAQFTSAICS	441	A*6802	22	0,41	9	15	22	22
528	538	11	LAQFTSAICSV	442	B*5101	13	1,40	19	15	22	22
528	538	11	LAQFTSAICSV	22	B*5201	12	22	16	15	22	22
529	538	10	AQFTSAICSV	443	A*0201	55	22	77	15	22	22
529	538	10	AQFTSAICSV	22	A*0206	85	22	119	15	22	22
529	538	10	AQFTSAICSV	22	B*1301	83	22	116	15	22	22
529	538	10	AQFTSAICSV	22	B*1302	46	22	65	15	22	22
529	538	10	AQFTSAICSV	22	B*3701	14	22	20	15	22	22
529	538	10	AQFTSAICSV	22	B*3901	10	22	15	15	22	22
529	538	10	AQFTSAICSV	22	B*4801	77	22	108	15	22	22
529	538	10	AQFTSAICSV	22	B*4901	30	22	43	15	22	22
529	538	10	AQFTSAICSV	22	B*5001	64	22	90	15	22	22
529	538	10	AQFTSAICSV	22	B*5201	82	22	115	15	22	22
531	538	8	FTSAICSV	444	A*2501	82	22	114	15	22	22
531	538	8	FTSAICSV	22	A*2601	49	22	68	15	22	22
529	539	11	AQFTSAICSVV	445	B*1301	75	1,34	100	15	22	22
529	539	11	AQFTSAICSVV	22	B*1302	41	22	55	15	22	22
529	539	11	AQFTSAICSVV	22	B*4002	20	22	27	15	22	22

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
529	539	11	AQFTSAICSVV	33	B*4801	62	33	83	15	33	33	
529	539	11	AQFTSAICSVV	33	B*4901	26	33	35	15	33	33	
529	539	11	AQFTSAICSVV	33	B*5001	60	33	81	15	33	33	
529	539	11	AQFTSAICSVV	33	B*5201	53	33	71	15	33	33	
531	539	9	FTSAICSVV	446	A*6802	49	33	65	15	33	33	
531	539	9	FTSAICSVV	33	B*4601	31	33	42	15	33	33	
531	539	9	FTSAICSVV	33	B*5201	2	33	3	15	33	33	
531	539	9	FTSAICSVV	33	B*5601	4	33	5	15	33	33	
530	540	11	QFTSAICSVVR	447	A*3303	30	1,19	35	15	33	33	
531	540	10	FTSAICSVVR	448	A*3101	38	33	45	15	33	33	
531	540	10	FTSAICSVVR	33	A*3303	92	33	109	15	33	33	
531	540	10	FTSAICSVVR	33	A*6801	100	33	119	15	33	33	
531	540	10	FTSAICSVVR	33	A*7401	68	33	81	15	33	33	
531	540	10	FTSAICSVVR	33	B*5701	23	33	27	15	33	33	
532	540	9	TSAICSVVR	449	A*6801	82	33	98	15	33	33	
533	540	8	SAICSVVR	450	A*3101	11	33	14	15	33	33	
533	540	8	SAICSVVR	33	A*3303	39	33	47	15	33	33	
533	540	8	SAICSVVR	33	A*6801	81	33	96	15	33	33	
531	541	11	FTSAICSVVRR	451	A*1101	2	1,69	4	15	33	33	
531	541	11	FTSAICSVVRR	33	A*3101	32	33	54	15	33	33	
531	541	11	FTSAICSVVRR	33	A*3303	96	33	162	15	33	33	
531	541	11	FTSAICSVVRR	33	A*7401	77	33	130	15	33	33	
532	541	10	TSAICSVVRR	452	A*3101	37	33	62	15	33	33	
532	541	10	TSAICSVVRR	33	A*6801	99	33	167	15	33	33	
533	541	9	SAICSVVRR	453	A*3101	6	33	11	15	33	33	
533	541	9	SAICSVVRR	33	A*3303	63	33	107	15	33	33	
533	541	9	SAICSVVRR	33	A*6801	85	33	144	15	33	33	
533	541	9	SAICSVVRR	33	A*7401	46	33	78	15	33	33	
534	541	8	AICSVVRR	454	A*3101	56	33	94	15	33	33	
534	541	8	AICSVVRR	33	A*7401	84	33	142	15	33	33	
533	543	11	SAICSVRRRAF	455	A*2501	10	1,06	11	15	33	33	
533	543	11	SAICSVRRRAF	33	B*0702	12	33	12	15	33	33	
533	543	11	SAICSVRRRAF	33	B*1501	78	33	83	15	33	33	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
533	543	11	SAICSVVRRAF	53	B*1502	94	52	100	15	53	55	
533	543	11	SAICSVVRRAF	53	B*1525	88	52	94	15	53	55	
533	543	11	SAICSVVRRAF	53	B*3501	71	52	75	15	53	55	
533	543	11	SAICSVVRRAF	53	B*3503	31	52	33	15	53	55	
533	543	11	SAICSVVRRAF	53	B*4601	90	52	96	15	53	55	
536	543	8	CSVVRRAF	456	B*1502	30	52	31	15	53	55	
536	543	8	CSVVRRAF	53	B*1525	3	52	4	15	53	55	
536	543	8	CSVVRRAF	53	B*4601	36	52	38	15	53	55	
536	545	10	CSVVRRAFPH	457	B*5801	8	0,14	1	15	53	55	
538	545	8	VVRRAFPH	458	A*3001	10	52	1	15	53	55	
537	546	10	SVVRRAFPHC	459	A*3001	28	0,21	6	15	53	55	
537	547	11	SVVRRAFPHCL	460	B*0801	71	1,96	140	15	53	55	
539	547	9	VRRAFPHCL	461	B*1402	28	52	56	15	53	55	
539	547	9	VRRAFPHCL	53	B*2702	51	52	99	15	53	55	
539	547	9	VRRAFPHCL	53	B*2705	3	52	6	15	53	55	
540	547	8	RRAFPHCL	462	B*1402	47	52	93	15	53	55	
540	547	8	RRAFPHCL	53	B*2702	96	52	189	15	53	55	
540	547	8	RRAFPHCL	53	B*2705	93	52	182	15	53	55	
540	547	8	RRAFPHCL	53	B*3901	9	52	18	15	53	55	
540	547	8	RRAFPHCL	53	B*4801	6	52	11	15	53	55	
538	548	11	VVRRAFPHCLA	463	A*3001	86	1,06	91	15	53	55	
540	548	9	RRAFPHCLA	464	B*2702	45	52	47	15	53	55	
540	548	9	RRAFPHCLA	53	B*2705	39	52	41	15	53	55	
541	548	8	RAFPHCLA	465	A*3001	68	52	72	15	53	55	
540	549	10	RRAFPHCLAF	466	B*2702	95	1,82	173	15	53	55	
540	549	10	RRAFPHCLAF	53	B*2705	91	52	165	15	53	55	
541	549	9	RAFPHCLAF	467	A*3201	73	52	132	15	53	55	
541	549	9	RAFPHCLAF	53	B*1301	79	52	143	15	53	55	
541	549	9	RAFPHCLAF	53	B*1402	66	52	119	15	53	55	
541	549	9	RAFPHCLAF	53	B*1501	84	52	153	15	53	55	
541	549	9	RAFPHCLAF	53	B*3501	68	52	124	15	53	55	
541	549	9	RAFPHCLAF	53	B*4601	97	52	176	15	53	55	
541	549	9	RAFPHCLAF	53	B*5201	75	52	135	15	53	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
541	549	9	RAFPCHLAF	33	B*5701	59	33	107	15	33	33
541	549	9	RAFPCHLAF	33	B*5801	81	33	148	15	33	33
542	549	8	AFPHCLAF	468	A*2301	71	33	128	15	33	33
542	549	8	AFPHCLAF	33	A*2402	70	33	128	15	33	33
543	550	8	FPHCLAFS	469	B*3501	67	0,25	17	15	33	33
543	550	8	FPHCLAFS	33	B*5501	17	33	4	15	33	33
543	550	8	FPHCLAFS	33	B*5601	56	33	14	15	33	33
541	551	11	RAFPCHLAFSY	470	A*0301	77	1,93	149	15	33	33
541	551	11	RAFPCHLAFSY	33	A*3201	94	33	182	15	33	33
541	551	11	RAFPCHLAFSY	33	B*1301	66	33	128	15	33	33
541	551	11	RAFPCHLAFSY	33	B*1501	91	33	175	15	33	33
541	551	11	RAFPCHLAFSY	33	B*1502	93	33	179	15	33	33
541	551	11	RAFPCHLAFSY	33	B*1525	95	33	183	15	33	33
541	551	11	RAFPCHLAFSY	33	B*5701	89	33	173	15	33	33
541	551	11	RAFPCHLAFSY	33	B*5802	86	33	165	15	33	33
542	551	10	AFPHCLAFSY	471	A*2902	94	33	181	15	33	33
543	551	9	FPHCLAFSY	472	B*3501	97	33	188	15	33	33
543	551	9	FPHCLAFSY	33	B*3503	91	33	175	15	33	33
543	551	9	FPHCLAFSY	33	B*5301	98	33	190	15	33	33
543	551	9	FPHCLAFSY	33	B*5501	83	33	160	15	33	33
542	552	11	AFPHCLAFSYM	473	A*2402	4	1,02	4	15	33	33
543	552	10	FPHCLAFSYM	474	B*0702	64	33	65	15	33	33
543	552	10	FPHCLAFSYM	33	B*1402	90	33	92	15	33	33
543	552	10	FPHCLAFSYM	33	B*3501	96	33	98	15	33	33
543	552	10	FPHCLAFSYM	33	B*3503	99	33	100	15	33	33
543	552	10	FPHCLAFSYM	33	B*3901	68	33	69	15	33	33
543	552	10	FPHCLAFSYM	33	B*5101	98	33	100	15	33	33
543	552	10	FPHCLAFSYM	33	B*5301	97	33	98	15	33	33
543	552	10	FPHCLAFSYM	33	B*5501	97	33	98	15	33	33
543	552	10	FPHCLAFSYM	33	B*5601	87	33	89	15	33	33
545	555	11	HCLAFSYMDDV	475	A*0201	73	0,60	44	15	33	33
547	555	9	LAFSYMDDV	476	B*5101	20	33	12	15	33	33
547	556	10	LAFSYMDDVV	477	B*5201	51	0,34	17	15	33	33

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
549	556	8	FSYMDDVV	478	B*4601	34	22	12	15	22	22
549	556	8	FSYMDDVV	22	B*5101	23	22	8	15	22	22
549	556	8	FSYMDDVV	22	B*5201	39	22	13	15	22	22
547	557	11	LAFSYMDDVV	479	B*3503	11	1,21	13	15	22	22
547	557	11	LAFSYMDDVV	22	B*3801	29	22	35	15	22	22
547	557	11	LAFSYMDDVV	22	B*3901	19	22	24	15	22	22
547	557	11	LAFSYMDDVV	22	B*4801	23	22	28	15	22	22
549	557	9	FSYMDDVV	480	B*3901	25	22	30	15	22	22
549	557	9	FSYMDDVV	22	B*4601	62	22	76	15	22	22
550	557	8	SYMDDVV	481	A*2301	38	22	46	15	22	22
550	557	8	SYMDDVV	22	A*2402	47	22	57	15	22	22
551	559	9	YMDDVV	482	A*0101	66	1,49	98	15	22	22
551	559	9	YMDDVV	22	A*0201	100	22	149	15	22	22
551	559	9	YMDDVV	22	A*0206	71	22	105	15	22	22
552	559	8	MDDVV	483	A*6802	34	22	50	15	22	22
					Cumulative Class I-BCI score:			11658			
565	572	8	RESLYTAV	486	B*1301	93	1,67	155	16	565	598
565	572	8	RESLYTAV	22	B*1302	31	22	52	16	22	22
565	572	8	RESLYTAV	22	B*3701	81	22	135	16	22	22
565	572	8	RESLYTAV	22	B*4001	91	22	153	16	22	22
565	572	8	RESLYTAV	22	B*4002	90	22	151	16	22	22
565	572	8	RESLYTAV	22	B*4402	65	22	109	16	22	22
565	572	8	RESLYTAV	22	B*4403	52	22	87	16	22	22
565	572	8	RESLYTAV	22	B*4801	44	22	74	16	22	22
565	572	8	RESLYTAV	22	B*4901	87	22	145	16	22	22
565	572	8	RESLYTAV	22	B*5001	88	22	147	16	22	22
565	573	9	RESLYTAVT	487	B*4002	40	1,11	45	16	22	22
565	573	9	RESLYTAVT	22	B*5001	56	22	62	16	22	22
565	574	10	RESLYTAVTN	488	B*4002	35	0,69	24	16	22	22
565	575	11	RESLYTAVTNF	489	B*1301	73	1,85	136	16	22	22
565	575	11	RESLYTAVTNF	22	B*1801	81	22	150	16	22	22
565	575	11	RESLYTAVTNF	22	B*4001	78	22	145	16	22	22

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
565	575	11	RESLYTAVTNF	55	B*4002	75	55	139	16	55	55	
565	575	11	RESLYTAVTNF	55	B*4402	96	55	178	16	55	55	
565	575	11	RESLYTAVTNF	55	B*4403	92	55	170	16	55	55	
565	575	11	RESLYTAVTNF	55	B*4901	70	55	129	16	55	55	
565	575	11	RESLYTAVTNF	55	B*5001	68	55	126	16	55	55	
566	575	10	ESLYTAVTNF	490	A*2601	95	55	176	16	55	55	
567	575	9	SLYTAVTNF	491	B*1501	64	55	119	16	55	55	
567	575	9	SLYTAVTNF	55	B*1525	86	55	160	16	55	55	
568	575	8	LYTAVTNF	492	A*2301	90	55	166	16	55	55	
568	575	8	LYTAVTNF	55	A*2402	91	55	169	16	55	55	
567	576	10	SLYTAVTNFL	493	A*0201	64	1,69	109	16	55	55	
568	576	9	LYTAVTNFL	494	A*2301	16	55	26	16	55	55	
568	576	9	LYTAVTNFL	55	A*2402	53	55	89	16	55	55	
569	576	8	YTAVTNFL	495	A*0101	2	55	3	16	55	55	
569	576	8	YTAVTNFL	55	A*2501	71	55	121	16	55	55	
569	576	8	YTAVTNFL	55	A*2601	59	55	100	16	55	55	
569	576	8	YTAVTNFL	55	B*4601	80	55	136	16	55	55	
567	577	11	SLYTAVTNFLL	496	A*3201	48	1,86	90	16	55	55	
568	577	10	LYTAVTNFLL	497	A*2301	60	55	112	16	55	55	
568	577	10	LYTAVTNFLL	55	A*2402	67	55	124	16	55	55	
568	577	10	LYTAVTNFLL	55	B*3801	8	55	15	16	55	55	
569	577	9	YTAVTNFLL	498	A*0101	70	55	130	16	55	55	
569	577	9	YTAVTNFLL	55	A*6802	28	55	52	16	55	55	
569	577	9	YTAVTNFLL	55	B*5801	41	55	75	16	55	55	
569	579	11	YTAVTNFLLSL	499	A*0101	58	1,91	112	16	55	55	
569	579	11	YTAVTNFLLSL	55	A*2501	69	55	132	16	55	55	
569	579	11	YTAVTNFLLSL	55	A*2601	56	55	108	16	55	55	
569	579	11	YTAVTNFLLSL	55	B*3801	43	55	82	16	55	55	
569	579	11	YTAVTNFLLSL	55	B*4601	89	55	169	16	55	55	
569	579	11	YTAVTNFLLSL	55	B*5801	14	55	26	16	55	55	
572	579	8	VTNFFLLSL	500	A*3201	26	55	49	16	55	55	
572	579	8	VTNFFLLSL	55	B*0702	23	55	44	16	55	55	
571	581	11	AVTNFLLSLGI	501	A*3201	9	1,49	14	16	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein								Peptide of invention (SLP)			
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
573	581	9	TNFLSLGI	502	B*5201	31	22	47	16	22	22
575	583	9	FLSLGIHL	503	A*0201	82	1,27	104	16	22	22
575	583	9	FLSLGIHL	22	A*0206	46	22	58	16	22	22
576	583	8	LLSLGIHL	504	B*0702	90	22	114	16	22	22
578	585	8	SLGIHLNP	505	A*0201	98	0,14	14	16	22	22
576	586	11	LLSLGIHLNPN	506	A*0206	75	0,09	7	16	22	22
577	587	11	LSLGIHLNPNK	507	A*0301	10	0,12	1	16	22	22
577	587	11	LSLGIHLNPNK	22	A*1101	50	22	6	16	22	22
578	587	10	SLGIHLNPNK	508	A*0301	30	22	3	16	22	22
578	587	10	SLGIHLNPNK	22	A*1101	24	22	3	16	22	22
580	587	8	GIHLNPNK	509	A*0301	26	22	3	16	22	22
580	587	8	GIHLNPNK	22	A*1101	17	22	2	16	22	22
582	589	8	HLNPNKTK	510	A*0301	51	1,61	82	16	22	22
582	590	9	HLNPNKTKR	511	A*3101	85	1,52	129	16	22	22
582	590	9	HLNPNKTKR	22	A*3303	54	22	81	16	22	22
582	590	9	HLNPNKTKR	22	A*7401	20	22	30	16	22	22
584	591	8	NPNTKRW	512	B*5301	46	1,80	83	16	22	22
585	594	10	PNKTKRWGYS	513	A*3201	55	0,53	29	16	22	22
587	594	8	KTKRWGYS	514	A*3001	67	22	36	16	22	22
586	595	10	NKTKRWGYSL	515	B*1402	46	1,81	84	16	22	22
587	595	9	KTKRWGYSL	516	A*3001	64	22	116	16	22	22
587	595	9	KTKRWGYSL	22	A*3201	85	22	154	16	22	22
587	595	9	KTKRWGYSL	22	B*5701	50	22	91	16	22	22
587	595	9	KTKRWGYSL	22	B*5802	52	22	94	16	22	22
588	595	8	KRWGYSL	517	B*1402	56	22	101	16	22	22
589	596	8	KRWGYSLN	518	B*2702	42	0,19	8	16	22	22
589	596	8	KRWGYSLN	22	B*2705	75	22	14	16	22	22
587	597	11	KTKRWGYSLNF	519	A*2402	2	1,95	3	16	22	22
587	597	11	KTKRWGYSLNF	22	A*3001	41	22	80	16	22	22
587	597	11	KTKRWGYSLNF	22	A*3002	41	22	80	16	22	22
587	597	11	KTKRWGYSLNF	22	A*3201	91	22	177	16	22	22
587	597	11	KTKRWGYSLNF	22	B*5701	77	22	150	16	22	22
587	597	11	KTKRWGYSLNF	22	B*5801	44	22	86	16	22	22

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
587	597	11	KTKRWGYSLNF	520	B*5802	81	52	158	16	52	52
589	597	9	KRWGYSLNF	520	A*3201	12	52	24	16	52	52
589	597	9	KRWGYSLNF	521	B*2705	96	52	186	16	52	52
590	597	8	RWGYSLNF	521	A*2301	88	52	171	16	52	52
590	597	8	RWGYSLNF	522	A*2402	89	52	174	16	52	52
590	597	8	RWGYSLNF	522	B*2705	63	52	122	16	52	52
589	598	10	KRWGYSLNFM	522	B*2702	100	0,84	84	16	52	52
589	598	10	KRWGYSLNFM	523	B*2705	43	52	36	16	52	52
589	598	10	KRWGYSLNFM	523	B*3901	5	52	4	16	52	52
590	598	9	RWGYSLNFM	523	A*2402	7	52	6	16	52	52
Cumulative Class I-BCI score:									8255		
585	594	10	PNKTKRWGYS	513	A*3201	55	0,53	29	17	584	617
587	594	8	KTKRWGYS	514	A*3001	67	52	36	17	52	52
586	595	10	NKTKRWGYSL	515	B*1402	46	1,81	84	17	52	52
587	595	9	KTKRWGYSL	516	A*3001	64	52	116	17	52	52
587	595	9	KTKRWGYSL	517	A*3201	85	52	154	17	52	52
587	595	9	KTKRWGYSL	518	B*5701	50	52	91	17	52	52
587	595	9	KTKRWGYSL	519	B*5802	52	52	94	17	52	52
588	595	8	TKRWGYSL	517	B*1402	56	52	101	17	52	52
589	596	8	KRWGYSLN	518	B*2702	42	0,19	8	17	52	52
589	596	8	KRWGYSLN	519	B*2705	75	52	14	17	52	52
587	597	11	KTKRWGYSLNF	519	A*2402	2	1,95	3	17	52	52
587	597	11	KTKRWGYSLNF	520	A*3001	41	52	80	17	52	52
587	597	11	KTKRWGYSLNF	521	A*3002	41	52	80	17	52	52
587	597	11	KTKRWGYSLNF	522	A*3201	91	52	177	17	52	52
587	597	11	KTKRWGYSLNF	523	B*5701	77	52	150	17	52	52
587	597	11	KTKRWGYSLNF	524	B*5801	44	52	86	17	52	52
587	597	11	KTKRWGYSLNF	525	B*5802	81	52	158	17	52	52
589	597	9	KRWGYSLNF	520	A*3201	12	52	24	17	52	52
589	597	9	KRWGYSLNF	521	B*2705	96	52	186	17	52	52
590	597	8	RWGYSLNF	521	A*2301	88	52	171	17	52	52
590	597	8	RWGYSLNF	522	A*2402	89	52	174	17	52	52

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
590	597	8	RWGYSLNF	522	B*2705	63	52	122	17	52	52	
589	598	10	KRWGYSLNFM	522	B*2702	100	0,84	84	17	52	52	
589	598	10	KRWGYSLNFM	522	B*2705	43	52	36	17	52	52	
589	598	10	KRWGYSLNFM	522	B*3901	5	52	4	17	52	52	
590	598	9	RWGYSLNFM	523	A*2402	7	52	6	17	52	52	
589	599	11	KRWGYSLNFMG	524	B*2702	57	0,64	36	17	52	52	
589	599	11	KRWGYSLNFMG	525	B*2705	24	52	15	17	52	52	
590	600	11	RWGYSLNFMGY	525	A*3002	82	1,89	155	17	52	52	
592	600	9	GYSLNFMGY	526	A*2902	73	52	138	17	52	52	
593	600	8	YSLNFMGY	527	A*0101	87	52	164	17	52	52	
593	600	8	YSLNFMGY	527	A*2501	88	52	166	17	52	52	
593	600	8	YSLNFMGY	527	A*2601	87	52	165	17	52	52	
593	600	8	YSLNFMGY	527	A*2902	100	52	189	17	52	52	
593	600	8	YSLNFMGY	527	A*3002	86	52	163	17	52	52	
593	600	8	YSLNFMGY	527	B*1501	42	52	80	17	52	52	
593	600	8	YSLNFMGY	527	B*1502	48	52	91	17	52	52	
593	600	8	YSLNFMGY	527	B*1525	37	52	71	17	52	52	
593	600	8	YSLNFMGY	527	B*4601	79	52	149	17	52	52	
593	600	8	YSLNFMGY	527	B*5801	27	52	51	17	52	52	
593	600	8	YSLNFMGY	527	B*5802	25	52	47	17	52	52	
591	601	11	WGYSLNFMGYI	528	B*1302	25	0,91	23	17	52	52	
591	601	11	WGYSLNFMGYI	528	B*5201	67	52	60	17	52	52	
593	601	9	YSLNFMGYI	529	A*2501	76	52	68	17	52	52	
593	601	9	YSLNFMGYI	529	B*4601	30	52	27	17	52	52	
593	601	9	YSLNFMGYI	529	B*5201	49	52	44	17	52	52	
593	601	9	YSLNFMGYI	529	B*5802	78	52	71	17	52	52	
594	601	8	SLNFMGYI	530	A*3201	39	52	36	17	52	52	
592	602	11	GYSLNFMGYII	531	A*2301	62	0,67	42	17	52	52	
592	602	11	GYSLNFMGYII	531	A*2402	68	52	46	17	52	52	
593	602	10	YSLNFMGYII	532	A*0206	52	52	35	17	52	52	
593	602	10	YSLNFMGYII	532	B*1301	62	52	42	17	52	52	
593	602	10	YSLNFMGYII	532	B*1302	39	52	27	17	52	52	
593	602	10	YSLNFMGYII	532	B*3801	20	52	14	17	52	52	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
593	602	10	YSLNFMGYII	53	B*5201	92	52	62	17	53	53
593	602	10	YSLNFMGYII	53	B*5802	4	52	3	17	53	53
594	602	9	SLNFMGYII	533	A*3201	71	52	48	17	53	53
595	602	8	LNFMGYII	534	B*1302	30	52	20	17	53	53
595	602	8	LNFMGYII	53	B*5101	7	52	4	17	53	53
595	602	8	LNFMGYII	53	B*5201	90	52	61	17	53	53
597	604	8	FMGYIIGS	535	A*0201	36	0,52	19	17	53	53
595	605	11	LNFMGYIIIGSW	536	B*5701	5	1,77	8	17	53	53
596	605	10	NFMGYIIIGSW	537	A*2301	50	52	88	17	53	53
596	605	10	NFMGYIIIGSW	538	B*4402	50	52	88	17	53	53
597	605	9	FMGYIIIGSW	538	B*4601	52	52	93	17	53	53
598	605	8	MGYIIIGSW	539	A*6802	25	52	44	17	53	53
598	605	8	MGYIIIGSW	53	B*5201	29	52	52	17	53	53
598	605	8	MGYIIIGSW	53	B*5301	56	52	99	17	53	53
598	605	8	MGYIIIGSW	53	B*5701	85	52	150	17	53	53
598	605	8	MGYIIIGSW	53	B*5801	78	52	138	17	53	53
598	605	8	MGYIIIGSW	53	B*5802	80	52	141	17	53	53
598	608	11	MGYIIIGSWGTL	540	B*1402	33	1,71	57	17	53	53
599	608	10	GYIIIGSWGTL	541	A*3201	83	52	142	17	53	53
600	608	9	YIIIGSWGTL	542	A*0206	2	52	4	17	53	53
600	608	9	YIIIGSWGTL	53	A*2501	92	52	157	17	53	53
600	608	9	YIIIGSWGTL	53	A*2601	28	52	48	17	53	53
600	608	9	YIIIGSWGTL	53	B*1502	67	52	114	17	53	53
607	614	8	TLPQDHIV	543	A*0201	4	0,56	2	17	53	53
606	616	11	GTLPQDHIVQK	544	A*0301	8	1,05	9	17	53	53
606	616	11	GTLPQDHIVQK	53	A*1101	63	52	66	17	53	53
608	617	10	LPQDHIVQKI	545	B*5101	82	1,83	150	17	53	53
608	617	10	LPQDHIVQKI	53	B*5301	26	52	48	17	53	53
					Cumulative BCI Class Score:			6396			
653	660	8	YPALMPLY	548	A*0101	36	1,81	65	18	653	691
653	660	8	YPALMPLY	53	A*2601	21	52	37	18	53	53
653	660	8	YPALMPLY	53	A*2902	41	52	75	18	53	53

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
653	660	8	YPALMPLY	55	B*3501	95	55	171	18	55	55
653	660	8	YPALMPLY	55	B*3503	84	55	151	18	55	55
653	660	8	YPALMPLY	55	B*5101	38	55	69	18	55	55
653	660	8	YPALMPLY	55	B*5301	89	55	160	18	55	55
653	660	8	YPALMPLY	55	B*5501	28	55	50	18	55	55
653	660	8	YPALMPLY	55	B*5601	37	55	67	18	55	55
652	661	10	GYPALMPLYA	549	A*2402	40	1,43	58	18	55	55
653	661	9	YPALMPLYA	550	B*0702	9	55	12	18	55	55
653	661	9	YPALMPLYA	55	B*3503	59	55	85	18	55	55
653	661	9	YPALMPLYA	55	B*5101	27	55	38	18	55	55
653	661	9	YPALMPLYA	55	B*5501	94	55	135	18	55	55
653	661	9	YPALMPLYA	55	B*5601	100	55	143	18	55	55
653	662	10	YPALMPLYAC	551	B*0702	4	0,21	1	18	55	55
653	662	10	YPALMPLYAC	55	B*3501	72	55	15	18	55	55
653	662	10	YPALMPLYAC	55	B*3503	69	55	14	18	55	55
653	662	10	YPALMPLYAC	55	B*5301	54	55	11	18	55	55
653	662	10	YPALMPLYAC	55	B*5501	70	55	15	18	55	55
653	662	10	YPALMPLYAC	55	B*5601	86	55	18	18	55	55
655	662	8	ALMPLYAC	552	A*0201	11	55	2	18	55	55
653	663	11	YPALMPLYACI	553	B*0702	54	1,19	64	18	55	55
653	663	11	YPALMPLYACI	55	B*1402	40	55	48	18	55	55
653	663	11	YPALMPLYACI	55	B*3501	33	55	40	18	55	55
653	663	11	YPALMPLYACI	55	B*3503	82	55	98	18	55	55
653	663	11	YPALMPLYACI	55	B*5101	100	55	119	18	55	55
653	663	11	YPALMPLYACI	55	B*5201	27	55	33	18	55	55
653	663	11	YPALMPLYACI	55	B*5301	87	55	104	18	55	55
653	663	11	YPALMPLYACI	55	B*5501	69	55	82	18	55	55
653	663	11	YPALMPLYACI	55	B*5601	77	55	92	18	55	55
655	663	9	ALMPLYACI	554	A*0201	67	55	80	18	55	55
657	664	8	MPLYACIQ	555	B*5501	12	0,20	2	18	55	55
657	664	8	MPLYACIQ	55	B*5601	8	55	2	18	55	55
657	665	9	MPLYACIQ A	556	B*3501	44	1,41	62	18	55	55
657	665	9	MPLYACIQ A	55	B*3503	49	55	68	18	55	55

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
657	665	9	MPLYACIQA	55	B*5101	80	55	112	18	55	55	
657	665	9	MPLYACIQA	55	B*5501	93	55	131	18	55	55	
657	665	9	MPLYACIQA	55	B*5601	99	55	139	18	55	55	
657	666	10	MPLYACIQAK	557	B*3501	43	1,01	43	18	55	55	
657	666	10	MPLYACIQAK	55	B*5601	3	55	3	18	55	55	
658	666	9	PLYACIQAK	558	A*0301	74	55	75	18	55	55	
659	669	11	LYACIQAKQAF	559	A*2301	86	1,07	92	18	55	55	
659	669	11	LYACIQAKQAF	55	A*2402	88	55	94	18	55	55	
660	669	10	YACIQAKQAF	560	B*1502	26	55	28	18	55	55	
663	671	9	IQAKQAFTF	561	A*2402	84	1,58	133	18	55	55	
663	671	9	IQAKQAFTF	55	B*1301	61	55	96	18	55	55	
663	671	9	IQAKQAFTF	55	B*1501	63	55	99	18	55	55	
663	671	9	IQAKQAFTF	55	B*1525	71	55	112	18	55	55	
664	671	8	QAKQAFTF	562	B*1501	8	55	12	18	55	55	
664	671	8	QAKQAFTF	55	B*1502	37	55	59	18	55	55	
664	671	8	QAKQAFTF	55	B*1525	14	55	21	18	55	55	
664	671	8	QAKQAFTF	55	B*5802	3	55	5	18	55	55	
666	675	10	KQAFTFSPTY	563	A*2902	27	1,81	49	18	55	55	
666	675	10	KQAFTFSPTY	55	A*3002	30	55	53	18	55	55	
666	675	10	KQAFTFSPTY	55	B*1501	89	55	161	18	55	55	
666	675	10	KQAFTFSPTY	55	B*1502	63	55	114	18	55	55	
666	675	10	KQAFTFSPTY	55	B*1525	85	55	153	18	55	55	
666	675	10	KQAFTFSPTY	55	B*5001	32	55	58	18	55	55	
667	675	9	QAFTFSPTY	564	A*2902	46	55	83	18	55	55	
667	675	9	QAFTFSPTY	55	A*3002	58	55	104	18	55	55	
667	675	9	QAFTFSPTY	55	B*1525	66	55	119	18	55	55	
667	675	9	QAFTFSPTY	55	B*3501	73	55	133	18	55	55	
667	675	9	QAFTFSPTY	55	B*5701	12	55	22	18	55	55	
668	675	8	AFTFSPTY	565	A*2902	60	55	109	18	55	55	
668	675	8	AFTFSPTY	55	A*3002	56	55	102	18	55	55	
666	676	11	KQAFTFSPTYK	566	A*0301	100	1,78	178	18	55	55	
666	676	11	KQAFTFSPTYK	55	A*1101	83	55	147	18	55	55	
666	676	11	KQAFTFSPTYK	55	A*3001	49	55	87	18	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
666	676	11	KQAFTFSPTYK	567	A*7401	60	52	106	18	52	52	
667	676	10	QAFTFSPTYK	567	A*0301	64	52	114	18	52	52	
667	676	10	QAFTFSPTYK	567	A*1101	78	52	139	18	52	52	
667	676	10	QAFTFSPTYK	567	A*6801	91	52	162	18	52	52	
667	676	10	QAFTFSPTYK	567	A*7401	59	52	104	18	52	52	
669	676	8	FTFSPTYK	568	A*0301	98	52	175	18	52	52	
669	676	8	FTFSPTYK	568	A*1101	96	52	170	18	52	52	
669	676	8	FTFSPTYK	568	A*3101	25	52	45	18	52	52	
669	676	8	FTFSPTYK	568	A*3303	69	52	123	18	52	52	
669	676	8	FTFSPTYK	568	A*7401	99	52	176	18	52	52	
669	677	9	FTFSPTYKA	569	A*0201	2	1,62	4	18	52	52	
669	677	9	FTFSPTYKA	569	A*6802	47	52	76	18	52	52	
669	677	9	FTFSPTYKA	569	B*5601	36	52	58	18	52	52	
668	678	11	AFTFSPTYKAF	570	A*2402	14	0,94	13	18	52	52	
669	678	10	FTFSPTYKAF	571	A*0101	64	52	60	18	52	52	
669	678	10	FTFSPTYKAF	569	A*2501	96	52	90	18	52	52	
669	678	10	FTFSPTYKAF	569	A*2601	92	52	87	18	52	52	
669	678	10	FTFSPTYKAF	569	B*1501	88	52	82	18	52	52	
669	678	10	FTFSPTYKAF	569	B*1502	100	52	94	18	52	52	
669	678	10	FTFSPTYKAF	569	B*1525	83	52	78	18	52	52	
669	678	10	FTFSPTYKAF	569	B*3501	36	52	34	18	52	52	
669	678	10	FTFSPTYKAF	569	B*3503	43	52	41	18	52	52	
669	678	10	FTFSPTYKAF	569	B*4601	98	52	92	18	52	52	
669	678	10	FTFSPTYKAF	569	B*5802	48	52	45	18	52	52	
670	678	9	TFSPTYKAF	572	A*2301	83	52	78	18	52	52	
670	678	9	TFSPTYKAF	569	A*2402	42	52	39	18	52	52	
669	679	11	FTFSPTYKAFL	573	A*2501	61	0,51	32	18	52	52	
669	679	11	FTFSPTYKAFL	569	A*2601	46	52	24	18	52	52	
669	679	11	FTFSPTYKAFL	569	B*4601	61	52	31	18	52	52	
672	679	8	SPTYKAFL	574	B*0801	39	52	20	18	52	52	
672	679	8	SPTYKAFL	569	B*3503	15	52	8	18	52	52	
672	679	8	SPTYKAFL	569	B*5501	1	52	1	18	52	52	
673	681	9	PTYKAFLSK	575	A*0301	72	1,52	110	18	52	52	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
673	681	9	PTYKAFLSK	576	A*1101	61	52	92	18	52	52	
674	681	8	TYKAFLSK	576	A*3001	77	52	117	18	52	52	
674	681	8	TYKAFLSK	577	A*3101	18	52	27	18	52	52	
673	683	11	PTYKAFLSKQY	577	A*0101	47	1,56	73	18	52	52	
673	683	11	PTYKAFLSKQY	578	A*2902	8	52	12	18	52	52	
673	683	11	PTYKAFLSKQY	578	A*3002	27	52	42	18	52	52	
674	683	10	TYKAFLSKQY	578	A*2902	67	52	104	18	52	52	
674	683	10	TYKAFLSKQY	579	A*3002	21	52	33	18	52	52	
676	683	8	KAFLSKQY	579	A*3002	51	52	79	18	52	52	
676	683	8	KAFLSKQY	580	B*1501	25	52	39	18	52	52	
676	683	8	KAFLSKQY	580	B*1502	11	52	17	18	52	52	
676	683	8	KAFLSKQY	580	B*1525	61	52	95	18	52	52	
676	683	8	KAFLSKQY	580	B*5701	71	52	111	18	52	52	
676	683	8	KAFLSKQY	580	B*5801	51	52	79	18	52	52	
676	683	8	KAFLSKQY	580	B*5802	62	52	97	18	52	52	
676	684	9	KAFLSKQYM	580	B*5701	82	1,51	124	18	52	52	
676	684	9	KAFLSKQYM	581	B*5801	46	52	69	18	52	52	
676	685	10	KAFLSKQYMN	581	A*3001	63	52	24	18	52	52	
676	686	11	KAFLSKQYMN	582	A*3001	48	1,83	88	18	52	52	
676	686	11	KAFLSKQYMN	582	A*3201	24	52	44	18	52	52	
676	686	11	KAFLSKQYMN	582	B*4801	13	52	25	18	52	52	
676	686	11	KAFLSKQYMN	582	B*5701	62	52	114	18	52	52	
676	686	11	KAFLSKQYMN	582	B*5801	19	52	34	18	52	52	
676	686	11	KAFLSKQYMN	582	B*5802	23	52	43	18	52	52	
678	686	9	FLSKQYMN	583	A*0201	33	52	61	18	52	52	
677	687	11	AFLSKQYMNLY	584	A*2902	84	1,58	133	18	52	52	
677	687	11	AFLSKQYMNLY	585	A*3002	55	52	87	18	52	52	
678	687	10	FLSKQYMNLY	585	A*0101	98	52	155	18	52	52	
678	687	10	FLSKQYMNLY	585	A*2501	67	52	106	18	52	52	
678	687	10	FLSKQYMNLY	585	A*3002	34	52	53	18	52	52	
678	687	10	FLSKQYMNLY	585	B*1501	23	52	37	18	52	52	
678	687	10	FLSKQYMNLY	585	B*1502	35	52	56	18	52	52	
678	687	10	FLSKQYMNLY	585	B*4601	18	52	28	18	52	52	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
679	687	9	LSKQYMNLY	586	A*0101	96	22	152	18	22	22	
679	687	9	LSKQYMNLY	22	A*3002	69	22	109	18	22	22	
679	687	9	LSKQYMNLY	22	B*1501	27	22	42	18	22	22	
680	687	8	SKQYMNLY	587	B*3501	21	22	34	18	22	22	
679	689	11	LSKQYMNLYPV	588	B*0801	37	0,93	35	18	22	22	
681	689	9	KQYMNLYPV	589	A*0201	89	22	83	18	22	22	
681	689	9	KQYMNLYPV	22	A*0206	96	22	89	18	22	22	
681	689	9	KQYMNLYPV	22	A*3201	44	22	41	18	22	22	
681	689	9	KQYMNLYPV	22	B*1301	72	22	67	18	22	22	
681	689	9	KQYMNLYPV	22	B*1302	38	22	35	18	22	22	
681	689	9	KQYMNLYPV	22	B*1525	29	22	27	18	22	22	
681	689	9	KQYMNLYPV	22	B*2702	48	22	45	18	22	22	
681	689	9	KQYMNLYPV	22	B*4801	88	22	82	18	22	22	
681	689	9	KQYMNLYPV	22	B*5001	48	22	45	18	22	22	
681	689	9	KQYMNLYPV	22	B*5201	73	22	67	18	22	22	
682	689	8	QYMNLYPV	590	A*2301	59	22	54	18	22	22	
682	689	8	QYMNLYPV	22	A*2402	61	22	57	18	22	22	
681	690	10	KQYMNLYPVA	591	B*1302	3	1,25	4	18	22	22	
681	690	10	KQYMNLYPVA	22	B*4801	42	22	53	18	22	22	
681	690	10	KQYMNLYPVA	22	B*5001	16	22	20	18	22	22	
681	691	11	KQYMNLYPVAR	592	A*0301	49	1,78	88	18	22	22	
681	691	11	KQYMNLYPVAR	22	A*3101	100	22	178	18	22	22	
681	691	11	KQYMNLYPVAR	22	A*3201	23	22	40	18	22	22	
681	691	11	KQYMNLYPVAR	22	A*7401	100	22	178	18	22	22	
682	691	10	QYMNLYPVAR	593	A*3101	84	22	149	18	22	22	
682	691	10	QYMNLYPVAR	22	A*3303	90	22	160	18	22	22	
683	691	9	YMNLYPVAR	594	A*3101	78	22	140	18	22	22	
683	691	9	YMNLYPVAR	22	A*3303	89	22	158	18	22	22	
683	691	9	YMNLYPVAR	22	A*7401	94	22	167	18	22	22	
684	691	8	MNLYPVAR	595	A*3101	16	22	29	18	22	22	
684	691	8	MNLYPVAR	22	A*3303	75	22	133	18	22	22	
					Cumulative Class I-BCI score:			12576				

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
657	665	9	MPLYACIQQA	556	B*3501	44	1,41	62	19	657	691	
657	665	9	MPLYACIQQA	"	B*3503	49	"	68	19	"	"	
657	665	9	MPLYACIQQA	"	B*5101	80	"	112	19	"	"	
657	665	9	MPLYACIQQA	"	B*5501	93	"	131	19	"	"	
657	665	9	MPLYACIQQA	"	B*5601	99	"	139	19	"	"	
657	666	10	MPLYACIQAK	557	B*3501	43	1,01	43	19	"	"	
657	666	10	MPLYACIQAK	"	B*5601	3	"	3	19	"	"	
658	666	9	PLYACIQAK	558	A*0301	74	"	75	19	"	"	
659	669	11	LYACIQAKQAF	559	A*2301	86	1,07	92	19	"	"	
659	669	11	LYACIQAKQAF	"	A*2402	88	"	94	19	"	"	
660	669	10	YACIQAKQAF	560	B*1502	26	"	28	19	"	"	
663	671	9	IQAKQAFTF	561	A*2402	84	1,58	133	19	"	"	
663	671	9	IQAKQAFTF	"	B*1301	61	"	96	19	"	"	
663	671	9	IQAKQAFTF	"	B*1501	63	"	99	19	"	"	
663	671	9	IQAKQAFTF	"	B*1525	71	"	112	19	"	"	
664	671	8	QAKQAFTF	562	B*1501	8	"	12	19	"	"	
664	671	8	QAKQAFTF	"	B*1502	37	"	59	19	"	"	
664	671	8	QAKQAFTF	"	B*1525	14	"	21	19	"	"	
664	671	8	QAKQAFTF	"	B*5802	3	"	5	19	"	"	
666	675	10	KQAFTFSPTY	563	A*2902	27	1,81	49	19	"	"	
666	675	10	KQAFTFSPTY	"	A*3002	30	"	53	19	"	"	
666	675	10	KQAFTFSPTY	"	B*1501	89	"	161	19	"	"	
666	675	10	KQAFTFSPTY	"	B*1502	63	"	114	19	"	"	
666	675	10	KQAFTFSPTY	"	B*1525	85	"	153	19	"	"	
666	675	10	KQAFTFSPTY	"	B*5001	32	"	58	19	"	"	
667	675	9	QAFTFSPTY	564	A*2902	46	"	83	19	"	"	
667	675	9	QAFTFSPTY	"	A*3002	58	"	104	19	"	"	
667	675	9	QAFTFSPTY	"	B*1525	66	"	119	19	"	"	
667	675	9	QAFTFSPTY	"	B*3501	73	"	133	19	"	"	
667	675	9	QAFTFSPTY	"	B*5701	12	"	22	19	"	"	
668	675	8	AFTFSPTY	565	A*2902	60	"	109	19	"	"	
668	675	8	AFTFSPTY	"	A*3002	56	"	102	19	"	"	
666	676	11	KQAFTFSPTYK	566	A*0301	100	1,78	178	19	"	"	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
666	676	11	KQAFTFSPTYK	55	A*1101	83	55	147	19	55	55	
666	676	11	KQAFTFSPTYK	55	A*3001	49	55	87	19	55	55	
666	676	11	KQAFTFSPTYK	55	A*7401	60	55	106	19	55	55	
667	676	10	QAFTFSPTYK	567	A*0301	64	55	114	19	55	55	
667	676	10	QAFTFSPTYK	55	A*1101	78	55	139	19	55	55	
667	676	10	QAFTFSPTYK	55	A*6801	91	55	162	19	55	55	
667	676	10	QAFTFSPTYK	55	A*7401	59	55	104	19	55	55	
669	676	8	FTFSPTYK	568	A*0301	98	55	175	19	55	55	
669	676	8	FTFSPTYK	55	A*1101	96	55	170	19	55	55	
669	676	8	FTFSPTYK	55	A*3101	25	55	45	19	55	55	
669	676	8	FTFSPTYK	55	A*3303	69	55	123	19	55	55	
669	676	8	FTFSPTYK	55	A*7401	99	55	176	19	55	55	
669	677	9	FTFSPTYKA	569	A*0201	2	1,62	4	19	55	55	
669	677	9	FTFSPTYKA	55	A*6802	47	55	76	19	55	55	
669	677	9	FTFSPTYKA	55	B*5601	36	55	58	19	55	55	
668	678	11	AFTFSPTYKAF	570	A*2402	14	0,94	13	19	55	55	
669	678	10	FTFSPTYKAF	571	A*0101	64	55	60	19	55	55	
669	678	10	FTFSPTYKAF	55	A*2501	96	55	90	19	55	55	
669	678	10	FTFSPTYKAF	55	A*2601	92	55	87	19	55	55	
669	678	10	FTFSPTYKAF	55	B*1501	88	55	82	19	55	55	
669	678	10	FTFSPTYKAF	55	B*1502	100	55	94	19	55	55	
669	678	10	FTFSPTYKAF	55	B*1525	83	55	78	19	55	55	
669	678	10	FTFSPTYKAF	55	B*3501	36	55	34	19	55	55	
669	678	10	FTFSPTYKAF	55	B*3503	43	55	41	19	55	55	
669	678	10	FTFSPTYKAF	55	B*4601	98	55	92	19	55	55	
669	678	10	FTFSPTYKAF	55	B*5802	48	55	45	19	55	55	
670	678	9	TESPTYKAF	572	A*2301	83	55	78	19	55	55	
670	678	9	TESPTYKAF	55	A*2402	42	55	39	19	55	55	
669	679	11	FTFSPTYKAFL	573	A*2501	61	0,51	32	19	55	55	
669	679	11	FTFSPTYKAFL	55	A*2601	46	55	24	19	55	55	
669	679	11	FTFSPTYKAFL	55	B*4601	61	55	31	19	55	55	
672	679	8	SPTYKAFL	574	B*0801	39	55	20	19	55	55	
672	679	8	SPTYKAFL	55	B*3503	15	55	8	19	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
672	679	8	SPTYKAFL	575	B*5501	1	52	1	19	55	55	
673	681	9	PTYKAFLSK	575	A*0301	72	1,52	110	19	55	55	
673	681	9	PTYKAFLSK	575	A*1101	61	52	92	19	55	55	
674	681	8	TYKAFLSK	576	A*3001	77	52	117	19	55	55	
674	681	8	TYKAFLSK	577	A*3101	18	52	27	19	55	55	
673	683	11	PTYKAFLSKQY	577	A*0101	47	1,56	73	19	55	55	
673	683	11	PTYKAFLSKQY	578	A*2902	8	52	12	19	55	55	
673	683	11	PTYKAFLSKQY	578	A*3002	27	52	42	19	55	55	
674	683	10	TYKAFLSKQY	578	A*2902	67	52	104	19	55	55	
674	683	10	TYKAFLSKQY	579	A*3002	21	52	33	19	55	55	
676	683	8	KAFLSKQY	579	A*3002	51	52	79	19	55	55	
676	683	8	KAFLSKQY	579	B*1501	25	52	39	19	55	55	
676	683	8	KAFLSKQY	579	B*1502	11	52	17	19	55	55	
676	683	8	KAFLSKQY	579	B*1525	61	52	95	19	55	55	
676	683	8	KAFLSKQY	579	B*5701	71	52	111	19	55	55	
676	683	8	KAFLSKQY	579	B*5801	51	52	79	19	55	55	
676	683	8	KAFLSKQY	579	B*5802	62	52	97	19	55	55	
676	684	9	KAFLSKQYM	580	B*5701	82	1,51	124	19	55	55	
676	684	9	KAFLSKQYM	581	B*5801	46	52	69	19	55	55	
676	685	10	KAFLSKQYMN	581	A*3001	63	52	24	19	55	55	
676	686	11	KAFLSKQYMN	582	A*3001	48	1,83	88	19	55	55	
676	686	11	KAFLSKQYMN	582	A*3201	24	52	44	19	55	55	
676	686	11	KAFLSKQYMN	582	B*4801	13	52	25	19	55	55	
676	686	11	KAFLSKQYMN	582	B*5701	62	52	114	19	55	55	
676	686	11	KAFLSKQYMN	582	B*5801	19	52	34	19	55	55	
676	686	11	KAFLSKQYMN	582	B*5802	23	52	43	19	55	55	
678	686	9	FLSKQYMN	583	A*0201	33	52	61	19	55	55	
677	687	11	AFLSKQYMN	584	A*2902	84	1,58	133	19	55	55	
677	687	11	AFLSKQYMN	585	A*3002	55	52	87	19	55	55	
678	687	10	FLSKQYMN	585	A*0101	98	52	155	19	55	55	
678	687	10	FLSKQYMN	585	A*2501	67	52	106	19	55	55	
678	687	10	FLSKQYMN	585	A*3002	34	52	53	19	55	55	
678	687	10	FLSKQYMN	585	B*1501	23	52	37	19	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
678	687	10	FLSKQYMNLY	55	B*1502	35	55	56	19	55	55
678	687	10	FLSKQYMNLY	55	B*4601	18	55	28	19	55	55
679	687	9	LSKQYMNLY	586	A*0101	96	55	152	19	55	55
679	687	9	LSKQYMNLY	55	A*3002	69	55	109	19	55	55
679	687	9	LSKQYMNLY	55	B*1501	27	55	42	19	55	55
680	687	8	SKQYMNLY	587	B*3501	21	55	34	19	55	55
679	689	11	LSKQYMNLYPV	588	B*0801	37	0,93	35	19	55	55
681	689	9	KQYMNLYPV	589	A*0201	89	55	83	19	55	55
681	689	9	KQYMNLYPV	55	A*0206	96	55	89	19	55	55
681	689	9	KQYMNLYPV	55	A*3201	44	55	41	19	55	55
681	689	9	KQYMNLYPV	55	B*1301	72	55	67	19	55	55
681	689	9	KQYMNLYPV	55	B*1302	38	55	35	19	55	55
681	689	9	KQYMNLYPV	55	B*1525	29	55	27	19	55	55
681	689	9	KQYMNLYPV	55	B*2702	48	55	45	19	55	55
681	689	9	KQYMNLYPV	55	B*4801	88	55	82	19	55	55
681	689	9	KQYMNLYPV	55	B*5001	48	55	45	19	55	55
681	689	9	KQYMNLYPV	55	B*5201	73	55	67	19	55	55
682	689	8	QYMNLYPV	590	A*2301	59	55	54	19	55	55
682	689	8	QYMNLYPV	55	A*2402	61	55	57	19	55	55
681	690	10	KQYMNLYPVA	591	B*1302	3	1,25	4	19	55	55
681	690	10	KQYMNLYPVA	55	B*4801	42	55	53	19	55	55
681	690	10	KQYMNLYPVA	55	B*5001	16	55	20	19	55	55
681	691	11	KQYMNLYPVAR	592	A*0301	49	1,78	88	19	55	55
681	691	11	KQYMNLYPVAR	55	A*3101	100	55	178	19	55	55
681	691	11	KQYMNLYPVAR	55	A*3201	23	55	40	19	55	55
681	691	11	KQYMNLYPVAR	55	A*7401	100	55	178	19	55	55
682	691	10	QYMNLYPVAR	593	A*3101	84	55	149	19	55	55
682	691	10	QYMNLYPVAR	55	A*3303	90	55	160	19	55	55
683	691	9	YMNLYPVAR	594	A*3101	78	55	140	19	55	55
683	691	9	YMNLYPVAR	55	A*3303	89	55	158	19	55	55
683	691	9	YMNLYPVAR	55	A*7401	94	55	167	19	55	55
684	691	8	MNLYPVAR	595	A*3101	16	55	29	19	55	55
684	691	8	MNLYPVAR	55	A*3303	75	55	133	19	55	55

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
					Cumulative Class I-BCI score: 10420							
716	723	8	RMRGTFVA	596	A*3001	92	1,41	130	20	715	746	
716	724	9	RMRGTFVAP	597	A*3001	7	0,12	1	20	715	746	
717	724	8	MRGTFVAP	598	A*0206	94	71	11	20	715	746	
715	725	11	QMRGTFVAPL	599	B*1402	89	0,99	88	20	715	746	
715	725	11	QMRGTFVAPL	71	B*2702	83	71	82	20	715	746	
715	725	11	QMRGTFVAPL	71	B*3801	57	71	57	20	715	746	
715	725	11	QMRGTFVAPL	71	B*3901	99	71	98	20	715	746	
715	725	11	QMRGTFVAPL	71	B*4801	29	71	29	20	715	746	
716	725	10	RMRGTFVAPL	600	B*0801	76	71	76	20	715	746	
716	725	10	RMRGTFVAPL	71	B*1402	65	71	64	20	715	746	
716	725	10	RMRGTFVAPL	71	B*1501	67	71	67	20	715	746	
716	725	10	RMRGTFVAPL	71	B*1525	47	71	47	20	715	746	
716	725	10	RMRGTFVAPL	71	B*4801	90	71	90	20	715	746	
717	725	9	MRGTFVAPL	601	B*1402	88	71	87	20	715	746	
717	725	9	MRGTFVAPL	71	B*2702	71	71	70	20	715	746	
717	725	9	MRGTFVAPL	71	B*3901	81	71	80	20	715	746	
716	726	11	RMRGTFVAPLP	602	A*3001	37	0,08	3	20	715	746	
718	726	9	RGTFVAPLP	603	B*5802	45	71	4	20	715	746	
717	727	11	MRGTFVAPLPI	604	B*1402	70	0,98	68	20	715	746	
717	727	11	MRGTFVAPLPI	71	B*2702	82	71	80	20	715	746	
717	727	11	MRGTFVAPLPI	71	B*3801	37	71	36	20	715	746	
717	727	11	MRGTFVAPLPI	71	B*3901	49	71	48	20	715	746	
717	727	11	MRGTFVAPLPI	71	B*5201	18	71	17	20	715	746	
719	727	9	GTFVAPLPI	605	A*3201	70	71	68	20	715	746	
719	727	9	GTFVAPLPI	71	B*5201	59	71	58	20	715	746	
720	727	8	TFVAPLPI	606	A*2301	19	71	19	20	715	746	
720	727	8	TFVAPLPI	71	A*2402	12	71	12	20	715	746	
719	728	10	GTFVAPLPIH	607	A*3001	97	0,37	36	20	715	746	
721	730	10	FVAPLPIHTA	608	A*0206	58	1,82	106	20	715	746	
721	730	10	FVAPLPIHTA	71	B*5601	51	71	94	20	715	746	
723	730	8	APLPIHTA	609	B*5501	67	71	123	20	715	746	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
723	730	8	APLPHTA	55	B*5601	76	55	138	20	55	55	
723	732	10	APLPHTAEL	610	B*0702	67	1,48	99	20	55	55	
723	732	10	APLPHTAEL	55	B*1402	69	55	102	20	55	55	
723	732	10	APLPHTAEL	55	B*3503	66	55	98	20	55	55	
723	732	10	APLPHTAEL	55	B*5501	53	55	79	20	55	55	
723	732	10	APLPHTAEL	55	B*5601	44	55	65	20	55	55	
725	732	8	LPIHTAEL	611	B*1402	76	55	112	20	55	55	
725	732	8	LPIHTAEL	55	B*3503	89	55	132	20	55	55	
725	732	8	LPIHTAEL	55	B*3901	48	55	71	20	55	55	
725	732	8	LPIHTAEL	55	B*5101	88	55	131	20	55	55	
725	732	8	LPIHTAEL	55	B*5301	77	55	114	20	55	55	
725	732	8	LPIHTAEL	55	B*5501	74	55	110	20	55	55	
725	732	8	LPIHTAEL	55	B*5601	71	55	104	20	55	55	
723	733	11	APLPHTAELL	612	B*0702	33	1,70	57	20	55	55	
723	733	11	APLPHTAELL	55	B*1402	39	55	67	20	55	55	
725	733	9	LPIHTAELL	613	B*0702	1	55	2	20	55	55	
725	733	9	LPIHTAELL	55	B*1402	38	55	65	20	55	55	
725	733	9	LPIHTAELL	55	B*3503	57	55	97	20	55	55	
725	733	9	LPIHTAELL	55	B*5101	78	55	133	20	55	55	
725	733	9	LPIHTAELL	55	B*5301	61	55	103	20	55	55	
725	733	9	LPIHTAELL	55	B*5501	10	55	18	20	55	55	
725	733	9	LPIHTAELL	55	B*5601	26	55	44	20	55	55	
725	734	10	LPIHTAELLA	614	B*3503	42	1,12	47	20	55	55	
725	734	10	LPIHTAELLA	55	B*5501	81	55	91	20	55	55	
725	734	10	LPIHTAELLA	55	B*5601	92	55	103	20	55	55	
725	735	11	LPIHTAELLAA	615	B*0702	45	1,10	49	20	55	55	
725	735	11	LPIHTAELLAA	55	B*3501	76	55	84	20	55	55	
725	735	11	LPIHTAELLAA	55	B*3503	65	55	71	20	55	55	
725	735	11	LPIHTAELLAA	55	B*5101	45	55	49	20	55	55	
725	735	11	LPIHTAELLAA	55	B*5501	92	55	101	20	55	55	
725	735	11	LPIHTAELLAA	55	B*5601	97	55	107	20	55	55	
728	735	8	HTAELLAA	616	A*2501	31	55	34	20	55	55	
728	735	8	HTAELLAA	55	A*2601	72	55	79	20	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
728	735	8	HTAELLAA	55	B*5501	9	55	10	20	55	55
728	735	8	HTAELLAA	55	B*5601	32	55	35	20	55	55
728	736	9	HTAELLAAAC	617	A*2501	86	0,20	18	20	55	55
728	736	9	HTAELLAAAC	55	A*2601	54	55	11	20	55	55
728	737	10	HTAELLAAACF	618	A*0101	32	1,63	52	20	55	55
728	737	10	HTAELLAAACF	55	A*2501	94	55	153	20	55	55
728	737	10	HTAELLAAACF	55	A*2601	85	55	138	20	55	55
728	737	10	HTAELLAAACF	55	B*1502	43	55	69	20	55	55
728	737	10	HTAELLAAACF	55	B*4601	72	55	117	20	55	55
728	737	10	HTAELLAAACF	55	B*5802	42	55	68	20	55	55
730	737	8	AELLAACF	619	B*1301	65	55	105	20	55	55
730	737	8	AELLAACF	55	B*1801	76	55	124	20	55	55
730	737	8	AELLAACF	55	B*4001	70	55	113	20	55	55
730	737	8	AELLAACF	55	B*4002	65	55	106	20	55	55
730	737	8	AELLAACF	55	B*4403	96	55	156	20	55	55
730	737	8	AELLAACF	55	B*4901	52	55	85	20	55	55
730	737	8	AELLAACF	55	B*5001	40	55	65	20	55	55
728	738	11	HTAELLAAACFA	620	A*2601	36	0,81	29	20	55	55
730	738	9	AELLAACFA	621	B*1301	59	55	48	20	55	55
730	738	9	AELLAACFA	55	B*1302	10	55	8	20	55	55
730	738	9	AELLAACFA	55	B*3701	29	55	23	20	55	55
730	738	9	AELLAACFA	55	B*4002	85	55	69	20	55	55
730	738	9	AELLAACFA	55	B*4402	73	55	59	20	55	55
730	738	9	AELLAACFA	55	B*4403	68	55	55	20	55	55
730	738	9	AELLAACFA	55	B*4901	65	55	53	20	55	55
730	738	9	AELLAACFA	55	B*5001	72	55	59	20	55	55
729	739	11	TAELLAACFAR	622	A*6801	54	1,51	82	20	55	55
730	739	10	AELLAACFAR	623	B*4002	45	55	68	20	55	55
731	739	9	ELLAACFAR	624	A*3303	80	55	121	20	55	55
731	739	9	ELLAACFAR	55	A*6801	71	55	107	20	55	55
731	739	9	ELLAACFAR	55	A*7401	18	55	28	20	55	55
732	739	8	LLAACFAR	625	A*3101	24	55	36	20	55	55
732	739	8	LLAACFAR	55	A*3303	66	55	100	20	55	55

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
732	739	8	LLAACFAR	..	A*6801	57	..	87	20	..	..	
732	739	8	LLAACFAR	..	A*7401	93	..	140	20	..	..	
730	740	11	AELLAACFARS	626	B*4402	12	0,24	3	20	..	..	
730	740	11	AELLAACFARS	..	B*4403	4	..	1	20	..	..	
733	740	8	LAACFARS	627	A*0206	13	..	3	20	..	..	
731	741	11	ELLAACFARSR	628	A*3303	37	1,17	43	20	..	..	
732	741	10	LLAACFARSR	629	A*3101	58	..	68	20	..	..	
732	741	10	LLAACFARSR	..	A*3303	6	..	7	20	..	..	
732	741	10	LLAACFARSR	..	A*7401	66	..	77	20	..	..	
733	741	9	LAACFARSR	630	A*3303	28	..	33	20	..	..	
733	741	9	LAACFARSR	..	A*6801	56	..	66	20	..	..	
734	741	8	AACFARSR	631	A*3101	15	..	18	20	..	..	
737	744	8	FARSRSGA	632	B*0801	85	0,75	63	20	..	..	
737	744	8	FARSRSGA	..	B*5501	59	..	44	20	..	..	
737	744	8	FARSRSGA	..	B*5601	1	..	1	20	..	..	
737	745	9	FARSRSGAK	633	A*3001	39	0,48	19	20	..	..	
737	745	9	FARSRSGAK	..	B*5501	16	..	8	20	..	..	
737	746	10	FARSRSGAKL	634	B*1402	25	1,60	41	20	..	..	
737	746	10	FARSRSGAKL	..	B*4601	3	..	5	20	..	..	
737	746	10	FARSRSGAKL	..	B*5501	15	..	24	20	..	..	
738	746	9	ARSRSGAKL	635	B*2702	12	..	19	20	..	..	
739	746	8	RSRSGAKL	636	A*3001	76	..	122	20	..	..	
					Cumulative BCI Class Score:				7869			
754	762	9	VLSRKYTSE	638	B*0801	68	1,77	120	21	754	791	
754	762	9	VLSRKYTSE	..	B*1501	17	..	30	21	..	..	
755	762	8	LSRKYTSE	639	B*0801	61	..	108	21	..	..	
755	762	8	LSRKYTSE	..	B*1501	98	..	174	21	..	..	
755	762	8	LSRKYTSE	..	B*1502	85	..	150	21	..	..	
755	762	8	LSRKYTSE	..	B*1525	81	..	144	21	..	..	
755	762	8	LSRKYTSE	..	B*4601	59	..	104	21	..	..	
755	762	8	LSRKYTSE	..	B*5701	61	..	107	21	..	..	
755	762	8	LSRKYTSE	..	B*5802	46	..	82	21	..	..	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
754	764	11	VLSRKYTSFPW	640	A*3201	17	0,99	16	21	55	55	
754	764	11	VLSRKYTSFPW	55	B*5701	55	55	54	21	55	55	
754	764	11	VLSRKYTSFPW	55	B*5801	56	55	55	21	55	55	
754	764	11	VLSRKYTSFPW	55	B*5802	22	55	21	21	55	55	
755	764	10	LSRKYTSFPW	641	B*1525	10	55	10	21	55	55	
755	764	10	LSRKYTSFPW	55	B*5802	96	55	94	21	55	55	
756	764	9	SRKYTSFPW	642	B*2702	81	55	80	21	55	55	
757	764	8	RKYTSFPW	643	B*1301	52	55	51	21	55	55	
757	764	8	RKYTSFPW	55	B*2702	94	55	93	21	55	55	
757	764	8	RKYTSFPW	55	B*4402	4	55	4	21	55	55	
757	764	8	RKYTSFPW	55	B*4403	12	55	12	21	55	55	
757	764	8	RKYTSFPW	55	B*5701	3	55	3	21	55	55	
757	764	8	RKYTSFPW	55	B*5802	12	55	11	21	55	55	
755	765	11	LSRKYTSEFWL	644	A*3001	36	1,24	45	21	55	55	
755	765	11	LSRKYTSEFWL	55	B*0801	36	55	44	21	55	55	
756	765	10	SRKYTSFPWL	645	A*3001	21	55	26	21	55	55	
756	765	10	SRKYTSFPWL	55	B*1402	24	55	30	21	55	55	
756	765	10	SRKYTSFPWL	55	B*2702	46	55	57	21	55	55	
756	765	10	SRKYTSFPWL	55	B*2705	10	55	13	21	55	55	
757	765	9	RKYTSFPWL	646	B*1402	8	55	10	21	55	55	
757	765	9	RKYTSFPWL	55	B*2702	4	55	4	21	55	55	
757	765	9	RKYTSFPWL	55	B*4801	87	55	108	21	55	55	
758	765	8	KYTSFPWL	647	A*2301	81	55	101	21	55	55	
758	765	8	KYTSFPWL	55	A*2402	77	55	96	21	55	55	
756	766	11	SRKYTSFPWLL	648	B*1402	64	1,92	122	21	55	55	
756	766	11	SRKYTSFPWLL	55	B*2702	80	55	152	21	55	55	
756	766	11	SRKYTSFPWLL	55	B*3901	26	55	50	21	55	55	
757	766	10	RKYTSFPWLL	649	B*1302	8	55	16	21	55	55	
757	766	10	RKYTSFPWLL	55	B*1402	63	55	120	21	55	55	
757	766	10	RKYTSFPWLL	55	B*2702	70	55	134	21	55	55	
757	766	10	RKYTSFPWLL	55	B*3901	17	55	32	21	55	55	
757	766	10	RKYTSFPWLL	55	B*4801	75	55	144	21	55	55	
758	766	9	KYTSFPWLL	650	A*2301	97	55	185	21	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
758	766	9	KYTSFPWLL	651	A*2402	96	22	185	21	22	22	
759	766	8	YTSFPWLL	651	A*0101	57	22	108	21	22	22	
759	766	8	YTSFPWLL	651	A*2601	18	22	34	21	22	22	
759	766	8	YTSFPWLL	651	B*5801	5	22	10	21	22	22	
757	767	11	RKYTSFPWLLG	652	B*2705	48	0,64	31	21	22	22	
758	767	10	KYTSFPWLLG	653	A*3201	11	22	7	21	22	22	
759	767	9	YTSFPWLLG	654	A*0101	9	22	6	21	22	22	
762	769	8	FPWLLGCT	655	B*3501	65	0,19	13	21	22	22	
762	769	8	FPWLLGCT	655	B*3503	8	22	2	21	22	22	
762	769	8	FPWLLGCT	655	B*5101	35	22	7	21	22	22	
762	769	8	FPWLLGCT	655	B*5501	66	22	13	21	22	22	
762	769	8	FPWLLGCT	655	B*5601	85	22	16	21	22	22	
762	770	9	FPWLLGCTA	656	B*1402	14	1,76	25	21	22	22	
762	770	9	FPWLLGCTA	656	B*3501	39	22	68	21	22	22	
762	770	9	FPWLLGCTA	656	B*3503	88	22	155	21	22	22	
762	770	9	FPWLLGCTA	656	B*5101	33	22	59	21	22	22	
762	771	10	FPWLLGCTAN	657	B*0702	7	0,39	3	21	22	22	
762	771	10	FPWLLGCTAN	657	B*3501	79	22	31	21	22	22	
762	771	10	FPWLLGCTAN	657	B*3503	24	22	9	21	22	22	
762	771	10	FPWLLGCTAN	657	B*5101	57	22	22	21	22	22	
762	771	10	FPWLLGCTAN	657	B*5301	52	22	20	21	22	22	
762	771	10	FPWLLGCTAN	657	B*5501	52	22	20	21	22	22	
762	771	10	FPWLLGCTAN	657	B*5601	69	22	27	21	22	22	
762	772	11	FPWLLGCTANW	658	B*1402	55	1,72	94	21	22	22	
762	772	11	FPWLLGCTANW	658	B*1801	48	22	82	21	22	22	
762	772	11	FPWLLGCTANW	658	B*3501	93	22	161	21	22	22	
762	772	11	FPWLLGCTANW	658	B*3503	81	22	140	21	22	22	
762	772	11	FPWLLGCTANW	658	B*3801	63	22	109	21	22	22	
762	772	11	FPWLLGCTANW	658	B*5101	87	22	149	21	22	22	
762	772	11	FPWLLGCTANW	658	B*5501	8	22	14	21	22	22	
762	772	11	FPWLLGCTANW	658	B*5601	50	22	86	21	22	22	
763	772	10	PWLLGCTANW	659	A*2301	67	22	116	21	22	22	
763	772	10	PWLLGCTANW	659	A*2402	32	22	54	21	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
764	772	9	WLLGCTANW	660	B*5701	26	22	44	21	22	22	
764	773	10	WLLGcTANWI	661	A*0201	91	0,22	20	21	22	22	
765	773	9	LLGCTANWI	662	A*0201	71	22	15	21	22	22	
764	774	11	WLLGCTANWIL	663	B*3801	18	1,41	26	21	22	22	
764	774	11	WLLGCTANWIL	22	B*3901	74	22	104	21	22	22	
764	774	11	WLLGCTANWIL	22	B*4801	40	22	57	21	22	22	
765	774	10	LLGcTANWIL	664	A*0201	64	22	90	21	22	22	
765	775	11	LLGCTANWILR	665	A*7401	30	1,01	31	21	22	22	
766	775	10	LGCTANWILR	666	A*3201	33	22	34	21	22	22	
768	775	8	CTANWILR	667	A*1101	72	22	72	21	22	22	
768	775	8	CTANWILR	22	A*3101	53	22	54	21	22	22	
768	775	8	CTANWILR	22	A*3303	79	22	80	21	22	22	
768	775	8	CTANWILR	22	A*6801	94	22	95	21	22	22	
768	775	8	CTANWILR	22	A*7401	74	22	75	21	22	22	
769	779	11	TANWILRGTSF	668	B*1502	33	1,20	40	21	22	22	
769	779	11	TANWILRGTSF	22	B*3501	11	22	13	21	22	22	
769	779	11	TANWILRGTSF	22	B*4601	25	22	29	21	22	22	
769	779	11	TANWILRGTSF	22	B*5802	20	22	24	21	22	22	
770	779	10	ANWILRGTSF	669	B*4402	8	22	9	21	22	22	
771	779	9	NWILRGTSF	670	A*2301	2	22	2	21	22	22	
771	779	9	NWILRGTSF	22	A*2402	30	22	36	21	22	22	
772	779	8	WILRGTSF	671	B*0801	7	22	8	21	22	22	
772	779	8	WILRGTSF	22	B*1501	52	22	62	21	22	22	
772	779	8	WILRGTSF	22	B*1502	81	22	97	21	22	22	
772	779	8	WILRGTSF	22	B*1525	63	22	75	21	22	22	
772	779	8	WILRGTSF	22	B*4601	39	22	47	21	22	22	
772	780	9	WILRGTSFV	672	A*0201	100	1,19	119	21	22	22	
772	780	9	WILRGTSFV	22	A*0206	69	22	82	21	22	22	
771	781	11	NWILRGTSFVY	673	A*2902	51	1,69	86	21	22	22	
771	781	11	NWILRGTSFVY	22	B*1801	24	22	40	21	22	22	
772	781	10	WILRGTSFVY	674	B*1502	59	22	100	21	22	22	
772	781	10	WILRGTSFVY	22	B*1525	8	22	14	21	22	22	
772	781	10	WILRGTSFVY	22	B*4601	2	22	3	21	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
773	781	9	ILRGTSFVY	675	A*0301	23	..	39	21	..	..
773	781	9	ILRGTSFVY	..	A*2902	63	..	108	21	..	..
773	781	9	ILRGTSFVY	..	A*3002	72	..	122	21	..	..
773	781	9	ILRGTSFVY	..	B*1501	83	..	140	21	..	..
773	781	9	ILRGTSFVY	..	B*1525	69	..	118	21	..	..
774	781	8	LRGTSFVY	676	B*2702	23	..	39	21	..	..
774	781	8	LRGTSFVY	..	B*2705	37	..	63	21	..	..
773	782	10	ILRGTSFVYV	677	A*0201	71	1,67	119	21	..	..
776	785	10	GTSEFVYVPSA	678	A*3001	73	1,35	98	21	..	..
776	785	10	GTSEFVYVPSA	..	B*5701	45	..	61	21	..	..
778	786	9	SFVYVPSAL	679	B*1402	7	1,57	11	21	..	..
779	786	8	FVYVPSAL	680	A*2501	27	..	42	21	..	..
779	786	8	FVYVPSAL	..	B*0801	5	..	8	21	..	..
779	786	8	FVYVPSAL	..	B*1402	75	..	118	21	..	..
779	786	8	FVYVPSAL	..	B*1502	54	..	85	21	..	..
779	786	8	FVYVPSAL	..	B*3503	41	..	64	21	..	..
779	786	8	FVYVPSAL	..	B*3801	41	..	64	21	..	..
779	786	8	FVYVPSAL	..	B*3901	73	..	114	21	..	..
779	786	8	FVYVPSAL	..	B*4601	77	..	121	21	..	..
779	786	8	FVYVPSAL	..	B*5501	45	..	71	21	..	..
779	786	8	FVYVPSAL	..	B*5601	24	..	38	21	..	..
781	788	8	YVPSALNP	681	A*0206	73	0,38	27	21	..	..
779	789	11	FVYVPSALNPA	682	A*6802	15	0,68	10	21	..	..
779	789	11	FVYVPSALNPA	..	B*4601	67	..	46	21	..	..
779	789	11	FVYVPSALNPA	..	B*5501	65	..	44	21	..	..
779	789	11	FVYVPSALNPA	..	B*5601	74	..	51	21	..	..
781	789	9	YVPSALNPA	683	A*0206	42	..	28	21	..	..
782	789	8	VPSALNPA	684	B*0702	22	..	15	21	..	..
782	789	8	VPSALNPA	..	B*3503	1	..	1	21	..	..
782	789	8	VPSALNPA	..	B*5101	5	..	3	21	..	..
782	789	8	VPSALNPA	..	B*5501	80	..	55	21	..	..
782	789	8	VPSALNPA	..	B*5601	91	..	62	21	..	..
781	790	10	YVPSALNPAD	685	A*3001	14	0,18	3	21	..	..

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein									Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
					Cumulative Class I-BCI score: 8555						
757	765	9	RKYTSFPWL	646	B*1402	8	1,24	10	22	757	792
757	765	9	RKYTSFPWL	„	B*2702	4	„	4	22	„	„
757	765	9	RKYTSFPWL	„	B*4801	87	„	108	22	„	„
758	765	8	KYTSFPWL	647	A*2301	81	„	101	22	„	„
758	765	8	KYTSFPWL	„	A*2402	77	„	96	22	„	„
756	766	11	SRKYTSFPWLL	648	B*1402	64	1,92	122	22	„	„
756	766	11	SRKYTSFPWLL	„	B*2702	80	„	152	22	„	„
756	766	11	SRKYTSFPWLL	„	B*3901	26	„	50	22	„	„
757	766	10	RKYTSFPWLL	649	B*1302	8	„	16	22	„	„
757	766	10	RKYTSFPWLL	„	B*1402	63	„	120	22	„	„
757	766	10	RKYTSFPWLL	„	B*2702	70	„	134	22	„	„
757	766	10	RKYTSFPWLL	„	B*3901	17	„	32	22	„	„
757	766	10	RKYTSFPWLL	„	B*4801	75	„	144	22	„	„
758	766	9	KYTSFPWLL	650	A*2301	97	„	185	22	„	„
758	766	9	KYTSFPWLL	„	A*2402	96	„	185	22	„	„
759	766	8	YTSFPWLL	651	A*0101	57	„	108	22	„	„
759	766	8	YTSFPWLL	„	A*2601	18	„	34	22	„	„
759	766	8	YTSFPWLL	„	B*5801	5	„	10	22	„	„
757	767	11	RKYTSFPWLLG	652	B*2705	48	0,64	31	22	„	„
758	767	10	KYTSFPWLLG	653	A*3201	11	„	7	22	„	„
759	767	9	YTSFPWLLG	654	A*0101	9	„	6	22	„	„
762	769	8	FPWLLGCT	655	B*3501	65	0,19	13	22	„	„
762	769	8	FPWLLGCT	„	B*3503	8	„	2	22	„	„
762	769	8	FPWLLGCT	„	B*5101	35	„	7	22	„	„
762	769	8	FPWLLGCT	„	B*5501	66	„	13	22	„	„
762	769	8	FPWLLGCT	„	B*5601	85	„	16	22	„	„
762	770	9	FPWLLGCTA	656	B*1402	14	1,76	25	22	„	„
762	770	9	FPWLLGCTA	„	B*3501	39	„	68	22	„	„
762	770	9	FPWLLGCTA	„	B*3503	88	„	155	22	„	„
762	770	9	FPWLLGCTA	„	B*5101	33	„	59	22	„	„
762	771	10	FPWLLGCTAN	657	B*0702	7	0,39	3	22	„	„

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
762	771	10	FPWLLGCTAN	55	B*3501	79	55	31	22	55	55	
762	771	10	FPWLLGCTAN	55	B*3503	24	55	9	22	55	55	
762	771	10	FPWLLGCTAN	55	B*5101	57	55	22	22	55	55	
762	771	10	FPWLLGCTAN	55	B*5301	52	55	20	22	55	55	
762	771	10	FPWLLGCTAN	55	B*5501	52	55	20	22	55	55	
762	771	10	FPWLLGCTAN	55	B*5601	69	55	27	22	55	55	
762	772	11	FPWLLGCTANW	658	B*1402	55	1,72	94	22	55	55	
762	772	11	FPWLLGCTANW	55	B*1801	48	55	82	22	55	55	
762	772	11	FPWLLGCTANW	55	B*3501	93	55	161	22	55	55	
762	772	11	FPWLLGCTANW	55	B*3503	81	55	140	22	55	55	
762	772	11	FPWLLGCTANW	55	B*3801	63	55	109	22	55	55	
762	772	11	FPWLLGCTANW	55	B*5101	87	55	149	22	55	55	
762	772	11	FPWLLGCTANW	55	B*5501	8	55	14	22	55	55	
762	772	11	FPWLLGCTANW	55	B*5601	50	55	86	22	55	55	
763	772	10	PWLLGCTANW	659	A*2301	67	55	116	22	55	55	
763	772	10	PWLLGCTANW	55	A*2402	32	55	54	22	55	55	
764	772	9	WLLGCTANW	660	B*5701	26	55	44	22	55	55	
764	773	10	WLLGcTANWI	661	A*0201	91	0,22	20	22	55	55	
765	773	9	LLGCTANWI	662	A*0201	71	55	15	22	55	55	
764	774	11	WLLGCTANWIL	663	B*3801	18	1,41	26	22	55	55	
764	774	11	WLLGCTANWIL	55	B*3901	74	55	104	22	55	55	
764	774	11	WLLGCTANWIL	55	B*4801	40	55	57	22	55	55	
765	774	10	LLGCTANWIL	664	A*0201	64	55	90	22	55	55	
765	775	11	LLGCTANWILR	665	A*7401	30	1,01	31	22	55	55	
766	775	10	LGCTANWILR	666	A*3201	33	55	34	22	55	55	
768	775	8	CTANWILR	667	A*1101	72	55	72	22	55	55	
768	775	8	CTANWILR	55	A*3101	53	55	54	22	55	55	
768	775	8	CTANWILR	55	A*3303	79	55	80	22	55	55	
768	775	8	CTANWILR	55	A*6801	94	55	95	22	55	55	
768	775	8	CTANWILR	55	A*7401	74	55	75	22	55	55	
769	779	11	TANWILRGTSF	668	B*1502	33	1,20	40	22	55	55	
769	779	11	TANWILRGTSF	55	B*3501	11	55	13	22	55	55	
769	779	11	TANWILRGTSF	55	B*4601	25	55	29	22	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
769	779	11	TANWILRGTSF	“	B*5802	20	“	24	22	“	“	
770	779	10	ANWILRGTSF	669	B*4402	8	“	9	22	“	“	
771	779	9	NWILRGTSF	670	A*2301	2	“	2	22	“	“	
771	779	9	NWILRGTSF	“	A*2402	30	“	36	22	“	“	
772	779	8	WILRGTSF	671	B*0801	7	“	8	22	“	“	
772	779	8	WILRGTSF	“	B*1501	52	“	62	22	“	“	
772	779	8	WILRGTSF	“	B*1502	81	“	97	22	“	“	
772	779	8	WILRGTSF	“	B*1525	63	“	75	22	“	“	
772	779	8	WILRGTSF	“	B*4601	39	“	47	22	“	“	
772	780	9	WILRGTSFV	672	A*0201	100	1,19	119	22	“	“	
772	780	9	WILRGTSFV	“	A*0206	69	“	82	22	“	“	
771	781	11	NWILRGTSFVY	673	A*2902	51	1,69	86	22	“	“	
771	781	11	NWILRGTSFVY	“	B*1801	24	“	40	22	“	“	
772	781	10	WILRGTSFVY	674	B*1502	59	“	100	22	“	“	
772	781	10	WILRGTSFVY	“	B*1525	8	“	14	22	“	“	
772	781	10	WILRGTSFVY	“	B*4601	2	“	3	22	“	“	
773	781	9	ILRGTSFVY	675	A*0301	23	“	39	22	“	“	
773	781	9	ILRGTSFVY	“	A*2902	63	“	108	22	“	“	
773	781	9	ILRGTSFVY	“	A*3002	72	“	122	22	“	“	
773	781	9	ILRGTSFVY	“	B*1501	83	“	140	22	“	“	
773	781	9	ILRGTSFVY	“	B*1525	69	“	118	22	“	“	
774	781	8	LRGTSFVY	676	B*2702	23	“	39	22	“	“	
774	781	8	LRGTSFVY	“	B*2705	37	“	63	22	“	“	
773	782	10	ILRGTSFVYV	677	A*0201	71	1,67	119	22	“	“	
776	785	10	GTSFVYVPSA	678	A*3001	73	1,35	98	22	“	“	
776	785	10	GTSFVYVPSA	“	B*5701	45	“	61	22	“	“	
778	786	9	SFVYVPSAL	679	B*1402	7	1,57	11	22	“	“	
779	786	8	FVYVPSAL	680	A*2501	27	“	42	22	“	“	
779	786	8	FVYVPSAL	“	B*0801	5	“	8	22	“	“	
779	786	8	FVYVPSAL	“	B*1402	75	“	118	22	“	“	
779	786	8	FVYVPSAL	“	B*1502	54	“	85	22	“	“	
779	786	8	FVYVPSAL	“	B*3503	41	“	64	22	“	“	
779	786	8	FVYVPSAL	“	B*3801	41	“	64	22	“	“	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
779	786	8	FVYVPSAL	73	B*3901	73	73	114	22	73	73	
779	786	8	FVYVPSAL	73	B*4601	77	77	121	22	73	73	
779	786	8	FVYVPSAL	73	B*5501	45	73	71	22	73	73	
779	786	8	FVYVPSAL	73	B*5601	24	73	38	22	73	73	
781	788	8	YVPSALNP	681	A*0206	73	0,38	27	22	73	73	
779	789	11	FVYVPSALNPA	682	A*6802	15	0,68	10	22	73	73	
779	789	11	FVYVPSALNPA	73	B*4601	67	73	46	22	73	73	
779	789	11	FVYVPSALNPA	73	B*5501	65	73	44	22	73	73	
779	789	11	FVYVPSALNPA	73	B*5601	74	73	51	22	73	73	
781	789	9	YVPSALNPA	683	A*0206	42	73	28	22	73	73	
782	789	8	VPSALNPA	684	B*0702	22	73	15	22	73	73	
782	789	8	VPSALNPA	73	B*3503	1	73	1	22	73	73	
782	789	8	VPSALNPA	73	B*5101	5	73	3	22	73	73	
782	789	8	VPSALNPA	73	B*5501	80	73	55	22	73	73	
782	789	8	VPSALNPA	73	B*5601	91	73	62	22	73	73	
781	790	10	YVPSALNPAD	685	A*3001	14	0,18	3	22	73	73	
					Cumulative Class I-BCI score:			6817				
754	762	9	VLSRKYTSE	638	B*0801	68	1,77	120	23	754	789	
754	762	9	VLSRKYTSE	73	B*1501	17	73	30	23	73	73	
755	762	8	LSRKYTSE	639	B*0801	61	73	108	23	73	73	
755	762	8	LSRKYTSE	73	B*1501	98	73	174	23	73	73	
755	762	8	LSRKYTSE	73	B*1502	85	73	150	23	73	73	
755	762	8	LSRKYTSE	73	B*1525	81	73	144	23	73	73	
755	762	8	LSRKYTSE	73	B*4601	59	73	104	23	73	73	
755	762	8	LSRKYTSE	73	B*5701	61	73	107	23	73	73	
755	762	8	LSRKYTSE	73	B*5802	46	73	82	23	73	73	
754	764	11	VLSRKYTSEFPW	640	A*3201	17	0,99	16	23	73	73	
754	764	11	VLSRKYTSEFPW	73	B*5701	55	73	54	23	73	73	
754	764	11	VLSRKYTSEFPW	73	B*5801	56	73	55	23	73	73	
754	764	11	VLSRKYTSEFPW	73	B*5802	22	73	21	23	73	73	
755	764	10	LSRKYTSEFPW	641	B*1525	10	73	10	23	73	73	
755	764	10	LSRKYTSEFPW	73	B*5802	96	73	94	23	73	73	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
756	764	9	SRKYTSFPW	642	B*2702	81	22	80	23	22	22	
757	764	8	RKYTSFPW	643	B*1301	52	22	51	23	22	22	
757	764	8	RKYTSFPW	22	B*2702	94	22	93	23	22	22	
757	764	8	RKYTSFPW	22	B*4402	4	22	4	23	22	22	
757	764	8	RKYTSFPW	22	B*4403	12	22	12	23	22	22	
757	764	8	RKYTSFPW	22	B*5701	3	22	3	23	22	22	
757	764	8	RKYTSFPW	22	B*5802	12	22	11	23	22	22	
755	765	11	LSRKYTSFPWL	644	A*3001	36	1,24	45	23	22	22	
755	765	11	LSRKYTSFPWL	22	B*0801	36	22	44	23	22	22	
756	765	10	SRKYTSFPWL	645	A*3001	21	22	26	23	22	22	
756	765	10	SRKYTSFPWL	22	B*1402	24	22	30	23	22	22	
756	765	10	SRKYTSFPWL	22	B*2702	46	22	57	23	22	22	
756	765	10	SRKYTSFPWL	22	B*2705	10	22	13	23	22	22	
757	765	9	RKYTSFPWL	646	B*1402	8	22	10	23	22	22	
757	765	9	RKYTSFPWL	22	B*2702	4	22	4	23	22	22	
757	765	9	RKYTSFPWL	22	B*4801	87	22	108	23	22	22	
758	765	8	KYTSFPWL	647	A*2301	81	22	101	23	22	22	
758	765	8	KYTSFPWL	22	A*2402	77	22	96	23	22	22	
756	766	11	SRKYTSFPWLL	648	B*1402	64	1,92	122	23	22	22	
756	766	11	SRKYTSFPWLL	22	B*2702	80	22	152	23	22	22	
756	766	11	SRKYTSFPWLL	22	B*3901	26	22	50	23	22	22	
757	766	10	RKYTSFPWLL	649	B*1302	8	22	16	23	22	22	
757	766	10	RKYTSFPWLL	22	B*1402	63	22	120	23	22	22	
757	766	10	RKYTSFPWLL	22	B*2702	70	22	134	23	22	22	
757	766	10	RKYTSFPWLL	22	B*3901	17	22	32	23	22	22	
757	766	10	RKYTSFPWLL	22	B*4801	75	22	144	23	22	22	
758	766	9	KYTSFPWLL	650	A*2301	97	22	185	23	22	22	
758	766	9	KYTSFPWLL	22	A*2402	96	22	185	23	22	22	
759	766	8	YTSFPWLL	651	A*0101	57	22	108	23	22	22	
759	766	8	YTSFPWLL	22	A*2601	18	22	34	23	22	22	
759	766	8	YTSFPWLL	22	B*5801	5	22	10	23	22	22	
757	767	11	RKYTSFPWLLG	652	B*2705	48	0,64	31	23	22	22	
758	767	10	KYTSFPWLLG	653	A*3201	11	22	7	23	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
759	767	9	YTSFPWLLG	654	A*0101	9	22	6	23	22	22	
762	769	8	FPWLLGCT	655	B*3501	65	0,19	13	23	22	22	
762	769	8	FPWLLGCT	22	B*3503	8	22	2	23	22	22	
762	769	8	FPWLLGCT	22	B*5101	35	22	7	23	22	22	
762	769	8	FPWLLGCT	22	B*5501	66	22	13	23	22	22	
762	769	8	FPWLLGCT	22	B*5601	85	22	16	23	22	22	
762	770	9	FPWLLGCTA	656	B*1402	14	1,76	25	23	22	22	
762	770	9	FPWLLGCTA	22	B*3501	39	22	68	23	22	22	
762	770	9	FPWLLGCTA	22	B*3503	88	22	155	23	22	22	
762	770	9	FPWLLGCTA	22	B*5101	33	22	59	23	22	22	
762	771	10	FPWLLGCTAN	657	B*0702	7	0,39	3	23	22	22	
762	771	10	FPWLLGCTAN	22	B*3501	79	22	31	23	22	22	
762	771	10	FPWLLGCTAN	22	B*3503	24	22	9	23	22	22	
762	771	10	FPWLLGCTAN	22	B*5101	57	22	22	23	22	22	
762	771	10	FPWLLGCTAN	22	B*5301	52	22	20	23	22	22	
762	771	10	FPWLLGCTAN	22	B*5501	52	22	20	23	22	22	
762	771	10	FPWLLGCTAN	22	B*5601	69	22	27	23	22	22	
762	772	11	FPWLLGCTANW	658	B*1402	55	1,72	94	23	22	22	
762	772	11	FPWLLGCTANW	22	B*1801	48	22	82	23	22	22	
762	772	11	FPWLLGCTANW	22	B*3501	93	22	161	23	22	22	
762	772	11	FPWLLGCTANW	22	B*3503	81	22	140	23	22	22	
762	772	11	FPWLLGCTANW	22	B*3801	63	22	109	23	22	22	
762	772	11	FPWLLGCTANW	22	B*5101	87	22	149	23	22	22	
762	772	11	FPWLLGCTANW	22	B*5501	8	22	14	23	22	22	
762	772	11	FPWLLGCTANW	22	B*5601	50	22	86	23	22	22	
763	772	10	PWLLGCTANW	659	A*2301	67	22	116	23	22	22	
763	772	10	PWLLGCTANW	22	A*2402	32	22	54	23	22	22	
764	772	9	WLLGCTANW	660	B*5701	26	22	44	23	22	22	
764	773	10	WLLGcTANWI	661	A*0201	91	0,22	20	23	22	22	
765	773	9	LLGCTANWI	662	A*0201	71	22	15	23	22	22	
764	774	11	WLLGCTANWIL	663	B*3801	18	1,41	26	23	22	22	
764	774	11	WLLGCTANWIL	22	B*3901	74	22	104	23	22	22	
764	774	11	WLLGCTANWIL	22	B*4801	40	22	57	23	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
765	774	10	LLGCTANWIL	664	A*0201	64	22	90	23	22	22	
765	775	11	LLGCTANWILR	665	A*7401	30	1,01	31	23	22	22	
766	775	10	LGCTANWILR	666	A*3201	33	22	34	23	22	22	
768	775	8	CTANWILR	667	A*1101	72	22	72	23	22	22	
768	775	8	CTANWILR	22	A*3101	53	22	54	23	22	22	
768	775	8	CTANWILR	22	A*3303	79	22	80	23	22	22	
768	775	8	CTANWILR	22	A*6801	94	22	95	23	22	22	
768	775	8	CTANWILR	22	A*7401	74	22	75	23	22	22	
769	779	11	TANWILRGTSF	668	B*1502	33	1,20	40	23	22	22	
769	779	11	TANWILRGTSF	22	B*3501	11	22	13	23	22	22	
769	779	11	TANWILRGTSF	22	B*4601	25	22	29	23	22	22	
769	779	11	TANWILRGTSF	22	B*5802	20	22	24	23	22	22	
770	779	10	ANWILRGTSF	669	B*4402	8	22	9	23	22	22	
771	779	9	NWILRGTSF	670	A*2301	2	22	2	23	22	22	
771	779	9	NWILRGTSF	22	A*2402	30	22	36	23	22	22	
772	779	8	WILRGTSF	671	B*0801	7	22	8	23	22	22	
772	779	8	WILRGTSF	22	B*1501	52	22	62	23	22	22	
772	779	8	WILRGTSF	22	B*1502	81	22	97	23	22	22	
772	779	8	WILRGTSF	22	B*1525	63	22	75	23	22	22	
772	779	8	WILRGTSF	22	B*4601	39	22	47	23	22	22	
772	780	9	WILRGTSFV	672	A*0201	100	1,19	119	23	22	22	
772	780	9	WILRGTSFV	22	A*0206	69	22	82	23	22	22	
771	781	11	NWILRGTSFVY	673	A*2902	51	1,69	86	23	22	22	
771	781	11	NWILRGTSFVY	22	B*1801	24	22	40	23	22	22	
772	781	10	WILRGTSFVY	674	B*1502	59	22	100	23	22	22	
772	781	10	WILRGTSFVY	22	B*1525	8	22	14	23	22	22	
772	781	10	WILRGTSFVY	22	B*4601	2	22	3	23	22	22	
773	781	9	ILRGTSFVY	675	A*0301	23	22	39	23	22	22	
773	781	9	ILRGTSFVY	22	A*2902	63	22	108	23	22	22	
773	781	9	ILRGTSFVY	22	A*3002	72	22	122	23	22	22	
773	781	9	ILRGTSFVY	22	B*1501	83	22	140	23	22	22	
773	781	9	ILRGTSFVY	22	B*1525	69	22	118	23	22	22	
774	781	8	LRGTSFVY	676	B*2702	23	22	39	23	22	22	

HLA class I binding peptides in SLP sequences derived from HBV Polymerase protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
774	781	8	LRGTSFVY	22	B*2705	37	22	63	23	22	22	
773	782	10	ILRGTSFVYV	677	A*0201	71	1,67	119	23	22	22	
776	785	10	GTSFVYVPSA	678	A*3001	73	1,35	98	23	22	22	
776	785	10	GTSFVYVPSA	22	B*5701	45	22	61	23	22	22	
778	786	9	SFVYVPSAL	679	B*1402	7	1,57	11	23	22	22	
779	786	8	FVYVPSAL	680	A*2501	27	22	42	23	22	22	
779	786	8	FVYVPSAL	22	B*0801	5	22	8	23	22	22	
779	786	8	FVYVPSAL	22	B*1402	75	22	118	23	22	22	
779	786	8	FVYVPSAL	22	B*1502	54	22	85	23	22	22	
779	786	8	FVYVPSAL	22	B*3503	41	22	64	23	22	22	
779	786	8	FVYVPSAL	22	B*3801	41	22	64	23	22	22	
779	786	8	FVYVPSAL	22	B*3901	73	22	114	23	22	22	
779	786	8	FVYVPSAL	22	B*4601	77	22	121	23	22	22	
779	786	8	FVYVPSAL	22	B*5501	45	22	71	23	22	22	
779	786	8	FVYVPSAL	22	B*5601	24	22	38	23	22	22	
781	788	8	YVPSALNP	681	A*0206	73	0,38	27	23	22	22	
779	789	11	FVYVPSALNPA	682	A*6802	15	0,68	10	23	22	22	
779	789	11	FVYVPSALNPA	22	B*4601	67	22	46	23	22	22	
779	789	11	FVYVPSALNPA	22	B*5501	65	22	44	23	22	22	
779	789	11	FVYVPSALNPA	22	B*5601	74	22	51	23	22	22	
781	789	9	YVPSALNPA	683	A*0206	42	22	28	23	22	22	
782	789	8	VPSALNPA	684	B*0702	22	22	15	23	22	22	
782	789	8	VPSALNPA	22	B*3503	1	22	1	23	22	22	
782	789	8	VPSALNPA	22	B*5101	5	22	3	23	22	22	
782	789	8	VPSALNPA	22	B*5501	80	22	55	23	22	22	
782	789	8	VPSALNPA	22	B*5601	91	22	62	23	22	22	
Cumulative Class I-BCI score:									8553			

“Start” and “End” are relative to the amino acid sequence of HBV polymerase as depicted in SEQ ID NO: 1

^A Peptide amino acid sequence. Each HLA class I binding peptide of HBV polymerase is listed separately for each HLA class I molecule to which it is predicted to bind, and can be listed multiple times for that reason.

^B Class I-B score. See *Material and Methods* (Examples section).

^C C-score. See *Material and Methods* (Examples section).

^D Class I-BCI score. See *Material and Methods* (Examples section).

^E Cumulative Class I-BCI score. See *Material and Methods* (Examples section).

Table 4b. Predicted HLA class II-restricted CD4⁺ T cell epitopes contained in SLP sequences from HBV polymerase protein.

HLA class II binding peptides in SLP sequences derived from HBV Polymerase						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
1	15	MPLSYQHFRKLLLLLD	686	*0701	79	1	1	30
1	15	MPLSYQHFRKLLLLLD	„	*1101	86	1	„	„
1	15	MPLSYQHFRKLLLLLD	„	*1501	9	1	„	„
2	16	PLSYQHFRKLLLLDD	687	*0701	40	1	„	„
2	16	PLSYQHFRKLLLLDD	„	*1101	84	1	„	„
2	16	PLSYQHFRKLLLLDD	„	*1501	4	1	„	„
3	17	LSYQHFRKLLLLDDG	688	*0701	9	1	„	„
3	17	LSYQHFRKLLLLDDG	„	*1101	83	1	„	„
3	17	LSYQHFRKLLLLDDG	„	*1501	3	1	„	„
4	18	SYQHFRKLLLLDDGT	689	*1101	81	1	„	„
5	19	YQHFRKLLLLDDGTE	690	*1101	80	1	„	„
6	20	QHFRKLLLLDDGTEA	691	*0301	31	1	„	„
6	20	QHFRKLLLLDDGTEA	„	*1101	56	1	„	„
7	21	HFRKLLLLDDGTEAG	692	*0301	30	1	„	„
8	22	FRKLLLLDDGTEAGP	693	*0301	29	1	„	„
9	23	RKLLLLDDGTEAGPL	694	*0301	27	1	„	„
10	24	KLLLLDDGTEAGPLE	695	*0301	26	1	„	„
11	25	LLLLDDGTEAGPLEE	696	*0301	24	1	„	„
		Cumulative Class II-B score^C:			780			
55	69	THKVGNETGLYSSTV	697	*0101	14	2	52	86
55	69	THKVGNETGLYSSTV	„	*1501	54	2	„	„
56	70	HKVGNETGLYSSTVP	698	*0101	10	2	„	„
56	70	HKVGNETGLYSSTVP	„	*1501	51	2	„	„
57	71	KVGNETGLYSSTVPI	699	*0101	64	2	„	„
57	71	KVGNETGLYSSTVPI	„	*0105	78	2	„	„
57	71	KVGNETGLYSSTVPI	„	*0107	78	2	„	„
57	71	KVGNETGLYSSTVPI	„	*0401	11	2	„	„
57	71	KVGNETGLYSSTVPI	„	*0701	26	2	„	„
57	71	KVGNETGLYSSTVPI	„	*1501	47	2	„	„
58	72	VGNETGLYSSTVPIF	700	*0101	93	2	„	„
58	72	VGNETGLYSSTVPIF	„	*0105	88	2	„	„
58	72	VGNETGLYSSTVPIF	„	*0107	88	2	„	„
58	72	VGNETGLYSSTVPIF	„	*0301	14	2	„	„
58	72	VGNETGLYSSTVPIF	„	*0401	23	2	„	„
58	72	VGNETGLYSSTVPIF	„	*0701	34	2	„	„
58	72	VGNETGLYSSTVPIF	„	*1501	59	2	„	„
59	73	GNFTGLYSSTVPIFN	701	*0101	80	2	„	„
59	73	GNFTGLYSSTVPIFN	„	*0105	55	2	„	„
59	73	GNFTGLYSSTVPIFN	„	*0107	55	2	„	„
59	73	GNFTGLYSSTVPIFN	„	*0301	16	2	„	„
59	73	GNFTGLYSSTVPIFN	„	*0401	24	2	„	„
59	73	GNFTGLYSSTVPIFN	„	*0701	54	2	„	„
60	74	NFTGLYSSTVPIFNP	702	*0101	57	2	„	„

HLA class II binding peptides in SLP sequences derived from HBV Polymerase						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
60	74	NFTGLYSSTVPIFNP	„	*0301	11	2	„	„
60	74	NFTGLYSSTVPIFNP	„	*0401	16	2	„	„
60	74	NFTGLYSSTVPIFNP	„	*0701	30	2	„	„
61	75	FTGLYSSTVPIFNPE	703	*0101	43	2	„	„
61	75	FTGLYSSTVPIFNPE	„	*0301	13	2	„	„
61	75	FTGLYSSTVPIFNPE	„	*0401	19	2	„	„
61	75	FTGLYSSTVPIFNPE	„	*0701	11	2	„	„
62	76	TGLYSSTVPIFNPEW	704	*0301	7	2	„	„
		Cumulative Class II-B score:				1323		
103	117	VNEKRRLKLIMPARF	705	*0101	47	3	103	135
103	117	VNEKRRLKLIMPARF	„	*0102	33	3	„	„
103	117	VNEKRRLKLIMPARF	„	*0104	8	3	„	„
103	117	VNEKRRLKLIMPARF	„	*0106	50	3	„	„
103	117	VNEKRRLKLIMPARF	„	*0301	36	3	„	„
103	117	VNEKRRLKLIMPARF	„	*0701	17	3	„	„
103	117	VNEKRRLKLIMPARF	„	*1301	7	3	„	„
103	117	VNEKRRLKLIMPARF	„	*1501	64	3	„	„
104	118	NEKRRLKLIMPARFY	706	*0101	53	3	„	„
104	118	NEKRRLKLIMPARFY	„	*0102	83	3	„	„
104	118	NEKRRLKLIMPARFY	„	*0104	78	3	„	„
104	118	NEKRRLKLIMPARFY	„	*0106	83	3	„	„
104	118	NEKRRLKLIMPARFY	„	*0701	27	3	„	„
104	118	NEKRRLKLIMPARFY	„	*1301	64	3	„	„
104	118	NEKRRLKLIMPARFY	„	*1501	76	3	„	„
105	119	EKRRLKLIMPARFYFYP	707	*0101	46	3	„	„
105	119	EKRRLKLIMPARFYFYP	„	*0102	93	3	„	„
105	119	EKRRLKLIMPARFYFYP	„	*0104	85	3	„	„
105	119	EKRRLKLIMPARFYFYP	„	*0106	85	3	„	„
105	119	EKRRLKLIMPARFYFYP	„	*0701	3	3	„	„
105	119	EKRRLKLIMPARFYFYP	„	*1101	8	3	„	„
105	119	EKRRLKLIMPARFYFYP	„	*1301	61	3	„	„
105	119	EKRRLKLIMPARFYFYP	„	*1501	71	3	„	„
106	120	KRRLKLIMPARFYPT	708	*0101	49	3	„	„
106	120	KRRLKLIMPARFYPT	„	*0102	100	3	„	„
106	120	KRRLKLIMPARFYPT	„	*0103	4	3	„	„
106	120	KRRLKLIMPARFYPT	„	*0104	100	3	„	„
106	120	KRRLKLIMPARFYPT	„	*0105	45	3	„	„
106	120	KRRLKLIMPARFYPT	„	*0106	93	3	„	„
106	120	KRRLKLIMPARFYPT	„	*0107	45	3	„	„
106	120	KRRLKLIMPARFYPT	„	*1101	25	3	„	„
106	120	KRRLKLIMPARFYPT	„	*1301	71	3	„	„
106	120	KRRLKLIMPARFYPT	„	*1501	73	3	„	„
107	121	RRLKLIMPARFYPTH	709	*0101	44	3	„	„
107	121	RRLKLIMPARFYPTH	„	*0102	80	3	„	„
107	121	RRLKLIMPARFYPTH	„	*0104	88	3	„	„
107	121	RRLKLIMPARFYPTH	„	*0106	78	3	„	„

HLA class II binding peptides in SLP sequences derived from HBV Polymerase						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
107	121	RRLKLIMPARFYPTH	„	*1301	32	3	„	„
107	121	RRLKLIMPARFYPTH	„	*1501	69	3	„	„
108	122	RLKLIMPARFYPTHT	710	*0102	53	3	„	„
108	122	RLKLIMPARFYPTHT	„	*0104	53	3	„	„
108	122	RLKLIMPARFYPTHT	„	*0106	60	3	„	„
108	122	RLKLIMPARFYPTHT	„	*1501	41	3	„	„
109	123	LKLIMPARFYPTHTK	711	*1501	40	3	„	„
111	125	LIMPARFYPTHTKYL	712	*0701	93	3	„	„
112	126	IMPARFYPTHTKYLPL	713	*0701	91	3	„	„
113	127	MPARFYPTHTKYLPL	714	*0701	96	3	„	„
114	128	PARFYPTHTKYLPLD	715	*0701	94	3	„	„
115	129	ARFYPTHTKYLPLDK	716	*0701	90	3	„	„
116	130	RFYPTHTKYLPLDKG	717	*0701	86	3	„	„
117	131	FYPTHTKYLPLDKGI	718	*0701	81	3	„	„
121	135	HTKYLPLDKGIKPY	719	*1101	23	3	„	„
Cumulative Class II-B score:					3070			
121	135	HTKYLPLDKGIKPY	719	*1101	23	4	118	150
122	136	TKYLPLDKGIKPY	720	*1101	21	4	„	„
130	144	GIKPYYPDQVNVHYF	721	*0401	26	4	„	„
131	145	IKPYYPDQVNVHYFQ	722	*0401	51	4	„	„
132	146	KPYYPDQVNVHYFQT	723	*0401	21	4	„	„
Cumulative Class II-B score:					143			
139	153	VNVHYFQTRHYLHTL	726	*1101	87	5	139	177
139	153	VNVHYFQTRHYLHTL	„	*1501	70	5	„	„
140	154	VNVHYFQTRHYLHTLW	727	*0701	70	5	„	„
140	154	VNVHYFQTRHYLHTLW	„	*1101	76	5	„	„
140	154	VNVHYFQTRHYLHTLW	„	*1501	58	5	„	„
141	155	NHYFQTRHYLHTLWK	728	*0701	40	5	„	„
141	155	NHYFQTRHYLHTLWK	„	*1101	79	5	„	„
141	155	NHYFQTRHYLHTLWK	„	*1501	28	5	„	„
142	156	HYFQTRHYLHTLWKA	729	*1101	54	5	„	„
142	156	HYFQTRHYLHTLWKA	„	*1501	30	5	„	„
143	157	YFQTRHYLHTLWKAG	730	*1101	24	5	„	„
144	158	FQTRHYLHTLWKAGI	731	*1101	55	5	„	„
144	158	FQTRHYLHTLWKAGI	„	*1501	5	5	„	„
145	159	QTRHYLHTLWKAGIL	732	*1101	78	5	„	„
145	159	QTRHYLHTLWKAGIL	„	*1501	38	5	„	„
146	160	TRHYLHTLWKAGILY	733	*1101	88	5	„	„
146	160	TRHYLHTLWKAGILY	„	*1501	45	5	„	„
147	161	RHYLHTLWKAGILYK	734	*1101	85	5	„	„
147	161	RHYLHTLWKAGILYK	„	*1501	40	5	„	„
148	162	HYLHTLWKAGILYKR	735	*1101	50	5	„	„
154	168	WKAGILYKRETTSA	736	*0401	81	5	„	„
155	169	KAGILYKRETTSA	737	*0401	83	5	„	„
156	170	AGILYKRETTSA	738	*0401	84	5	„	„

HLA class II binding peptides in SLP sequences derived from HBV Polymerase						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
157	171	GILYKRETTTSASFC	739	*0401	80	5	..	..
158	172	ILYKRETTTSASFCG	740	*0401	79	5	..	..
159	173	LYKRETTTSASFCGS	741	*0401	14	5	..	..
		Cumulative Class II-B score:				1519		
143	157	YFQTRHYLHTLWKAG	730	*1101	24	6	143	177
144	158	FQTRHYLHTLWKAGI	731	*1101	55	6	..	..
144	158	FQTRHYLHTLWKAGI	..	*1501	5	6	..	..
145	159	QTRHYLHTLWKAGIL	732	*1101	78	6	..	..
145	159	QTRHYLHTLWKAGIL	..	*1501	38	6	..	..
146	160	TRHYLHTLWKAGILY	733	*1101	88	6	..	..
146	160	TRHYLHTLWKAGILY	..	*1501	45	6	..	..
147	161	RHYLHTLWKAGILYK	734	*1101	85	6	..	..
147	161	RHYLHTLWKAGILYK	..	*1501	40	6	..	..
148	162	HYLHTLWKAGILYKR	735	*1101	50	6	..	..
154	168	WKAGILYKRETTTSA	736	*0401	81	6	..	..
155	169	KAGILYKRETTTSAS	737	*0401	83	6	..	..
156	170	AGILYKRETTTSASF	738	*0401	84	6	..	..
157	171	GILYKRETTTSASFC	739	*0401	80	6	..	..
158	172	ILYKRETTTSASFCG	740	*0401	79	6	..	..
159	173	LYKRETTTSASFCGS	741	*0401	14	6	..	..
		Cumulative Class II-B score:				928		
137	151	DQVFNHYFQTRHYLH	724	*0701	53	7	137	170
137	151	DQVFNHYFQTRHYLH	..	*1101	75	7	..	..
137	151	DQVFNHYFQTRHYLH	..	*1501	63	7	..	..
138	152	QVFNHYFQTRHYLHT	725	*0701	63	7	..	..
138	152	QVFNHYFQTRHYLHT	..	*1101	59	7	..	..
138	152	QVFNHYFQTRHYLHT	..	*1501	73	7	..	..
139	153	VFNHYFQTRHYLHTL	726	*0701	88	7	..	..
139	153	VFNHYFQTRHYLHTL	..	*1101	87	7	..	..
139	153	VFNHYFQTRHYLHTL	..	*1501	70	7	..	..
140	154	VNHYFQTRHYLHTLW	727	*0701	70	7	..	..
140	154	VNHYFQTRHYLHTLW	..	*1101	76	7	..	..
140	154	VNHYFQTRHYLHTLW	..	*1501	58	7	..	..
141	155	NHYFQTRHYLHTLWK	728	*0701	40	7	..	..
141	155	NHYFQTRHYLHTLWK	..	*1101	79	7	..	..
141	155	NHYFQTRHYLHTLWK	..	*1501	28	7	..	..
142	156	HYFQTRHYLHTLWKA	729	*1101	54	7	..	..
142	156	HYFQTRHYLHTLWKA	..	*1501	30	7	..	..
143	157	YFQTRHYLHTLWKAG	730	*1101	24	7	..	..
144	158	FQTRHYLHTLWKAGI	731	*1101	55	7	..	..
144	158	FQTRHYLHTLWKAGI	..	*1501	5	7	..	..
145	159	QTRHYLHTLWKAGIL	732	*1101	78	7	..	..
145	159	QTRHYLHTLWKAGIL	..	*1501	38	7	..	..
146	160	TRHYLHTLWKAGILY	733	*1101	88	7	..	..
146	160	TRHYLHTLWKAGILY	..	*1501	45	7	..	..

HLA class II binding peptides in SLP sequences derived from HBV Polymerase						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
147	161	RHYLHTLWKAGILYK	734	*1101	85	7	„	„
147	161	RHYLHTLWKAGILYK	„	*1501	40	7	„	„
148	162	HYLHTLWKAGILYKR	735	*1101	50	7	„	„
154	168	WKAGILYKRETTTSA	736	*0401	81	7	„	„
155	169	KAGILYKRETTTSAS	737	*0401	83	7	„	„
156	170	AGILYKRETTTSASF	738	*0401	84	7	„	„
		Cumulative Class II-B score:			1817			
324	338	SCWWLQFRNSKPCSE	742	*0401	3	8	316	347
385	399	TAESRLVVDFSQFSR	743	*0301	97	9	385	417
386	400	AESRLVVDFSQFSRG	744	*0301	87	9	„	„
387	401	ESRLVVDFSQFSRGI	745	*0301	96	9	„	„
388	402	SRLVVDFSQFSRGIS	746	*0301	94	9	„	„
389	403	RLVVDFSQFSRGISR	747	*0301	77	9	„	„
390	404	LVVDFSQFSRGISRV	748	*0301	76	9	„	„
		Cumulative Class II-B score:			527			
421	435	LSSNLSWLSLDVSAA	749	*0401	27	10	419	456
422	436	SSNLSWLSLDVSAAF	750	*0301	57	10	„	„
422	436	SSNLSWLSLDVSAAF	„	*0401	71	10	„	„
423	437	SNLSWLSLDVSAAFY	751	*0301	56	10	„	„
423	437	SNLSWLSLDVSAAFY	„	*0401	70	10	„	„
424	438	NLSWLSLDVSAAFYH	752	*0301	54	10	„	„
424	438	NLSWLSLDVSAAFYH	„	*0401	69	10	„	„
425	439	LSWLSLDVSAAFYHI	753	*0301	53	10	„	„
425	439	LSWLSLDVSAAFYHI	„	*0401	67	10	„	„
425	439	LSWLSLDVSAAFYHI	„	*1301	18	10	„	„
426	440	SWLSLDVSAAFYHIP	754	*0301	51	10	„	„
426	440	SWLSLDVSAAFYHIP	„	*0401	66	10	„	„
427	441	WLSLDVSAAFYHIPL	755	*0301	50	10	„	„
427	441	WLSLDVSAAFYHIPL	„	*0401	17	10	„	„
428	442	LSLDVSAAFYHIPLH	756	*0301	49	10	„	„
432	446	VSAAFYHIPLHPAAM	757	*0101	8	10	„	„
432	446	VSAAFYHIPLHPAAM	„	*0105	8	10	„	„
432	446	VSAAFYHIPLHPAAM	„	*0107	8	10	„	„
433	447	SAAFYHIPLHPAAMP	758	*0101	35	10	„	„
433	447	SAAFYHIPLHPAAMP	„	*0105	35	10	„	„
433	447	SAAFYHIPLHPAAMP	„	*0107	35	10	„	„
433	447	SAAFYHIPLHPAAMP	„	*1101	3	10	„	„
434	448	AAFYHIPLHPAAMPH	759	*0101	13	10	„	„
434	448	AAFYHIPLHPAAMPH	„	*0105	13	10	„	„
434	448	AAFYHIPLHPAAMPH	„	*0107	13	10	„	„
		Cumulative Class II-B score:			943			
422	436	SSNLSWLSLDVSAAF	750	*0301	57	11	422	459
422	436	SSNLSWLSLDVSAAF	„	*0401	71	11	„	„

HLA class II binding peptides in SLP sequences derived from HBV Polymerase						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
423	437	SNLSWLSLDVSAAFY	751	*0301	56	11	„	„
423	437	SNLSWLSLDVSAAFY	„	*0401	70	11	„	„
424	438	NLSWLSLDVSAAFYH	752	*0301	54	11	„	„
424	438	NLSWLSLDVSAAFYH	„	*0401	69	11	„	„
425	439	LSWLSLDVSAAFYHI	753	*0301	53	11	„	„
425	439	LSWLSLDVSAAFYHI	„	*0401	67	11	„	„
425	439	LSWLSLDVSAAFYHI	„	*1301	18	11	„	„
426	440	SWLSLDVSAAFYHIP	754	*0301	51	11	„	„
426	440	SWLSLDVSAAFYHIP	„	*0401	66	11	„	„
427	441	WLSLDVSAAFYHIPL	755	*0301	50	11	„	„
427	441	WLSLDVSAAFYHIPL	„	*0401	17	11	„	„
428	442	LSLDVSAAFYHIPLH	756	*0301	49	11	„	„
432	446	VSAAFYHIPLHPAAM	757	*0101	8	11	„	„
432	446	VSAAFYHIPLHPAAM	„	*0105	8	11	„	„
432	446	VSAAFYHIPLHPAAM	„	*0107	8	11	„	„
433	447	SAAFYHIPLHPAAMP	758	*0101	35	11	„	„
433	447	SAAFYHIPLHPAAMP	„	*0105	35	11	„	„
433	447	SAAFYHIPLHPAAMP	„	*0107	35	11	„	„
433	447	SAAFYHIPLHPAAMP	„	*1101	3	11	„	„
434	448	AAFYHIPLHPAAMPH	759	*0101	13	11	„	„
434	448	AAFYHIPLHPAAMPH	„	*0105	13	11	„	„
434	448	AAFYHIPLHPAAMPH	„	*0107	13	11	„	„
444	458	AAMPHLLIGSSGLSR	760	*0101	9	11	„	„
444	458	AAMPHLLIGSSGLSR	„	*0301	64	11	„	„
445	459	AMPHLLIGSSGLSRY	761	*0101	7	11	„	„
445	459	AMPHLLIGSSGLSRY	„	*0301	63	11	„	„
Cumulative Class II-B score:					1058			
427	441	WLSLDVSAAFYHIPL	755	*0301	50	12	427	459
427	441	WLSLDVSAAFYHIPL	„	*0401	17	12	„	„
428	442	LSLDVSAAFYHIPLH	756	*0301	49	12	„	„
432	446	VSAAFYHIPLHPAAM	757	*0101	8	12	„	„
432	446	VSAAFYHIPLHPAAM	„	*0105	8	12	„	„
432	446	VSAAFYHIPLHPAAM	„	*0107	8	12	„	„
433	447	SAAFYHIPLHPAAMP	758	*0101	35	12	„	„
433	447	SAAFYHIPLHPAAMP	„	*0105	35	12	„	„
433	447	SAAFYHIPLHPAAMP	„	*0107	35	12	„	„
433	447	SAAFYHIPLHPAAMP	„	*1101	3	12	„	„
434	448	AAFYHIPLHPAAMPH	759	*0101	13	12	„	„
434	448	AAFYHIPLHPAAMPH	„	*0105	13	12	„	„
434	448	AAFYHIPLHPAAMPH	„	*0107	13	12	„	„
444	458	AAMPHLLIGSSGLSR	760	*0101	9	12	„	„
444	458	AAMPHLLIGSSGLSR	„	*0301	64	12	„	„
445	459	AMPHLLIGSSGLSRY	761	*0101	7	12	„	„
445	459	AMPHLLIGSSGLSRY	„	*0301	63	12	„	„
Cumulative Class II-B score:					426			

HLA class II binding peptides in SLP sequences derived from HBV Polymerase						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
483	497	SCSRQLYVSLMLLYK	762	*1101	94	13	481	514
484	498	CSRQLYVSLMLLYKT	763	*1101	93	13	„	„
484	498	CSRQLYVSLMLLYKT	„	*1501	20	13	„	„
485	499	SRQLYVSLMLLYKTY	764	*1101	91	13	„	„
485	499	SRQLYVSLMLLYKTY	„	*1501	10	13	„	„
486	500	RQLYVSLMLLYKTYG	765	*0301	47	13	„	„
486	500	RQLYVSLMLLYKTYG	„	*1101	100	13	„	„
486	500	RQLYVSLMLLYKTYG	„	*1301	21	13	„	„
486	500	RQLYVSLMLLYKTYG	„	*1501	23	13	„	„
487	501	QLYVSLMLLYKTYGW	766	*0301	10	13	„	„
487	501	QLYVSLMLLYKTYGW	„	*1101	99	13	„	„
487	501	QLYVSLMLLYKTYGW	„	*1301	20	13	„	„
487	501	QLYVSLMLLYKTYGW	„	*1501	61	13	„	„
488	502	LYVSLMLLYKTYGWK	767	*0301	9	13	„	„
488	502	LYVSLMLLYKTYGWK	„	*1101	97	13	„	„
488	502	LYVSLMLLYKTYGWK	„	*1301	19	13	„	„
488	502	LYVSLMLLYKTYGWK	„	*1501	60	13	„	„
489	503	YVSLMLLYKTYGWKL	768	*0701	100	13	„	„
489	503	YVSLMLLYKTYGWKL	„	*1101	96	13	„	„
489	503	YVSLMLLYKTYGWKL	„	*1301	17	13	„	„
489	503	YVSLMLLYKTYGWKL	„	*1501	99	13	„	„
490	504	VSLMLLYKTYGWKLH	769	*0701	99	13	„	„
490	504	VSLMLLYKTYGWKLH	„	*1301	16	13	„	„
490	504	VSLMLLYKTYGWKLH	„	*1501	100	13	„	„
491	505	SIMLLYKTYGWKLHL	770	*0701	97	13	„	„
491	505	SIMLLYKTYGWKLHL	„	*1301	14	13	„	„
491	505	SIMLLYKTYGWKLHL	„	*1501	97	13	„	„
492	506	IMLLYKTYGWKLHLY	771	*0106	3	13	„	„
492	506	IMLLYKTYGWKLHLY	„	*0701	89	13	„	„
492	506	IMLLYKTYGWKLHLY	„	*1101	5	13	„	„
492	506	IMLLYKTYGWKLHLY	„	*1301	13	13	„	„
492	506	IMLLYKTYGWKLHLY	„	*1501	77	13	„	„
493	507	MLLYKTYGWKLHLYS	772	*0701	87	13	„	„
493	507	MLLYKTYGWKLHLYS	„	*1101	9	13	„	„
493	507	MLLYKTYGWKLHLYS	„	*1501	66	13	„	„
494	508	LLYKTYGWKLHLYSH	773	*0701	84	13	„	„
494	508	LLYKTYGWKLHLYSH	„	*1101	7	13	„	„
494	508	LLYKTYGWKLHLYSH	„	*1501	85	13	„	„
495	509	LYKTYGWKLHLYSHP	774	*0701	74	13	„	„
495	509	LYKTYGWKLHLYSHP	„	*1101	6	13	„	„
495	509	LYKTYGWKLHLYSHP	„	*1501	13	13	„	„
496	510	YKTYGWKLHLYSHPI	775	*1101	4	13	„	„
497	511	KTYGWKLHLYSHPIV	776	*0101	30	13	„	„
497	511	KTYGWKLHLYSHPIV	„	*0701	13	13	„	„
497	511	KTYGWKLHLYSHPIV	„	*1101	3	13	„	„
497	511	KTYGWKLHLYSHPIV	„	*1501	90	13	„	„
498	512	TYGWKLHLYSHPIVL	777	*0101	70	13	„	„

HLA class II binding peptides in SLP sequences derived from HBV Polymerase						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
498	512	TYGWKLHLYSHPIVL	„	*0701	71	13	„	„
498	512	TYGWKLHLYSHPIVL	„	*1101	1	13	„	„
498	512	TYGWKLHLYSHPIVL	„	*1501	89	13	„	„
499	513	YGWKLHLYSHPIVLG	778	*0101	81	13	„	„
499	513	YGWKLHLYSHPIVLG	„	*0701	24	13	„	„
499	513	YGWKLHLYSHPIVLG	„	*1301	50	13	„	„
499	513	YGWKLHLYSHPIVLG	„	*1501	87	13	„	„
500	514	GWKLHLYSHPIVLGF	779	*0101	66	13	„	„
500	514	GWKLHLYSHPIVLGF	„	*0701	7	13	„	„
500	514	GWKLHLYSHPIVLGF	„	*1301	49	13	„	„
500	514	GWKLHLYSHPIVLGF	„	*1501	86	13	„	„
		Cumulative Class II-B score:				3046		
524	538	SPFLLAQFTSAICSV	780	*0101	61	14	524	559
524	538	SPFLLAQFTSAICSV	„	*0401	43	14	„	„
524	538	SPFLLAQFTSAICSV	„	*1501	16	14	„	„
525	539	PFLLAQFTSAICSVV	781	*0101	24	14	„	„
525	539	PFLLAQFTSAICSVV	„	*0401	41	14	„	„
525	539	PFLLAQFTSAICSVV	„	*0701	59	14	„	„
525	539	PFLLAQFTSAICSVV	„	*1501	14	14	„	„
526	540	FLLAQFTSAICSVVR	782	*0401	13	14	„	„
526	540	FLLAQFTSAICSVVR	„	*0701	53	14	„	„
527	541	LLAQFTSAICSVVRR	783	*0701	49	14	„	„
528	542	LAQFTSAICSVVRR	784	*0701	43	14	„	„
529	543	AQFTSAICSVVRR	785	*0701	51	14	„	„
533	547	SAICSVVRRAPPHCL	786	*0701	47	14	„	„
533	547	SAICSVVRRAPPHCL	„	*1301	60	14	„	„
534	548	AICSVVRRAPPHCLA	787	*0701	16	14	„	„
534	548	AICSVVRRAPPHCLA	„	*1301	59	14	„	„
535	549	ICSVVRRAPPHCLAF	788	*0106	10	14	„	„
535	549	ICSVVRRAPPHCLAF	„	*0701	21	14	„	„
535	549	ICSVVRRAPPHCLAF	„	*1301	57	14	„	„
536	550	CSVVRRAPPHCLAFS	789	*0103	30	14	„	„
536	550	CSVVRRAPPHCLAFS	„	*0106	30	14	„	„
536	550	CSVVRRAPPHCLAFS	„	*1301	56	14	„	„
537	551	SVVRRAPPHCLAFSY	790	*1301	54	14	„	„
538	552	VVRRAPPHCLAFSYM	791	*1301	53	14	„	„
539	553	VRRAPPHCLAFSYM	792	*1301	51	14	„	„
545	559	HCLAFSYMDDVVLGA	793	*0401	30	14	„	„
		Cumulative Class II-B score:				1042		
526	540	FLLAQFTSAICSVVR	782	*0401	13	15	526	559
526	540	FLLAQFTSAICSVVR	„	*0701	53	15	„	„
527	541	LLAQFTSAICSVVRR	783	*0701	49	15	„	„
528	542	LAQFTSAICSVVRR	784	*0701	43	15	„	„
529	543	AQFTSAICSVVRR	785	*0701	51	15	„	„
533	547	SAICSVVRRAPPHCL	786	*0701	47	15	„	„

HLA class II binding peptides in SLP sequences derived from HBV Polymerase						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
533	547	SAICSVVRRAFPCL	„	*1301	60	15	„	„
534	548	AICSVVRRAFPCL	787	*0701	16	15	„	„
534	548	AICSVVRRAFPCL	„	*1301	59	15	„	„
535	549	ICSVVRRAFPCLAF	788	*0106	10	15	„	„
535	549	ICSVVRRAFPCLAF	„	*0701	21	15	„	„
535	549	ICSVVRRAFPCLAF	„	*1301	57	15	„	„
536	550	CSVVRRAFPCLAFS	789	*0103	30	15	„	„
536	550	CSVVRRAFPCLAFS	„	*0106	30	15	„	„
536	550	CSVVRRAFPCLAFS	„	*1301	56	15	„	„
537	551	SVVRRAFPCLAFSY	790	*1301	54	15	„	„
538	552	VVRRAFPCLAFSYM	791	*1301	53	15	„	„
539	553	VRRAFPCLAFSYM	792	*1301	51	15	„	„
545	559	HCLAFSYMDDVVLGA	793	*0401	30	15	„	„
		Cumulative Class II-B score:				783		
565	579	RESLYTAVTNFLLSL	794	*0103	9	16	565	598
565	579	RESLYTAVTNFLLSL	„	*0701	67	16	„	„
566	580	ESLYTAVTNFLLSLG	795	*0701	66	16	„	„
567	581	SLYTAVTNFLLSLGI	796	*0701	64	16	„	„
568	582	LYTAVTNFLLSLGIH	797	*0701	63	16	„	„
569	583	YTAVTNFLLSLGIHL	798	*0101	90	16	„	„
569	583	YTAVTNFLLSLGIHL	„	*0701	61	16	„	„
569	583	YTAVTNFLLSLGIHL	„	*1501	37	16	„	„
570	584	TAVTNFLLSLGIHLN	799	*0101	91	16	„	„
570	584	TAVTNFLLSLGIHLN	„	*0102	28	16	„	„
570	584	TAVTNFLLSLGIHLN	„	*0104	23	16	„	„
570	584	TAVTNFLLSLGIHLN	„	*1501	49	16	„	„
571	585	AVTNFLLSLGIHLNP	800	*0101	89	16	„	„
571	585	AVTNFLLSLGIHLNP	„	*0102	35	16	„	„
571	585	AVTNFLLSLGIHLNP	„	*0104	25	16	„	„
571	585	AVTNFLLSLGIHLNP	„	*1501	46	16	„	„
572	586	VTNFLLSLGIHLNPN	801	*0101	84	16	„	„
572	586	VTNFLLSLGIHLNPN	„	*0102	38	16	„	„
572	586	VTNFLLSLGIHLNPN	„	*0104	38	16	„	„
572	586	VTNFLLSLGIHLNPN	„	*0106	5	16	„	„
572	586	VTNFLLSLGIHLNPN	„	*1501	63	16	„	„
573	587	TNFLLSLGIHLNPKN	802	*0101	83	16	„	„
573	587	TNFLLSLGIHLNPKN	„	*0102	10	16	„	„
573	587	TNFLLSLGIHLNPKN	„	*0104	5	16	„	„
573	587	TNFLLSLGIHLNPKN	„	*0401	4	16	„	„
573	587	TNFLLSLGIHLNPKN	„	*1501	43	16	„	„
574	588	NFLLSLGIHLNPKNKT	803	*0101	33	16	„	„
574	588	NFLLSLGIHLNPKNKT	„	*1501	30	16	„	„
575	589	FLSLGIHLNPKNKTK	804	*0101	23	16	„	„
575	589	FLSLGIHLNPKNKTK	„	*1501	29	16	„	„
576	590	LLSLGIHLNPKNKTKR	805	*1301	25	16	„	„
577	591	LSLGIHLNPKNKTKRW	806	*1301	50	16	„	„

HLA class II binding peptides in SLP sequences derived from HBV Polymerase						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
578	592	SLGIHLNPNKTKRWG	807	*1301	43	16	„	„
579	593	LGIHLNPNKTKRWGY	808	*1301	36	16	„	„
		Cumulative Class II-B score:				1482		
589	603	KRWGYSLNFMGYIIG	809	*1501	57	17	584	617
590	604	RWGYSLNFMGYIIGS	810	*1501	56	17	„	„
591	605	WGYSLNFMGYIIGSW	811	*1501	34	17	„	„
592	606	GYSLNFMGYIIGSWG	812	*1501	21	17	„	„
593	607	YSLNFMGYIIGSWGTL	813	*1501	24	17	„	„
594	608	SLNFMGYIIGSWGTL	814	*1501	11	17	„	„
595	609	LNFMGYIIGSWGTL	815	*1501	19	17	„	„
		Cumulative Class II-B score:				223		
653	667	YPALMPYACIQAKQ	816	*1101	11	18	653	691
656	670	LMPLYACIQAKQAFT	817	*0101	58	18	„	„
656	670	LMPLYACIQAKQAFT	„	*0105	58	18	„	„
656	670	LMPLYACIQAKQAFT	„	*0107	58	18	„	„
657	671	MPLYACIQAKQAFTF	818	*0101	75	18	„	„
657	671	MPLYACIQAKQAFTF	„	*0105	75	18	„	„
657	671	MPLYACIQAKQAFTF	„	*0107	75	18	„	„
657	671	MPLYACIQAKQAFTF	„	*1301	41	18	„	„
658	672	PLYACIQAKQAFTFS	819	*0101	48	18	„	„
658	672	PLYACIQAKQAFTFS	„	*0105	48	18	„	„
658	672	PLYACIQAKQAFTFS	„	*0107	48	18	„	„
658	672	PLYACIQAKQAFTFS	„	*1301	40	18	„	„
659	673	LYACIQAKQAFTFSP	820	*1301	39	18	„	„
660	674	YACIQAKQAFTFSPT	821	*1301	37	18	„	„
661	675	ACIQAKQAFTFSPTY	822	*1301	36	18	„	„
662	676	CIQAKQAFTFSPTYK	823	*1301	34	18	„	„
663	677	IQAKQAFTFSPTYKA	824	*0701	6	18	„	„
663	677	IQAKQAFTFSPTYKA	„	*1301	33	18	„	„
664	678	QAKQAFTFSPTYKAF	825	*0401	44	18	„	„
664	678	QAKQAFTFSPTYKAF	„	*0701	37	18	„	„
665	679	AKQAFTFSPTYKAFL	826	*0401	79	18	„	„
665	679	AKQAFTFSPTYKAFL	„	*0701	77	18	„	„
666	680	KQAFTFSPTYKAFLS	827	*0401	33	18	„	„
666	680	KQAFTFSPTYKAFLS	„	*0701	60	18	„	„
666	680	KQAFTFSPTYKAFLS	„	*1101	13	18	„	„
666	680	KQAFTFSPTYKAFLS	„	*1501	8	18	„	„
667	681	QAFTFSPTYKAFLSK	828	*0401	54	18	„	„
667	681	QAFTFSPTYKAFLSK	„	*0701	46	18	„	„
668	682	AFTFSPTYKAFLSKQ	829	*0701	14	18	„	„
669	683	FTFSPTYKAFLSKQY	830	*0701	19	18	„	„
672	686	SPTYKAFLSKQYMN	831	*1501	3	18	„	„
673	687	PTYKAFLSKQYMNLY	832	*1501	23	18	„	„
677	691	AFLSKQYMNLYPVAR	833	*0101	40	18	„	„
		Cumulative Class II-B score:				1365		

HLA class II binding peptides in SLP sequences derived from HBV Polymerase						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
657	671	MPLYACIQAKQAFTF	818	*0101	75	19	657	691
657	671	MPLYACIQAKQAFTF	„	*0105	75	19	„	„
657	671	MPLYACIQAKQAFTF	„	*0107	75	19	„	„
657	671	MPLYACIQAKQAFTF	„	*1301	41	19	„	„
658	672	PLYACIQAKQAFTFS	819	*0101	48	19	„	„
658	672	PLYACIQAKQAFTFS	„	*0105	48	19	„	„
658	672	PLYACIQAKQAFTFS	„	*0107	48	19	„	„
658	672	PLYACIQAKQAFTFS	„	*1301	40	19	„	„
659	673	LYACIQAKQAFTFSP	820	*1301	39	19	„	„
660	674	YACIQAKQAFTFSPT	821	*1301	37	19	„	„
661	675	ACIQAKQAFTFSPTY	822	*1301	36	19	„	„
662	676	CIQAKQAFTFSPTYK	823	*1301	34	19	„	„
663	677	IQAKQAFTFSPTYKA	824	*0701	6	19	„	„
663	677	IQAKQAFTFSPTYKA	„	*1301	33	19	„	„
664	678	QAKQAFTFSPTYKAF	825	*0401	44	19	„	„
664	678	QAKQAFTFSPTYKAF	„	*0701	37	19	„	„
665	679	AKQAFTFSPTYKAFL	826	*0401	79	19	„	„
665	679	AKQAFTFSPTYKAFL	„	*0701	77	19	„	„
666	680	KQAFTFSPTYKAFLS	827	*0401	33	19	„	„
666	680	KQAFTFSPTYKAFLS	„	*0701	60	19	„	„
666	680	KQAFTFSPTYKAFLS	„	*1101	13	19	„	„
666	680	KQAFTFSPTYKAFLS	„	*1501	8	19	„	„
667	681	QAFTFSPTYKAFLSK	828	*0401	54	19	„	„
667	681	QAFTFSPTYKAFLSK	„	*0701	46	19	„	„
668	682	AFTFSPTYKAFLSKQ	829	*0701	14	19	„	„
669	683	FTFSPTYKAFLSKQY	830	*0701	19	19	„	„
672	686	SPTYKAFLSKQYMN	831	*1501	3	19	„	„
673	687	PTYKAFLSKQYMNLY	832	*1501	23	19	„	„
677	691	AFLSKQYMNLYPVAR	833	*0101	40	19	„	„
Cumulative Class II-B score:					1181			
717	731	MRGTFVAPLPIHTAE	834	*0101	10	20	715	746
717	731	MRGTFVAPLPIHTAE	„	*0105	10	20	„	„
717	731	MRGTFVAPLPIHTAE	„	*0107	10	20	„	„
718	732	RGTFVAPLPIHTAEL	835	*0101	4	20	„	„
718	732	RGTFVAPLPIHTAEL	„	*0102	20	20	„	„
718	732	RGTFVAPLPIHTAEL	„	*0104	30	20	„	„
718	732	RGTFVAPLPIHTAEL	„	*0105	60	20	„	„
718	732	RGTFVAPLPIHTAEL	„	*0106	33	20	„	„
718	732	RGTFVAPLPIHTAEL	„	*0107	60	20	„	„
719	733	GTFVAPLPIHTAELL	836	*0101	6	20	„	„
732	746	LLAACFARSRS GAKL	837	*0701	1	20	„	„
Cumulative Class II-B score:					244			
767	781	GCTANWILRGTSFVY	838	*1501	1	21	754	791
768	782	CTANWILRGTSFVYV	839	*1301	21	21	„	„

HLA class II binding peptides in SLP sequences derived from HBV Polymerase						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
768	782	CTANWILRGTSFVYV	„	*1501	10	21	„	„
773	787	ILRGTSFVYVPSALN	840	*0101	100	21	„	„
773	787	ILRGTSFVYVPSALN	„	*0401	23	21	„	„
773	787	ILRGTSFVYVPSALN	„	*0701	31	21	„	„
774	788	LRGTSFVYVPSALNP	841	*0101	96	21	„	„
774	788	LRGTSFVYVPSALNP	„	*0105	40	21	„	„
774	788	LRGTSFVYVPSALNP	„	*0107	40	21	„	„
774	788	LRGTSFVYVPSALNP	„	*0401	56	21	„	„
774	788	LRGTSFVYVPSALNP	„	*0701	23	21	„	„
775	789	RGTSFVYVPSALNPA	842	*0101	99	21	„	„
775	789	RGTSFVYVPSALNPA	„	*0102	30	21	„	„
775	789	RGTSFVYVPSALNPA	„	*0104	43	21	„	„
775	789	RGTSFVYVPSALNPA	„	*0105	93	21	„	„
775	789	RGTSFVYVPSALNPA	„	*0107	93	21	„	„
775	789	RGTSFVYVPSALNPA	„	*0401	76	21	„	„
775	789	RGTSFVYVPSALNPA	„	*0701	29	21	„	„
776	790	GTSFVYVPSALNPAD	843	*0101	97	21	„	„
776	790	GTSFVYVPSALNPAD	„	*0102	13	21	„	„
776	790	GTSFVYVPSALNPAD	„	*0104	28	21	„	„
776	790	GTSFVYVPSALNPAD	„	*0105	85	21	„	„
776	790	GTSFVYVPSALNPAD	„	*0107	85	21	„	„
776	790	GTSFVYVPSALNPAD	„	*0401	74	21	„	„
776	790	GTSFVYVPSALNPAD	„	*0701	4	21	„	„
777	791	TSFVYVPSALNPADD	844	*0101	94	21	„	„
777	791	TSFVYVPSALNPADD	„	*0105	68	21	„	„
777	791	TSFVYVPSALNPADD	„	*0107	68	21	„	„
777	791	TSFVYVPSALNPADD	„	*0401	73	21	„	„
Cumulative Class II-B score:					1591			
767	781	GCTANWILRGTSFVY	838	*1501	1	22	757	792
768	782	CTANWILRGTSFVYV	839	*1301	21	22	„	„
768	782	CTANWILRGTSFVYV	„	*1501	10	22	„	„
773	787	ILRGTSFVYVPSALN	840	*0101	100	22	„	„
773	787	ILRGTSFVYVPSALN	„	*0401	23	22	„	„
773	787	ILRGTSFVYVPSALN	„	*0701	31	22	„	„
774	788	LRGTSFVYVPSALNP	841	*0101	96	22	„	„
774	788	LRGTSFVYVPSALNP	„	*0105	40	22	„	„
774	788	LRGTSFVYVPSALNP	„	*0107	40	22	„	„
774	788	LRGTSFVYVPSALNP	„	*0401	56	22	„	„
774	788	LRGTSFVYVPSALNP	„	*0701	23	22	„	„
775	789	RGTSFVYVPSALNPA	842	*0101	99	22	„	„
775	789	RGTSFVYVPSALNPA	„	*0102	30	22	„	„
775	789	RGTSFVYVPSALNPA	„	*0104	43	22	„	„
775	789	RGTSFVYVPSALNPA	„	*0105	93	22	„	„
775	789	RGTSFVYVPSALNPA	„	*0107	93	22	„	„
775	789	RGTSFVYVPSALNPA	„	*0401	76	22	„	„
775	789	RGTSFVYVPSALNPA	„	*0701	29	22	„	„

HLA class II binding peptides in SLP sequences derived from HBV Polymerase						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
776	790	GTSEFVYVPSALNPAD	843	*0101	97	22	„	„
776	790	GTSEFVYVPSALNPAD	„	*0102	13	22	„	„
776	790	GTSEFVYVPSALNPAD	„	*0104	28	22	„	„
776	790	GTSEFVYVPSALNPAD	„	*0105	85	22	„	„
776	790	GTSEFVYVPSALNPAD	„	*0107	85	22	„	„
776	790	GTSEFVYVPSALNPAD	„	*0401	74	22	„	„
776	790	GTSEFVYVPSALNPAD	„	*0701	4	22	„	„
777	791	TSFVYVPSALNPADD	844	*0101	94	22	„	„
777	791	TSFVYVPSALNPADD	„	*0105	68	22	„	„
777	791	TSFVYVPSALNPADD	„	*0107	68	22	„	„
777	791	TSFVYVPSALNPADD	„	*0401	73	22	„	„
778	792	SFVYVPSALNPADDP	845	*0101	54	22	„	„
778	792	SFVYVPSALNPADDP	„	*0401	64	22	„	„
Cumulative Class II-B score:					1709			
767	781	GCTANWILRGTSFVY	838	*1501	1	23	754	789
768	782	CTANWILRGTSFVYV	839	*1301	21	23	„	„
768	782	CTANWILRGTSFVYV	„	*1501	10	23	„	„
773	787	ILRGTSFVYVPSALN	840	*0101	100	23	„	„
773	787	ILRGTSFVYVPSALN	„	*0401	23	23	„	„
773	787	ILRGTSFVYVPSALN	„	*0701	31	23	„	„
774	788	LRGTSFVYVPSALNP	841	*0101	96	23	„	„
774	788	LRGTSFVYVPSALNP	„	*0105	40	23	„	„
774	788	LRGTSFVYVPSALNP	„	*0107	40	23	„	„
774	788	LRGTSFVYVPSALNP	„	*0401	56	23	„	„
774	788	LRGTSFVYVPSALNP	„	*0701	23	23	„	„
775	789	RGTSFVYVPSALNPA	842	*0101	99	23	„	„
775	789	RGTSFVYVPSALNPA	„	*0102	30	23	„	„
775	789	RGTSFVYVPSALNPA	„	*0104	43	23	„	„
775	789	RGTSFVYVPSALNPA	„	*0105	93	23	„	„
775	789	RGTSFVYVPSALNPA	„	*0107	93	23	„	„
775	789	RGTSFVYVPSALNPA	„	*0401	76	23	„	„
775	789	RGTSFVYVPSALNPA	„	*0701	29	23	„	„
Cumulative Class II-B score:					903			

“Start” and “End” are relative to the amino acid sequence of human HBV polymerase as depicted in SEQ ID NO: 1

^A Peptide amino acid sequence. Each HLA-DRB1 binding peptide of HBV polymerase is listed separately for each HLA class II molecule to which it is predicted to bind, and each peptide can be listed multiple times for that reason.

^B Class II-B score. See *Material and Methods* (Examples section). ^C Cumulative Class II-B score. See *Material and Methods* (Examples section).

Table 5a. Predicted HLA class I-restricted CD8⁺ cytotoxic T cell epitopes contained in SLP sequences from HBV Core protein.

HLA class I binding peptides in SLP sequences derived from HBV Core protein							Peptide of invention (SLP)				
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
107	117	11	DPASRDLLVNY	846	B*3501	100	1,68	168	24	107	141
107	117	11	DPASRDLLVNY	⁂	B*3503	30	⁂	50	24	⁂	⁂
107	117	11	DPASRDLLVNY	⁂	B*5301	79	⁂	132	24	⁂	⁂
108	117	10	PASRDLLVNY	847	B*5701	100	⁂	168	24	⁂	⁂
108	117	10	PASRDLLVNY	⁂	B*5801	100	⁂	168	24	⁂	⁂
109	117	9	ASRDLLVNY	848	A*3002	45	⁂	76	24	⁂	⁂
109	117	9	ASRDLLVNY	⁂	B*1501	40	⁂	67	24	⁂	⁂
109	117	9	ASRDLLVNY	⁂	B*1525	10	⁂	17	24	⁂	⁂
111	118	8	RDLLVNYV	849	B*1302	63	1,72	108	24	⁂	⁂
113	122	10	LVVNYVNTNV	850	A*0206	29	1,04	30	24	⁂	⁂
113	122	10	LVVNYVNTNV	⁂	A*6802	75	⁂	78	24	⁂	⁂
114	122	9	VVNYVNTNV	851	A*6802	38	⁂	39	24	⁂	⁂
113	123	11	LVVNYVNTNVG	852	A*6802	25	0,09	2	24	⁂	⁂
116	124	9	NYVNTNVGL	853	A*2301	63	1,89	118	24	⁂	⁂
117	125	9	YVNTNVGLK	854	A*0301	100	0,33	33	24	⁂	⁂
117	125	9	YVNTNVGLK	⁂	A*1101	100	⁂	33	24	⁂	⁂
117	125	9	YVNTNVGLK	⁂	A*6801	62	⁂	20	24	⁂	⁂
116	126	11	NYVNTNVGLKI	855	A*2301	44	1,53	67	24	⁂	⁂
116	126	11	NYVNTNVGLKI	⁂	A*2402	63	⁂	96	24	⁂	⁂
120	129	10	TNVGLKIRQL	856	B*0801	50	1,67	83	24	⁂	⁂
121	129	9	NVGLKIRQL	857	B*0702	75	⁂	125	24	⁂	⁂
121	130	10	NVGLKIRQLL	858	B*0702	83	1,23	103	24	⁂	⁂
123	130	8	GLKIRQLL	859	B*0801	70	⁂	86	24	⁂	⁂
122	131	10	VGLKIRQLLW	860	B*5802	55	1,66	91	24	⁂	⁂
123	132	10	GLKIRQLLWF	861	A*0301	25	1,02	25	24	⁂	⁂
125	132	8	KIRQLLWF	862	A*3201	75	⁂	76	24	⁂	⁂
125	132	8	KIRQLLWF	⁂	B*1501	20	⁂	20	24	⁂	⁂
125	132	8	KIRQLLWF	⁂	B*1525	40	⁂	41	24	⁂	⁂
126	134	9	IRQLLWFHI	863	B*2702	86	1,69	145	24	⁂	⁂
126	134	9	IRQLLWFHI	⁂	B*2705	84	⁂	142	24	⁂	⁂
127	134	8	RQLLWFHI	864	A*2301	81	⁂	138	24	⁂	⁂

HLA class I binding peptides in SLP sequences derived from HBV Core protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
127	134	8	RQLLWFHI	865	A*2402	69	55	116	24	55	55	
127	134	8	RQLLWFHI	866	A*3201	63	55	106	24	55	55	
127	134	8	RQLLWFHI	867	B*1301	90	55	152	24	55	55	
127	134	8	RQLLWFHI	868	B*2702	100	55	169	24	55	55	
127	134	8	RQLLWFHI	869	B*3701	73	55	124	24	55	55	
127	134	8	RQLLWFHI	870	B*4002	57	55	97	24	55	55	
127	134	8	RQLLWFHI	871	B*4801	100	55	169	24	55	55	
127	134	8	RQLLWFHI	872	B*4901	47	55	80	24	55	55	
127	134	8	RQLLWFHI	873	B*5001	47	55	79	24	55	55	
127	134	8	RQLLWFHI	874	B*5201	78	55	132	24	55	55	
126	135	10	IRQLLWFHIS	865	B*2705	3	0,55	2	24	55	55	
127	135	9	RQLLWFHIS	866	B*4801	14	55	8	24	55	55	
127	136	10	RQLLWFHISC	867	B*4801	29	0,82	24	24	55	55	
128	136	9	QLLWFHISC	868	A*0201	75	55	62	24	55	55	
129	136	8	LLWFHISC	869	A*0201	60	55	49	24	55	55	
127	137	11	RQLLWFHISCL	870	B*1301	35	1,95	68	24	55	55	
127	137	11	RQLLWFHISCL	871	B*1302	50	55	98	24	55	55	
127	137	11	RQLLWFHISCL	872	B*1402	38	55	75	24	55	55	
127	137	11	RQLLWFHISCL	873	B*2702	71	55	139	24	55	55	
127	137	11	RQLLWFHISCL	874	B*3701	40	55	78	24	55	55	
127	137	11	RQLLWFHISCL	875	B*3901	64	55	125	24	55	55	
127	137	11	RQLLWFHISCL	876	B*4001	7	55	13	24	55	55	
127	137	11	RQLLWFHISCL	877	B*4002	14	55	28	24	55	55	
128	137	10	QLLWFHISCL	871	A*0201	20	55	39	24	55	55	
129	137	9	LLWFHISCL	872	A*0201	50	55	98	24	55	55	
129	137	9	LLWFHISCL	873	B*0801	50	55	98	24	55	55	
130	137	8	LWFHISCL	874	A*2301	13	55	24	24	55	55	
130	137	8	LWFHISCL	875	A*2402	13	55	24	24	55	55	
129	138	10	LLWFHISCLT	876	A*0201	56	0,32	18	24	55	55	
129	139	11	LLWFHISCLTF	877	A*3201	81	1,49	121	24	55	55	
129	139	11	LLWFHISCLTF	878	B*1501	100	55	149	24	55	55	
129	139	11	LLWFHISCLTF	879	B*1502	78	55	116	24	55	55	
129	139	11	LLWFHISCLTF	880	B*1525	100	55	149	24	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Core protein										Peptide of invention (SLP)			
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
130	139	10	LWFHISCLTF	876	A*2301	100	55	149	24	55	55		
130	139	10	LWFHISCLTF	55	A*2402	100	55	149	24	55	55		
130	139	10	LWFHISCLTF	55	A*2902	86	55	127	24	55	55		
130	139	10	LWFHISCLTF	55	B*2702	43	55	64	24	55	55		
132	139	8	FHISCLTF	877	A*2301	56	55	84	24	55	55		
132	139	8	FHISCLTF	55	B*1402	54	55	80	24	55	55		
132	139	8	FHISCLTF	55	B*3503	40	55	59	24	55	55		
132	139	8	FHISCLTF	55	B*3801	100	55	149	24	55	55		
132	139	8	FHISCLTF	55	B*3901	57	55	85	24	55	55		
131	141	11	WFHISCLTFGR	878	A*3101	29	1,41	42	24	55	55		
131	141	11	WFHISCLTFGR	55	A*3303	52	55	74	24	55	55		
132	141	10	FHISCLTFGR	879	A*3101	35	55	50	24	55	55		
133	141	9	HISCLTFGR	880	A*3101	82	55	116	24	55	55		
133	141	9	HISCLTFGR	55	A*3303	95	55	135	24	55	55		
133	141	9	HISCLTFGR	55	A*6801	85	55	120	24	55	55		
133	141	9	HISCLTFGR	55	A*7401	100	55	141	24	55	55		
134	141	8	ISCLTFGR	881	A*3101	88	55	125	24	55	55		
134	141	8	ISCLTFGR	55	A*3303	29	55	40	24	55	55		
134	141	8	ISCLTFGR	55	A*6801	31	55	43	24	55	55		
134	141	8	ISCLTFGR	55	A*7401	50	55	71	24	55	55		
					Cumulative Class I-BCI score ^E :						7277		
136	145	10	CLTFGRETVL	882	B*0801	100	1,87	187	25	136	169		
137	147	11	LTFGRETVLEY	883	A*0101	80	1,68	134	25	55	55		
137	147	11	LTFGRETVLEY	55	A*0301	67	55	112	25	55	55		
137	147	11	LTFGRETVLEY	55	A*2501	80	55	134	25	55	55		
137	147	11	LTFGRETVLEY	55	A*2601	60	55	101	25	55	55		
137	147	11	LTFGRETVLEY	55	A*2902	100	55	168	25	55	55		
137	147	11	LTFGRETVLEY	55	A*3002	100	55	168	25	55	55		
137	147	11	LTFGRETVLEY	55	B*1501	90	55	151	25	55	55		
137	147	11	LTFGRETVLEY	55	B*1502	100	55	168	25	55	55		
137	147	11	LTFGRETVLEY	55	B*4601	67	55	112	25	55	55		
137	147	11	LTFGRETVLEY	55	B*5701	38	55	63	25	55	55		

HLA class I binding peptides in SLP sequences derived from HBV Core protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
137	147	11	LTFGRETVLEY	884	B*5802	36	55	61	25	55	55	
139	147	9	FGRETVLEY	884	B*1525	90	55	151	25	55	55	
139	147	9	FGRETVLEY	885	B*4601	100	55	168	25	55	55	
138	148	11	TFGRETVLEYL	885	A*2301	6	1,23	8	25	55	55	
138	148	11	TFGRETVLEYL	886	A*2402	31	55	38	25	55	55	
139	148	10	FGRETVLEYL	886	B*0702	100	55	123	25	55	55	
140	148	9	GRETVLEYL	887	B*2702	21	55	26	25	55	55	
141	148	8	RETVLEYL	888	B*1301	60	55	74	25	55	55	
141	148	8	RETVLEYL	888	B*3701	33	55	41	25	55	55	
141	148	8	RETVLEYL	888	B*4001	100	55	123	25	55	55	
141	148	8	RETVLEYL	888	B*4002	93	55	114	25	55	55	
141	148	8	RETVLEYL	888	B*4402	8	55	10	25	55	55	
141	148	8	RETVLEYL	888	B*4403	54	55	66	25	55	55	
141	148	8	RETVLEYL	888	B*4801	7	55	9	25	55	55	
141	148	8	RETVLEYL	888	B*4901	6	55	7	25	55	55	
139	149	11	FGRETVLEYLV	889	A*0201	45	1,23	55	25	55	55	
141	149	9	RETVLEYLV	890	B*1301	30	55	37	25	55	55	
141	149	9	RETVLEYLV	889	B*1302	38	55	46	25	55	55	
141	149	9	RETVLEYLV	889	B*3701	27	55	33	25	55	55	
141	149	9	RETVLEYLV	889	B*4001	67	55	82	25	55	55	
141	149	9	RETVLEYLV	889	B*4002	79	55	96	25	55	55	
141	149	9	RETVLEYLV	889	B*4901	71	55	87	25	55	55	
141	149	9	RETVLEYLV	889	B*5001	27	55	33	25	55	55	
142	149	8	ETVLEYLV	891	A*2501	20	55	25	25	55	55	
142	149	8	ETVLEYLV	889	A*2601	50	55	61	25	55	55	
141	150	10	RETVLEYLVS	892	B*4002	7	0,57	4	25	55	55	
141	151	11	RETVLEYLVSF	893	B*1301	45	1,50	67	25	55	55	
141	151	11	RETVLEYLVSF	889	B*1801	88	55	131	25	55	55	
141	151	11	RETVLEYLVSF	889	B*2702	50	55	75	25	55	55	
141	151	11	RETVLEYLVSF	889	B*4001	80	55	120	25	55	55	
141	151	11	RETVLEYLVSF	889	B*4002	86	55	128	25	55	55	
141	151	11	RETVLEYLVSF	889	B*4402	67	55	100	25	55	55	
141	151	11	RETVLEYLVSF	889	B*4403	77	55	115	25	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Core protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
141	151	11	RETVLEYLVSF	894	B*4901	35	53	25	25	25	25	
141	151	11	RETVLEYLVSF	894	B*5001	60	90	25	25	25	25	
142	151	10	ETVLEYLVSF	894	A*2501	100	150	25	25	25	25	
142	151	10	ETVLEYLVSF	894	A*2601	100	150	25	25	25	25	
143	151	9	TVLEYLVSF	895	A*3201	50	75	25	25	25	25	
143	151	9	TVLEYLVSF	895	B*1525	20	30	25	25	25	25	
145	152	8	LEYLVSG	896	B*4901	18	0,48	8	25	25	25	
143	153	11	TVLEYLVSGV	897	A*0201	90	1,80	162	25	25	25	
143	153	11	TVLEYLVSGV	897	A*6802	100	180	25	25	25	25	
144	153	10	VLEYLVSGV	898	A*0201	65	117	25	25	25	25	
145	153	9	LEYLVSGV	899	A*0201	67	120	25	25	25	25	
145	153	9	LEYLVSGV	899	B*1301	75	135	25	25	25	25	
145	153	9	LEYLVSGV	899	B*1801	63	113	25	25	25	25	
145	153	9	LEYLVSGV	899	B*3701	67	120	25	25	25	25	
145	153	9	LEYLVSGV	899	B*4001	73	132	25	25	25	25	
145	153	9	LEYLVSGV	899	B*4002	29	51	25	25	25	25	
145	153	9	LEYLVSGV	899	B*4402	42	75	25	25	25	25	
145	153	9	LEYLVSGV	899	B*4901	94	170	25	25	25	25	
145	153	9	LEYLVSGV	899	B*5001	87	156	25	25	25	25	
145	153	9	LEYLVSGV	899	B*5201	56	100	25	25	25	25	
145	154	10	LEYLVSGVW	900	B*1301	65	1,34	87	25	25	25	
145	154	10	LEYLVSGVW	900	B*1302	13	17	25	25	25	25	
145	154	10	LEYLVSGVW	900	B*3801	11	15	25	25	25	25	
145	154	10	LEYLVSGVW	900	B*4402	92	123	25	25	25	25	
145	154	10	LEYLVSGVW	900	B*4403	92	124	25	25	25	25	
145	154	10	LEYLVSGVW	900	B*4901	88	118	25	25	25	25	
145	154	10	LEYLVSGVW	900	B*5201	22	30	25	25	25	25	
146	154	9	EYLVSGVW	901	A*2301	69	92	25	25	25	25	
146	154	9	EYLVSGVW	901	A*2402	81	109	25	25	25	25	
147	154	8	YLVSGVW	902	B*5701	13	17	25	25	25	25	
147	154	8	YLVSGVW	902	B*5801	36	48	25	25	25	25	
145	155	11	LEYLVSGVWI	903	B*1301	85	1,63	139	25	25	25	
145	155	11	LEYLVSGVWI	903	B*1302	88	143	25	25	25	25	

HLA class I binding peptides in SLP sequences derived from HBV Core protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
145	155	11	LEYLVSGVWI	904	B*1801	50	55	82	25	55	55	
145	155	11	LEYLVSGVWI	905	B*3701	80	55	130	25	55	55	
145	155	11	LEYLVSGVWI	906	B*3801	78	55	127	25	55	55	
145	155	11	LEYLVSGVWI	907	B*4001	60	55	98	25	55	55	
145	155	11	LEYLVSGVWI	908	B*4002	43	55	70	25	55	55	
145	155	11	LEYLVSGVWI	909	B*4402	50	55	82	25	55	55	
145	155	11	LEYLVSGVWI	910	B*4403	62	55	100	25	55	55	
145	155	11	LEYLVSGVWI	911	B*4901	100	55	163	25	55	55	
145	155	11	LEYLVSGVWI	912	B*5001	80	55	130	25	55	55	
145	155	11	LEYLVSGVWI	913	B*5201	89	55	145	25	55	55	
147	155	9	YLVSGVWI	914	A*0201	75	55	122	25	55	55	
146	156	11	EYLVSGVWIR	915	A*3303	71	1,61	115	25	55	55	
147	156	10	YLVSGVWIR	916	A*0301	100	55	161	25	55	55	
147	156	10	YLVSGVWIR	917	A*6801	54	55	87	25	55	55	
148	156	9	LVSGVWIR	918	A*3101	12	55	19	25	55	55	
148	156	9	LVSGVWIR	919	A*3303	38	55	61	25	55	55	
148	156	9	LVSGVWIR	920	A*6801	23	55	37	25	55	55	
148	156	9	LVSGVWIR	921	A*7401	40	55	64	25	55	55	
149	156	8	VSGVWIR	922	A*1101	13	55	20	25	55	55	
149	156	8	VSGVWIR	923	A*3101	59	55	95	25	55	55	
149	156	8	VSGVWIR	924	A*3303	48	55	77	25	55	55	
149	156	8	VSGVWIR	925	A*6801	77	55	124	25	55	55	
149	156	8	VSGVWIR	926	A*7401	80	55	129	25	55	55	
148	157	10	LVSGVWIRT	927	A*3201	88	0,42	37	25	55	55	
148	158	11	LVSGVWIRTP	928	A*6802	63	0,28	17	25	55	55	
151	160	10	FGVWIRTPPA	929	B*5501	55	0,99	54	25	55	55	
151	160	10	FGVWIRTPPA	930	B*5601	64	55	63	25	55	55	
151	161	11	FGVWIRTPPAY	931	A*2902	57	1,46	83	25	55	55	
151	161	11	FGVWIRTPPAY	932	B*1502	56	55	81	25	55	55	
151	161	11	FGVWIRTPPAY	933	B*3501	89	55	130	25	55	55	
151	161	11	FGVWIRTPPAY	934	B*4601	33	55	49	25	55	55	
152	161	10	GVWIRTPPAY	935	A*3001	67	55	97	25	55	55	
152	161	10	GVWIRTPPAY	936	B*1502	22	55	32	25	55	55	

HLA class I binding peptides in SLP sequences derived from HBV Core protein										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
153	161	9	VWIRTPPAY	914	A*2902	79	..	114	25	..	..	
153	161	9	VWIRTPPAY	..	A*3002	91	..	132	25	..	..	
154	161	8	WIRTPPAY	915	A*2601	30	..	44	25	..	..	
154	161	8	WIRTPPAY	..	A*2902	14	..	21	25	..	..	
154	161	8	WIRTPPAY	..	B*1501	70	..	102	25	..	..	
154	161	8	WIRTPPAY	..	B*1502	89	..	130	25	..	..	
154	161	8	WIRTPPAY	..	B*1525	50	..	73	25	..	..	
152	162	11	GVWIRTPPAYR	916	A*0301	33	0,95	32	25	..	..	
152	162	11	GVWIRTPPAYR	..	A*1101	38	..	36	25	..	..	
152	162	11	GVWIRTPPAYR	..	A*3101	100	..	95	25	..	..	
152	162	11	GVWIRTPPAYR	..	A*3303	76	..	72	25	..	..	
152	162	11	GVWIRTPPAYR	..	A*7401	90	..	86	25	..	..	
153	162	10	VWIRTPPAYR	917	A*3101	6	..	6	25	..	..	
153	162	10	VWIRTPPAYR	..	A*3303	33	..	32	25	..	..	
154	162	9	WIRTPPAYR	918	A*3303	90	..	86	25	..	..	
154	162	9	WIRTPPAYR	..	A*7401	70	..	67	25	..	..	
156	165	10	RTPPAYRPPN	919	A*3001	83	0,09	7	25	..	..	
158	168	11	PPAYRPPNAPI	920	B*0702	17	1,00	17	25	..	..	
160	168	9	AYRPPNAPI	921	A*2402	25	..	25	25	..	..	
160	168	9	AYRPPNAPI	..	A*3001	42	..	41	25	..	..	
160	169	10	AYRPPNAPIL	922	A*2402	6	1,90	12	25	..	..	
160	169	10	AYRPPNAPIL	..	B*0702	50	..	95	25	..	..	
161	169	9	YRPPNAPIL	923	B*3901	36	..	68	25	..	..	
					Cumulative BCI Class I-score:				11331			

“Start” and “End” are relative to the amino acid sequence of HBV core protein as depicted in SEQ ID NO: 4

^A Peptide amino acid sequence. Each HLA class I binding peptide of HBV core protein is listed separately for each HLA class I molecule to which it is predicted to bind, and can be listed multiple times for that reason.

^B Class I-B score. See *Material and Methods* of Examples section.

^C C-score. See *Material and Methods* of Examples section.

^D Class I-BCI score. See *Material and Methods* (Examples section).

^E Cumulative Class I-BCI score. See *Material and Methods* (Examples section).

Table 5b. Predicted HLA class II-restricted CD4⁺ T cell epitopes contained in SLP sequences from HBV Core protein.

HLA class II binding peptides in SLP sequences derived from HBV Core protein						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
107	121	DPASRDLVVNYVNTN	924	*0301	46	24	107	141
108	122	PASRDLVVNYVNTNV	925	*0401	69	24	..	..
108	122	PASRDLVVNYVNTNV	..	*1301	10	24	..	..
109	123	ASRDLVVNYVNTNVG	926	*0401	85	24	..	..
109	123	ASRDLVVNYVNTNVG	..	*1301	20	24	..	..
110	124	SRDLVVNYVNTNVGL	927	*0401	92	24	..	..
110	124	SRDLVVNYVNTNVGL	..	*1301	40	24	..	..
111	125	RDLVVNYVNTNVGLK	928	*0103	17	24	..	..
111	125	RDLVVNYVNTNVGLK	..	*0401	100	24	..	..
111	125	RDLVVNYVNTNVGLK	..	*1301	50	24	..	..
112	126	DLVVNYVNTNVGLKI	929	*0103	50	24	..	..
112	126	DLVVNYVNTNVGLKI	..	*0106	25	24	..	..
112	126	DLVVNYVNTNVGLKI	..	*0301	62	24	..	..
112	126	DLVVNYVNTNVGLKI	..	*0401	77	24	..	..
112	126	DLVVNYVNTNVGLKI	..	*0701	15	24	..	..
112	126	DLVVNYVNTNVGLKI	..	*1301	80	24	..	..
113	127	LVVNYVNTNVGLKIR	930	*0103	100	24	..	..
113	127	LVVNYVNTNVGLKIR	..	*0104	35	24	..	..
113	127	LVVNYVNTNVGLKIR	..	*0106	75	24	..	..
113	127	LVVNYVNTNVGLKIR	..	*0301	69	24	..	..
113	127	LVVNYVNTNVGLKIR	..	*0701	50	24	..	..
113	127	LVVNYVNTNVGLKIR	..	*1301	100	24	..	..
114	128	VVNYVNTNVGLKIRQ	931	*0103	83	24	..	..
114	128	VVNYVNTNVGLKIRQ	..	*0104	45	24	..	..
114	128	VVNYVNTNVGLKIRQ	..	*0106	80	24	..	..
114	128	VVNYVNTNVGLKIRQ	..	*1301	90	24	..	..
115	129	VNYVNTNVGLKIRQQL	932	*0101	21	24	..	..
115	129	VNYVNTNVGLKIRQQL	..	*0102	10	24	..	..
115	129	VNYVNTNVGLKIRQQL	..	*0103	67	24	..	..
115	129	VNYVNTNVGLKIRQQL	..	*0104	65	24	..	..
115	129	VNYVNTNVGLKIRQQL	..	*0105	19	24	..	..
115	129	VNYVNTNVGLKIRQQL	..	*0106	85	24	..	..
115	129	VNYVNTNVGLKIRQQL	..	*0107	21	24	..	..
115	129	VNYVNTNVGLKIRQQL	..	*0701	33	24	..	..
115	129	VNYVNTNVGLKIRQQL	..	*1301	70	24	..	..
116	130	NYVNTNVGLKIRQQLL	933	*0103	33	24	..	..
116	130	NYVNTNVGLKIRQQLL	..	*0104	25	24	..	..
116	130	NYVNTNVGLKIRQQLL	..	*0106	65	24	..	..
116	130	NYVNTNVGLKIRQQLL	..	*1301	60	24	..	..
117	131	YVNTNVGLKIRQQLLW	934	*1101	54	24	..	..
117	131	YVNTNVGLKIRQQLLW	..	*1301	30	24	..	..
118	132	VNTNVGLKIRQQLLWF	935	*0301	38	24	..	..
118	132	VNTNVGLKIRQQLLWF	..	*1301	46	24	..	..
119	133	NTNVGLKIRQQLLWFH	936	*0301	31	24	..	..

HLA class II binding peptides in SLP sequences derived from HBV Core protein						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
119	133	NTNVGLKIRQLLWFH	„	*1301	38	24	„	„
120	134	TNVGLKIRQLLWFHI	937	*0102	70	24	„	„
120	134	TNVGLKIRQLLWFHI	„	*0104	55	24	„	„
120	134	TNVGLKIRQLLWFHI	„	*0106	40	24	„	„
120	134	TNVGLKIRQLLWFHI	„	*0301	23	24	„	„
120	134	TNVGLKIRQLLWFHI	„	*0701	38	24	„	„
120	134	TNVGLKIRQLLWFHI	„	*1301	31	24	„	„
120	134	TNVGLKIRQLLWFHI	„	*1501	38	24	„	„
121	135	NVGLKIRQLLWFHIS	938	*0101	11	24	„	„
121	135	NVGLKIRQLLWFHIS	„	*0102	85	24	„	„
121	135	NVGLKIRQLLWFHIS	„	*0104	75	24	„	„
121	135	NVGLKIRQLLWFHIS	„	*0105	10	24	„	„
121	135	NVGLKIRQLLWFHIS	„	*0106	50	24	„	„
121	135	NVGLKIRQLLWFHIS	„	*0107	11	24	„	„
121	135	NVGLKIRQLLWFHIS	„	*0301	15	24	„	„
121	135	NVGLKIRQLLWFHIS	„	*0701	23	24	„	„
121	135	NVGLKIRQLLWFHIS	„	*1301	23	24	„	„
121	135	NVGLKIRQLLWFHIS	„	*1501	85	24	„	„
122	136	VGLKIRQLLWFHISC	939	*0102	65	24	„	„
122	136	VGLKIRQLLWFHISC	„	*0104	50	24	„	„
122	136	VGLKIRQLLWFHISC	„	*0106	20	24	„	„
122	136	VGLKIRQLLWFHISC	„	*0301	8	24	„	„
122	136	VGLKIRQLLWFHISC	„	*1301	15	24	„	„
122	136	VGLKIRQLLWFHISC	„	*1501	46	24	„	„
123	137	GLKIRQLLWFHISCL	940	*0101	31	24	„	„
123	137	GLKIRQLLWFHISCL	„	*0102	75	24	„	„
123	137	GLKIRQLLWFHISCL	„	*0104	80	24	„	„
123	137	GLKIRQLLWFHISCL	„	*0106	55	24	„	„
123	137	GLKIRQLLWFHISCL	„	*0701	100	24	„	„
123	137	GLKIRQLLWFHISCL	„	*1301	8	24	„	„
123	137	GLKIRQLLWFHISCL	„	*1501	100	24	„	„
124	138	LKIRQLLWFHISCLT	941	*0101	26	24	„	„
124	138	LKIRQLLWFHISCLT	„	*0102	80	24	„	„
124	138	LKIRQLLWFHISCLT	„	*0104	70	24	„	„
124	138	LKIRQLLWFHISCLT	„	*0105	24	24	„	„
124	138	LKIRQLLWFHISCLT	„	*0106	60	24	„	„
124	138	LKIRQLLWFHISCLT	„	*0107	26	24	„	„
124	138	LKIRQLLWFHISCLT	„	*0701	92	24	„	„
124	138	LKIRQLLWFHISCLT	„	*1501	92	24	„	„
125	139	KIRQLLWFHISCLTF	942	*0101	5	24	„	„
125	139	KIRQLLWFHISCLTF	„	*0102	50	24	„	„
125	139	KIRQLLWFHISCLTF	„	*0104	40	24	„	„
125	139	KIRQLLWFHISCLTF	„	*0105	5	24	„	„
125	139	KIRQLLWFHISCLTF	„	*0106	35	24	„	„
125	139	KIRQLLWFHISCLTF	„	*0107	5	24	„	„
125	139	KIRQLLWFHISCLTF	„	*0701	85	24	„	„
125	139	KIRQLLWFHISCLTF	„	*1501	31	24	„	„

HLA class II binding peptides in SLP sequences derived from HBV Core protein						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
126	140	IRQLLWFHISCLTFG	943	*0102	40	24	„	„
126	140	IRQLLWFHISCLTFG	„	*0701	46	24	„	„
126	140	IRQLLWFHISCLTFG	„	*1101	69	24	„	„
127	141	RQLLWFHISCLTFGR	944	*0701	8	24	„	„
127	141	RQLLWFHISCLTFGR	„	*1101	46	24	„	„
		Cumulative Class II-B score ^C:			4649			
139	153	FGRETVLEYLVSFGV	945	*0101	42	25	136	169
139	153	FGRETVLEYLVSFGV	„	*0102	35	25	„	„
139	153	FGRETVLEYLVSFGV	„	*0105	38	25	„	„
139	153	FGRETVLEYLVSFGV	„	*0107	42	25	„	„
139	153	FGRETVLEYLVSFGV	„	*0701	69	25	„	„
139	153	FGRETVLEYLVSFGV	„	*1501	23	25	„	„
140	154	GRETVLEYLVSFGVW	946	*0101	46	25	„	„
140	154	GRETVLEYLVSFGVW	„	*0102	55	25	„	„
140	154	GRETVLEYLVSFGVW	„	*0104	60	25	„	„
140	154	GRETVLEYLVSFGVW	„	*0105	67	25	„	„
140	154	GRETVLEYLVSFGVW	„	*0106	45	25	„	„
140	154	GRETVLEYLVSFGVW	„	*0107	74	25	„	„
140	154	GRETVLEYLVSFGVW	„	*0701	62	25	„	„
140	154	GRETVLEYLVSFGVW	„	*1501	15	25	„	„
141	155	RETVLEYLVSFGVWI	947	*0101	92	25	„	„
141	155	RETVLEYLVSFGVWI	„	*0102	95	25	„	„
141	155	RETVLEYLVSFGVWI	„	*0104	90	25	„	„
141	155	RETVLEYLVSFGVWI	„	*0105	81	25	„	„
141	155	RETVLEYLVSFGVWI	„	*0106	90	25	„	„
141	155	RETVLEYLVSFGVWI	„	*0107	89	25	„	„
141	155	RETVLEYLVSFGVWI	„	*0701	77	25	„	„
141	155	RETVLEYLVSFGVWI	„	*1501	8	25	„	„
142	156	ETVLEYLVSFGVWIR	948	*0101	100	25	„	„
142	156	ETVLEYLVSFGVWIR	„	*0102	100	25	„	„
142	156	ETVLEYLVSFGVWIR	„	*0104	100	25	„	„
142	156	ETVLEYLVSFGVWIR	„	*0105	90	25	„	„
142	156	ETVLEYLVSFGVWIR	„	*0106	100	25	„	„
142	156	ETVLEYLVSFGVWIR	„	*0107	100	25	„	„
142	156	ETVLEYLVSFGVWIR	„	*0701	54	25	„	„
142	156	ETVLEYLVSFGVWIR	„	*1301	100	25	„	„
142	156	ETVLEYLVSFGVWIR	„	*1501	77	25	„	„
143	157	TVLEYLVSFGVWIRT	949	*0101	85	25	„	„
143	157	TVLEYLVSFGVWIRT	„	*0102	90	25	„	„
143	157	TVLEYLVSFGVWIRT	„	*0104	95	25	„	„
143	157	TVLEYLVSFGVWIRT	„	*0105	86	25	„	„
143	157	TVLEYLVSFGVWIRT	„	*0106	95	25	„	„
143	157	TVLEYLVSFGVWIRT	„	*0107	95	25	„	„
143	157	TVLEYLVSFGVWIRT	„	*0701	31	25	„	„
143	157	TVLEYLVSFGVWIRT	„	*1301	92	25	„	„
143	157	TVLEYLVSFGVWIRT	„	*1501	69	25	„	„

HLA class II binding peptides in SLP sequences derived from HBV Core protein						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
144	158	VLEYLVSFSGVWIRTP	950	*0101	69	25	..	..
144	158	VLEYLVSFSGVWIRTP	..	*0102	60	25	..	..
144	158	VLEYLVSFSGVWIRTP	..	*0104	85	25	..	..
144	158	VLEYLVSFSGVWIRTP	..	*0105	76	25	..	..
144	158	VLEYLVSFSGVWIRTP	..	*0106	70	25	..	..
144	158	VLEYLVSFSGVWIRTP	..	*0107	84	25	..	..
144	158	VLEYLVSFSGVWIRTP	..	*1301	85	25	..	..
144	158	VLEYLVSFSGVWIRTP	..	*1501	62	25	..	..
145	159	LEYLVSFSGVWIRTPP	951	*0101	62	25	..	..
145	159	LEYLVSFSGVWIRTPP	..	*0102	15	25	..	..
145	159	LEYLVSFSGVWIRTPP	..	*0104	20	25	..	..
145	159	LEYLVSFSGVWIRTPP	..	*0105	48	25	..	..
145	159	LEYLVSFSGVWIRTPP	..	*0107	53	25	..	..
145	159	LEYLVSFSGVWIRTPP	..	*1301	77	25	..	..
145	159	LEYLVSFSGVWIRTPP	..	*1501	54	25	..	..
146	160	EYLVSFSGVWIRTPPA	952	*1301	69	25	..	..
147	161	YLVSFSGVWIRTPPAY	953	*1301	62	25	..	..
148	162	LVSFSGVWIRTPPAYR	954	*0101	32	25	..	..
148	162	LVSFSGVWIRTPPAYR	..	*0105	29	25	..	..
148	162	LVSFSGVWIRTPPAYR	..	*0107	32	25	..	..
148	162	LVSFSGVWIRTPPAYR	..	*0401	40	25	..	..
148	162	LVSFSGVWIRTPPAYR	..	*1301	54	25	..	..
149	163	VSFSGVWIRTPPAYRP	955	*0101	63	25	..	..
149	163	VSFSGVWIRTPPAYRP	..	*0102	25	25	..	..
149	163	VSFSGVWIRTPPAYRP	..	*0105	57	25	..	..
149	163	VSFSGVWIRTPPAYRP	..	*0107	63	25	..	..
149	163	VSFSGVWIRTPPAYRP	..	*0401	60	25	..	..
149	163	VSFSGVWIRTPPAYRP	..	*1101	25	25	..	..
150	164	SFGVWIRTPPAYRPP	956	*0101	68	25	..	..
150	164	SFGVWIRTPPAYRPP	..	*0102	30	25	..	..
150	164	SFGVWIRTPPAYRPP	..	*0105	62	25	..	..
150	164	SFGVWIRTPPAYRPP	..	*0107	68	25	..	..
150	164	SFGVWIRTPPAYRPP	..	*0401	80	25	..	..
150	164	SFGVWIRTPPAYRPP	..	*1101	75	25	..	..
151	165	FGVWIRTPPAYRPPN	957	*0101	79	25	..	..
151	165	FGVWIRTPPAYRPPN	..	*0102	45	25	..	..
151	165	FGVWIRTPPAYRPPN	..	*0104	30	25	..	..
151	165	FGVWIRTPPAYRPPN	..	*0105	71	25	..	..
151	165	FGVWIRTPPAYRPPN	..	*0106	5	25	..	..
151	165	FGVWIRTPPAYRPPN	..	*0107	79	25	..	..
151	165	FGVWIRTPPAYRPPN	..	*0401	100	25	..	..
151	165	FGVWIRTPPAYRPPN	..	*1101	100	25	..	..
152	166	GVWIRTPPAYRPPNA	958	*0101	58	25	..	..
152	166	GVWIRTPPAYRPPNA	..	*0105	52	25	..	..
152	166	GVWIRTPPAYRPPNA	..	*0107	58	25	..	..
152	166	GVWIRTPPAYRPPNA	..	*1101	50	25	..	..
Cumulative Class II-B score:					5493			

“Start” and “End” are relative to the amino acid sequence of human HBV core protein as depicted in SEQ ID NO: 4

^A Peptide amino acid sequence. Each HLA-DRB1 binding peptide of HBV core is listed separately for each HLA class II molecule to which it is predicted to bind, and each peptide can be listed multiple times for that reason.

^B Class II-B score. See *Material and Methods* (Examples section).

^C Cumulative Class II-B score. See *Material and Methods* (Examples section).

Table 6a. Predicted HLA class I-restricted CD8⁺ cytotoxic T cell epitopes contained in SLP sequences from HBV X protein (consensus sequence).

HLA class I binding peptides in SLP sequences derived from HBV X protein (consensus sequence)							Peptide of invention (SLP)				
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
36	44	9	ALPSPSPSA	959	A*0201	20	0,97	19	26	36	68
37	44	8	LPSPSPSA	960	B*3501	92	..	89	26	..	..
37	44	8	LPSPSPSA	..	B*5101	82	..	79	26	..	..
37	44	8	LPSPSPSA	..	B*5501	63	..	61	26	..	..
37	44	8	LPSPSPSA	..	B*5601	92	..	89	26	..	..
36	45	10	ALPSPSPSAV	961	A*0201	90	1,49	134	26	..	..
37	45	9	LPSPSPSAV	962	B*3503	75	..	112	26	..	..
37	45	9	LPSPSPSAV	..	B*5101	100	..	149	26	..	..
37	45	9	LPSPSPSAV	..	B*5501	94	..	139	26	..	..
37	45	9	LPSPSPSAV	..	B*5601	46	..	69	26	..	..
37	45	9	LPSPSPSAV	..	B*0701	50	..	74	26	..	..
37	47	11	LPSPSPSAVPA	963	A*6802	20	1,05	21	26	..	..
37	47	11	LPSPSPSAVPA	..	B*3501	33	..	35	26	..	..
37	47	11	LPSPSPSAVPA	..	B*3503	58	..	61	26	..	..
37	47	11	LPSPSPSAVPA	..	B*5101	55	..	57	26	..	..
37	47	11	LPSPSPSAVPA	..	B*5501	88	..	92	26	..	..
37	47	11	LPSPSPSAVPA	..	B*5601	77	..	81	26	..	..
37	47	11	LPSPSPSAVPA	..	B*0701	25	..	26	26	..	..
39	47	9	SPSPSAVPA	964	B*5501	56	..	59	26	..	..
39	47	9	SPSPSAVPA	..	B*5601	85	..	89	26	..	..
41	51	11	SPSAVPADHGA	965	B*5501	6	1,30	8	26	..	..
41	51	11	SPSAVPADHGA	..	B*5601	8	..	10	26	..	..
44	53	10	AVPADHGAHL	966	B*0701	75	1,87	140	26	..	..
45	53	9	VPADHGAHL	967	B*1402	43	..	80	26	..	..
45	53	9	VPADHGAHL	..	B*3503	42	..	78	26	..	..
45	53	9	VPADHGAHL	..	B*5501	31	..	59	26	..	..
45	53	9	VPADHGAHL	..	B*0701	100	..	187	26	..	..
45	55	11	VPADHGAHLSL	968	B*1402	93	1,93	180	26	..	..
45	55	11	VPADHGAHLSL	..	B*3501	67	..	129	26	..	..

HLA class I binding peptides in SLP sequences derived from HBV X protein (consensus sequence)							Peptide of invention (SLP)				
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
45	55	11	VPADHGAHLSL	969	B*3503	100	96	193	26	96	96
45	55	11	VPADHGAHLSL	970	B*5101	73	96	141	26	96	96
45	55	11	VPADHGAHLSL	971	B*5301	29	96	55	26	96	96
45	55	11	VPADHGAHLSL	972	B*5501	50	96	97	26	96	96
45	55	11	VPADHGAHLSL	973	B*0701	100	96	193	26	96	96
47	55	9	ADHGAHLSL	974	B*4002	14	96	28	26	96	96
48	55	8	DHGAHLSL	975	B*1402	79	96	152	26	96	96
49	56	8	HGAHLSLR	976	A*3303	73	0,63	46	26	96	96
49	56	8	HGAHLSLR	977	A*6801	33	96	21	26	96	96
50	58	9	GAHLSLRGL	978	B*0701	25	1,33	33	26	96	96
51	58	8	AHLSLRGL	979	B*1402	29	96	38	26	96	96
51	58	8	AHLSLRGL	980	B*3901	9	96	12	26	96	96
51	60	10	AHLSLRGLPV	981	B*1402	71	1,05	75	26	96	96
51	60	10	AHLSLRGLPV	982	B*3901	36	96	38	26	96	96
52	60	9	HLSLRGLPV	983	B*0801	40	96	42	26	96	96
53	60	8	LSLRGLPV	984	A*0201	36	96	38	26	96	96
53	60	8	LSLRGLPV	985	B*5201	33	96	35	26	96	96
52	61	10	HLSLRGLPVC	986	A*3001	88	0,87	77	26	96	96
53	61	9	LSLRGLPVC	987	B*5802	10	96	9	26	96	96
53	63	11	LSLRGLPVCAF	988	B*1502	71	1,48	106	26	96	96
53	63	11	LSLRGLPVCAF	989	B*1525	85	96	125	26	96	96
53	63	11	LSLRGLPVCAF	990	B*4601	50	96	74	26	96	96
53	63	11	LSLRGLPVCAF	991	B*5701	100	96	148	26	96	96
53	63	11	LSLRGLPVCAF	992	B*5801	90	96	133	26	96	96
53	63	11	LSLRGLPVCAF	993	B*5802	30	96	44	26	96	96
54	63	10	SLRGIPVCAF	994	A*0301	100	96	148	26	96	96
54	63	10	SLRGIPVCAF	995	B*1501	86	96	127	26	96	96
54	63	10	SLRGIPVCAF	996	B*1502	86	96	127	26	96	96
54	63	10	SLRGIPVCAF	997	B*1525	54	96	80	26	96	96
54	63	10	SLRGIPVCAF	998	B*4601	36	96	53	26	96	96
56	63	8	RGLPVCAF	999	A*2301	25	96	37	26	96	96
56	63	8	RGLPVCAF	1000	A*3201	20	96	30	26	96	96
58	65	8	LPVCAFSS	1001	B*5101	45	0,59	27	26	96	96

HLA class I binding peptides in SLP sequences derived from HBV X protein (consensus sequence)										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
58	65	8	LPVCAFSS	“	B*5501	13	“	7	26	“	“	
58	65	8	LPVCAFSS	“	B*5601	31	“	18	26	“	“	
56	66	11	RGLPVCAFSSA	984	A*3001	29	0,95	28	26	“	“	
57	66	10	GLPVCAFSSA	985	A*0201	20	“	19	26	“	“	
58	66	9	LPVCAFSSA	986	B*3503	83	“	79	26	“	“	
58	66	9	LPVCAFSSA	“	B*5101	91	“	86	26	“	“	
58	66	9	LPVCAFSSA	“	B*5501	100	“	95	26	“	“	
58	66	9	LPVCAFSSA	“	B*5601	100	“	95	26	“	“	
58	67	10	LPVCAFSSAG	987	B*3501	58	0,11	6	26	“	“	
58	67	10	LPVCAFSSAG	“	B*3503	8	“	1	26	“	“	
58	67	10	LPVCAFSSAG	“	B*5501	19	“	2	26	“	“	
					Cumulative Class I-BCI score ^E :				5422			
61	70	10	CAFSSAGPCA	988	A*3001	76	0,45	35	27	61	95	
61	71	11	CAFSSAGPCAL	989	B*1402	57	1,74	99	27	“	“	
61	71	11	CAFSSAGPCAL	“	B*3901	64	“	111	27	“	“	
61	71	11	CAFSSAGPCAL	“	B*4801	57	“	99	27	“	“	
63	71	9	FSSAGPCAL	990	B*3901	100	“	174	27	“	“	
63	71	9	FSSAGPCAL	“	B*4601	71	“	124	27	“	“	
62	72	11	AFSSAGPCALR	991	A*3101	40	1,24	50	27	“	“	
63	72	10	FSSAGPCALR	992	A*3303	60	“	74	27	“	“	
63	72	10	FSSAGPCALR	“	A*6801	100	“	124	27	“	“	
64	72	9	SSAGPCALR	993	A*3303	87	“	107	27	“	“	
64	72	9	SSAGPCALR	“	A*6801	56	“	69	27	“	“	
63	73	11	FSSAGPCALRF	994	A*0101	38	1,58	59	27	“	“	
63	73	11	FSSAGPCALRF	“	B*1501	14	“	23	27	“	“	
63	73	11	FSSAGPCALRF	“	B*1502	43	“	68	27	“	“	
63	73	11	FSSAGPCALRF	“	B*1525	15	“	24	27	“	“	
63	73	11	FSSAGPCALRF	“	B*3501	50	“	79	27	“	“	
63	73	11	FSSAGPCALRF	“	B*4601	86	“	136	27	“	“	
63	73	11	FSSAGPCALRF	“	B*5301	86	“	136	27	“	“	
63	73	11	FSSAGPCALRF	“	B*5701	67	“	105	27	“	“	
63	73	11	FSSAGPCALRF	“	B*5801	100	“	158	27	“	“	

HLA class I binding peptides in SLP sequences derived from HBV X protein (consensus sequence)										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
63	73	11	FSSAGPCALRF	"	B*5802	50	"	79	27	"	"
64	73	10	SSAGPCALRF	995	B*5802	20	"	32	27	"	"
65	73	9	SAGPCALRF	996	A*0101	25	"	40	27	"	"
65	73	9	SAGPCALRF	"	B*5701	17	"	26	27	"	"
69	77	9	CALRFTSAR	997	A*3101	30	1,06	32	27	"	"
69	77	9	CALRFTSAR	"	A*3303	100	"	106	27	"	"
69	77	9	CALRFTSAR	"	A*6801	11	"	12	27	"	"
69	77	9	CALRFTSAR	"	A*7401	100	"	106	27	"	"
70	77	8	ALRFTSAR	998	A*3001	18	"	19	27	"	"
70	77	8	ALRFTSAR	"	A*3101	70	"	74	27	"	"
70	77	8	ALRFTSAR	"	A*3303	53	"	56	27	"	"
70	77	8	ALRFTSAR	"	A*7401	90	"	95	27	"	"
70	77	8	ALRFTSAR	"	A*0301	81	"	86	27	"	"
69	78	10	CALRFTSARR	999	A*3101	90	1,59	143	27	"	"
69	78	10	CALRFTSARR	"	A*3303	93	"	148	27	"	"
69	78	10	CALRFTSARR	"	A*7401	60	"	95	27	"	"
70	78	9	ALRFTSARR	1000	A*3101	20	"	32	27	"	"
70	78	9	ALRFTSARR	"	A*3303	7	"	11	27	"	"
70	78	9	ALRFTSARR	"	A*7401	80	"	127	27	"	"
70	78	9	ALRFTSARR	"	A*0301	50	"	80	27	"	"
71	78	8	LRFTSARR	1001	B*2705	10	"	16	27	"	"
70	79	10	ALRFTSARRM	1002	B*0701	50	1,80	90	27	"	"
70	79	10	ALRFTSARRM	"	B*0801	67	"	120	27	"	"
71	79	9	LRFTSARRM	1003	B*1402	7	"	13	27	"	"
71	79	9	LRFTSARRM	"	B*2702	75	"	135	27	"	"
71	79	9	LRFTSARRM	"	B*2705	60	"	108	27	"	"
77	84	8	RRMETTVN	1004	B*2702	38	0,84	31	27	"	"
75	85	11	SARRMETTVNA	1005	A*3001	6	1,44	8	27	"	"
77	85	9	RRMETTVNA	1006	B*2702	50	"	72	27	"	"
77	85	9	RRMETTVNA	"	B*2705	40	"	58	27	"	"
77	86	10	RRMETTVNAH	1007	B*2702	63	0,74	46	27	"	"
79	86	8	METTVNAH	1008	A*6802	60	"	44	27	"	"
79	86	8	METTVNAH	"	B*1801	67	"	49	27	"	"

HLA class I binding peptides in SLP sequences derived from HBV X protein (consensus sequence)										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
79	86	8	METTVAH	"	B*4403	33	"	25	27	"	"
77	87	11	RRMETTVNAHQ	1009	B*2702	25	0,30	7	27	"	"
79	87	9	METTVAH	1010	B*4403	44	"	13	27	"	"
78	88	11	RMETTVNAHQI	1011	A*3201	40	0,68	27	27	"	"
79	88	10	METTVAHQI	1012	B*1301	100	"	68	27	"	"
79	88	10	METTVAHQI	"	B*1302	67	"	45	27	"	"
79	88	10	METTVAHQI	"	B*1801	33	"	23	27	"	"
79	88	10	METTVAHQI	"	B*3701	100	"	68	27	"	"
79	88	10	METTVAHQI	"	B*3801	100	"	68	27	"	"
79	88	10	METTVAHQI	"	B*4901	100	"	68	27	"	"
79	88	10	METTVAHQI	"	B*5001	100	"	68	27	"	"
79	88	10	METTVAHQI	"	B*5201	100	"	68	27	"	"
80	88	9	ETTVAHQI	1013	A*6802	40	"	27	27	"	"
79	89	11	METTVAHQIL	1014	B*1301	75	0,67	50	27	"	"
79	89	11	METTVAHQIL	"	B*1801	100	"	67	27	"	"
79	89	11	METTVAHQIL	"	B*3701	92	"	61	27	"	"
79	89	11	METTVAHQIL	"	B*3801	80	"	53	27	"	"
79	89	11	METTVAHQIL	"	B*4001	90	"	60	27	"	"
79	89	11	METTVAHQIL	"	B*4002	43	"	29	27	"	"
79	89	11	METTVAHQIL	"	B*4402	40	"	27	27	"	"
79	89	11	METTVAHQIL	"	B*4403	67	"	45	27	"	"
79	89	11	METTVAHQIL	"	B*4801	43	"	29	27	"	"
79	89	11	METTVAHQIL	"	B*4901	78	"	52	27	"	"
79	89	11	METTVAHQIL	"	B*5001	20	"	13	27	"	"
80	89	10	ETTVAHQIL	1015	A*2501	40	"	27	27	"	"
81	91	11	TTVNAHQILPK	1016	A*1101	67	0,39	26	27	"	"
81	91	11	TTVNAHQILPK	"	A*6801	44	"	17	27	"	"
81	91	11	TTVNAHQILPK	"	A*0301	6	"	2	27	"	"
82	91	10	TVNAHQILPK	1017	A*1101	92	"	36	27	"	"
82	91	10	TVNAHQILPK	"	A*0301	100	"	39	27	"	"
82	92	11	TVNAHQILPKV	1018	A*0201	27	1,32	36	27	"	"
84	93	10	NAHQILPKVL	1019	B*0701	25	1,59	40	27	"	"
85	93	9	AHQILPKVL	1020	B*3801	60	"	95	27	"	"

HLA class I binding peptides in SLP sequences derived from HBV X protein (consensus sequence)										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
85	93	9	AHQILPKVL	”	B*3901	18	”	29	27	”	”	
86	93	8	HQILPKVL	1021	B*3901	91	”	144	27	”	”	
86	93	8	HQILPKVL	”	B*4801	100	”	159	27	”	”	
86	95	10	HQILPKVLHK	1022	A*1101	42	1,60	67	27	”	”	
86	95	10	HQILPKVLHK	”	A*0301	33	”	53	27	”	”	
87	95	9	QILPKVLHK	1023	A*1101	50	”	80	27	”	”	
87	95	9	QILPKVLHK	”	A*0101	75	”	120	27	”	”	
87	95	9	QILPKVLHK	”	A*0301	100	”	160	27	”	”	
88	95	8	ILPKVLHK	1024	A*0201	82	”	131	27	”	”	
88	95	8	ILPKVLHK	”	A*0301	63	”	100	27	”	”	
						Cumulative Class I-BCI score: 6468						
86	93	8	HQILPKVL	1021	B*3901	91	”	144	28	86	120	
86	93	8	HQILPKVL	”	B*4801	100	”	159	28	”	”	
86	95	10	HQILPKVLHK	1022	A*1101	42	1,60	67	28	”	”	
86	95	10	HQILPKVLHK	”	A*0301	33	”	53	28	”	”	
87	95	9	QILPKVLHK	1023	A*1101	50	”	80	28	”	”	
87	95	9	QILPKVLHK	”	A*0101	75	”	120	28	”	”	
87	95	9	QILPKVLHK	”	A*0301	100	”	160	28	”	”	
88	95	8	ILPKVLHK	1024	A*0201	82	”	131	28	”	”	
88	95	8	ILPKVLHK	”	A*0301	63	”	100	28	”	”	
86	96	11	HQILPKVLHKKR	1025	A*3101	50	1,87	94	28	”	”	
86	96	11	HQILPKVLHKKR	”	A*3303	47	”	87	28	”	”	
87	96	10	QILPKVLHKKR	1026	A*3101	60	”	112	28	”	”	
87	96	10	QILPKVLHKKR	”	A*3303	67	”	125	28	”	”	
88	96	9	ILPKVLHKKR	1027	A*3303	27	”	50	28	”	”	
88	96	9	ILPKVLHKKR	”	A*0301	75	”	141	28	”	”	
89	96	8	LPKVLHKKR	1028	B*0701	42	”	78	28	”	”	
88	97	10	ILPKVLHKKRT	1029	A*0201	30	0,47	14	28	”	”	
89	98	10	LPKVLHKKRTL	1030	B*5101	64	1,61	103	28	”	”	
89	98	10	LPKVLHKKRTL	”	B*0701	88	”	141	28	”	”	
89	98	10	LPKVLHKKRTL	”	B*0801	100	”	161	28	”	”	
91	98	8	KVLHKKRTL	1031	B*0801	10	”	16	28	”	”	

HLA class I binding peptides in SLP sequences derived from HBV X protein (consensus sequence)										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
91	100	10	KVLHKRTLGL	1032	A*0201	70	1,91	134	28	55	55
91	100	10	KVLHKRTLGL	55	B*0701	38	55	72	28	55	55
91	100	10	KVLHKRTLGL	55	B*0801	33	55	64	28	55	55
92	100	9	VLHKRTLGL	1033	A*0201	90	55	172	28	55	55
92	100	9	VLHKRTLGL	55	B*0801	100	55	191	28	55	55
92	102	11	VLHKRTLGLSA	1034	B*0801	70	1,09	76	28	55	55
95	102	8	KRTLGLSA	1035	B*2702	13	55	14	28	55	55
93	103	11	LHKRTLGLSAM	1036	B*1402	86	1,72	148	28	55	55
93	103	11	LHKRTLGLSAM	55	B*0801	20	55	34	28	55	55
94	103	10	HKRTLGLSAM	1037	B*1402	50	55	86	28	55	55
95	103	9	KRTLGLSAM	1038	B*2702	88	55	151	28	55	55
96	103	8	RTLGLSAM	1039	A*2501	20	55	34	28	55	55
96	103	8	RTLGLSAM	55	A*3201	100	55	172	28	55	55
96	103	8	RTLGLSAM	55	B*1502	29	55	49	28	55	55
96	103	8	RTLGLSAM	55	B*1525	23	55	40	28	55	55
96	103	8	RTLGLSAM	55	B*4601	93	55	160	28	55	55
96	103	8	RTLGLSAM	55	B*5701	33	55	57	28	55	55
96	103	8	RTLGLSAM	55	B*5801	80	55	138	28	55	55
97	104	8	TLGLSAMS	1040	A*0201	9	0,51	5	28	55	55
97	105	9	TLGLSAMST	1041	A*0201	50	0,88	44	28	55	55
97	106	10	TLGLSAMSTT	1042	A*0201	40	0,27	11	28	55	55
99	108	10	GLSAMSTTDL	1043	A*0201	50	1,60	80	28	55	55
100	110	11	LSAMSTTDLEA	1044	A*0206	100	1,07	107	28	55	55
101	111	11	SAMSTTDLEA	1045	A*2902	75	0,70	53	28	55	55
101	111	11	SAMSTTDLEA	55	A*3002	100	55	70	28	55	55
101	111	11	SAMSTTDLEA	55	B*1501	100	55	70	28	55	55
101	111	11	SAMSTTDLEA	55	B*1502	100	55	70	28	55	55
101	111	11	SAMSTTDLEA	55	B*1525	100	55	70	28	55	55
101	111	11	SAMSTTDLEA	55	B*4601	100	55	70	28	55	55
101	111	11	SAMSTTDLEA	55	B*5301	57	55	40	28	55	55
101	111	11	SAMSTTDLEA	55	B*5801	60	55	42	28	55	55
102	111	10	AMSTTDLEA	1046	A*0301	50	55	35	28	55	55
103	111	9	MSTTDLEA	1047	A*2601	25	55	18	28	55	55

HLA class I binding peptides in SLP sequences derived from HBV X protein (consensus sequence)							Peptide of invention (SLP)				
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
103	111	9	MSTTDLEAY	55	A*0101	88	55	62	28	55	55
103	111	9	MSTTDLEAY	55	B*3501	83	55	59	28	55	55
104	111	8	STTDLEAY	1048	A*2501	100	55	70	28	55	55
102	112	11	AMSTTDLEAYF	1049	A*3002	20	1,45	29	28	55	55
102	112	11	AMSTTDLEAYF	55	B*1501	71	55	104	28	55	55
102	112	11	AMSTTDLEAYF	55	B*1502	14	55	21	28	55	55
102	112	11	AMSTTDLEAYF	55	B*1525	62	55	89	28	55	55
102	112	11	AMSTTDLEAYF	55	B*4601	7	55	10	28	55	55
103	112	10	MSTTDLEAYF	1050	A*0101	13	55	18	28	55	55
103	112	10	MSTTDLEAYF	55	B*3501	42	55	61	28	55	55
103	112	10	MSTTDLEAYF	55	B*4601	43	55	62	28	55	55
103	112	10	MSTTDLEAYF	55	B*5301	14	55	21	28	55	55
103	112	10	MSTTDLEAYF	55	B*5802	40	55	58	28	55	55
104	112	9	STTDLEAYF	1051	A*2501	60	55	87	28	55	55
104	112	9	STTDLEAYF	55	A*2601	50	55	73	28	55	55
105	112	8	TTDLEAYF	1052	A*0101	75	55	109	28	55	55
103	113	11	MSTTDLEAYFK	1053	A*1101	75	0,43	32	28	55	55
103	113	11	MSTTDLEAYFK	55	A*6801	67	55	29	28	55	55
104	113	10	STTDLEAYFK	1054	A*1101	100	55	43	28	55	55
104	113	10	STTDLEAYFK	55	A*6801	89	55	38	28	55	55
104	113	10	STTDLEAYFK	55	A*0301	19	55	8	28	55	55
105	113	9	TTDLEAYFK	1055	A*1101	83	55	36	28	55	55
105	113	9	TTDLEAYFK	55	A*6801	22	55	10	28	55	55
105	113	9	TTDLEAYFK	55	A*0101	100	55	43	28	55	55
105	113	9	TTDLEAYFK	55	A*0301	25	55	11	28	55	55
106	116	11	TDLEAYFKDCV	1056	A*0201	64	0,18	12	28	55	55
106	116	11	TDLEAYFKDCV	55	B*3701	33	55	6	28	55	55
108	116	9	LEAYFKDCV	1057	A*0201	10	55	2	28	55	55
108	116	9	LEAYFKDCV	55	B*1301	25	55	5	28	55	55
108	116	9	LEAYFKDCV	55	B*3701	75	55	14	28	55	55
108	116	9	LEAYFKDCV	55	B*4001	40	55	7	28	55	55
108	116	9	LEAYFKDCV	55	B*4901	89	55	16	28	55	55
108	116	9	LEAYFKDCV	55	B*5001	80	55	15	28	55	55

HLA class I binding peptides in SLP sequences derived from HBV X protein (consensus sequence)										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
109	116	8	EAYFKDCV	1058	B*0801	40	55	7	28	55	55	
108	117	10	LEAYFKDCVF	1059	B*1301	63	1,37	85	28	55	55	
108	117	10	LEAYFKDCVF	55	B*3701	42	55	57	28	55	55	
108	117	10	LEAYFKDCVF	55	B*4001	20	55	27	28	55	55	
108	117	10	LEAYFKDCVF	55	B*4402	80	55	109	28	55	55	
108	117	10	LEAYFKDCVF	55	B*4403	89	55	121	28	55	55	
108	117	10	LEAYFKDCVF	55	B*4901	67	55	91	28	55	55	
108	117	10	LEAYFKDCVF	55	B*5001	60	55	82	28	55	55	
110	117	8	AYFKDCVF	1060	A*2301	100	55	137	28	55	55	
110	117	8	AYFKDCVF	55	A*2402	100	55	137	28	55	55	
109	118	10	EAYFKDCVFK	1061	A*1101	25	1,38	34	28	55	55	
109	118	10	EAYFKDCVFK	55	A*6801	78	55	107	28	55	55	
110	118	9	AYFKDCVFK	1062	A*1101	8	55	11	28	55	55	
111	118	8	YFKDCVFK	1063	A*3101	10	55	14	28	55	55	
111	118	8	YFKDCVFK	55	A*3303	80	55	110	28	55	55	
110	120	11	AYFKDCVFKDW	1064	A*2301	75	1,74	131	28	55	55	
110	120	11	AYFKDCVFKDW	55	A*2402	67	55	116	28	55	55	
						Cumulative Class I-BCI score:						
								7354				
108	117	10	LEAYFKDCVF	1059	B*1301	63	1,37	85	29	108	141	
108	117	10	LEAYFKDCVF	55	B*3701	42	55	57	29	55	55	
108	117	10	LEAYFKDCVF	55	B*4001	20	55	27	29	55	55	
108	117	10	LEAYFKDCVF	55	B*4402	80	55	109	29	55	55	
108	117	10	LEAYFKDCVF	55	B*4403	89	55	121	29	55	55	
108	117	10	LEAYFKDCVF	55	B*4901	67	55	91	29	55	55	
108	117	10	LEAYFKDCVF	55	B*5001	60	55	82	29	55	55	
110	117	8	AYFKDCVF	1060	A*2301	100	55	137	29	55	55	
110	117	8	AYFKDCVF	55	A*2402	100	55	137	29	55	55	
109	118	10	EAYFKDCVFK	1061	A*1101	25	1,38	34	29	55	55	
109	118	10	EAYFKDCVFK	55	A*6801	78	55	107	29	55	55	
110	118	9	AYFKDCVFK	1062	A*1101	8	55	11	29	55	55	
111	118	8	YFKDCVFK	1063	A*3101	10	55	14	29	55	55	
111	118	8	YFKDCVFK	55	A*3303	80	55	110	29	55	55	

HLA class I binding peptides in SLP sequences derived from HBV X protein (consensus sequence)										Peptide of invention (SLP)	
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
110	120	11	AYFKDCVFKDW	1064	A*2301	75	1,74	131	29	29	29
110	120	11	AYFKDCVFKDW	29	A*2402	67	29	116	29	29	29
114	123	10	DCVFKDWEEL	1065	A*3201	60	1,30	78	29	29	29
115	123	9	CVFKDWEEL	1066	A*0201	40	29	52	29	29	29
115	123	9	CVFKDWEEL	29	B*0701	50	29	65	29	29	29
118	127	10	KDWEELGEEI	1067	B*1301	88	0,73	63	29	29	29
118	127	10	KDWEELGEEI	29	B*1302	100	29	73	29	29	29
118	127	10	KDWEELGEEI	29	B*5201	67	29	48	29	29	29
120	127	8	WEELGEEI	1068	B*1301	50	29	36	29	29	29
120	127	8	WEELGEEI	29	B*4001	70	29	51	29	29	29
120	127	8	WEELGEEI	29	B*4901	56	29	40	29	29	29
119	129	11	DWEELGEEIRL	1069	A*0201	55	1,70	93	29	29	29
120	129	10	WEELGEEIRL	1070	B*3801	20	29	34	29	29	29
120	129	10	WEELGEEIRL	29	B*4001	10	29	17	29	29	29
121	129	9	EELGEEIRL	1071	B*4001	60	29	102	29	29	29
121	129	9	EELGEEIRL	29	B*4403	22	29	38	29	29	29
121	131	11	EELGEEIRLKV	1072	B*1801	17	1,00	17	29	29	29
121	131	11	EELGEEIRLKV	29	B*3701	50	29	50	29	29	29
122	131	10	ELGEEIRLKV	1073	A*0201	60	29	60	29	29	29
124	131	8	GEEIRLKV	1074	B*4901	11	29	11	29	29	29
123	132	10	LGEIIRLKVVF	1075	A*0101	50	1,36	68	29	29	29
124	132	9	GEEIRLKVVF	1076	B*4402	60	29	82	29	29	29
124	132	9	GEEIRLKVVF	29	B*4403	11	29	15	29	29	29
125	132	8	EEIRLKVVF	1077	B*1801	83	29	113	29	29	29
125	132	8	EEIRLKVVF	29	B*4402	20	29	27	29	29	29
125	132	8	EEIRLKVVF	29	B*4403	56	29	75	29	29	29
123	133	11	LGEIIRLKVVFV	1078	A*0206	50	1,07	54	29	29	29
123	133	11	LGEIIRLKVVFV	29	A*0201	91	29	98	29	29	29
125	133	9	EEIRLKVVFV	1079	B*3701	58	29	63	29	29	29
125	133	9	EEIRLKVVFV	29	B*4001	30	29	32	29	29	29
125	133	9	EEIRLKVVFV	29	B*4403	78	29	84	29	29	29
126	133	8	EIRLKVVFV	1080	B*0801	100	29	107	29	29	29
125	134	10	EEIRLKVVFVL	1081	B*1801	50	1,85	93	29	29	29

HLA class I binding peptides in SLP sequences derived from HBV X protein (consensus sequence)							Peptide of invention (SLP)				
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I-B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End
125	134	10	EEIRLKVFL	”	B*3701	83	”	154	29	”	”
125	134	10	EEIRLKVFL	”	B*3801	40	”	74	29	”	”
125	134	10	EEIRLKVFL	”	B*4001	100	”	185	29	”	”
125	134	10	EEIRLKVFL	”	B*4002	71	”	132	29	”	”
125	134	10	EEIRLKVFL	”	B*4402	100	”	185	29	”	”
125	134	10	EEIRLKVFL	”	B*4403	100	”	185	29	”	”
126	134	9	EIRLKVFL	1082	B*0701	63	”	116	29	”	”
126	134	9	EIRLKVFL	”	B*0801	100	”	185	29	”	”
127	134	8	IRLKVFL	1083	A*0206	25	”	46	29	”	”
127	134	8	IRLKVFL	”	B*1402	64	”	119	29	”	”
127	134	8	IRLKVFL	”	B*2702	100	”	185	29	”	”
127	134	8	IRLKVFL	”	B*3901	82	”	151	29	”	”
129	136	8	LKVFLGG	1084	A*0206	75	0,47	35	29	”	”
128	138	11	RLKVFLGGCR	1085	A*3101	80	0,64	51	29	”	”
128	138	11	RLKVFLGGCR	”	A*7401	30	”	19	29	”	”
128	138	11	RLKVFLGGCR	”	A*0301	13	”	8	29	”	”
130	138	9	KVFLGGCR	1086	A*3101	100	”	64	29	”	”
130	138	9	KVFLGGCR	”	A*7401	50	”	32	29	”	”
130	140	11	KVFLGGCRHK	1087	A*1101	58	1,05	61	29	”	”
130	140	11	KVFLGGCRHK	”	A*3001	94	”	99	29	”	”
130	140	11	KVFLGGCRHK	”	A*0301	94	”	98	29	”	”
133	140	8	VLGGCRHK	1088	A*0201	18	”	19	29	”	”
133	140	8	VLGGCRHK	”	A*0301	44	”	46	29	”	”
132	141	10	FVLGGCRHKL	1089	A*0201	80	1,66	133	29	”	”
132	141	10	FVLGGCRHKL	”	B*0701	63	”	104	29	”	”
133	141	9	VLGGCRHKL	1090	A*0201	100	”	166	29	”	”
					Cumulative Class I-BCI score:			5862			

“Start” and “End” are relative to the amino acid sequence of HBV X protein, consensus sequence, as depicted in SEQ ID NO: 45

^A Peptide amino acid sequence. Each HLA class I binding peptide of HBV X protein is listed separately for each HLA class I molecule to which it is predicted to bind, and can be listed

5 multiple times for that reason.

^B Class I-B score. See *Material and Methods* (Examples section).

^C C-score. See *Material and Methods* (Examples section). ^D Class I-BCI score. See *Material and Methods* (Examples section).

^E Cumulative Class I-BCI score. See *Material and Methods* (Examples section).

Table 6b. Predicted HLA class II-restricted CD4⁺ T cell epitopes contained in SLP sequences from HBV X protein (consensus sequence).

HLA class II binding peptides in SLP derived from HBV X protein (consens. seq.)						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
46	60	PADHGAHLSLRGLPV	1091	*0701	8	26	36	68
47	61	ADHGAHLSLRGLPVC	1092	*0101	13	26	„	„
47	61	ADHGAHLSLRGLPVC	„	*0102	20	26	„	„
47	61	ADHGAHLSLRGLPVC	„	*0105	13	26	„	„
47	61	ADHGAHLSLRGLPVC	„	*0107	13	26	„	„
48	62	DHGAHLSLRGLPVCA	1093	*0101	87	26	„	„
48	62	DHGAHLSLRGLPVCA	„	*0102	67	26	„	„
48	62	DHGAHLSLRGLPVCA	„	*0104	43	26	„	„
48	62	DHGAHLSLRGLPVCA	„	*0105	87	26	„	„
48	62	DHGAHLSLRGLPVCA	„	*0106	53	26	„	„
48	62	DHGAHLSLRGLPVCA	„	*0107	87	26	„	„
49	63	HGAHLSLRGLPVCAF	1094	*0101	100	26	„	„
49	63	HGAHLSLRGLPVCAF	„	*0102	93	26	„	„
49	63	HGAHLSLRGLPVCAF	„	*0103	40	26	„	„
49	63	HGAHLSLRGLPVCAF	„	*0104	90	26	„	„
49	63	HGAHLSLRGLPVCAF	„	*0105	90	26	„	„
49	63	HGAHLSLRGLPVCAF	„	*0106	90	26	„	„
49	63	HGAHLSLRGLPVCAF	„	*0107	90	26	„	„
49	63	HGAHLSLRGLPVCAF	„	*1101	85	26	„	„
49	63	HGAHLSLRGLPVCAF	„	*1301	100	26	„	„
49	63	HGAHLSLRGLPVCAF	„	*1501	46	26	„	„
50	64	GAHLSLRGLPVCAFS	1095	*0101	77	26	„	„
50	64	GAHLSLRGLPVCAFS	„	*0102	97	26	„	„
50	64	GAHLSLRGLPVCAFS	„	*0103	70	26	„	„
50	64	GAHLSLRGLPVCAFS	„	*0104	93	26	„	„
50	64	GAHLSLRGLPVCAFS	„	*0105	93	26	„	„
50	64	GAHLSLRGLPVCAFS	„	*0106	97	26	„	„
50	64	GAHLSLRGLPVCAFS	„	*0107	93	26	„	„
50	64	GAHLSLRGLPVCAFS	„	*1101	77	26	„	„
50	64	GAHLSLRGLPVCAFS	„	*1301	92	26	„	„
50	64	GAHLSLRGLPVCAFS	„	*1501	54	26	„	„
51	65	AHLSLRGLPVCAFSS	1096	*0101	100	26	„	„
51	65	AHLSLRGLPVCAFSS	„	*0102	100	26	„	„
51	65	AHLSLRGLPVCAFSS	„	*0103	100	26	„	„
51	65	AHLSLRGLPVCAFSS	„	*0104	100	26	„	„
51	65	AHLSLRGLPVCAFSS	„	*0105	100	26	„	„
51	65	AHLSLRGLPVCAFSS	„	*0106	100	26	„	„
51	65	AHLSLRGLPVCAFSS	„	*0107	100	26	„	„
51	65	AHLSLRGLPVCAFSS	„	*1301	85	26	„	„
52	66	HLSLRGLPVCAFSSA	1097	*0101	97	26	„	„
52	66	HLSLRGLPVCAFSSA	„	*0102	90	26	„	„
52	66	HLSLRGLPVCAFSSA	„	*0103	90	26	„	„
52	66	HLSLRGLPVCAFSSA	„	*0104	97	26	„	„
52	66	HLSLRGLPVCAFSSA	„	*0105	97	26	„	„

HLA class II binding peptides in SLP derived from HBV X protein (consens. seq.)						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA- DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
52	66	HLSLRGLPVCAFSSA	„	*0106	93	26	„	„
52	66	HLSLRGLPVCAFSSA	„	*0107	97	26	„	„
52	66	HLSLRGLPVCAFSSA	„	*1301	77	26	„	„
53	67	LSLRGLPVCAFSSAG	1098	*0101	83	26	„	„
53	67	LSLRGLPVCAFSSAG	„	*0102	50	26	„	„
53	67	LSLRGLPVCAFSSAG	„	*0104	77	26	„	„
53	67	LSLRGLPVCAFSSAG	„	*0105	83	26	„	„
53	67	LSLRGLPVCAFSSAG	„	*0106	73	26	„	„
53	67	LSLRGLPVCAFSSAG	„	*0107	83	26	„	„
53	67	LSLRGLPVCAFSSAG	„	*1301	69	26	„	„
54	68	SLRGLPVCAFSSAGP	1099	*0101	37	26	„	„
54	68	SLRGLPVCAFSSAGP	„	*0102	7	26	„	„
54	68	SLRGLPVCAFSSAGP	„	*0104	30	26	„	„
54	68	SLRGLPVCAFSSAGP	„	*0105	37	26	„	„
54	68	SLRGLPVCAFSSAGP	„	*0106	7	26	„	„
54	68	SLRGLPVCAFSSAGP	„	*0107	37	26	„	„
54	68	SLRGLPVCAFSSAGP	„	*1301	62	26	„	„
		Cumulative Class II-B score^C:			4414			
61	75	CAFSSAGPCALRFTS	1100	*0101	20	27	61	95
61	75	CAFSSAGPCALRFTS	„	*0105	20	27	„	„
61	75	CAFSSAGPCALRFTS	„	*0107	20	27	„	„
61	75	CAFSSAGPCALRFTS	„	*0701	15	27	„	„
64	78	SSAGPCALRFTSARR	1101	*1501	69	27	„	„
65	79	SAGPCALRFTSARRM	1102	*0101	23	27	„	„
65	79	SAGPCALRFTSARRM	„	*0102	23	27	„	„
65	79	SAGPCALRFTSARRM	„	*0104	27	27	„	„
65	79	SAGPCALRFTSARRM	„	*0106	23	27	„	„
65	79	SAGPCALRFTSARRM	„	*0401	31	27	„	„
65	79	SAGPCALRFTSARRM	„	*0701	85	27	„	„
65	79	SAGPCALRFTSARRM	„	*1301	46	27	„	„
65	79	SAGPCALRFTSARRM	„	*1501	92	27	„	„
66	80	AGPCALRFTSARRME	1103	*0101	69	27	„	„
66	80	AGPCALRFTSARRME	„	*0102	37	27	„	„
66	80	AGPCALRFTSARRME	„	*0104	40	27	„	„
66	80	AGPCALRFTSARRME	„	*0105	3	27	„	„
66	80	AGPCALRFTSARRME	„	*0106	37	27	„	„
66	80	AGPCALRFTSARRME	„	*0107	3	27	„	„
66	80	AGPCALRFTSARRME	„	*0401	46	27	„	„
66	80	AGPCALRFTSARRME	„	*0701	69	27	„	„
66	80	AGPCALRFTSARRME	„	*1301	38	27	„	„
66	80	AGPCALRFTSARRME	„	*1501	85	27	„	„
67	81	GPCALRFTSARRMET	1104	*0101	62	27	„	„
67	81	GPCALRFTSARRMET	„	*0102	57	27	„	„
67	81	GPCALRFTSARRMET	„	*0104	70	27	„	„
67	81	GPCALRFTSARRMET	„	*0105	43	27	„	„
67	81	GPCALRFTSARRMET	„	*0106	80	27	„	„

HLA class II binding peptides in SLP derived from HBV X protein (consens. seq.)						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA- DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
67	81	GPCALRFTSARRMET	„	*0107	43	27	„	„
67	81	GPCALRFTSARRMET	„	*0301	46	27	„	„
67	81	GPCALRFTSARRMET	„	*0401	92	27	„	„
67	81	GPCALRFTSARRMET	„	*0701	77	27	„	„
67	81	GPCALRFTSARRMET	„	*1101	8	27	„	„
67	81	GPCALRFTSARRMET	„	*1301	31	27	„	„
67	81	GPCALRFTSARRMET	„	*1501	100	27	„	„
68	82	PCALRFTSARRMETT	1105	*0101	54	27	„	„
68	82	PCALRFTSARRMETT	„	*0102	60	27	„	„
68	82	PCALRFTSARRMETT	„	*0104	83	27	„	„
68	82	PCALRFTSARRMETT	„	*0105	57	27	„	„
68	82	PCALRFTSARRMETT	„	*0106	83	27	„	„
68	82	PCALRFTSARRMETT	„	*0107	57	27	„	„
68	82	PCALRFTSARRMETT	„	*0301	38	27	„	„
68	82	PCALRFTSARRMETT	„	*0401	69	27	„	„
68	82	PCALRFTSARRMETT	„	*0701	100	27	„	„
68	82	PCALRFTSARRMETT	„	*1101	31	27	„	„
68	82	PCALRFTSARRMETT	„	*1301	23	27	„	„
68	82	PCALRFTSARRMETT	„	*1501	77	27	„	„
69	83	CALRFTSARRMETTV	1106	*0101	46	27	„	„
69	83	CALRFTSARRMETTV	„	*0102	43	27	„	„
69	83	CALRFTSARRMETTV	„	*0104	67	27	„	„
69	83	CALRFTSARRMETTV	„	*0105	47	27	„	„
69	83	CALRFTSARRMETTV	„	*0106	57	27	„	„
69	83	CALRFTSARRMETTV	„	*0107	47	27	„	„
69	83	CALRFTSARRMETTV	„	*0301	31	27	„	„
69	83	CALRFTSARRMETTV	„	*0401	23	27	„	„
69	83	CALRFTSARRMETTV	„	*0701	92	27	„	„
69	83	CALRFTSARRMETTV	„	*1101	38	27	„	„
69	83	CALRFTSARRMETTV	„	*1301	15	27	„	„
69	83	CALRFTSARRMETTV	„	*1501	62	27	„	„
70	84	ALRFTSARRMETTVN	1107	*0101	38	27	„	„
70	84	ALRFTSARRMETTVN	„	*0102	17	27	„	„
70	84	ALRFTSARRMETTVN	„	*0104	37	27	„	„
70	84	ALRFTSARRMETTVN	„	*0106	3	27	„	„
70	84	ALRFTSARRMETTVN	„	*0301	62	27	„	„
70	84	ALRFTSARRMETTVN	„	*0401	8	27	„	„
70	84	ALRFTSARRMETTVN	„	*0701	62	27	„	„
70	84	ALRFTSARRMETTVN	„	*1101	46	27	„	„
70	84	ALRFTSARRMETTVN	„	*1301	8	27	„	„
70	84	ALRFTSARRMETTVN	„	*1501	23	27	„	„
71	85	LRFTSARRMETTVNA	1108	*0301	23	27	„	„
71	85	LRFTSARRMETTVNA	„	*0401	15	27	„	„
71	85	LRFTSARRMETTVNA	„	*0701	54	27	„	„
71	85	LRFTSARRMETTVNA	„	*1101	23	27	„	„
73	87	FTSARRMETTVNAHQ	1109	*0401	85	27	„	„
74	88	TSARRMETTVNAHQI	1110	*0401	100	27	„	„

HLA class II binding peptides in SLP derived from HBV X protein (consens. seq.)						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA- DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
75	89	SARRMETTVNAHQIL	1111	*0401	38	27	„	„
75	89	SARRMETTVNAHQIL	„	*1301	40	27	„	„
76	90	ARRMETTVNAHQILP	1112	*0401	80	27	„	„
76	90	ARRMETTVNAHQILP	„	*1301	10	27	„	„
77	91	RRMETTVNAHQILPK	1113	*1301	50	27	„	„
78	92	RMETTVNAHQILPKV	1114	*1301	20	27	„	„
81	95	TTVNAHQILPKVLHK	1115	*1101	15	27	„	„
		Cumulative Class II-B score:				3788		
86	100	HQILPKVLHKRTLGL	1116	*1101	54	28	86	120
87	101	QILPKVLHKRTLGLS	1117	*0102	10	28	„	„
87	101	QILPKVLHKRTLGLS	„	*1101	22	28	„	„
87	101	QILPKVLHKRTLGLS	„	*1301	70	28	„	„
88	102	ILPKVLHKRTLGLSA	1118	*0102	53	28	„	„
88	102	ILPKVLHKRTLGLSA	„	*0104	17	28	„	„
88	102	ILPKVLHKRTLGLSA	„	*0106	33	28	„	„
88	102	ILPKVLHKRTLGLSA	„	*1101	44	28	„	„
88	102	ILPKVLHKRTLGLSA	„	*1301	80	28	„	„
89	103	LPKVLHKRTLGLSAM	1119	*0101	10	28	„	„
89	103	LPKVLHKRTLGLSAM	„	*0102	77	28	„	„
89	103	LPKVLHKRTLGLSAM	„	*0104	60	28	„	„
89	103	LPKVLHKRTLGLSAM	„	*0105	10	28	„	„
89	103	LPKVLHKRTLGLSAM	„	*0106	77	28	„	„
89	103	LPKVLHKRTLGLSAM	„	*0107	10	28	„	„
89	103	LPKVLHKRTLGLSAM	„	*0701	10	28	„	„
89	103	LPKVLHKRTLGLSAM	„	*1101	78	28	„	„
89	103	LPKVLHKRTLGLSAM	„	*1301	100	28	„	„
89	103	LPKVLHKRTLGLSAM	„	*1501	40	28	„	„
90	104	PKVLHKRTLGLSAMS	1120	*0101	33	28	„	„
90	104	PKVLHKRTLGLSAMS	„	*0102	73	28	„	„
90	104	PKVLHKRTLGLSAMS	„	*0104	63	28	„	„
90	104	PKVLHKRTLGLSAMS	„	*0105	33	28	„	„
90	104	PKVLHKRTLGLSAMS	„	*0106	67	28	„	„
90	104	PKVLHKRTLGLSAMS	„	*0107	33	28	„	„
90	104	PKVLHKRTLGLSAMS	„	*1101	72	28	„	„
90	104	PKVLHKRTLGLSAMS	„	*1301	90	28	„	„
91	105	KVLHKRTLGLSAMST	1121	*0101	63	28	„	„
91	105	KVLHKRTLGLSAMST	„	*0102	70	28	„	„
91	105	KVLHKRTLGLSAMST	„	*0104	50	28	„	„
91	105	KVLHKRTLGLSAMST	„	*0105	63	28	„	„
91	105	KVLHKRTLGLSAMST	„	*0106	60	28	„	„
91	105	KVLHKRTLGLSAMST	„	*0107	63	28	„	„
91	105	KVLHKRTLGLSAMST	„	*1101	11	28	„	„
91	105	KVLHKRTLGLSAMST	„	*1301	60	28	„	„
92	106	VLHKRTLGLSAMSTT	1122	*0101	15	28	„	„
92	106	VLHKRTLGLSAMSTT	„	*0102	47	28	„	„
92	106	VLHKRTLGLSAMSTT	„	*0104	23	28	„	„

HLA class II binding peptides in SLP derived from HBV X protein (consens. seq.)						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA- DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
92	106	VLHKRTLGLSAMSTT	„	*0105	73	28	„	„
92	106	VLHKRTLGLSAMSTT	„	*0106	43	28	„	„
92	106	VLHKRTLGLSAMSTT	„	*0107	73	28	„	„
93	107	LHKRTLGLSAMSTTD	1123	*0101	60	28	„	„
93	107	LHKRTLGLSAMSTTD	„	*0102	27	28	„	„
93	107	LHKRTLGLSAMSTTD	„	*0105	60	28	„	„
93	107	LHKRTLGLSAMSTTD	„	*0107	60	28	„	„
94	108	HKRTLGLSAMSTTDL	1124	*0101	92	28	„	„
94	108	HKRTLGLSAMSTTDL	„	*0102	33	28	„	„
94	108	HKRTLGLSAMSTTDL	„	*0104	3	28	„	„
94	108	HKRTLGLSAMSTTDL	„	*0105	67	28	„	„
94	108	HKRTLGLSAMSTTDL	„	*0106	40	28	„	„
94	108	HKRTLGLSAMSTTDL	„	*0107	67	28	„	„
94	108	HKRTLGLSAMSTTDL	„	*0401	77	28	„	„
95	109	KRTLGLSAMSTTDLE	1125	*0101	31	28	„	„
95	109	KRTLGLSAMSTTDLE	„	*0105	23	28	„	„
95	109	KRTLGLSAMSTTDLE	„	*0106	17	28	„	„
95	109	KRTLGLSAMSTTDLE	„	*0107	23	28	„	„
95	109	KRTLGLSAMSTTDLE	„	*0401	54	28	„	„
96	110	RTLGLSAMSTTDLEA	1126	*0101	8	28	„	„
96	110	RTLGLSAMSTTDLEA	„	*0105	30	28	„	„
96	110	RTLGLSAMSTTDLEA	„	*0106	27	28	„	„
96	110	RTLGLSAMSTTDLEA	„	*0107	30	28	„	„
96	110	RTLGLSAMSTTDLEA	„	*0401	62	28	„	„
97	111	TLGLSAMSTTDLEAY	1127	*0101	17	28	„	„
97	111	TLGLSAMSTTDLEAY	„	*0105	17	28	„	„
97	111	TLGLSAMSTTDLEAY	„	*0106	20	28	„	„
97	111	TLGLSAMSTTDLEAY	„	*0107	17	28	„	„
97	111	TLGLSAMSTTDLEAY	„	*0401	50	28	„	„
105	119	TTDLEAYFKDCVFKD	1128	*0301	69	28	„	„
106	120	TDLEAYFKDCVFKDW	1129	*0301	54	28	„	„
Cumulative Class II-B score:					3170			
108	122	LEAYFKDCVFKDWEE	1130	*0301	15	29	108	141
110	124	AYFKDCVFKDWEEELG	1131	*0301	100	29	„	„
111	125	YFKDCVFKDWEEELGE	1132	*0301	92	29	„	„
119	133	DWEEELGEEIRLKV FV	1133	*0301	77	29	„	„
120	134	WEELGEEIRLKV FVL	1134	*0301	85	29	„	„
120	134	WEELGEEIRLKV FVL	„	*1501	8	29	„	„
121	135	EELGEEIRLKV FVLG	1135	*1501	31	29	„	„
123	137	LGEEIRLKV FVLGGC	1136	*1501	15	29	„	„
124	138	GEEIRLKV FVLGGCR	1137	*1501	38	29	„	„
125	139	EEIRLKV FVLGGCRH	1138	*0102	3	29	„	„
126	140	EIRLKV FVLGGCRHK	1139	*0102	40	29	„	„
126	140	EIRLKV FVLGGCRHK	„	*0104	20	29	„	„
126	140	EIRLKV FVLGGCRHK	„	*1501	10	29	„	„
127	141	IRLKV FVLGGCRHKL	1140	*0101	40	29	„	„

HLA class II binding peptides in SLP derived from HBV X protein (consens. seq.)						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
127	141	IRLKVFVLGGCRHKL	„	*0102	80	29	„	„
127	141	IRLKVFVLGGCRHKL	„	*0104	73	29	„	„
127	141	IRLKVFVLGGCRHKL	„	*0105	40	29	„	„
127	141	IRLKVFVLGGCRHKL	„	*0106	70	29	„	„
127	141	IRLKVFVLGGCRHKL	„	*0107	40	29	„	„
127	141	IRLKVFVLGGCRHKL	„	*1101	56	29	„	„
127	141	IRLKVFVLGGCRHKL	„	*1501	90	29	„	„
Cumulative Class II-B score:					1024			

“Start” and “End” are relative to the amino acid sequence of human HBV X protein as depicted in SEQ ID NO: 45

^A Peptide amino acid sequence. Each HLA-DRB1 binding peptide of HBV X protein is listed

5 separately for each HLA class II molecule to which it is predicted to bind, and each peptide can be listed multiple times for that reason.

^B Class II-B score. See *Material and Methods* (Examples section).

^C Cumulative Class II-B score. See *Material and Methods* (Examples section).

Table 7a. Predicted HLA class I-restricted CD8⁺ cytotoxic T cell epitopes contained in SLP sequences from HBV large surface protein.

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
175	182	8	MENITSGF	1146	B*4901	40	1,40	56	30	175	210		
175	182	8	MENITSGF	"	B*5001	35	1,40	49	"	"	"		
175	182	8	MENITSGF	"	B*1801	30	1,40	42	"	"	"		
175	183	9	MENITSGFL	1147	B*4403	90	0,93	84	"	"	"		
175	183	9	MENITSGFL	"	B*4402	85	0,93	79	"	"	"		
175	183	9	MENITSGFL	"	B*4001	75	0,93	70	"	"	"		
175	183	9	MENITSGFL	"	B*5001	25	0,93	23	"	"	"		
175	183	9	MENITSGFL	"	B*4901	20	0,93	19	"	"	"		
175	184	10	MENITSGFLG	1148	B*4402	75	0,59	44	"	"	"		
175	184	10	MENITSGFLG	"	B*4403	60	0,59	35	"	"	"		
175	185	11	MENITSGFLGP	1149	B*4402	35	0,19	7	"	"	"		
175	186	12	MENITSGFLGPL	1150	B*4001	90	0,80	72	"	"	"		
175	186	12	MENITSGFLGPL	"	B*4002	80	0,80	64	"	"	"		
175	186	12	MENITSGFLGPL	"	B*4402	80	0,80	64	"	"	"		
175	186	12	MENITSGFLGPL	"	B*4403	80	0,80	64	"	"	"		
175	186	12	MENITSGFLGPL	"	B*1801	70	0,80	56	"	"	"		
175	186	12	MENITSGFLGPL	"	B*3701	60	0,80	48	"	"	"		
175	186	12	MENITSGFLGPL	"	B*5001	55	0,80	44	"	"	"		
175	186	12	MENITSGFLGPL	"	B*4901	30	0,80	24	"	"	"		
176	186	11	ENITSGFLGPL	1151	A*6802	20	0,80	16	"	"	"		
175	187	13	MENITSGFLGPLL	1152	B*4402	95	0,77	73	"	"	"		
175	187	13	MENITSGFLGPLL	"	B*4403	95	0,77	73	"	"	"		
175	187	13	MENITSGFLGPLL	"	B*4001	85	0,77	66	"	"	"		
175	187	13	MENITSGFLGPLL	"	B*5001	75	0,77	58	"	"	"		
175	187	13	MENITSGFLGPLL	"	B*3701	70	0,77	54	"	"	"		
175	187	13	MENITSGFLGPLL	"	B*4002	65	0,77	50	"	"	"		
175	187	13	MENITSGFLGPLL	"	B*4901	60	0,77	46	"	"	"		
175	187	13	MENITSGFLGPLL	"	B*1801	40	0,77	31	"	"	"		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
175	187	13	MENITSGFLGPLL	”	B*1301	25	0,77	19	”	”	”		
178	187	10	ITSGFLGPLL	1153	A*3001	15	0,77	12	”	”	”		
175	188	14	MENITSGFLGPLLV	1154	B*4901	95	1,48	141	”	”	”		
175	188	14	MENITSGFLGPLLV	”	B*4402	90	1,48	133	”	”	”		
175	188	14	MENITSGFLGPLLV	”	B*4403	85	1,48	126	”	”	”		
175	188	14	MENITSGFLGPLLV	”	B*5001	80	1,48	119	”	”	”		
175	188	14	MENITSGFLGPLLV	”	B*4001	65	1,48	96	”	”	”		
175	188	14	MENITSGFLGPLLV	”	B*3701	50	1,48	74	”	”	”		
175	188	14	MENITSGFLGPLLV	”	B*4002	10	1,48	15	”	”	”		
182	193	12	FLGPLLVLQAGF	1155	B*1501	30	1,17	35	”	”	”		
186	193	8	LLVLQAGF	1156	B*1501	10	1,17	12	”	”	”		
187	194	8	LVLQAGFF	1157	A*2601	15	0,99	15	”	”	”		
182	195	14	FLGPLLVLQAGFFL	1158	A*0201	63	1,59	100	”	”	”		
182	195	14	FLGPLLVLQAGFFL	”	A*0206	55	1,59	87	”	”	”		
186	195	10	LLVLqAGFFL	1159	A*0201	66	1,59	104	”	”	”		
187	195	9	LVLQAGFFL	1160	A*0201	20	1,59	32	”	”	”		
187	196	10	LVLQAGFFLL	1161	A*0206	20	1,85	37	”	”	”		
188	196	9	VLQAGFFLL	1162	A*0201	26	1,85	48	”	”	”		
189	196	8	LQAGFFLL	1163	B*3701	85	1,85	157	”	”	”		
189	196	8	LQAGFFLL	”	B*4801	60	1,85	111	”	”	”		
189	196	8	LQAGFFLL	”	B*1301	50	1,85	92	”	”	”		
189	196	8	LQAGFFLL	”	B*3901	45	1,85	83	”	”	”		
189	196	8	LQAGFFLL	”	B*1302	40	1,85	74	”	”	”		
189	196	8	LQAGFFLL	”	B*3801	35	1,85	65	”	”	”		
189	196	8	LQAGFFLL	”	B*5001	30	1,85	55	”	”	”		
187	198	12	LVLQAGFFLLLTR	1164	A*7401	30	1,36	41	”	”	”		
187	198	12	LVLQAGFFLLLTR	”	A*3101	10	1,36	14	”	”	”		
187	198	12	LVLQAGFFLLLTR	”	A*1101	5	1,36	7	”	”	”		
188	198	11	VLQAGFFLLLTR	1165	A*7401	90	1,36	122	”	”	”		
189	198	10	LQAGFFLLLTR	1166	A*3101	80	1,36	109	”	”	”		
189	198	10	LQAGFFLLLTR	”	A*7401	65	1,36	88	”	”	”		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
189	198	10	LQAGFFLLTR	..	A*1101	15	1,36	20	..	..	..		
190	198	9	QAGFFLLTR	1167	A*7401	10	1,36	14	..	..	..		
191	198	8	AGFFLLTR	1168	A*7401	70	1,36	95	..	..	..		
189	199	11	LQAGFFLLTRI	1169	B*5201	95	1,36	129	..	..	..		
189	199	11	LQAGFFLLTRI	..	B*1302	85	1,36	115	..	..	..		
189	199	11	LQAGFFLLTRI	..	B*4901	50	1,36	68	..	..	..		
189	199	11	LQAGFFLLTRI	..	B*1301	30	1,36	41	..	..	..		
189	199	11	LQAGFFLLTRI	..	B*4001	25	1,36	34	..	..	..		
189	199	11	LQAGFFLLTRI	..	B*5001	15	1,36	20	..	..	..		
189	199	11	LQAGFFLLTRI	..	B*3701	10	1,36	14	..	..	..		
189	200	12	LQAGFFLLTRIL	1170	B*4001	60	1,90	114	..	..	..		
189	200	12	LQAGFFLLTRIL	..	B*3701	40	1,90	76	..	..	..		
189	200	12	LQAGFFLLTRIL	..	B*4801	40	1,90	76	..	..	..		
189	200	12	LQAGFFLLTRIL	..	B*3901	30	1,90	57	..	..	..		
189	200	12	LQAGFFLLTRIL	..	B*5001	5	1,90	9	..	..	..		
189	202	14	LQAGFFLLTRILTI	1171	B*5201	80	1,73	139	..	..	..		
189	202	14	LQAGFFLLTRILTI	..	B*4901	65	1,73	113	..	..	..		
189	202	14	LQAGFFLLTRILTI	..	B*5001	65	1,73	113	..	..	..		
189	202	14	LQAGFFLLTRILTI	..	B*1301	60	1,73	104	..	..	..		
189	202	14	LQAGFFLLTRILTI	..	B*1302	55	1,73	95	..	..	..		
189	202	14	LQAGFFLLTRILTI	..	A*0206	50	1,73	87	..	..	..		
189	202	14	LQAGFFLLTRILTI	..	B*3701	45	1,73	78	..	..	..		
189	202	14	LQAGFFLLTRILTI	..	B*4001	45	1,73	78	..	..	..		
191	202	12	AGFFLLTRILTI	1172	B*5201	50	1,73	87	..	..	..		
194	202	9	FLLTRILTI	1173	B*0801	80	1,73	139	..	..	..		
194	202	9	FLLTRILTI	..	A*0201	37	1,73	64	..	..	..		
194	206	13	FLLTRILTI PQSL	1174	B*0801	100	1,23	123	..	..	..		
194	206	13	FLLTRILTI PQSL	..	A*0201	29	1,23	35	..	..	..		
195	206	12	L LTRILTI PQSL	1175	B*1402	70	1,23	86	..	..	..		
196	206	11	LTRILTI PQSL	1176	A*3001	25	1,23	31	..	..	..		
196	206	11	LTRILTI PQSL	..	B*1402	10	1,23	12	..	..	..		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
197	206	10	TRILTIPQSL	1177	B*3901	100	1,23	123	22	22	22	
197	206	10	TRILTIPQSL	22	B*2705	5	1,23	6	22	22	22	
196	209	14	LTRILTIPQSLDSW	1178	B*5701	75	1,47	111	22	22	22	
196	209	14	LTRILTIPQSLDSW	22	B*5802	40	1,47	59	22	22	22	
198	209	12	RILTIPQSLDSW	1179	B*5801	65	1,47	96	22	22	22	
198	209	12	RILTIPQSLDSW	22	A*3201	60	1,47	88	22	22	22	
198	209	12	RILTIPQSLDSW	22	B*5701	50	1,47	74	22	22	22	
200	209	10	LTIPQSLDSW	1180	B*5802	90	1,47	133	22	22	22	
200	209	10	LTIPQSLDSW	22	A*2501	40	1,47	59	22	22	22	
197	210	14	TRILTIPQSLDSWW	1181	B*4402	20	0,79	16	22	22	22	
197	210	14	TRILTIPQSLDSWW	22	B*4403	15	0,79	12	22	22	22	
198	210	13	RILTIPQSLDSWW	1182	B*5801	60	0,79	47	22	22	22	
198	210	13	RILTIPQSLDSWW	22	B*5701	40	0,79	31	22	22	22	
200	210	11	LTIPQSLDSWW	1183	B*5802	75	0,79	59	22	22	22	
200	210	11	LTIPQSLDSWW	22	B*5801	40	0,79	31	22	22	22	
202	210	9	IPQSLDSWW	1184	B*5301	50	0,79	39	22	22	22	
						Cumulative Class I-BCI score:						
						6882						

239	246	8	CPPICPGY	1185	B*3501	45	1,44	65	31	239	274
239	248	10	CPPICPGYRW	1186	B*5301	85	1,94	165	22	22	22
240	251	12	PPICPGYRWML	1187	B*3503	50	1,46	73	22	22	22
243	251	9	CPGYRWML	1188	B*0801	75	1,46	110	22	22	22
243	251	9	CPGYRWML	22	B*1402	50	1,46	73	22	22	22
243	252	10	CPGYRWMLR	1189	A*3303	5	1,04	5	22	22	22
244	252	9	PGYRWMLR	1190	A*3101	5	1,04	5	22	22	22
245	252	8	GYRWMLR	1191	A*3101	95	1,04	99	22	22	22
245	252	8	GYRWMLR	22	A*3303	10	1,04	10	22	22	22
245	253	9	GYRWMLRR	1192	A*3101	45	0,95	43	22	22	22
245	254	10	GYRWMLRRF	1193	A*2402	10	1,01	10	22	22	22

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
246	254	9	YRWMCLRRF	1194	B*2702	40	1,01	41	55	55	55		
246	254	9	YRWMCLRRF	55	B*2705	40	1,01	41	55	55	55		
245	255	11	GYRWMCLRRFI	1195	A*3001	35	0,99	35	55	55	55		
246	255	10	YRWMCLRRFI	1196	B*1402	90	0,99	89	55	55	55		
246	255	10	YRWMCLRRFI	55	B*2702	85	0,99	84	55	55	55		
246	255	10	YRWMCLRRFI	55	B*2705	20	0,99	20	55	55	55		
243	256	14	CPGYRWMCLRRFII	1197	B*0801	65	0,86	56	55	55	55		
243	256	14	CPGYRWMCLRRFII	55	B*5101	25	0,86	21	55	55	55		
246	256	11	YRWMCLRRFII	1198	B*2702	100	0,86	86	55	55	55		
246	256	11	YRWMCLRRFII	55	B*1402	75	0,86	64	55	55	55		
246	256	11	YRWMCLRRFII	55	B*2705	65	0,86	56	55	55	55		
246	256	11	YRWMCLRRFII	55	B*3801	60	0,86	51	55	55	55		
247	256	10	RWMCLRRFII	1199	A*2402	55	0,86	47	55	55	55		
247	256	10	RWMCLRRFII	55	A*2301	35	0,86	30	55	55	55		
245	257	13	GYRWMCLRRFIIF	1200	A*2301	85	1,08	92	55	55	55		
246	257	12	YRWMCLRRFIIF	1201	B*1402	100	1,08	108	55	55	55		
246	257	12	YRWMCLRRFIIF	55	B*2702	75	1,08	81	55	55	55		
246	257	12	YRWMCLRRFIIF	55	B*2705	60	1,08	65	55	55	55		
247	257	11	RWMCLRRFIIF	1202	A*2402	50	1,08	54	55	55	55		
249	257	9	MCLRRFIIF	1203	B*0801	55	1,08	59	55	55	55		
245	258	14	GYRWMCLRRFIIFL	1204	A*3001	45	1,61	72	55	55	55		
246	258	13	YRWMCLRRFIIFL	1205	B*1402	95	1,61	153	55	55	55		
246	258	13	YRWMCLRRFIIFL	55	B*2705	85	1,61	137	55	55	55		
246	258	13	YRWMCLRRFIIFL	55	B*2702	60	1,61	96	55	55	55		
246	258	13	YRWMCLRRFIIFL	55	B*3801	20	1,61	32	55	55	55		
249	258	10	MCLRRFIIFL	1206	B*0801	15	1,61	24	55	55	55		
251	258	8	LRRFIIFL	1207	B*1402	60	1,61	96	55	55	55		
246	259	14	YRWMCLRRFIIFLF	1208	B*2702	55	1,73	95	55	55	55		
246	259	14	YRWMCLRRFIIFLF	55	B*2705	45	1,73	78	55	55	55		
246	259	14	YRWMCLRRFIIFLF	55	B*3801	40	1,73	69	55	55	55		
247	259	13	RWMCLRRFIIFLF	1209	A*2402	100	1,73	173	55	55	55		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
247	259	13	RMCLRRFIIFLF	..	A*2301	80	1,73	138	..	..	..		
249	259	11	MCLRRFIIFLF	1210	B*1801	50	1,73	86	..	..	..		
251	259	9	LRFIIFLF	1211	B*2705	25	1,73	43	..	..	..		
252	259	8	RFIIFLF	1212	B*2702	90	1,73	155	..	..	..		
252	259	8	RFIIFLF	..	B*2705	70	1,73	121	..	..	..		
252	259	8	RFIIFLF	..	B*3801	70	1,73	121	..	..	..		
247	260	14	RMCLRRFIIFLFI	1213	A*2402	65	1,60	104	..	..	..		
248	260	13	WMCLRRFIIFLFI	1214	B*0801	5	1,60	8	..	..	..		
249	260	12	MCLRRFIIFLFI	1215	B*0801	90	1,60	144	..	..	..		
250	260	11	CLRRFIIFLFI	1216	A*3001	60	1,60	96	..	..	..		
251	260	10	LRFIIFLFI	1217	B*1402	25	1,60	40	..	..	..		
252	260	9	RFIIFLFI	1218	B*2705	75	1,60	120	..	..	..		
252	260	9	RFIIFLFI	..	B*3801	50	1,60	80	..	..	..		
252	260	9	RFIIFLFI	..	B*2702	35	1,60	56	..	..	..		
248	261	14	WMCLRRFIIFLFIL	1219	B*0801	20	1,79	36	..	..	..		
249	261	13	MCLRRFIIFLFIL	1220	B*0801	70	1,79	126	..	..	..		
250	261	12	CLRRFIIFLFIL	1221	B*0801	25	1,79	45	..	..	..		
251	261	11	LRFIIFLFIL	1222	B*1402	35	1,79	63	..	..	..		
252	261	10	RFIIFLFIL	1223	B*2705	100	1,79	179	..	..	..		
252	261	10	RFIIFLFIL	..	B*3801	85	1,79	152	..	..	..		
252	261	10	RFIIFLFIL	..	B*2702	80	1,79	144	..	..	..		
252	261	10	RFIIFLFIL	..	B*4801	50	1,79	90	..	..	..		
252	261	10	RFIIFLFIL	..	B*4001	10	1,79	18	..	..	..		
252	261	10	RFIIFLFIL	..	B*4002	5	1,79	9	..	..	..		
253	261	9	RFIIFLFIL	1224	B*4001	15	1,79	27	..	..	..		
254	261	8	FIIFLFIL	1225	A*2501	10	1,79	18	..	..	..		
249	262	14	MCLRRFIIFLFILL	1226	B*0801	60	1,50	90	..	..	..		
250	262	13	CLRRFIIFLFILL	1227	A*3001	5	1,50	7	..	..	..		
251	262	12	LRRFIIFLFILL	1228	B*2705	35	1,50	52	..	..	..		
251	262	12	LRRFIIFLFILL	..	B*1402	5	1,50	7	..	..	..		
252	262	11	RFIIFLFILL	1229	B*2702	95	1,50	142	..	..	..		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
252	262	11	RRFIIFLFILL	„	B*2705	95	1,50	142	„	„	„		
252	262	11	RRFIIFLFILL	„	B*3801	80	1,50	120	„	„	„		
252	262	11	RRFIIFLFILL	„	B*4002	60	1,50	90	„	„	„		
252	262	11	RRFIIFLFILL	„	B*4801	45	1,50	67	„	„	„		
253	262	10	RFIIFLFILL	1230	B*4001	20	1,50	30	„	„	„		
254	262	9	FIIFLFILL	1231	A*6802	60	1,50	90	„	„	„		
254	262	9	FIIFLFILL	„	A*2601	30	1,50	45	„	„	„		
251	263	13	LRRFIIFLFILL	1232	B*2705	50	1,90	95	„	„	„		
252	263	12	RRFIIFLFILL	1233	B*2705	90	1,90	171	„	„	„		
252	263	12	RRFIIFLFILL	„	B*3801	90	1,90	171	„	„	„		
252	263	12	RRFIIFLFILL	„	B*2702	70	1,90	133	„	„	„		
252	263	12	RRFIIFLFILL	„	B*4002	40	1,90	76	„	„	„		
252	263	12	RRFIIFLFILL	„	B*4801	5	1,90	10	„	„	„		
254	263	10	FIIFLFILL	1234	A*2601	65	1,90	124	„	„	„		
252	264	13	RRFIIFLFILLCL	1235	B*2705	30	0,75	22	„	„	„		
252	265	14	RRFIIFLFILLCL	1236	B*2705	80	1,60	128	„	„	„		
252	265	14	RRFIIFLFILLCL	„	B*2702	50	1,60	80	„	„	„		
252	265	14	RRFIIFLFILLCL	„	B*4002	25	1,60	40	„	„	„		
252	265	14	RRFIIFLFILLCL	„	B*3801	10	1,60	16	„	„	„		
257	265	9	FLFILLCL	1237	A*0201	60	1,60	96	„	„	„		
254	266	13	FIIFLFILLCLLI	1238	A*6802	40	0,76	30	„	„	„		
257	266	10	FLFILLCLLI	1239	A*0201	31	0,76	24	„	„	„		
257	266	10	FLFILLCLLI	„	B*5101	15	0,76	11	„	„	„		
254	267	14	FIIFLFILLCLLIF	1240	A*2501	80	1,24	99	„	„	„		
254	267	14	FIIFLFILLCLLIF	„	A*2601	70	1,24	86	„	„	„		
254	267	14	FIIFLFILLCLLIF	„	B*1501	50	1,24	62	„	„	„		
254	267	14	FIIFLFILLCLLIF	„	B*4601	35	1,24	43	„	„	„		
254	267	14	FIIFLFILLCLLIF	„	A*2902	20	1,24	25	„	„	„		
255	267	13	IIFLFILLCLLIF	1241	A*3201	20	1,24	25	„	„	„		
256	267	12	IFLFILLCLLIF	1242	A*2301	95	1,24	117	„	„	„		
256	267	12	IFLFILLCLLIF	„	A*2902	30	1,24	37	„	„	„		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
257	267	11	FLFILLCLIF	1243	B*4601	80	1,24	99	55	55	55		
257	267	11	FLFILLCLIF	55	B*1501	65	1,24	80	55	55	55		
257	267	11	FLFILLCLIF	55	B*1502	65	1,24	80	55	55	55		
258	267	10	LFILLCLIF	1244	A*2301	50	1,24	62	55	55	55		
256	268	13	IFLILLCLIFL	1245	A*2301	10	1,44	14	55	55	55		
257	268	12	FLFILLCLIFL	1246	A*0201	40	1,44	57	55	55	55		
259	268	10	FILLCLIFL	1247	A*0201	49	1,44	70	55	55	55		
259	268	10	FILLCLIFL	55	A*0206	5	1,44	7	55	55	55		
260	268	9	ILLCLIFL	1248	A*0201	71	1,44	103	55	55	55		
256	269	14	IFLILLCLIFLL	1249	A*2301	65	1,83	119	55	55	55		
257	269	13	FLFILLCLIFLL	1250	A*0201	23	1,83	42	55	55	55		
260	269	10	ILLCLIFLL	1251	A*0201	77	1,83	141	55	55	55		
261	269	9	LLCLIFLL	1252	A*0201	83	1,83	152	55	55	55		
259	270	12	FILLCLIFLLV	1253	A*0206	40	1,71	68	55	55	55		
260	270	11	ILLCLIFLLV	1254	A*0206	45	1,71	77	55	55	55		
261	270	10	LLCLIFLLV	1255	A*0206	65	1,71	111	55	55	55		
261	270	10	LLCLIFLLV	55	A*0201	54	1,71	93	55	55	55		
262	270	9	LLCLIFLLV	1256	A*0201	6	1,71	10	55	55	55		
261	271	11	LLCLIFLLVL	1257	A*0206	85	1,61	136	55	55	55		
261	274	14	LLCLIFLLVLLDY	1258	A*2902	80	1,83	147	55	55	55		
262	274	13	LLCLIFLLVLLDY	1259	A*2902	90	1,83	165	55	55	55		
262	274	13	LLCLIFLLVLLDY	55	A*0101	75	1,83	138	55	55	55		
264	274	11	CLIFLLVLLDY	1260	A*0101	85	1,83	156	55	55	55		
265	274	10	LIFLLVLLDY	1261	A*0101	55	1,83	101	55	55	55		
265	274	10	LIFLLVLLDY	55	A*0301	35	1,83	64	55	55	55		
266	274	9	IFLLVLLDY	1262	A*2902	70	1,83	128	55	55	55		
267	274	8	FLLVLLDY	1263	B*1502	60	1,83	110	55	55	55		
						Cumulative Class I-BCI score:							
								10214					

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
324	331	8	IPIPSSWA	1264	B*5601	85	0,15	13	32	323	358		
324	331	8	IPIPSSWA	"	B*5501	55	0,16	9	"	"	"		
324	332	9	IPIPSSWAF	1265	B*3501	70	1,87	131	"	"	"		
324	332	9	IPIPSSWAF	"	B*3503	55	1,87	103	"	"	"		
324	332	9	IPIPSSWAF	"	B*5301	45	1,87	84	"	"	"		
324	333	10	IPIPSSWAF	1266	B*5601	100	1,02	102	"	"	"		
324	333	10	IPIPSSWAF	"	B*5501	85	1,02	87	"	"	"		
326	333	8	IPSSWAF	1267	B*5601	45	1,02	46	"	"	"		
326	333	8	IPSSWAF	"	B*5501	40	1,02	41	"	"	"		
323	334	12	CIPIPSSWAF	1268	A*0301	80	1,04	83	"	"	"		
323	334	12	CIPIPSSWAF	"	A*1101	30	1,04	31	"	"	"		
324	334	11	IPIPSSWAF	1269	B*3501	15	1,04	16	"	"	"		
326	334	9	IPSSWAF	1270	A*1101	10	1,04	10	"	"	"		
327	334	8	PSSWAF	1271	A*0301	45	1,04	47	"	"	"		
324	335	12	IPIPSSWAF	1272	B*3503	85	1,90	161	"	"	"		
324	335	12	IPIPSSWAF	"	B*3501	80	1,90	152	"	"	"		
324	335	12	IPIPSSWAF	"	B*5301	25	1,90	47	"	"	"		
325	335	11	PIPSSWAF	1273	A*2501	30	1,90	57	"	"	"		
326	335	10	IPSSWAF	1274	B*3501	35	1,90	66	"	"	"		
327	335	9	PSSWAF	1275	A*0101	65	1,90	123	"	"	"		
327	335	9	PSSWAF	"	A*3002	45	1,90	85	"	"	"		
328	335	8	SSWAF	1276	A*2501	75	1,90	142	"	"	"		
328	335	8	SSWAF	"	A*3002	75	1,90	142	"	"	"		
328	335	8	SSWAF	"	A*2902	55	1,90	104	"	"	"		
324	336	13	IPIPSSWAF	1277	B*3503	80	1,06	85	"	"	"		
324	336	13	IPIPSSWAF	"	B*5101	65	1,06	69	"	"	"		
324	337	14	IPIPSSWAF	1278	B*5301	55	1,58	87	"	"	"		
324	337	14	IPIPSSWAF	"	B*5101	20	1,58	32	"	"	"		
324	337	14	IPIPSSWAF	"	B*5701	5	1,58	8	"	"	"		
326	337	12	IPSSWAF	1279	B*5301	100	1,58	158	"	"	"		
326	337	12	IPSSWAF	"	B*5802	10	1,58	16	"	"	"		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
328	337	10	SSWAFAKYLW	1280	B*5802	100	1,58	158	55	55	55		
328	337	10	SSWAFAKYLW	55	B*5701	95	1,58	150	55	55	55		
328	337	10	SSWAFAKYLW	55	B*4403	45	1,58	71	55	55	55		
328	337	10	SSWAFAKYLW	55	B*5801	35	1,58	55	55	55	55		
328	337	10	SSWAFAKYLW	55	B*4402	15	1,58	24	55	55	55		
330	337	8	WAFAKYLW	1281	B*5801	85	1,58	134	55	55	55		
330	337	8	WAFAKYLW	55	B*5701	65	1,58	103	55	55	55		
330	337	8	WAFAKYLW	55	B*5802	50	1,58	79	55	55	55		
326	339	14	IPSSWAFAKYLWEW	1282	B*5301	95	1,83	174	55	55	55		
328	339	12	SSWAFAKYLWEW	1283	B*5701	100	1,83	183	55	55	55		
328	339	12	SSWAFAKYLWEW	55	B*5801	95	1,83	174	55	55	55		
328	339	12	SSWAFAKYLWEW	55	B*5802	65	1,83	119	55	55	55		
328	339	12	SSWAFAKYLWEW	55	A*3201	55	1,83	101	55	55	55		
328	339	12	SSWAFAKYLWEW	55	B*4403	50	1,83	91	55	55	55		
328	339	12	SSWAFAKYLWEW	55	B*4402	10	1,83	18	55	55	55		
330	339	10	WAFAKYLWEW	1284	B*5802	85	1,83	156	55	55	55		
330	339	10	WAFAKYLWEW	55	B*5201	70	1,83	128	55	55	55		
331	339	9	AFAKYLWEW	1285	B*4402	50	1,83	91	55	55	55		
331	339	9	AFAKYLWEW	55	B*4403	40	1,83	73	55	55	55		
332	339	8	FAKYLWEW	1286	B*4601	40	1,83	73	55	55	55		
332	339	8	FAKYLWEW	55	B*5701	30	1,83	55	55	55	55		
330	342	13	WAFAKYLWEWASV	1287	A*6802	85	1,92	164	55	55	55		
330	342	13	WAFAKYLWEWASV	55	B*1402	20	1,92	38	55	55	55		
332	342	11	FAKYLWEWASV	1288	B*4601	50	1,92	96	55	55	55		
330	343	14	WAFAKYLWEWASVR	1289	A*3303	80	1,07	85	55	55	55		
330	343	14	WAFAKYLWEWASVR	55	A*6801	50	1,07	53	55	55	55		
330	343	14	WAFAKYLWEWASVR	55	A*7401	15	1,07	16	55	55	55		
331	343	13	AFAKYLWEWASVR	1290	A*3101	70	1,07	75	55	55	55		
331	343	13	AFAKYLWEWASVR	55	A*3303	35	1,07	37	55	55	55		
332	343	12	FAKYLWEWASVR	1291	A*3303	85	1,07	91	55	55	55		
332	343	12	FAKYLWEWASVR	55	A*6801	60	1,07	64	55	55	55		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
332	343	12	FAKYLWEWASVR	..	A*3101	55	1,07	59	..	..	..		
334	343	10	KYLWEWASVR	1292	A*3101	100	1,07	107	..	..	..		
335	343	9	YLWEWASVR	1293	A*7401	85	1,07	91	..	..	..		
335	343	9	YLWEWASVR	..	A*3303	40	1,07	43	..	..	..		
335	343	9	YLWEWASVR	..	A*3101	35	1,07	37	..	..	..		
335	343	9	YLWEWASVR	..	A*0301	20	1,07	21	..	..	..		
331	344	14	FAKYLWEWASVRF	1294	A*2402	30	1,86	56	..	..	..		
331	344	14	FAKYLWEWASVRF	..	A*2301	5	1,86	9	..	..	..		
332	344	13	FAKYLWEWASVRF	1295	B*4601	75	1,86	139	..	..	..		
335	344	10	YLWEWASVRF	1296	B*1502	90	1,86	167	..	..	..		
335	344	10	YLWEWASVRF	..	B*1525	45	1,86	84	..	..	..		
337	344	8	WEWASVRF	1297	B*3701	80	1,86	149	..	..	..		
337	344	8	WEWASVRF	..	B*4901	80	1,86	149	..	..	..		
337	344	8	WEWASVRF	..	B*5001	50	1,86	93	..	..	..		
337	344	8	WEWASVRF	..	B*1301	45	1,86	84	..	..	..		
337	344	8	WEWASVRF	..	B*4403	5	1,86	9	..	..	..		
337	345	9	WEWASVRFS	1298	B*4403	65	0,50	33	..	..	..		
337	345	9	WEWASVRFS	..	B*5001	60	0,50	30	..	..	..		
337	345	9	WEWASVRFS	..	B*4002	55	0,50	28	..	..	..		
337	345	9	WEWASVRFS	..	B*4901	15	0,50	8	..	..	..		
333	346	14	AKYLWEWASVRFSW	1299	B*4403	35	1,50	52	..	..	..		
334	346	13	KYLWEWASVRFSW	1300	A*2402	95	1,50	142	..	..	..		
334	346	13	KYLWEWASVRFSW	..	A*2301	75	1,50	112	..	..	..		
335	346	12	YLWEWASVRFSW	1301	A*3201	80	1,50	120	..	..	..		
335	346	12	YLWEWASVRFSW	..	B*1302	75	1,50	112	..	..	..		
335	346	12	YLWEWASVRFSW	..	B*5201	45	1,50	67	..	..	..		
337	346	10	WEWASVRFSW	1302	B*1301	100	1,50	150	..	..	..		
337	346	10	WEWASVRFSW	..	B*4402	100	1,50	150	..	..	..		
337	346	10	WEWASVRFSW	..	B*4403	100	1,50	150	..	..	..		
337	346	10	WEWASVRFSW	..	B*1302	90	1,50	135	..	..	..		
337	346	10	WEWASVRFSW	..	B*4002	90	1,50	135	..	..	..		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
337	346	10	WEWASVRFWS	..	B*4901	75	1,50	112	..	..	..		
339	346	8	WASVRFWS	1303	B*5801	50	1,50	75	..	..	..		
334	347	14	KYLWEWASVRFWSL	1304	A*2402	90	1,37	123	..	..	..		
334	347	14	KYLWEWASVRFWSL	..	A*2301	40	1,37	55	..	..	..		
335	347	13	YLWEWASVRFWSL	1305	A*0201	100	1,37	137	..	..	..		
335	347	13	YLWEWASVRFWSL	..	A*0206	60	1,37	82	..	..	..		
337	347	11	WEWASVRFWSL	1306	B*4001	95	1,37	130	..	..	..		
337	347	11	WEWASVRFWSL	..	B*3701	90	1,37	123	..	..	..		
337	347	11	WEWASVRFWSL	..	B*5001	90	1,37	123	..	..	..		
337	347	11	WEWASVRFWSL	..	B*4002	85	1,37	117	..	..	..		
337	347	11	WEWASVRFWSL	..	B*4901	85	1,37	117	..	..	..		
337	347	11	WEWASVRFWSL	..	B*1301	80	1,37	110	..	..	..		
337	347	11	WEWASVRFWSL	..	B*4402	55	1,37	75	..	..	..		
337	347	11	WEWASVRFWSL	..	B*1302	10	1,37	14	..	..	..		
339	347	9	WASVRFWSL	1307	B*0801	50	1,37	69	..	..	..		
337	348	12	WEWASVRFWSLS	1308	B*1801	80	0,54	43	..	..	..		
337	348	12	WEWASVRFWSLS	..	B*4002	70	0,54	38	..	..	..		
337	348	12	WEWASVRFWSLS	..	B*4901	45	0,54	24	..	..	..		
337	348	12	WEWASVRFWSLS	..	B*5001	45	0,54	24	..	..	..		
337	348	12	WEWASVRFWSLS	..	B*4403	20	0,54	11	..	..	..		
337	348	12	WEWASVRFWSLS	..	B*3701	5	0,54	3	..	..	..		
341	348	8	SVRFWSLS	1309	A*3001	40	0,54	22	..	..	..		
337	349	13	WEWASVRFWSLSL	1310	B*1801	100	1,61	161	..	..	..		
337	349	13	WEWASVRFWSLSL	..	B*3701	100	1,61	161	..	..	..		
337	349	13	WEWASVRFWSLSL	..	B*4001	100	1,61	161	..	..	..		
337	349	13	WEWASVRFWSLSL	..	B*4002	100	1,61	161	..	..	..		
337	349	13	WEWASVRFWSLSL	..	B*4901	100	1,61	161	..	..	..		
337	349	13	WEWASVRFWSLSL	..	B*5001	100	1,61	161	..	..	..		
337	349	13	WEWASVRFWSLSL	..	B*1301	90	1,61	145	..	..	..		
337	349	13	WEWASVRFWSLSL	..	B*4403	75	1,61	120	..	..	..		
337	349	13	WEWASVRFWSLSL	..	B*4402	70	1,61	112	..	..	..		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
339	349	11	WASVRFWSLSL	1311	B*1402	85	1,61	137	55	55	55		
341	349	9	SVRFWSLSL	1312	A*3001	90	1,61	145	55	55	55		
341	349	9	SVRFWSLSL	55	B*0702	80	1,61	129	55	55	55		
342	349	8	VRFWSLSL	1313	B*3901	70	1,61	112	55	55	55		
337	350	14	WEWASVRFWSLSLL	1314	B*3701	95	1,15	109	55	55	55		
337	350	14	WEWASVRFWSLSLL	55	B*4002	95	1,15	109	55	55	55		
337	350	14	WEWASVRFWSLSLL	55	B*5001	95	1,15	109	55	55	55		
337	350	14	WEWASVRFWSLSLL	55	B*1801	90	1,15	104	55	55	55		
337	350	14	WEWASVRFWSLSLL	55	B*4901	90	1,15	104	55	55	55		
337	350	14	WEWASVRFWSLSLL	55	B*1301	85	1,15	98	55	55	55		
337	350	14	WEWASVRFWSLSLL	55	B*4001	80	1,15	92	55	55	55		
337	350	14	WEWASVRFWSLSLL	55	B*4403	70	1,15	81	55	55	55		
337	350	14	WEWASVRFWSLSLL	55	B*4801	70	1,15	81	55	55	55		
337	350	14	WEWASVRFWSLSLL	55	B*4402	60	1,15	69	55	55	55		
337	350	14	WEWASVRFWSLSLL	55	B*1302	50	1,15	58	55	55	55		
342	350	9	VRFWSLSL	1315	B*3801	65	1,15	75	55	55	55		
342	350	9	VRFWSLSL	55	B*2702	20	1,15	23	55	55	55		
339	351	13	WASVRFWSLSLLV	1316	B*5101	30	1,47	44	55	55	55		
341	351	11	SVRFWSLSLLV	1317	A*3001	85	1,47	125	55	55	55		
340	353	14	ASVRFWSLSLLVPF	1318	B*4601	30	0,19	6	55	55	55		
340	353	14	ASVRFWSLSLLVPF	55	B*1525	15	0,19	3	55	55	55		
341	353	13	SVRFWSLSLLVPF	1319	B*1501	80	0,19	15	55	55	55		
341	353	13	SVRFWSLSLLVPF	55	B*1525	60	0,19	11	55	55	55		
341	353	13	SVRFWSLSLLVPF	55	B*1502	25	0,19	5	55	55	55		
341	353	13	SVRFWSLSLLVPF	55	A*3001	20	0,19	4	55	55	55		
342	353	12	VRFWSLSLLVPF	1320	B*2702	65	0,19	12	55	55	55		
342	353	12	VRFWSLSLLVPF	55	B*2705	55	0,19	10	55	55	55		
343	353	11	RFSWLSLLVPF	1321	A*3201	85	0,19	16	55	55	55		
343	353	11	RFSWLSLLVPF	55	A*2402	80	0,19	15	55	55	55		
344	353	10	FSWLSLLVPF	1322	B*4601	100	0,19	19	55	55	55		
344	353	10	FSWLSLLVPF	55	B*1525	55	0,19	10	55	55	55		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
346	353	8	WLSLLVPF	1323	B*1502	10	0,19	2	55	55	55	
341	354	14	SVRFWSLSLLVPFV	1324	A*3001	95	1,30	124	55	55	55	
342	354	13	VRFSWLSLLVPFV	1325	B*2705	15	1,30	20	55	55	55	
346	354	9	WLSLLVPFV	1326	A*0201	94	1,30	123	55	55	55	
343	356	14	RFWSLSLLVPFVQW	1327	A*2402	25	1,92	48	55	55	55	
344	356	13	FSWLSLLVPFVQW	1328	B*5801	90	1,92	173	55	55	55	
344	356	13	FSWLSLLVPFVQW	55	B*5701	85	1,92	163	55	55	55	
344	356	13	FSWLSLLVPFVQW	55	B*5802	60	1,92	115	55	55	55	
344	356	13	FSWLSLLVPFVQW	55	B*5201	40	1,92	77	55	55	55	
347	356	10	LSLLVPFVQW	1329	B*5802	80	1,92	154	55	55	55	
344	357	14	FSWLSLLVPFVQWF	1330	B*4601	65	1,38	89	55	55	55	
345	357	13	SWLSLLVPFVQWF	1331	A*2301	45	1,38	62	55	55	55	
345	357	13	SWLSLLVPFVQWF	55	A*2402	35	1,38	48	55	55	55	
347	357	11	LSLLVPFVQWF	1332	B*5802	20	1,38	28	55	55	55	
348	357	10	SLLVPFVQWF	1333	B*1502	50	1,38	69	55	55	55	
349	357	9	LLVPFVQWF	1334	B*1501	45	1,38	62	55	55	55	
349	357	9	LLVPFVQWF	55	B*1525	10	1,38	14	55	55	55	
346	358	13	WLSLLVPFVQWFV	1335	A*0201	80	1,65	132	55	55	55	
346	358	13	WLSLLVPFVQWFV	55	A*0206	25	1,65	41	55	55	55	
349	358	10	LLVPFVQWFV	1336	A*0201	97	1,65	161	55	55	55	
349	358	10	LLVPFVQWFV	55	A*0206	90	1,65	149	55	55	55	
350	358	9	LVPFVQWFV	1337	A*6802	100	1,65	165	55	55	55	
350	358	9	LVPFVQWFV	55	A*0201	43	1,65	71	55	55	55	
						Cumulative Class I-BCI score:						
								14976				

327	334	8	PSSWAFAK	1271	A*0301	45	1,04	47	33	327	358
327	335	9	PSSWAFAKY	1275	A*0101	65	1,90	123	55	55	55
327	335	9	PSSWAFAKY	55	A*3002	45	1,90	85	55	55	55
328	335	8	SSWAFAKY	1276	A*2501	75	1,90	142	55	55	55

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
328	335	8	SSWAFAKY	“	A*3002	75	1,90	142	“	“	“		
328	335	8	SSWAFAKY	“	A*2902	55	1,90	104	“	“	“		
328	337	10	SSWAFAKYLW	1280	B*5802	100	1,58	158	“	“	“		
328	337	10	SSWAFAKYLW	“	B*5701	95	1,58	150	“	“	“		
328	337	10	SSWAFAKYLW	“	B*4403	45	1,58	71	“	“	“		
328	337	10	SSWAFAKYLW	“	B*5801	35	1,58	55	“	“	“		
328	337	10	SSWAFAKYLW	“	B*4402	15	1,58	24	“	“	“		
330	337	8	WAFAKYLW	1281	B*5801	85	1,58	134	“	“	“		
330	337	8	WAFAKYLW	“	B*5701	65	1,58	103	“	“	“		
330	337	8	WAFAKYLW	“	B*5802	50	1,58	79	“	“	“		
328	339	12	SSWAFAKYLWEW	1283	B*5701	100	1,83	183	“	“	“		
328	339	12	SSWAFAKYLWEW	“	B*5801	95	1,83	174	“	“	“		
328	339	12	SSWAFAKYLWEW	“	B*5802	65	1,83	119	“	“	“		
328	339	12	SSWAFAKYLWEW	“	A*3201	55	1,83	101	“	“	“		
328	339	12	SSWAFAKYLWEW	“	B*4403	50	1,83	91	“	“	“		
328	339	12	SSWAFAKYLWEW	“	B*4402	10	1,83	18	“	“	“		
330	339	10	WAFAKYLWEW	1284	B*5802	85	1,83	156	“	“	“		
330	339	10	WAFAKYLWEW	“	B*5201	70	1,83	128	“	“	“		
331	339	9	AFAKYLWEW	1285	B*4402	50	1,83	91	“	“	“		
331	339	9	AFAKYLWEW	“	B*4403	40	1,83	73	“	“	“		
332	339	8	FAKYLWEW	1286	B*4601	40	1,83	73	“	“	“		
332	339	8	FAKYLWEW	“	B*5701	30	1,83	55	“	“	“		
330	342	13	WAFAKYLWEWASV	1287	A*6802	85	1,92	164	“	“	“		
330	342	13	WAFAKYLWEWASV	“	B*1402	20	1,92	38	“	“	“		
332	342	11	FAKYLWEWASV	1288	B*4601	50	1,92	96	“	“	“		
330	343	14	WAFAKYLWEWASVR	1289	A*3303	80	1,07	85	“	“	“		
330	343	14	WAFAKYLWEWASVR	“	A*6801	50	1,07	53	“	“	“		
330	343	14	WAFAKYLWEWASVR	“	A*7401	15	1,07	16	“	“	“		
331	343	13	AFAKYLWEWASVR	1290	A*3101	70	1,07	75	“	“	“		
331	343	13	AFAKYLWEWASVR	“	A*3303	35	1,07	37	“	“	“		
332	343	12	FAKYLWEWASVR	1291	A*3303	85	1,07	91	“	“	“		
332	343	12	FAKYLWEWASVR	“	A*6801	60	1,07	64	“	“	“		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
332	343	12	FAKYLWEWASVR	..	A*3101	55	1,07	59	..	..	..		
334	343	10	KYLWEWASVR	1292	A*3101	100	1,07	107	..	..	..		
335	343	9	YLWEWASVR	1293	A*7401	85	1,07	91	..	..	..		
335	343	9	YLWEWASVR	..	A*3303	40	1,07	43	..	..	..		
335	343	9	YLWEWASVR	..	A*3101	35	1,07	37	..	..	..		
335	343	9	YLWEWASVR	..	A*0301	20	1,07	21	..	..	..		
331	344	14	AFAKYLWEWASVRF	1294	A*2402	30	1,86	56	..	..	..		
331	344	14	AFAKYLWEWASVRF	..	A*2301	5	1,86	9	..	..	..		
332	344	13	FAKYLWEWASVRF	1295	B*4601	75	1,86	139	..	..	..		
335	344	10	YLWEWASVRF	1296	B*1502	90	1,86	167	..	..	..		
335	344	10	YLWEWASVRF	..	B*1525	45	1,86	84	..	..	..		
337	344	8	WEWASVRF	1297	B*3701	80	1,86	149	..	..	..		
337	344	8	WEWASVRF	..	B*4901	80	1,86	149	..	..	..		
337	344	8	WEWASVRF	..	B*5001	50	1,86	93	..	..	..		
337	344	8	WEWASVRF	..	B*1301	45	1,86	84	..	..	..		
337	344	8	WEWASVRF	..	B*4403	5	1,86	9	..	..	..		
337	345	9	WEWASVRFS	1298	B*4403	65	0,50	33	..	..	..		
337	345	9	WEWASVRFS	..	B*5001	60	0,50	30	..	..	..		
337	345	9	WEWASVRFS	..	B*4002	55	0,50	28	..	..	..		
337	345	9	WEWASVRFS	..	B*4901	15	0,50	8	..	..	..		
333	346	14	AKYLWEWASVRFSW	1299	B*4403	35	1,50	52	..	..	..		
334	346	13	KYLWEWASVRFSW	1300	A*2402	95	1,50	142	..	..	..		
334	346	13	KYLWEWASVRFSW	..	A*2301	75	1,50	112	..	..	..		
335	346	12	YLWEWASVRFSW	1301	A*3201	80	1,50	120	..	..	..		
335	346	12	YLWEWASVRFSW	..	B*1302	75	1,50	112	..	..	..		
335	346	12	YLWEWASVRFSW	..	B*5201	45	1,50	67	..	..	..		
337	346	10	WEWASVRFSW	1302	B*1301	100	1,50	150	..	..	..		
337	346	10	WEWASVRFSW	..	B*4402	100	1,50	150	..	..	..		
337	346	10	WEWASVRFSW	..	B*4403	100	1,50	150	..	..	..		
337	346	10	WEWASVRFSW	..	B*1302	90	1,50	135	..	..	..		
337	346	10	WEWASVRFSW	..	B*4002	90	1,50	135	..	..	..		
337	346	10	WEWASVRFSW	..	B*4901	75	1,50	112	..	..	..		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
339	346	8	WASVRFSW	1303	B*5801	50	1,50	75	55	55	55		
334	347	14	KYLWEWASVRFSL	1304	A*2402	90	1,37	123	55	55	55		
334	347	14	KYLWEWASVRFSL	55	A*2301	40	1,37	55	55	55	55		
335	347	13	YLWEWASVRFSL	1305	A*0201	100	1,37	137	55	55	55		
335	347	13	YLWEWASVRFSL	55	A*0206	60	1,37	82	55	55	55		
337	347	11	WEWASVRFSL	1306	B*4001	95	1,37	130	55	55	55		
337	347	11	WEWASVRFSL	55	B*3701	90	1,37	123	55	55	55		
337	347	11	WEWASVRFSL	55	B*5001	90	1,37	123	55	55	55		
337	347	11	WEWASVRFSL	55	B*4002	85	1,37	117	55	55	55		
337	347	11	WEWASVRFSL	55	B*4901	85	1,37	117	55	55	55		
337	347	11	WEWASVRFSL	55	B*1301	80	1,37	110	55	55	55		
337	347	11	WEWASVRFSL	55	B*4402	55	1,37	75	55	55	55		
337	347	11	WEWASVRFSL	55	B*1302	10	1,37	14	55	55	55		
339	347	9	WASVRFSL	1307	B*0801	50	1,37	69	55	55	55		
337	348	12	WEWASVRFSL	1308	B*1801	80	0,54	43	55	55	55		
337	348	12	WEWASVRFSL	55	B*4002	70	0,54	38	55	55	55		
337	348	12	WEWASVRFSL	55	B*4901	45	0,54	24	55	55	55		
337	348	12	WEWASVRFSL	55	B*5001	45	0,54	24	55	55	55		
337	348	12	WEWASVRFSL	55	B*4403	20	0,54	11	55	55	55		
337	348	12	WEWASVRFSL	55	B*3701	5	0,54	3	55	55	55		
341	348	8	SVRFSL	1309	A*3001	40	0,54	22	55	55	55		
337	349	13	WEWASVRFSL	1310	B*1801	100	1,61	161	55	55	55		
337	349	13	WEWASVRFSL	55	B*3701	100	1,61	161	55	55	55		
337	349	13	WEWASVRFSL	55	B*4001	100	1,61	161	55	55	55		
337	349	13	WEWASVRFSL	55	B*4002	100	1,61	161	55	55	55		
337	349	13	WEWASVRFSL	55	B*4901	100	1,61	161	55	55	55		
337	349	13	WEWASVRFSL	55	B*5001	100	1,61	161	55	55	55		
337	349	13	WEWASVRFSL	55	B*1301	90	1,61	145	55	55	55		
337	349	13	WEWASVRFSL	55	B*4403	75	1,61	120	55	55	55		
337	349	13	WEWASVRFSL	55	B*4402	70	1,61	112	55	55	55		
339	349	11	WASVRFSL	1311	B*1402	85	1,61	137	55	55	55		
341	349	9	SVRFSL	1312	A*3001	90	1,61	145	55	55	55		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
341	349	9	SVRFWSLSL	“	B*0702	80	1,61	129	“	“	“		
342	349	8	VRFSWLSL	1313	B*3901	70	1,61	112	“	“	“		
337	350	14	WEWASVRFWSLSLL	1314	B*3701	95	1,15	109	“	“	“		
337	350	14	WEWASVRFWSLSLL	“	B*4002	95	1,15	109	“	“	“		
337	350	14	WEWASVRFWSLSLL	“	B*5001	95	1,15	109	“	“	“		
337	350	14	WEWASVRFWSLSLL	“	B*1801	90	1,15	104	“	“	“		
337	350	14	WEWASVRFWSLSLL	“	B*4901	90	1,15	104	“	“	“		
337	350	14	WEWASVRFWSLSLL	“	B*1301	85	1,15	98	“	“	“		
337	350	14	WEWASVRFWSLSLL	“	B*4001	80	1,15	92	“	“	“		
337	350	14	WEWASVRFWSLSLL	“	B*4403	70	1,15	81	“	“	“		
337	350	14	WEWASVRFWSLSLL	“	B*4801	70	1,15	81	“	“	“		
337	350	14	WEWASVRFWSLSLL	“	B*4402	60	1,15	69	“	“	“		
337	350	14	WEWASVRFWSLSLL	“	B*1302	50	1,15	58	“	“	“		
342	350	9	VRFSWLSLL	1315	B*3801	65	1,15	75	“	“	“		
342	350	9	VRFSWLSLL	“	B*2702	20	1,15	23	“	“	“		
339	351	13	WASVRFWSLSLLV	1316	B*5101	30	1,47	44	“	“	“		
341	351	11	SVRFWSLSLLV	1317	A*3001	85	1,47	125	“	“	“		
340	353	14	ASVRFWSLSLLVPF	1318	B*4601	30	0,19	6	“	“	“		
340	353	14	ASVRFWSLSLLVPF	“	B*1525	15	0,19	3	“	“	“		
341	353	13	SVRFWSLSLLVPF	1319	B*1501	80	0,19	15	“	“	“		
341	353	13	SVRFWSLSLLVPF	“	B*1525	60	0,19	11	“	“	“		
341	353	13	SVRFWSLSLLVPF	“	B*1502	25	0,19	5	“	“	“		
341	353	13	SVRFWSLSLLVPF	“	A*3001	20	0,19	4	“	“	“		
342	353	12	VRFSWLSLLVPF	1320	B*2702	65	0,19	12	“	“	“		
342	353	12	VRFSWLSLLVPF	“	B*2705	55	0,19	10	“	“	“		
343	353	11	RFWSLSLLVPF	1321	A*3201	85	0,19	16	“	“	“		
343	353	11	RFWSLSLLVPF	“	A*2402	80	0,19	15	“	“	“		
344	353	10	FSWLSLLVPF	1322	B*4601	100	0,19	19	“	“	“		
344	353	10	FSWLSLLVPF	“	B*1525	55	0,19	10	“	“	“		
346	353	8	WLSLLVPF	1323	B*1502	10	0,19	2	“	“	“		
341	354	14	SVRFWSLSLLVPFV	1324	A*3001	95	1,30	124	“	“	“		
342	354	13	VRFSWLSLLVPFV	1325	B*2705	15	1,30	20	“	“	“		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
346	354	9	WLSLLVPFV	1326	A*0201	94	1,30	123	55	55	55		
343	356	14	RFSWLSLLVPFVQW	1327	A*2402	25	1,92	48	55	55	55		
344	356	13	FSWLSLLVPFVQW	1328	B*5801	90	1,92	173	55	55	55		
344	356	13	FSWLSLLVPFVQW	55	B*5701	85	1,92	163	55	55	55		
344	356	13	FSWLSLLVPFVQW	55	B*5802	60	1,92	115	55	55	55		
344	356	13	FSWLSLLVPFVQW	55	B*5201	40	1,92	77	55	55	55		
347	356	10	LSLLVPFVQW	1329	B*5802	80	1,92	154	55	55	55		
344	357	14	FSWLSLLVPFVQWF	1330	B*4601	65	1,38	89	55	55	55		
345	357	13	SWLSLLVPFVQWF	1331	A*2301	45	1,38	62	55	55	55		
345	357	13	SWLSLLVPFVQWF	55	A*2402	35	1,38	48	55	55	55		
347	357	11	LSLLVPFVQWF	1332	B*5802	20	1,38	28	55	55	55		
348	357	10	SLLVPFVQWF	1333	B*1502	50	1,38	69	55	55	55		
349	357	9	LLVPFVQWF	1334	B*1501	45	1,38	62	55	55	55		
349	357	9	LLVPFVQWF	55	B*1525	10	1,38	14	55	55	55		
346	358	13	WLSLLVPFVQWFV	1335	A*0201	80	1,65	132	55	55	55		
346	358	13	WLSLLVPFVQWFV	55	A*0206	25	1,65	41	55	55	55		
349	358	10	LLVPFVQWFV	1336	A*0201	97	1,65	161	55	55	55		
349	358	10	LLVPFVQWFV	55	A*0206	90	1,65	149	55	55	55		
350	358	9	LVPFVQWFV	1337	A*6802	100	1,65	165	55	55	55		
350	358	9	LVPFVQWFV	55	A*0201	43	1,65	71	55	55	55		
						Cumulative Class I-BCI score:							
						13107							

328	335	8	SSWAFAKY	1276	A*2501	75	1,90	142	34	328	358
328	335	8	SSWAFAKY	55	A*3002	75	1,90	142	55	55	55
328	335	8	SSWAFAKY	55	A*2902	55	1,90	104	55	55	55
328	337	10	SSWAFAKYLV	1280	B*5802	100	1,58	158	55	55	55
328	337	10	SSWAFAKYLV	55	B*5701	95	1,58	150	55	55	55
328	337	10	SSWAFAKYLV	55	B*4403	45	1,58	71	55	55	55
328	337	10	SSWAFAKYLV	55	B*5801	35	1,58	55	55	55	55
328	337	10	SSWAFAKYLV	55	B*4402	15	1,58	24	55	55	55

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
330	337	8	WAFACYLW	1281	B*5801	85	1,58	134	55	55	55		
330	337	8	WAFACYLW	55	B*5701	65	1,58	103	55	55	55		
330	337	8	WAFACYLW	55	B*5802	50	1,58	79	55	55	55		
328	339	12	SSWAFACYLW	1283	B*5701	100	1,83	183	55	55	55		
328	339	12	SSWAFACYLW	55	B*5801	95	1,83	174	55	55	55		
328	339	12	SSWAFACYLW	55	B*5802	65	1,83	119	55	55	55		
328	339	12	SSWAFACYLW	55	A*3201	55	1,83	101	55	55	55		
328	339	12	SSWAFACYLW	55	B*4403	50	1,83	91	55	55	55		
328	339	12	SSWAFACYLW	55	B*4402	10	1,83	18	55	55	55		
330	339	10	WAFACYLW	1284	B*5802	85	1,83	156	55	55	55		
330	339	10	WAFACYLW	55	B*5201	70	1,83	128	55	55	55		
331	339	9	AFACYLW	1285	B*4402	50	1,83	91	55	55	55		
331	339	9	AFACYLW	55	B*4403	40	1,83	73	55	55	55		
332	339	8	FACYLW	1286	B*4601	40	1,83	73	55	55	55		
332	339	8	FACYLW	55	B*5701	30	1,83	55	55	55	55		
330	342	13	WAFACYLW	1287	A*6802	85	1,92	164	55	55	55		
330	342	13	WAFACYLW	55	B*1402	20	1,92	38	55	55	55		
332	342	11	FACYLW	1288	B*4601	50	1,92	96	55	55	55		
330	343	14	WAFACYLW	1289	A*3303	80	1,07	85	55	55	55		
330	343	14	WAFACYLW	55	A*6801	50	1,07	53	55	55	55		
330	343	14	WAFACYLW	55	A*7401	15	1,07	16	55	55	55		
331	343	13	AFACYLW	1290	A*3101	70	1,07	75	55	55	55		
331	343	13	AFACYLW	55	A*3303	35	1,07	37	55	55	55		
332	343	12	FACYLW	1291	A*3303	85	1,07	91	55	55	55		
332	343	12	FACYLW	55	A*6801	60	1,07	64	55	55	55		
332	343	12	FACYLW	55	A*3101	55	1,07	59	55	55	55		
334	343	10	KYLW	1292	A*3101	100	1,07	107	55	55	55		
335	343	9	YLW	1293	A*7401	85	1,07	91	55	55	55		
335	343	9	YLW	55	A*3303	40	1,07	43	55	55	55		
335	343	9	YLW	55	A*3101	35	1,07	37	55	55	55		
335	343	9	YLW	55	A*0301	20	1,07	21	55	55	55		
331	344	14	AFACYLW	1294	A*2402	30	1,86	56	55	55	55		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
331	344	14	AFAKYLWEWASVRF	“	A*2301	5	1,86	9	“	“	“		
332	344	13	FAKYLWEWASVRF	1295	B*4601	75	1,86	139	“	“	“		
335	344	10	YLWEWASVRF	1296	B*1502	90	1,86	167	“	“	“		
335	344	10	YLWEWASVRF	“	B*1525	45	1,86	84	“	“	“		
337	344	8	WEWASVRF	1297	B*3701	80	1,86	149	“	“	“		
337	344	8	WEWASVRF	“	B*4901	80	1,86	149	“	“	“		
337	344	8	WEWASVRF	“	B*5001	50	1,86	93	“	“	“		
337	344	8	WEWASVRF	“	B*1301	45	1,86	84	“	“	“		
337	344	8	WEWASVRF	“	B*4403	5	1,86	9	“	“	“		
337	345	9	WEWASVRFS	1298	B*4403	65	0,50	33	“	“	“		
337	345	9	WEWASVRFS	“	B*5001	60	0,50	30	“	“	“		
337	345	9	WEWASVRFS	“	B*4002	55	0,50	28	“	“	“		
337	345	9	WEWASVRFS	“	B*4901	15	0,50	8	“	“	“		
333	346	14	AKYLWEWASVRFSW	1299	B*4403	35	1,50	52	“	“	“		
334	346	13	KYLWEWASVRFSW	1300	A*2402	95	1,50	142	“	“	“		
334	346	13	KYLWEWASVRFSW	“	A*2301	75	1,50	112	“	“	“		
335	346	12	YLWEWASVRFSW	1301	A*3201	80	1,50	120	“	“	“		
335	346	12	YLWEWASVRFSW	“	B*1302	75	1,50	112	“	“	“		
335	346	12	YLWEWASVRFSW	“	B*5201	45	1,50	67	“	“	“		
337	346	10	WEWASVRFSW	1302	B*1301	100	1,50	150	“	“	“		
337	346	10	WEWASVRFSW	“	B*4402	100	1,50	150	“	“	“		
337	346	10	WEWASVRFSW	“	B*4403	100	1,50	150	“	“	“		
337	346	10	WEWASVRFSW	“	B*1302	90	1,50	135	“	“	“		
337	346	10	WEWASVRFSW	“	B*4002	90	1,50	135	“	“	“		
337	346	10	WEWASVRFSW	“	B*4901	75	1,50	112	“	“	“		
339	346	8	WASVRFSW	1303	B*5801	50	1,50	75	“	“	“		
334	347	14	KYLWEWASVRFSWL	1304	A*2402	90	1,37	123	“	“	“		
334	347	14	KYLWEWASVRFSWL	“	A*2301	40	1,37	55	“	“	“		
335	347	13	YLWEWASVRFSWL	1305	A*0201	100	1,37	137	“	“	“		
335	347	13	YLWEWASVRFSWL	“	A*0206	60	1,37	82	“	“	“		
337	347	11	WEWASVRFSWL	1306	B*4001	95	1,37	130	“	“	“		
337	347	11	WEWASVRFSWL	“	B*3701	90	1,37	123	“	“	“		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
337	347	11	WEWASVRFSWL	33	B*5001	90	1,37	123	33	33	33		
337	347	11	WEWASVRFSWL	33	B*4002	85	1,37	117	33	33	33		
337	347	11	WEWASVRFSWL	33	B*4901	85	1,37	117	33	33	33		
337	347	11	WEWASVRFSWL	33	B*1301	80	1,37	110	33	33	33		
337	347	11	WEWASVRFSWL	33	B*4402	55	1,37	75	33	33	33		
337	347	11	WEWASVRFSWL	33	B*1302	10	1,37	14	33	33	33		
339	347	9	WASVRFSWL	1307	B*0801	50	1,37	69	33	33	33		
337	348	12	WEWASVRFSWLS	1308	B*1801	80	0,54	43	33	33	33		
337	348	12	WEWASVRFSWLS	33	B*4002	70	0,54	38	33	33	33		
337	348	12	WEWASVRFSWLS	33	B*4901	45	0,54	24	33	33	33		
337	348	12	WEWASVRFSWLS	33	B*5001	45	0,54	24	33	33	33		
337	348	12	WEWASVRFSWLS	33	B*4403	20	0,54	11	33	33	33		
337	348	12	WEWASVRFSWLS	33	B*3701	5	0,54	3	33	33	33		
341	348	8	SVRFSWLS	1309	A*3001	40	0,54	22	33	33	33		
337	349	13	WEWASVRFSWLSL	1310	B*1801	100	1,61	161	33	33	33		
337	349	13	WEWASVRFSWLSL	33	B*3701	100	1,61	161	33	33	33		
337	349	13	WEWASVRFSWLSL	33	B*4001	100	1,61	161	33	33	33		
337	349	13	WEWASVRFSWLSL	33	B*4002	100	1,61	161	33	33	33		
337	349	13	WEWASVRFSWLSL	33	B*4901	100	1,61	161	33	33	33		
337	349	13	WEWASVRFSWLSL	33	B*5001	100	1,61	161	33	33	33		
337	349	13	WEWASVRFSWLSL	33	B*1301	90	1,61	145	33	33	33		
337	349	13	WEWASVRFSWLSL	33	B*4403	75	1,61	120	33	33	33		
337	349	13	WEWASVRFSWLSL	33	B*4402	70	1,61	112	33	33	33		
339	349	11	WASVRFSWLSL	1311	B*1402	85	1,61	137	33	33	33		
341	349	9	SVRFSWLSL	1312	A*3001	90	1,61	145	33	33	33		
341	349	9	SVRFSWLSL	33	B*0702	80	1,61	129	33	33	33		
342	349	8	VRFSWLSL	1313	B*3901	70	1,61	112	33	33	33		
337	350	14	WEWASVRFSWLSLL	1314	B*3701	95	1,15	109	33	33	33		
337	350	14	WEWASVRFSWLSLL	33	B*4002	95	1,15	109	33	33	33		
337	350	14	WEWASVRFSWLSLL	33	B*5001	95	1,15	109	33	33	33		
337	350	14	WEWASVRFSWLSLL	33	B*1801	90	1,15	104	33	33	33		
337	350	14	WEWASVRFSWLSLL	33	B*4901	90	1,15	104	33	33	33		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
337	350	14	WEWASVRFWSLSLL	„	B*1301	85	1,15	98	„	„	„		
337	350	14	WEWASVRFWSLSLL	„	B*4001	80	1,15	92	„	„	„		
337	350	14	WEWASVRFWSLSLL	„	B*4403	70	1,15	81	„	„	„		
337	350	14	WEWASVRFWSLSLL	„	B*4801	70	1,15	81	„	„	„		
337	350	14	WEWASVRFWSLSLL	„	B*4402	60	1,15	69	„	„	„		
337	350	14	WEWASVRFWSLSLL	„	B*1302	50	1,15	58	„	„	„		
342	350	9	VRFWSLSLL	1315	B*3801	65	1,15	75	„	„	„		
342	350	9	VRFWSLSLL	„	B*2702	20	1,15	23	„	„	„		
339	351	13	WASVRFWSLSLLV	1316	B*5101	30	1,47	44	„	„	„		
341	351	11	SVRFWSLSLLV	1317	A*3001	85	1,47	125	„	„	„		
340	353	14	ASVRFWSLSLLVPF	1318	B*4601	30	0,19	6	„	„	„		
340	353	14	ASVRFWSLSLLVPF	„	B*1525	15	0,19	3	„	„	„		
341	353	13	SVRFWSLSLLVPF	1319	B*1501	80	0,19	15	„	„	„		
341	353	13	SVRFWSLSLLVPF	„	B*1525	60	0,19	11	„	„	„		
341	353	13	SVRFWSLSLLVPF	„	B*1502	25	0,19	5	„	„	„		
341	353	13	SVRFWSLSLLVPF	„	A*3001	20	0,19	4	„	„	„		
342	353	12	VRFWSLSLLVPF	1320	B*2702	65	0,19	12	„	„	„		
342	353	12	VRFWSLSLLVPF	„	B*2705	55	0,19	10	„	„	„		
343	353	11	RFSWLSLLVPF	1321	A*3201	85	0,19	16	„	„	„		
343	353	11	RFSWLSLLVPF	„	A*2402	80	0,19	15	„	„	„		
344	353	10	FSWLSLLVPF	1322	B*4601	100	0,19	19	„	„	„		
344	353	10	FSWLSLLVPF	„	B*1525	55	0,19	10	„	„	„		
346	353	8	WLSLLVPF	1323	B*1502	10	0,19	2	„	„	„		
341	354	14	SVRFWSLSLLVPFV	1324	A*3001	95	1,30	124	„	„	„		
342	354	13	VRFWSLSLLVPFV	1325	B*2705	15	1,30	20	„	„	„		
346	354	9	WLSLLVPFV	1326	A*0201	94	1,30	123	„	„	„		
343	356	14	RFSWLSLLVPFVQW	1327	A*2402	25	1,92	48	„	„	„		
344	356	13	FSWLSLLVPFVQW	1328	B*5801	90	1,92	173	„	„	„		
344	356	13	FSWLSLLVPFVQW	„	B*5701	85	1,92	163	„	„	„		
344	356	13	FSWLSLLVPFVQW	„	B*5802	60	1,92	115	„	„	„		
344	356	13	FSWLSLLVPFVQW	„	B*5201	40	1,92	77	„	„	„		
347	356	10	LSLLVPFVQW	1329	B*5802	80	1,92	154	„	„	„		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
344	357	14	FSWLSLLVPFVQWF	1330	B*4601	65	1,38	89	35	35	35	
345	357	13	SWLSLLVPFVQWF	1331	A*2301	45	1,38	62	35	35	35	
345	357	13	SWLSLLVPFVQWF	35	A*2402	35	1,38	48	35	35	35	
347	357	11	LSLLVPFVQWF	1332	B*5802	20	1,38	28	35	35	35	
348	357	10	SLVPFVQWF	1333	B*1502	50	1,38	69	35	35	35	
349	357	9	LLVPFVQWF	1334	B*1501	45	1,38	62	35	35	35	
349	357	9	LLVPFVQWF	35	B*1525	10	1,38	14	35	35	35	
346	358	13	WLSLLVPFVQWFV	1335	A*0201	80	1,65	132	35	35	35	
346	358	13	WLSLLVPFVQWFV	35	A*0206	25	1,65	41	35	35	35	
349	358	10	LLVPFVQWFV	1336	A*0201	97	1,65	161	35	35	35	
349	358	10	LLVPFVQWFV	35	A*0206	90	1,65	149	35	35	35	
350	358	9	LVPFVQWFV	1337	A*6802	100	1,65	165	35	35	35	
350	358	9	LVPFVQWFV	35	A*0201	43	1,65	71	35	35	35	
						Cumulative Class I-BCI score:						
						12851						

366	373	8	LSAIWMW	1338	B*5801	100	1,78	178	35	365	400
366	373	8	LSAIWMW	35	B*5701	60	1,78	107	35	35	35
366	373	8	LSAIWMW	35	B*5802	45	1,78	80	35	35	35
365	374	10	WLSAIWMWY	1339	A*0101	90	1,38	124	35	35	35
365	374	10	WLSAIWMWY	35	A*0301	70	1,38	96	35	35	35
366	374	9	LSAIWMWY	1340	A*0101	100	1,38	138	35	35	35
367	374	8	SAIWMWY	1341	A*2501	90	1,38	124	35	35	35
367	374	8	SAIWMWY	35	A*3002	60	1,38	83	35	35	35
366	375	10	LSAIWMWYW	1342	B*5802	95	1,46	139	35	35	35
366	375	10	LSAIWMWYW	35	B*5801	75	1,46	110	35	35	35
367	375	9	SAIWMWYW	1343	B*5801	80	1,46	117	35	35	35
367	375	9	SAIWMWYW	35	B*4403	55	1,46	81	35	35	35
367	375	9	SAIWMWYW	35	B*5701	55	1,46	81	35	35	35
367	375	9	SAIWMWYW	35	B*4402	45	1,46	66	35	35	35
367	375	9	SAIWMWYW	35	B*5301	40	1,46	59	35	35	35

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
368	375	8	AIWMWYW	1344	B*5701	25	1,46	37	55	55	55		
370	379	10	WMWYWGPSL	1345	B*0801	95	1,46	138	55	55	55		
370	379	10	WMWYWGPSL	55	B*3801	95	1,46	138	55	55	55		
370	379	10	WMWYWGPSL	55	B*3901	95	1,46	138	55	55	55		
370	379	10	WMWYWGPSL	55	B*4801	80	1,46	117	55	55	55		
370	379	10	WMWYWGPSL	55	B*3701	65	1,46	95	55	55	55		
370	379	10	WMWYWGPSL	55	B*1301	40	1,46	58	55	55	55		
370	379	10	WMWYWGPSL	55	B*1525	20	1,46	29	55	55	55		
371	379	9	MMWYWGPSL	1346	B*4801	85	1,46	124	55	55	55		
371	379	9	MMWYWGPSL	55	B*1525	75	1,46	109	55	55	55		
371	379	9	MMWYWGPSL	55	A*0201	46	1,46	67	55	55	55		
371	379	9	MMWYWGPSL	55	A*3201	45	1,46	66	55	55	55		
371	379	9	MMWYWGPSL	55	B*1501	40	1,46	58	55	55	55		
371	379	9	MMWYWGPSL	55	B*3901	40	1,46	58	55	55	55		
367	380	14	SAIWMWYWGPSLY	1347	A*2601	95	1,93	183	55	55	55		
367	380	14	SAIWMWYWGPSLY	55	A*1101	80	1,93	154	55	55	55		
367	380	14	SAIWMWYWGPSLY	55	B*3501	75	1,93	145	55	55	55		
368	380	13	AIWMWYWGPSLY	1348	A*3002	85	1,93	164	55	55	55		
370	380	11	WMWYWGPSLY	1349	B*1502	100	1,93	193	55	55	55		
370	380	11	WMWYWGPSLY	55	A*0101	95	1,93	183	55	55	55		
370	380	11	WMWYWGPSLY	55	B*1501	75	1,93	145	55	55	55		
371	380	10	MMWYWGPSLY	1350	A*0301	100	1,93	193	55	55	55		
371	380	10	MMWYWGPSLY	55	A*3002	90	1,93	174	55	55	55		
371	380	10	MMWYWGPSLY	55	B*1525	90	1,93	174	55	55	55		
371	380	10	MMWYWGPSLY	55	A*7401	80	1,93	154	55	55	55		
371	380	10	MMWYWGPSLY	55	A*2902	65	1,93	125	55	55	55		
372	380	9	MMWYGPSLY	1351	A*2902	100	1,93	193	55	55	55		
369	382	14	IWMWYWGPSLYSI	1352	A*2402	85	0,77	65	55	55	55		
369	382	14	IWMWYWGPSLYSI	55	A*2301	60	0,77	46	55	55	55		
370	382	13	WMWYWGPSLYSI	1353	A*0206	100	0,77	77	55	55	55		
370	382	13	WMWYWGPSLYSI	55	B*0801	85	0,77	65	55	55	55		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
370	382	13	WMWYWGPSLYSI	..	B*3801	75	0,77	58	..	..	..	
370	382	13	WMWYWGPSLYSI	..	A*0201	74	0,77	57	..	..	..	
371	382	12	MMWYGPSLYSI	1354	A*3201	100	0,77	77	..	..	..	
371	382	12	MMWYGPSLYSI	..	B*5201	100	0,77	77	..	..	..	
371	382	12	MMWYGPSLYSI	..	B*1302	95	0,77	73	..	..	..	
371	382	12	MMWYGPSLYSI	..	A*0201	86	0,77	66	..	..	..	
371	382	12	MMWYGPSLYSI	..	A*7401	75	0,77	58	..	..	..	
371	382	12	MMWYGPSLYSI	..	B*4801	75	0,77	58	..	..	..	
371	382	12	MMWYGPSLYSI	..	B*1301	70	0,77	54	..	..	..	
370	383	14	WMWYWGPSLYSIV	1355	A*0206	70	0,79	55	..	..	..	
370	383	14	WMWYWGPSLYSIV	..	A*0201	51	0,79	40	..	..	..	
370	383	14	WMWYWGPSLYSIV	..	B*0801	45	0,79	35	..	..	..	
370	383	14	WMWYWGPSLYSIV	..	B*3901	10	0,79	8	..	..	..	
370	383	14	WMWYWGPSLYSIV	..	B*3801	5	0,79	4	..	..	..	
371	383	13	MMWYGPSLYSIV	1356	A*0201	69	0,79	54	..	..	..	
371	383	13	MMWYGPSLYSIV	..	B*1302	25	0,79	20	..	..	..	
371	383	13	MMWYGPSLYSIV	..	B*4801	25	0,79	20	..	..	..	
373	386	14	WYWGPSLYSIVSPF	1357	B*1502	80	0,72	58	..	..	..	
373	386	14	WYWGPSLYSIVSPF	..	A*2301	55	0,72	40	..	..	..	
373	386	14	WYWGPSLYSIVSPF	..	A*2402	20	0,72	14	..	..	..	
373	386	14	WYWGPSLYSIVSPF	..	A*2902	15	0,72	11	..	..	..	
374	386	13	YWGPSLYSIVSPF	1358	A*2301	70	0,72	51	..	..	..	
374	386	13	YWGPSLYSIVSPF	..	A*2402	70	0,72	51	..	..	..	
377	386	10	PSLYSIVSPF	1359	A*3201	35	0,72	25	..	..	..	
378	386	9	SLYSIVSPF	1360	B*1525	95	0,72	69	..	..	..	
378	386	9	SLYSIVSPF	..	A*3201	90	0,72	65	..	..	..	
378	386	9	SLYSIVSPF	..	B*1501	85	0,72	61	..	..	..	
378	386	9	SLYSIVSPF	..	B*4601	20	0,72	14	..	..	..	
378	386	9	SLYSIVSPF	..	A*2601	10	0,72	7	..	..	..	
374	387	14	YWGPSLYSIVSPFI	1361	A*2402	15	1,16	17	..	..	..	
378	387	10	SLYSIVSPFI	1362	A*0201	3	1,16	3	..	..	..	

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
376	389	14	GPSLYSIVSPFIPL	1363	B*0702	65	0,42	27	55	55	55		
378	389	12	SLYISVSPFIPL	1364	A*3201	75	0,42	32	55	55	55		
378	389	12	SLYISVSPFIPL	55	A*0201	34	0,42	14	55	55	55		
378	389	12	SLYISVSPFIPL	55	B*1502	30	0,42	13	55	55	55		
378	389	12	SLYISVSPFIPL	55	B*1501	5	0,42	2	55	55	55		
380	389	10	YSIVSPFIPL	1365	B*3901	65	0,42	27	55	55	55		
380	389	10	YSIVSPFIPL	55	A*6802	45	0,42	19	55	55	55		
380	389	10	YSIVSPFIPL	55	B*4001	40	0,42	17	55	55	55		
378	390	13	SLYISVSPFIPL	1366	A*0201	17	1,76	30	55	55	55		
379	392	14	LYSIVSPFIPL	1367	A*2402	60	1,07	64	55	55	55		
380	392	13	YSIVSPFIPL	1368	B*4601	45	1,07	48	55	55	55		
380	392	13	YSIVSPFIPL	55	B*5201	30	1,07	32	55	55	55		
381	392	12	SIVSPFIPL	1369	A*6802	25	1,07	27	55	55	55		
382	392	11	IVSPFIPL	1370	A*6802	30	1,07	32	55	55	55		
384	392	9	SPFIPL	1371	B*5501	90	1,07	96	55	55	55		
384	392	9	SPFIPL	55	B*5201	75	1,07	80	55	55	55		
384	392	9	SPFIPL	55	B*5101	70	1,07	75	55	55	55		
384	392	9	SPFIPL	55	B*5601	10	1,07	11	55	55	55		
380	393	14	YSIVSPFIPL	1372	B*4601	85	0,82	69	55	55	55		
380	393	14	YSIVSPFIPL	55	B*5801	55	0,82	45	55	55	55		
380	393	14	YSIVSPFIPL	55	A*2501	45	0,82	37	55	55	55		
380	393	14	YSIVSPFIPL	55	B*1525	30	0,82	25	55	55	55		
380	393	14	YSIVSPFIPL	55	B*1501	15	0,82	12	55	55	55		
381	393	13	SIVSPFIPL	1373	B*1525	40	0,82	33	55	55	55		
381	393	13	SIVSPFIPL	55	A*2601	5	0,82	4	55	55	55		
384	393	10	SPFIPL	1374	B*3501	65	0,82	53	55	55	55		
384	393	10	SPFIPL	55	B*3503	65	0,82	53	55	55	55		
384	393	10	SPFIPL	55	B*5101	45	0,82	37	55	55	55		
385	393	9	PFIFL	1375	A*2301	15	0,82	12	55	55	55		
386	393	8	FIFL	1376	A*2501	20	0,82	16	55	55	55		
384	394	11	SPFIPL	1377	B*3503	100	1,11	111	55	55	55		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
387	394	8	IPLLPIFF	1378	B*3503	70	1,11	78	55	55	55		
386	395	10	FIPLLPIFFC	1379	A*0201	9	0,98	8	55	55	55		
384	396	13	SPFIPLLPPIFFCL	1380	B*3503	75	1,93	145	55	55	55		
387	396	10	IPLLPIFFCL	1381	B*5101	10	1,93	19	55	55	55		
384	397	14	SPFIPLLPPIFFCLW	1382	B*3503	60	1,67	100	55	55	55		
384	397	14	SPFIPLLPPIFFCLW	55	B*5301	15	1,67	25	55	55	55		
387	397	11	IPLLPIFFCLW	1383	B*5101	55	1,67	92	55	55	55		
387	398	12	IPLLPIFFCLWV	1384	B*5101	100	1,51	151	55	55	55		
389	398	10	LLPIFFCLWV	1385	A*0201	89	1,51	134	55	55	55		
390	398	9	LPIFFCLWV	1386	B*5101	85	1,51	129	55	55	55		
386	399	14	FIPLLPIFFCLWVY	1387	A*2501	50	1,83	92	55	55	55		
386	399	14	FIPLLPIFFCLWVY	55	A*0101	35	1,83	64	55	55	55		
386	399	14	FIPLLPIFFCLWVY	55	A*2601	20	1,83	37	55	55	55		
387	399	13	IPLLPIFFCLWVY	1388	B*3501	60	1,83	110	55	55	55		
388	399	12	PLLPPIFFCLWVY	1389	A*2902	25	1,83	46	55	55	55		
388	399	12	PLLPPIFFCLWVY	55	A*3002	25	1,83	46	55	55	55		
389	399	11	LLPIFFCLWVY	1390	A*0101	60	1,83	110	55	55	55		
390	399	10	LPIFFCLWVY	1391	B*3501	95	1,83	174	55	55	55		
390	399	10	LPIFFCLWVY	55	B*5101	35	1,83	64	55	55	55		
390	399	10	LPIFFCLWVY	55	B*5301	35	1,83	64	55	55	55		
391	399	9	PIFFCLWVY	1392	A*3002	40	1,83	73	55	55	55		
391	399	9	PIFFCLWVY	55	A*2501	25	1,83	46	55	55	55		
392	399	8	IFFCLWVY	1393	A*3002	35	1,83	64	55	55	55		
387	400	14	IPLLPIFFCLWVYI	1394	B*5101	90	1,45	131	55	55	55		
387	400	14	IPLLPIFFCLWVYI	55	B*5201	20	1,45	29	55	55	55		
390	400	11	LPIFFCLWVYI	1395	B*3503	5	1,45	7	55	55	55		
						Cumulative Class I-BCI score:							
								9736					

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen												Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End			
371	380	10	MMWYWGPSLY	1350	A*0301	100	1,93	193	36	371	400			
371	380	10	MMWYWGPSLY	"	A*3002	90	1,93	174	"	"	"			
371	380	10	MMWYWGPSLY	"	B*1525	90	1,93	174	"	"	"			
371	380	10	MMWYWGPSLY	"	A*7401	80	1,93	154	"	"	"			
371	380	10	MMWYWGPSLY	"	A*2902	65	1,93	125	"	"	"			
372	380	9	MMWYWGPSLY	1351	A*2902	100	1,93	193	"	"	"			
371	382	12	MMWYWGPSLYSI	1354	A*3201	100	0,77	77	"	"	"			
371	382	12	MMWYWGPSLYSI	"	B*5201	100	0,77	77	"	"	"			
371	382	12	MMWYWGPSLYSI	"	B*1302	95	0,77	73	"	"	"			
371	382	12	MMWYWGPSLYSI	"	A*0201	86	0,77	66	"	"	"			
371	382	12	MMWYWGPSLYSI	"	A*7401	75	0,77	58	"	"	"			
371	382	12	MMWYWGPSLYSI	"	B*4801	75	0,77	58	"	"	"			
371	382	12	MMWYWGPSLYSI	"	B*1301	70	0,77	54	"	"	"			
370	383	14	MMWYWGPSLYSIV	1355	A*0206	70	0,79	55	"	"	"			
370	383	14	MMWYWGPSLYSIV	"	A*0201	51	0,79	40	"	"	"			
370	383	14	MMWYWGPSLYSIV	"	B*0801	45	0,79	35	"	"	"			
370	383	14	MMWYWGPSLYSIV	"	B*3901	10	0,79	8	"	"	"			
370	383	14	MMWYWGPSLYSIV	"	B*3801	5	0,79	4	"	"	"			
371	383	13	MMWYWGPSLYSIV	1356	A*0201	69	0,79	54	"	"	"			
371	383	13	MMWYWGPSLYSIV	"	B*1302	25	0,79	20	"	"	"			
371	383	13	MMWYWGPSLYSIV	"	B*4801	25	0,79	20	"	"	"			
373	386	14	WYWGPSLYSIVSPF	1357	B*1502	80	0,72	58	"	"	"			
373	386	14	WYWGPSLYSIVSPF	"	A*2301	55	0,72	40	"	"	"			
373	386	14	WYWGPSLYSIVSPF	"	A*2402	20	0,72	14	"	"	"			
373	386	14	WYWGPSLYSIVSPF	"	A*2902	15	0,72	11	"	"	"			
374	386	13	YWGPSLYSIVSPF	1358	A*2301	70	0,72	51	"	"	"			
374	386	13	YWGPSLYSIVSPF	"	A*2402	70	0,72	51	"	"	"			
377	386	10	PSLYSIVSPF	1359	A*3201	35	0,72	25	"	"	"			
378	386	9	SLYSIVSPF	1360	B*1525	95	0,72	69	"	"	"			
378	386	9	SLYSIVSPF	"	A*3201	90	0,72	65	"	"	"			
378	386	9	SLYSIVSPF	"	B*1501	85	0,72	61	"	"	"			
378	386	9	SLYSIVSPF	"	B*4601	20	0,72	14	"	"	"			

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
378	386	9	SLYSIVSPF	“	A*2601	10	0,72	7	“	“	“		
374	387	14	YWGPSLYSIVSPFI	1361	A*2402	15	1,16	17	“	“	“		
378	387	10	SLYSiVSPFI	1362	A*0201	3	1,16	3	“	“	“		
376	389	14	GPSLYSIVSPFIPL	1363	B*0702	65	0,42	27	“	“	“		
378	389	12	SLYSIVSPFIPL	1364	A*3201	75	0,42	32	“	“	“		
378	389	12	SLYSIVSPFIPL	“	A*0201	34	0,42	14	“	“	“		
378	389	12	SLYSIVSPFIPL	“	B*1502	30	0,42	13	“	“	“		
378	389	12	SLYSIVSPFIPL	“	B*1501	5	0,42	2	“	“	“		
380	389	10	YSIVSPFIPL	1365	B*3901	65	0,42	27	“	“	“		
380	389	10	YSIVSPFIPL	“	A*6802	45	0,42	19	“	“	“		
380	389	10	YSIVSPFIPL	“	B*4001	40	0,42	17	“	“	“		
378	390	13	SLYSIVSPFIPL	1366	A*0201	17	1,76	30	“	“	“		
379	392	14	LYSIVSPFIPL	1367	A*2402	60	1,07	64	“	“	“		
380	392	13	YSIVSPFIPL	1368	B*4601	45	1,07	48	“	“	“		
380	392	13	YSIVSPFIPL	“	B*5201	30	1,07	32	“	“	“		
381	392	12	SIVSPFIPL	1369	A*6802	25	1,07	27	“	“	“		
382	392	11	IVSPFIPL	1370	A*6802	30	1,07	32	“	“	“		
384	392	9	SPFIPL	1371	B*5501	90	1,07	96	“	“	“		
384	392	9	SPFIPL	“	B*5201	75	1,07	80	“	“	“		
384	392	9	SPFIPL	“	B*5101	70	1,07	75	“	“	“		
384	392	9	SPFIPL	“	B*5601	10	1,07	11	“	“	“		
380	393	14	YSIVSPFIPL	1372	B*4601	85	0,82	69	“	“	“		
380	393	14	YSIVSPFIPL	“	B*5801	55	0,82	45	“	“	“		
380	393	14	YSIVSPFIPL	“	A*2501	45	0,82	37	“	“	“		
380	393	14	YSIVSPFIPL	“	B*1525	30	0,82	25	“	“	“		
380	393	14	YSIVSPFIPL	“	B*1501	15	0,82	12	“	“	“		
381	393	13	SIVSPFIPL	1373	B*1525	40	0,82	33	“	“	“		
381	393	13	SIVSPFIPL	“	A*2601	5	0,82	4	“	“	“		
384	393	10	SPFIPL	1374	B*3501	65	0,82	53	“	“	“		
384	393	10	SPFIPL	“	B*3503	65	0,82	53	“	“	“		
384	393	10	SPFIPL	“	B*5101	45	0,82	37	“	“	“		
385	393	9	PFIP	1375	A*2301	15	0,82	12	“	“	“		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
386	393	8	FIPLLPIF	1376	A*2501	20	0,82	16	55	55	55	
384	394	11	SPFIPLLPIFF	1377	B*3503	100	1,11	111	55	55	55	
387	394	8	IPLLPIFF	1378	B*3503	70	1,11	78	55	55	55	
386	395	10	FIPLLPIFFC	1379	A*0201	9	0,98	8	55	55	55	
384	396	13	SPFIPLLPIFFCL	1380	B*3503	75	1,93	145	55	55	55	
387	396	10	IPLLPIFFCL	1381	B*5101	10	1,93	19	55	55	55	
384	397	14	SPFIPLLPIFFCLW	1382	B*3503	60	1,67	100	55	55	55	
384	397	14	SPFIPLLPIFFCLW	55	B*5301	15	1,67	25	55	55	55	
387	397	11	IPLLPIFFCLW	1383	B*5101	55	1,67	92	55	55	55	
387	398	12	IPLLPIFFCLWV	1384	B*5101	100	1,51	151	55	55	55	
389	398	10	LLPIFFCLWV	1385	A*0201	89	1,51	134	55	55	55	
390	398	9	LPIFFCLWV	1386	B*5101	85	1,51	129	55	55	55	
386	399	14	FIPLLPIFFCLWVY	1387	A*2501	50	1,83	92	55	55	55	
386	399	14	FIPLLPIFFCLWVY	55	A*0101	35	1,83	64	55	55	55	
386	399	14	FIPLLPIFFCLWVY	55	A*2601	20	1,83	37	55	55	55	
387	399	13	IPLLPIFFCLWVY	1388	B*3501	60	1,83	110	55	55	55	
388	399	12	PLLPIFFCLWVY	1389	A*2902	25	1,83	46	55	55	55	
388	399	12	PLLPIFFCLWVY	55	A*3002	25	1,83	46	55	55	55	
389	399	11	LLPIFFCLWVY	1390	A*0101	60	1,83	110	55	55	55	
390	399	10	LPIFFCLWVY	1391	B*3501	95	1,83	174	55	55	55	
390	399	10	LPIFFCLWVY	55	B*5101	35	1,83	64	55	55	55	
390	399	10	LPIFFCLWVY	55	B*5301	35	1,83	64	55	55	55	
391	399	9	PIFFCLWVY	1392	A*3002	40	1,83	73	55	55	55	
391	399	9	PIFFCLWVY	55	A*2501	25	1,83	46	55	55	55	
392	399	8	IFFCLWVY	1393	A*3002	35	1,83	64	55	55	55	
387	400	14	IPLLPIFFCLWVYI	1394	B*5101	90	1,45	131	55	55	55	
387	400	14	IPLLPIFFCLWVYI	55	B*5201	20	1,45	29	55	55	55	
390	400	11	LPIFFCLWVYI	1395	B*3503	5	1,45	7	55	55	55	
Cumulative Class I-BCI score:									5389			

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
370	379	10	WMWYWGPSL	1345	B*0801	95	1,46	138	37	370	400		
370	379	10	WMWYWGPSL	⁂	B*3801	95	1,46	138	⁂	⁂	⁂		
370	379	10	WMWYWGPSL	⁂	B*3901	95	1,46	138	⁂	⁂	⁂		
370	379	10	WMWYWGPSL	⁂	B*4801	80	1,46	117	⁂	⁂	⁂		
370	379	10	WMWYWGPSL	⁂	B*3701	65	1,46	95	⁂	⁂	⁂		
370	379	10	WMWYWGPSL	⁂	B*1301	40	1,46	58	⁂	⁂	⁂		
370	379	10	WMWYWGPSL	⁂	B*1525	20	1,46	29	⁂	⁂	⁂		
370	380	11	WMWYWGPSLY	1349	B*1502	100	1,93	193	⁂	⁂	⁂		
370	380	11	WMWYWGPSLY	⁂	A*0101	95	1,93	183	⁂	⁂	⁂		
370	380	11	WMWYWGPSLY	⁂	B*1501	75	1,93	145	⁂	⁂	⁂		
371	380	10	MMWYWGPSLY	1350	A*0301	100	1,93	193	⁂	⁂	⁂		
371	380	10	MMWYWGPSLY	⁂	A*3002	90	1,93	174	⁂	⁂	⁂		
371	380	10	MMWYWGPSLY	⁂	B*1525	90	1,93	174	⁂	⁂	⁂		
371	380	10	MMWYWGPSLY	⁂	A*7401	80	1,93	154	⁂	⁂	⁂		
371	380	10	MMWYWGPSLY	⁂	A*2902	65	1,93	125	⁂	⁂	⁂		
372	380	9	MWYWGPSLY	1351	A*2902	100	1,93	193	⁂	⁂	⁂		
370	382	13	WMWYWGPSLYSI	1353	A*0206	100	0,77	77	⁂	⁂	⁂		
370	382	13	WMWYWGPSLYSI	⁂	B*0801	85	0,77	65	⁂	⁂	⁂		
370	382	13	WMWYWGPSLYSI	⁂	B*3801	75	0,77	58	⁂	⁂	⁂		
370	382	13	WMWYWGPSLYSI	⁂	A*0201	74	0,77	57	⁂	⁂	⁂		
371	382	12	MMWYWGPSLYSI	1354	A*3201	100	0,77	77	⁂	⁂	⁂		
371	382	12	MMWYWGPSLYSI	⁂	B*5201	100	0,77	77	⁂	⁂	⁂		
371	382	12	MMWYWGPSLYSI	⁂	B*1302	95	0,77	73	⁂	⁂	⁂		
371	382	12	MMWYWGPSLYSI	⁂	A*0201	86	0,77	66	⁂	⁂	⁂		
371	382	12	MMWYWGPSLYSI	⁂	A*7401	75	0,77	58	⁂	⁂	⁂		
371	382	12	MMWYWGPSLYSI	⁂	B*4801	75	0,77	58	⁂	⁂	⁂		
371	382	12	MMWYWGPSLYSI	⁂	B*1301	70	0,77	54	⁂	⁂	⁂		
370	383	14	WMWYWGPSLYSIV	1355	A*0206	70	0,79	55	⁂	⁂	⁂		
370	383	14	WMWYWGPSLYSIV	⁂	A*0201	51	0,79	40	⁂	⁂	⁂		
370	383	14	WMWYWGPSLYSIV	⁂	B*0801	45	0,79	35	⁂	⁂	⁂		
370	383	14	WMWYWGPSLYSIV	⁂	B*3901	10	0,79	8	⁂	⁂	⁂		
370	383	14	WMWYWGPSLYSIV	⁂	B*3801	5	0,79	4	⁂	⁂	⁂		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
371	383	13	MMWYWGPSLYSIV	1356	A*0201	69	0,79	54	55	55	55		
371	383	13	MMWYWGPSLYSIV	55	B*1302	25	0,79	20	55	55	55		
371	383	13	MMWYWGPSLYSIV	55	B*4801	25	0,79	20	55	55	55		
373	386	14	WYWGPSLYSIVSPF	1357	B*1502	80	0,72	58	55	55	55		
373	386	14	WYWGPSLYSIVSPF	55	A*2301	55	0,72	40	55	55	55		
373	386	14	WYWGPSLYSIVSPF	55	A*2402	20	0,72	14	55	55	55		
373	386	14	WYWGPSLYSIVSPF	55	A*2902	15	0,72	11	55	55	55		
374	386	13	YWGPSLYSIVSPF	1358	A*2301	70	0,72	51	55	55	55		
374	386	13	YWGPSLYSIVSPF	55	A*2402	70	0,72	51	55	55	55		
377	386	10	PSLYSIVSPF	1359	A*3201	35	0,72	25	55	55	55		
378	386	9	SLYSIVSPF	1360	B*1525	95	0,72	69	55	55	55		
378	386	9	SLYSIVSPF	55	A*3201	90	0,72	65	55	55	55		
378	386	9	SLYSIVSPF	55	B*1501	85	0,72	61	55	55	55		
378	386	9	SLYSIVSPF	55	B*4601	20	0,72	14	55	55	55		
378	386	9	SLYSIVSPF	55	A*2601	10	0,72	7	55	55	55		
374	387	14	YWGPSLYSIVSPFI	1361	A*2402	15	1,16	17	55	55	55		
378	387	10	SLYSIVSPFI	1362	A*0201	3	1,16	3	55	55	55		
376	389	14	GPSLYSIVSPFIPL	1363	B*0702	65	0,42	27	55	55	55		
378	389	12	SLYSIVSPFIPL	1364	A*3201	75	0,42	32	55	55	55		
378	389	12	SLYSIVSPFIPL	55	A*0201	34	0,42	14	55	55	55		
378	389	12	SLYSIVSPFIPL	55	B*1502	30	0,42	13	55	55	55		
378	389	12	SLYSIVSPFIPL	55	B*1501	5	0,42	2	55	55	55		
380	389	10	YSIVSPFIPL	1365	B*3901	65	0,42	27	55	55	55		
380	389	10	YSIVSPFIPL	55	A*6802	45	0,42	19	55	55	55		
380	389	10	YSIVSPFIPL	55	B*4001	40	0,42	17	55	55	55		
378	390	13	SLYSIVSPFIPLL	1366	A*0201	17	1,76	30	55	55	55		
379	392	14	LYSIVSPFIPLLPI	1367	A*2402	60	1,07	64	55	55	55		
380	392	13	YSIVSPFIPLLPI	1368	B*4601	45	1,07	48	55	55	55		
380	392	13	YSIVSPFIPLLPI	55	B*5201	30	1,07	32	55	55	55		
381	392	12	SIVSPFIPLLPI	1369	A*6802	25	1,07	27	55	55	55		
382	392	11	IVSPFIPLLPI	1370	A*6802	30	1,07	32	55	55	55		
384	392	9	SPFIPLLPI	1371	B*5501	90	1,07	96	55	55	55		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen											Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End		
384	392	9	SPFIFLLPI	"	B*5201	75	1,07	80	"	"	"		
384	392	9	SPFIFLLPI	"	B*5101	70	1,07	75	"	"	"		
384	392	9	SPFIFLLPI	"	B*5601	10	1,07	11	"	"	"		
380	393	14	YSIVSPFIFLLPIF	1372	B*4601	85	0,82	69	"	"	"		
380	393	14	YSIVSPFIFLLPIF	"	B*5801	55	0,82	45	"	"	"		
380	393	14	YSIVSPFIFLLPIF	"	A*2501	45	0,82	37	"	"	"		
380	393	14	YSIVSPFIFLLPIF	"	B*1525	30	0,82	25	"	"	"		
380	393	14	YSIVSPFIFLLPIF	"	B*1501	15	0,82	12	"	"	"		
381	393	13	SIVSPFIFLLPIF	1373	B*1525	40	0,82	33	"	"	"		
381	393	13	SIVSPFIFLLPIF	"	A*2601	5	0,82	4	"	"	"		
384	393	10	SPFIFLLPIF	1374	B*3501	65	0,82	53	"	"	"		
384	393	10	SPFIFLLPIF	"	B*3503	65	0,82	53	"	"	"		
384	393	10	SPFIFLLPIF	"	B*5101	45	0,82	37	"	"	"		
385	393	9	PFIFLLPIF	1375	A*2301	15	0,82	12	"	"	"		
386	393	8	FIFLLPIF	1376	A*2501	20	0,82	16	"	"	"		
384	394	11	SPFIFLLPIFF	1377	B*3503	100	1,11	111	"	"	"		
387	394	8	IPLLPIFF	1378	B*3503	70	1,11	78	"	"	"		
386	395	10	FIFLLPIFFC	1379	A*0201	9	0,98	8	"	"	"		
384	396	13	SPFIFLLPIFFCL	1380	B*3503	75	1,93	145	"	"	"		
387	396	10	IPLLPIFFCL	1381	B*5101	10	1,93	19	"	"	"		
384	397	14	SPFIFLLPIFFCLW	1382	B*3503	60	1,67	100	"	"	"		
384	397	14	SPFIFLLPIFFCLW	"	B*5301	15	1,67	25	"	"	"		
387	397	11	IPLLPIFFCLW	1383	B*5101	55	1,67	92	"	"	"		
387	398	12	IPLLPIFFCLWV	1384	B*5101	100	1,51	151	"	"	"		
389	398	10	LLPIFFCLWV	1385	A*0201	89	1,51	134	"	"	"		
390	398	9	LPIFFCLWV	1386	B*5101	85	1,51	129	"	"	"		
386	399	14	FIFLLPIFFCLWVY	1387	A*2501	50	1,83	92	"	"	"		
386	399	14	FIFLLPIFFCLWVY	"	A*0101	35	1,83	64	"	"	"		
386	399	14	FIFLLPIFFCLWVY	"	A*2601	20	1,83	37	"	"	"		
387	399	13	IPLLPIFFCLWVY	1388	B*3501	60	1,83	110	"	"	"		
388	399	12	PLLPIFFCLWVY	1389	A*2902	25	1,83	46	"	"	"		
388	399	12	PLLPIFFCLWVY	"	A*3002	25	1,83	46	"	"	"		

HLA class I binding peptides contained in SLP sequences derived from HBV Surface antigen										Peptide of invention (SLP)		
Start	End	Length	Sequence ^A	SEQ ID NO:	HLA class I molecule	Class I- B score ^B	C-score ^C	Class I-BCI score ^D	SLP#	SLP Start	SLP End	
389	399	11	LLPIFFCLWVY	1390	A*0101	60	1,83	110	22	22	22	
390	399	10	LPIFFCLWVY	1391	B*3501	95	1,83	174	22	22	22	
390	399	10	LPIFFCLWVY	22	B*5101	35	1,83	64	22	22	22	
390	399	10	LPIFFCLWVY	22	B*5301	35	1,83	64	22	22	22	
391	399	9	PIFFCLWVY	1392	A*3002	40	1,83	73	22	22	22	
391	399	9	PIFFCLWVY	22	A*2501	25	1,83	46	22	22	22	
392	399	8	IFFCLWVY	1393	A*3002	35	1,83	64	22	22	22	
387	400	14	IPLLPIFFCLWVYI	1394	B*5101	90	1,45	131	22	22	22	
387	400	14	IPLLPIFFCLWVYI	22	B*5201	20	1,45	29	22	22	22	
390	400	11	LPIFFCLWVYI	1395	B*3503	5	1,45	7	22	22	22	
Cumulative Class I-BCI score:									6880			

“Start” and “End” are relative to the amino acid sequence of HBV large surface protein as depicted in SEQ ID NO: 1141

^A Peptide amino acid sequence. Each HLA class I binding peptide of HBV large surface protein is listed separately for each HLA class I molecule to which it is predicted to bind, and can be listed multiple times for that reason.

^B Class I-B score. See *Material and Methods* (Examples section).

^C C-score. See *Material and Methods* (Examples section).

^D Class I-BCI score. See *Material and Methods* (Examples section).

^E Cumulative Class I-BCI score. See *Material and Methods* (Examples section).

Table 7b. Predicted HLA class II-restricted CD4⁺ T cell epitopes contained in SLP sequences from HBV large surface protein.

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
181	195	GFLGPLLVLQAGFFL	1396	*1501	85	30	175	210
181	195	GFLGPLLVLQAGFFL	„	*0101	60	„	„	„
181	195	GFLGPLLVLQAGFFL	„	*1301	53	„	„	„
181	195	GFLGPLLVLQAGFFL	„	*0102	8	„	„	„
182	196	FLGPLLVLQAGFFLL	1397	*0101	93	„	„	„
182	196	FLGPLLVLQAGFFLL	„	*1501	83	„	„	„
182	196	FLGPLLVLQAGFFLL	„	*1301	50	„	„	„
182	196	FLGPLLVLQAGFFLL	„	*0102	35	„	„	„
182	196	FLGPLLVLQAGFFLL	„	*0104	28	„	„	„
182	196	FLGPLLVLQAGFFLL	„	*0106	20	„	„	„
183	197	LGPLLVLQAGFFLLT	1398	*0101	90	„	„	„
183	197	LGPLLVLQAGFFLLT	„	*1501	80	„	„	„
183	197	LGPLLVLQAGFFLLT	„	*1301	48	„	„	„
183	197	LGPLLVLQAGFFLLT	„	*0104	30	„	„	„
183	197	LGPLLVLQAGFFLLT	„	*0102	13	„	„	„
183	197	LGPLLVLQAGFFLLT	„	*0106	8	„	„	„
184	198	GPLLVLQAGFFLLTR	1399	*1501	78	„	„	„
184	198	GPLLVLQAGFFLLTR	„	*0101	58	„	„	„
184	198	GPLLVLQAGFFLLTR	„	*1301	45	„	„	„
184	198	GPLLVLQAGFFLLTR	„	*0104	33	„	„	„
184	198	GPLLVLQAGFFLLTR	„	*0102	10	„	„	„
184	198	GPLLVLQAGFFLLTR	„	*0106	3	„	„	„
185	199	PLLVLQAGFFLLTRI	1400	*1501	75	„	„	„
185	199	PLLVLQAGFFLLTRI	„	*1301	43	„	„	„
185	199	PLLVLQAGFFLLTRI	„	*0101	13	„	„	„
186	200	LLVLQAGFFLLTRIL	1401	*1301	40	„	„	„
186	200	LLVLQAGFFLLTRIL	„	*1501	25	„	„	„
187	201	LVLQAGFFLLTRILT	1402	*1101	83	„	„	„
187	201	LVLQAGFFLLTRILT	„	*0101	40	„	„	„
187	201	LVLQAGFFLLTRILT	„	*0701	40	„	„	„
187	201	LVLQAGFFLLTRILT	„	*1301	38	„	„	„
187	201	LVLQAGFFLLTRILT	„	*1501	15	„	„	„
187	201	LVLQAGFFLLTRILT	„	*0301	10	„	„	„
188	202	VLQAGFFLLTRILTI	1403	*0401	93	„	„	„
188	202	VLQAGFFLLTRILTI	„	*0701	80	„	„	„
188	202	VLQAGFFLLTRILTI	„	*1101	80	„	„	„
188	202	VLQAGFFLLTRILTI	„	*0101	70	„	„	„
188	202	VLQAGFFLLTRILTI	„	*0104	20	„	„	„
188	202	VLQAGFFLLTRILTI	„	*0102	15	„	„	„
189	203	LQAGFFLLTRILTIP	1404	*0401	90	„	„	„
189	203	LQAGFFLLTRILTIP	„	*0701	78	„	„	„
189	203	LQAGFFLLTRILTIP	„	*1101	78	„	„	„
189	203	LQAGFFLLTRILTIP	„	*0101	50	„	„	„
189	203	LQAGFFLLTRILTIP	„	*0104	35	„	„	„
189	203	LQAGFFLLTRILTIP	„	*0102	33	„	„	„
190	204	QAGFFLLTRILTIPQ	1405	*0401	100	„	„	„
190	204	QAGFFLLTRILTIPQ	„	*0701	75	„	„	„

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
190	204	QAGFFLLTRILTIPQ	„	*1101	75	„	„	„
190	204	QAGFFLLTRILTIPQ	„	*0101	68	„	„	„
190	204	QAGFFLLTRILTIPQ	„	*0102	63	„	„	„
190	204	QAGFFLLTRILTIPQ	„	*0104	58	„	„	„
190	204	QAGFFLLTRILTIPQ	„	*1501	20	„	„	„
190	204	QAGFFLLTRILTIPQ	„	*0105	8	„	„	„
190	204	QAGFFLLTRILTIPQ	„	*0107	8	„	„	„
191	205	AGFFLLTRILTIPQS	1406	*0401	98	„	„	„
191	205	AGFFLLTRILTIPQS	„	*0701	73	„	„	„
191	205	AGFFLLTRILTIPQS	„	*1101	73	„	„	„
191	205	AGFFLLTRILTIPQS	„	*0102	70	„	„	„
191	205	AGFFLLTRILTIPQS	„	*0104	65	„	„	„
191	205	AGFFLLTRILTIPQS	„	*0101	55	„	„	„
191	205	AGFFLLTRILTIPQS	„	*0106	23	„	„	„
191	205	AGFFLLTRILTIPQS	„	*0105	10	„	„	„
191	205	AGFFLLTRILTIPQS	„	*0107	10	„	„	„
192	206	GFFLLTRILTIPQSL	1407	*0401	95	„	„	„
192	206	GFFLLTRILTIPQSL	„	*1301	85	„	„	„
192	206	GFFLLTRILTIPQSL	„	*0102	83	„	„	„
192	206	GFFLLTRILTIPQSL	„	*0104	80	„	„	„
192	206	GFFLLTRILTIPQSL	„	*0701	70	„	„	„
192	206	GFFLLTRILTIPQSL	„	*1101	70	„	„	„
192	206	GFFLLTRILTIPQSL	„	*0106	50	„	„	„
192	206	GFFLLTRILTIPQSL	„	*0105	28	„	„	„
192	206	GFFLLTRILTIPQSL	„	*0107	28	„	„	„
192	206	GFFLLTRILTIPQSL	„	*0101	18	„	„	„
192	206	GFFLLTRILTIPQSL	„	*1501	10	„	„	„
193	207	FLLTRILTIPQSLD	1408	*0401	88	„	„	„
193	207	FLLTRILTIPQSLD	„	*0102	75	„	„	„
193	207	FLLTRILTIPQSLD	„	*1301	75	„	„	„
193	207	FLLTRILTIPQSLD	„	*0701	68	„	„	„
193	207	FLLTRILTIPQSLD	„	*1101	68	„	„	„
193	207	FLLTRILTIPQSLD	„	*0104	63	„	„	„
193	207	FLLTRILTIPQSLD	„	*0106	48	„	„	„
193	207	FLLTRILTIPQSLD	„	*0101	18	„	„	„
193	207	FLLTRILTIPQSLD	„	*0105	18	„	„	„
193	207	FLLTRILTIPQSLD	„	*0107	18	„	„	„
194	208	FLLTRILTIPQSLDS	1409	*0401	85	„	„	„
194	208	FLLTRILTIPQSLDS	„	*1301	65	„	„	„
194	208	FLLTRILTIPQSLDS	„	*0102	58	„	„	„
194	208	FLLTRILTIPQSLDS	„	*1101	53	„	„	„
194	208	FLLTRILTIPQSLDS	„	*0106	43	„	„	„
194	208	FLLTRILTIPQSLDS	„	*0104	40	„	„	„
194	208	FLLTRILTIPQSLDS	„	*0701	3	„	„	„
195	209	LLTRILTIPQSLDSW	„	*1301	70	„	„	„
195	209	LLTRILTIPQSLDSW	„	*0102	45	„	„	„
195	209	LLTRILTIPQSLDSW	„	*0106	35	„	„	„
195	209	LLTRILTIPQSLDSW	1410	*0401	15	„	„	„
196	210	LTRILTIPQSLDSWW	1411	*1301	45	„	„	„
					4798			

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
Cumulative Class II-B score:								

240	254	PPICPGYRWMCLRRF	1412	*1301	83	31	239	274
240	254	PPICPGYRWMCLRRF	„	*1101	70	„	„	„
241	255	PICPGYRWMCLRRFI	1413	*1301	80	„	„	„
241	255	PICPGYRWMCLRRFI	„	*1101	80	„	„	„
241	255	PICPGYRWMCLRRFI	„	*1501	60	„	„	„
241	255	PICPGYRWMCLRRFI	„	*0701	35	„	„	„
242	256	ICPGYRWMCLRRFII	1414	*1301	78	„	„	„
242	256	ICPGYRWMCLRRFII	„	*1501	95	„	„	„
242	256	ICPGYRWMCLRRFII	„	*1101	90	„	„	„
242	256	ICPGYRWMCLRRFII	„	*0701	85	„	„	„
242	256	ICPGYRWMCLRRFII	„	*0104	70	„	„	„
242	256	ICPGYRWMCLRRFII	„	*0102	68	„	„	„
242	256	ICPGYRWMCLRRFII	„	*0101	50	„	„	„
242	256	ICPGYRWMCLRRFII	„	*0105	50	„	„	„
242	256	ICPGYRWMCLRRFII	„	*0107	50	„	„	„
242	256	ICPGYRWMCLRRFII	„	*0301	35	„	„	„
243	257	CPGYRWMCLRRFIIF	1415	*1301	75	„	„	„
243	257	CPGYRWMCLRRFIIF	„	*1101	5	„	„	„
243	257	CPGYRWMCLRRFIIF	„	*1501	100	„	„	„
243	257	CPGYRWMCLRRFIIF	„	*0701	95	„	„	„
243	257	CPGYRWMCLRRFIIF	„	*0104	85	„	„	„
243	257	CPGYRWMCLRRFIIF	„	*0102	80	„	„	„
243	257	CPGYRWMCLRRFIIF	„	*0101	58	„	„	„
243	257	CPGYRWMCLRRFIIF	„	*0105	58	„	„	„
243	257	CPGYRWMCLRRFIIF	„	*0107	58	„	„	„
243	257	CPGYRWMCLRRFIIF	„	*0301	40	„	„	„
244	258	PGYRWMCLRRFIIFL	1416	*1301	73	„	„	„
244	258	PGYRWMCLRRFIIFL	„	*1101	95	„	„	„
244	258	PGYRWMCLRRFIIFL	„	*1501	90	„	„	„
244	258	PGYRWMCLRRFIIFL	„	*0701	80	„	„	„
244	258	PGYRWMCLRRFIIFL	„	*0104	75	„	„	„
244	258	PGYRWMCLRRFIIFL	„	*0102	73	„	„	„
244	258	PGYRWMCLRRFIIFL	„	*0101	45	„	„	„
244	258	PGYRWMCLRRFIIFL	„	*0105	45	„	„	„
244	258	PGYRWMCLRRFIIFL	„	*0107	45	„	„	„
244	258	PGYRWMCLRRFIIFL	„	*0301	15	„	„	„
245	259	GYRWMCLRRFIIFLF	1417	*1301	100	„	„	„
245	259	GYRWMCLRRFIIFLF	„	*0701	48	„	„	„
245	259	GYRWMCLRRFIIFLF	„	*1501	20	„	„	„
245	259	GYRWMCLRRFIIFLF	„	*1101	85	„	„	„
245	259	GYRWMCLRRFIIFLF	„	*0102	60	„	„	„
245	259	GYRWMCLRRFIIFLF	„	*0104	60	„	„	„
245	259	GYRWMCLRRFIIFLF	„	*0101	30	„	„	„
245	259	GYRWMCLRRFIIFLF	„	*0105	30	„	„	„
245	259	GYRWMCLRRFIIFLF	„	*0107	30	„	„	„
246	260	YRWMCLRRFIIFLFI	1418	*1301	98	„	„	„
246	260	YRWMCLRRFIIFLFI	„	*0701	50	„	„	„

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
246	260	YRWMCLRRFIIIFLFI	„	*1501	23	„	„	„
246	260	YRWMCLRRFIIIFLFI	„	*1101	75	„	„	„
247	261	RWMCLRRFIIIFLFIL	1419	*1301	95	„	„	„
247	261	RWMCLRRFIIIFLFIL	„	*0701	30	„	„	„
247	261	RWMCLRRFIIIFLFIL	„	*1501	10	„	„	„
247	261	RWMCLRRFIIIFLFIL	„	*1101	45	„	„	„
248	262	WMCLRRFIIIFLFILL	1420	*1301	93	„	„	„
248	262	WMCLRRFIIIFLFILL	„	*1501	73	„	„	„
248	262	WMCLRRFIIIFLFILL	„	*0701	60	„	„	„
248	262	WMCLRRFIIIFLFILL	„	*0301	28	„	„	„
249	263	MCLRRFIIIFLFILLL	1421	*1501	95	„	„	„
249	263	MCLRRFIIIFLFILLL	„	*1301	90	„	„	„
249	263	MCLRRFIIIFLFILLL	„	*0301	80	„	„	„
249	263	MCLRRFIIIFLFILLL	„	*0701	58	„	„	„
249	263	MCLRRFIIIFLFILLL	„	*0101	53	„	„	„
249	263	MCLRRFIIIFLFILLL	„	*1101	50	„	„	„
249	263	MCLRRFIIIFLFILLL	„	*0401	3	„	„	„
250	264	CLRRFIIIFLFILLLC	1422	*1301	88	„	„	„
250	264	CLRRFIIIFLFILLLC	„	*0301	78	„	„	„
250	264	CLRRFIIIFLFILLLC	„	*1501	68	„	„	„
250	264	CLRRFIIIFLFILLLC	„	*0701	55	„	„	„
250	264	CLRRFIIIFLFILLLC	„	*0101	48	„	„	„
250	264	CLRRFIIIFLFILLLC	„	*1101	48	„	„	„
251	265	LRRFIIIFLFILLLCL	1423	*1501	100	„	„	„
251	265	LRRFIIIFLFILLLCL	„	*1301	85	„	„	„
251	265	LRRFIIIFLFILLLCL	„	*0101	83	„	„	„
251	265	LRRFIIIFLFILLLCL	„	*0301	83	„	„	„
251	265	LRRFIIIFLFILLLCL	„	*1101	58	„	„	„
251	265	LRRFIIIFLFILLLCL	„	*0701	53	„	„	„
252	266	RRFIIIFLFILLLCLI	1424	*1501	98	„	„	„
252	266	RRFIIIFLFILLLCLI	„	*0101	80	„	„	„
252	266	RRFIIIFLFILLLCLI	„	*1101	55	„	„	„
252	266	RRFIIIFLFILLLCLI	„	*0301	40	„	„	„
252	266	RRFIIIFLFILLLCLI	„	*0701	38	„	„	„
252	266	RRFIIIFLFILLLCLI	„	*1301	35	„	„	„
253	267	RFIIIFLFILLLCLIF	1425	*1101	100	„	„	„
253	267	RFIIIFLFILLLCLIF	„	*0101	78	„	„	„
253	267	RFIIIFLFILLLCLIF	„	*1501	60	„	„	„
253	267	RFIIIFLFILLLCLIF	„	*0301	38	„	„	„
253	267	RFIIIFLFILLLCLIF	„	*0701	35	„	„	„
253	267	RFIIIFLFILLLCLIF	„	*1301	33	„	„	„
253	267	RFIIIFLFILLLCLIF	„	*0401	8	„	„	„
254	268	FIIFLFILLLCLIFL	1426	*1101	98	„	„	„
254	268	FIIFLFILLLCLIFL	„	*1501	88	„	„	„
254	268	FIIFLFILLLCLIFL	„	*0101	65	„	„	„
254	268	FIIFLFILLLCLIFL	„	*0301	35	„	„	„
254	268	FIIFLFILLLCLIFL	„	*1301	30	„	„	„
254	268	FIIFLFILLLCLIFL	„	*0401	13	„	„	„
255	269	IIFLFILLLCLIFLL	1427	*1101	95	„	„	„
255	269	IIFLFILLLCLIFLL	„	*1501	93	„	„	„

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
255	269	IIFLFILLLLCLIFLL	„	*0301	70	„	„	„
255	269	IIFLFILLLLCLIFLL	„	*0101	35	„	„	„
255	269	IIFLFILLLLCLIFLL	„	*0401	35	„	„	„
255	269	IIFLFILLLLCLIFLL	„	*1301	28	„	„	„
256	270	IFLFILLLLCLIFLLV	1428	*1101	93	„	„	„
256	270	IFLFILLLLCLIFLLV	„	*0301	68	„	„	„
256	270	IFLFILLLLCLIFLLV	„	*1501	53	„	„	„
256	270	IFLFILLLLCLIFLLV	„	*0101	30	„	„	„
256	270	IFLFILLLLCLIFLLV	„	*1301	25	„	„	„
256	270	IFLFILLLLCLIFLLV	„	*0401	10	„	„	„
257	271	FLFILLLLCLIFLLVL	1429	*1101	90	„	„	„
257	271	FLFILLLLCLIFLLVL	„	*0301	65	„	„	„
257	271	FLFILLLLCLIFLLVL	„	*1501	58	„	„	„
257	271	FLFILLLLCLIFLLVL	„	*0101	28	„	„	„
257	271	FLFILLLLCLIFLLVL	„	*1301	23	„	„	„
257	271	FLFILLLLCLIFLLVL	„	*0401	18	„	„	„
258	272	LFILLLLCLIFLLVLL	1430	*1101	88	„	„	„
258	272	LFILLLLCLIFLLVLL	„	*0301	63	„	„	„
258	272	LFILLLLCLIFLLVLL	„	*1501	50	„	„	„
258	272	LFILLLLCLIFLLVLL	„	*0101	25	„	„	„
258	272	LFILLLLCLIFLLVLL	„	*1301	20	„	„	„
259	273	FILLLLCLIFLLVLLD	1431	*1101	85	„	„	„
259	273	FILLLLCLIFLLVLLD	„	*0301	55	„	„	„
259	273	FILLLLCLIFLLVLLD	„	*1501	30	„	„	„
259	273	FILLLLCLIFLLVLLD	„	*0101	23	„	„	„
259	273	FILLLLCLIFLLVLLD	„	*1301	18	„	„	„
260	274	ILLLCLIFLLVLLDY	1432	*1101	45	„	„	„
260	274	ILLLCLIFLLVLLDY	„	*1301	15	„	„	„
260	274	ILLLCLIFLLVLLDY	„	*1501	13	„	„	„
Cumulative Class II-B score:					7238			

330	344	WAFAKYLWEWASVRF	1433	*1501	5	32	323	358
331	345	AFAKYLWEWASVRFS	1434	*0401	65	„	„	„
331	345	AFAKYLWEWASVRFS	„	*0301	30	„	„	„
331	345	AFAKYLWEWASVRFS	„	*1501	15	„	„	„
331	345	AFAKYLWEWASVRFS	„	*1101	5	„	„	„
332	346	FAKYLWEWASVRFSW	1435	*0401	80	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0301	55	„	„	„
332	346	FAKYLWEWASVRFSW	„	*1501	50	„	„	„
332	346	FAKYLWEWASVRFSW	„	*1101	40	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0104	25	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0101	23	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0105	23	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0107	23	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0701	15	„	„	„
333	347	AKYLWEWASVRFSWL	1436	*0701	28	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0401	60	„	„	„

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
333	347	AKYLWEWASVRFSWL	„	*0301	25	„	„	„
333	347	AKYLWEWASVRFSWL	„	*1101	25	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0101	3	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0105	3	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0107	3	„	„	„
334	348	KYLWEWASVRFSWLS	1437	*0701	25	„	„	„
334	348	KYLWEWASVRFSWLS	„	*0401	5	„	„	„
336	350	LWEWASVRFSWLSLL	1438	*0301	33	„	„	„
337	351	WEWASVRFSWLSLLV	1439	*0301	73	„	„	„
337	351	WEWASVRFSWLSLLV	„	*1501	45	„	„	„
337	351	WEWASVRFSWLSLLV	„	*1301	25	„	„	„
338	352	EWASVRFSWLSLLVP	1440	*0301	30	„	„	„
338	352	EWASVRFSWLSLLVP	„	*1501	40	„	„	„
338	352	EWASVRFSWLSLLVP	„	*1301	35	„	„	„
339	353	WASVRFSWLSLLVPF	1441	*0301	58	„	„	„
339	353	WASVRFSWLSLLVPF	„	*1501	55	„	„	„
339	353	WASVRFSWLSLLVPF	„	*1301	50	„	„	„
339	353	WASVRFSWLSLLVPF	„	*0104	38	„	„	„
339	353	WASVRFSWLSLLVPF	„	*0102	5	„	„	„
340	354	ASVRFSWLSLLVPFV	1442	*0301	75	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*0401	33	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*1101	18	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*0104	53	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*1501	30	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*0102	28	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*1301	20	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*0106	10	„	„	„
341	355	SVRFSWLSLLVPFVQ	1443	*0401	30	„	„	„
341	355	SVRFSWLSLLVPFVQ	„	*1101	15	„	„	„
341	355	SVRFSWLSLLVPFVQ	„	*0104	50	„	„	„
341	355	SVRFSWLSLLVPFVQ	„	*0102	23	„	„	„
341	355	SVRFSWLSLLVPFVQ	„	*0106	5	„	„	„
342	356	VRFSWLSLLVPFVQW	1444	*0401	28	„	„	„
342	356	VRFSWLSLLVPFVQW	„	*0101	15	„	„	„
342	356	VRFSWLSLLVPFVQW	„	*1101	13	„	„	„
342	356	VRFSWLSLLVPFVQW	„	*0104	15	„	„	„
343	357	RFSWLSLLVPFVQWF	1445	*0401	25	„	„	„
343	357	RFSWLSLLVPFVQWF	„	*0101	20	„	„	„
343	357	RFSWLSLLVPFVQWF	„	*1101	10	„	„	„
344	358	FSWLSLLVPFVQWFV	1446	*1501	90	„	„	„
344	358	FSWLSLLVPFVQWFV	„	*1301	70	„	„	„
344	358	FSWLSLLVPFVQWFV	„	*0401	23	„	„	„
344	358	FSWLSLLVPFVQWFV	„	*1101	8	„	„	„
Cumulative Class II-B score:					1815			

330	344	WAFAKYLWEWASVRF	1433	*1501	5	33	327	358
331	345	AFAKYLWEWASVRFS	1434	*0401	65	„	„	„
331	345	AFAKYLWEWASVRFS	„	*0301	30	„	„	„
331	345	AFAKYLWEWASVRFS	„	*1501	15	„	„	„

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
331	345	AFAYLWEWASVRFS	„	*1101	5	„	„	„
332	346	FAKYLWEWASVRFSW	1435	*0401	80	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0301	55	„	„	„
332	346	FAKYLWEWASVRFSW	„	*1501	50	„	„	„
332	346	FAKYLWEWASVRFSW	„	*1101	40	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0104	25	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0101	23	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0105	23	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0107	23	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0701	15	„	„	„
333	347	AKYLWEWASVRFSWL	1436	*0701	28	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0401	60	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0301	25	„	„	„
333	347	AKYLWEWASVRFSWL	„	*1101	25	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0101	3	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0105	3	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0107	3	„	„	„
334	348	KYLWEWASVRFSWLS	1437	*0701	25	„	„	„
334	348	KYLWEWASVRFSWLS	„	*0401	5	„	„	„
336	350	LWEWASVRFSWLSLL	1438	*0301	33	„	„	„
337	351	WEWASVRFSWLSLLV	1439	*0301	73	„	„	„
337	351	WEWASVRFSWLSLLV	„	*1501	45	„	„	„
337	351	WEWASVRFSWLSLLV	„	*1301	25	„	„	„
338	352	EWASVRFSWLSLLVP	1440	*0301	30	„	„	„
338	352	EWASVRFSWLSLLVP	„	*1501	40	„	„	„
338	352	EWASVRFSWLSLLVP	„	*1301	35	„	„	„
339	353	WASVRFSWLSLLVPF	1441	*0301	58	„	„	„
339	353	WASVRFSWLSLLVPF	„	*1501	55	„	„	„
339	353	WASVRFSWLSLLVPF	„	*1301	50	„	„	„
339	353	WASVRFSWLSLLVPF	„	*0104	38	„	„	„
339	353	WASVRFSWLSLLVPF	„	*0102	5	„	„	„
340	354	ASVRFSWLSLLVPFV	1442	*0301	75	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*0401	33	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*1101	18	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*0104	53	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*1501	30	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*0102	28	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*1301	20	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*0106	10	„	„	„
341	355	SVRFSWLSLLVPFVQ	1443	*0401	30	„	„	„
341	355	SVRFSWLSLLVPFVQ	„	*1101	15	„	„	„
341	355	SVRFSWLSLLVPFVQ	„	*0104	50	„	„	„
341	355	SVRFSWLSLLVPFVQ	„	*0102	23	„	„	„
341	355	SVRFSWLSLLVPFVQ	„	*0106	5	„	„	„
342	356	VRFSWLSLLVPFVQW	1444	*0401	28	„	„	„
342	356	VRFSWLSLLVPFVQW	„	*0101	15	„	„	„
342	356	VRFSWLSLLVPFVQW	„	*1101	13	„	„	„
342	356	VRFSWLSLLVPFVQW	„	*0104	15	„	„	„
343	357	RFSWLSLLVPFVQWF	1445	*0401	25	„	„	„
343	357	RFSWLSLLVPFVQWF	„	*0101	20	„	„	„

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
343	357	RFSWLSLLVPFVQWF	„	*1101	10	„	„	„
344	358	FSWLSLLVPFVQWFV	1446	*1501	90	„	„	„
344	358	FSWLSLLVPFVQWFV	„	*1301	70	„	„	„
344	358	FSWLSLLVPFVQWFV	„	*0401	23	„	„	„
344	358	FSWLSLLVPFVQWFV	„	*1101	8	„	„	„
Cumulative Class II-B score:					1815			

330	344	WAFAKYLWEWASVRF	1433	*1501	5	34	328	358
331	345	AFAKYLWEWASVRFS	1434	*0401	65	„	„	„
331	345	AFAKYLWEWASVRFS	„	*0301	30	„	„	„
331	345	AFAKYLWEWASVRFS	„	*1501	15	„	„	„
331	345	AFAKYLWEWASVRFS	„	*1101	5	„	„	„
332	346	FAKYLWEWASVRFSW	1435	*0401	80	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0301	55	„	„	„
332	346	FAKYLWEWASVRFSW	„	*1501	50	„	„	„
332	346	FAKYLWEWASVRFSW	„	*1101	40	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0104	25	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0101	23	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0105	23	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0107	23	„	„	„
332	346	FAKYLWEWASVRFSW	„	*0701	15	„	„	„
333	347	AKYLWEWASVRFSWL	1436	*0701	28	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0401	60	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0301	25	„	„	„
333	347	AKYLWEWASVRFSWL	„	*1101	25	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0101	3	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0105	3	„	„	„
333	347	AKYLWEWASVRFSWL	„	*0107	3	„	„	„
334	348	KYLWEWASVRFSWLS	1437	*0701	25	„	„	„
334	348	KYLWEWASVRFSWLS	„	*0401	5	„	„	„
336	350	LWEWASVRFSWLSLL	1438	*0301	33	„	„	„
337	351	WEWASVRFSWLSLLV	1439	*0301	73	„	„	„
337	351	WEWASVRFSWLSLLV	„	*1501	45	„	„	„
337	351	WEWASVRFSWLSLLV	„	*1301	25	„	„	„
338	352	EWASVRFSWLSLLVP	1440	*0301	30	„	„	„
338	352	EWASVRFSWLSLLVP	„	*1501	40	„	„	„
338	352	EWASVRFSWLSLLVP	„	*1301	35	„	„	„
339	353	WASVRFSWLSLLVPF	1441	*0301	58	„	„	„
339	353	WASVRFSWLSLLVPF	„	*1501	55	„	„	„
339	353	WASVRFSWLSLLVPF	„	*1301	50	„	„	„
339	353	WASVRFSWLSLLVPF	„	*0104	38	„	„	„
339	353	WASVRFSWLSLLVPF	„	*0102	5	„	„	„
340	354	ASVRFSWLSLLVPFV	1442	*0301	75	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*0401	33	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*1101	18	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*0104	53	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*1501	30	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*0102	28	„	„	„
340	354	ASVRFSWLSLLVPFV	„	*1301	20	„	„	„

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
340	354	ASVRFSWLSLLVPFV	„	*0106	10	„	„	„
341	355	SVRFSWLSLLVPFVQ	1443	*0401	30	„	„	„
341	355	SVRFSWLSLLVPFVQ	„	*1101	15	„	„	„
341	355	SVRFSWLSLLVPFVQ	„	*0104	50	„	„	„
341	355	SVRFSWLSLLVPFVQ	„	*0102	23	„	„	„
341	355	SVRFSWLSLLVPFVQ	„	*0106	5	„	„	„
342	356	VRFSWLSLLVPFVQW	1444	*0401	28	„	„	„
342	356	VRFSWLSLLVPFVQW	„	*0101	15	„	„	„
342	356	VRFSWLSLLVPFVQW	„	*1101	13	„	„	„
342	356	VRFSWLSLLVPFVQW	„	*0104	15	„	„	„
343	357	RFSWLSLLVPFVQWF	1445	*0401	25	„	„	„
343	357	RFSWLSLLVPFVQWF	„	*0101	20	„	„	„
343	357	RFSWLSLLVPFVQWF	„	*1101	10	„	„	„
344	358	FSWLSLLVPFVQWFV	1446	*1501	90	„	„	„
344	358	FSWLSLLVPFVQWFV	„	*1301	70	„	„	„
344	358	FSWLSLLVPFVQWFV	„	*0401	23	„	„	„
344	358	FSWLSLLVPFVQWFV	„	*1101	8	„	„	„
Cumulative Class II-B score:					1815			

365	379	WLSAIWMMWYWGPSL	1447	*1501	35	35	365	400
366	380	LSAIWMMWYWGPSLY	1448	*1501	48	„	„	„
367	381	SAIWMMWYWGPSLYS	1449	*1501	40	„	„	„
368	382	AIWMMWYWGPSLYSI	1450	*1501	45	„	„	„
369	383	IWMMWYWGPSLYSIV	1451	*1501	38	„	„	„
369	383	IWMMWYWGPSLYSIV	„	*0101	20	„	„	„
369	383	IWMMWYWGPSLYSIV	„	*0105	20	„	„	„
369	383	IWMMWYWGPSLYSIV	„	*0107	20	„	„	„
370	384	WMMWYWGPSLYSIVS	1452	*1501	28	„	„	„
370	384	WMMWYWGPSLYSIVS	„	*0101	33	„	„	„
370	384	WMMWYWGPSLYSIVS	„	*0105	33	„	„	„
370	384	WMMWYWGPSLYSIVS	„	*0107	33	„	„	„
371	385	MMWYWGPSLYSIVSP	1453	*1501	8	„	„	„
373	387	WYWGPSLYSIVSPFI	1454	*0701	90	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0401	40	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0106	45	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0101	43	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0105	43	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0107	43	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0102	18	„	„	„
374	388	YWGPSLYSIVSPFIP	1455	*0701	65	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0101	60	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0105	60	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0107	60	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0401	55	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0106	53	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0102	48	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0104	43	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*1501	25	„	„	„
375	389	WGPSLYSIVSPFIPL	1456	*0701	85	„	„	„

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
375	389	WGPSLYSIVSPFIPL	„	*0401	20	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*1501	18	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0104	88	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0102	85	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0101	83	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0105	83	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0106	83	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0107	83	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0103	15	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*1101	15	„	„	„
376	390	GPSLYSIVSPFIPLL	1457	*0701	83	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0401	43	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*1501	43	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0101	33	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0104	100	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0102	98	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0105	93	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0107	93	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0106	90	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0103	50	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*1101	35	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*1301	15	„	„	„
377	391	PSLYSIVSPFIPLLP	1458	*0701	63	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*1501	33	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0101	10	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0401	5	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0104	93	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0102	90	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0106	85	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0105	80	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0107	80	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0103	20	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*1101	20	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*1301	10	„	„	„
378	392	SLYSIVSPFIPLLPI	1459	*0701	43	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0104	83	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0102	78	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0106	73	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0101	63	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0105	63	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0107	63	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*1501	35	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0401	20	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0103	5	„	„	„
379	393	LYSIVSPFIPLLPIF	1460	*0701	33	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0106	63	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0102	55	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0104	55	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0101	53	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0105	53	„	„	„

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
379	393	LYSIVSPFIPLLPFI	„	*0107	53	„	„	„
380	394	YSIVSPFIPLLPFI	1461	*1101	35	„	„	„
380	394	YSIVSPFIPLLPFI	„	*0101	8	„	„	„
380	394	YSIVSPFIPLLPFI	„	*0104	23	„	„	„
380	394	YSIVSPFIPLLPFI	„	*0106	18	„	„	„
380	394	YSIVSPFIPLLPFI	„	*0105	5	„	„	„
380	394	YSIVSPFIPLLPFI	„	*0107	5	„	„	„
381	395	SIVSPFIPLLPFI	1462	*1101	33	„	„	„
381	395	SIVSPFIPLLPFI	„	*0101	5	„	„	„
382	396	IVSPFIPLLPFI	1463	*1101	30	„	„	„
382	396	IVSPFIPLLPFI	„	*0101	3	„	„	„
382	396	IVSPFIPLLPFI	„	*0104	18	„	„	„
382	396	IVSPFIPLLPFI	„	*0105	15	„	„	„
382	396	IVSPFIPLLPFI	„	*0107	15	„	„	„
382	396	IVSPFIPLLPFI	„	*0102	3	„	„	„
383	397	VSPFIPLLPFI	1464	*1101	28	„	„	„
383	397	VSPFIPLLPFI	„	*0101	13	„	„	„
383	397	VSPFIPLLPFI	„	*0105	13	„	„	„
383	397	VSPFIPLLPFI	„	*0107	13	„	„	„
383	397	VSPFIPLLPFI	„	*0104	10	„	„	„
384	398	SPFIPLLPFI	1465	*1101	25	„	„	„
384	398	SPFIPLLPFI	„	*1501	5	„	„	„
386	400	FIPLLPIFFCLWVYI	1466	*1101	23	„	„	„
Cumulative Class II-B score:					4425			

371	385	MMWYWGPSLYSIVSP	1453	*1501	8	36	371	400
373	387	WYWGPSLYSIVSPFI	1454	*0701	90	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0401	40	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0106	45	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0101	43	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0105	43	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0107	43	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0102	18	„	„	„
374	388	YWGPSLYSIVSPFIP	1455	*0701	65	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0101	60	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0105	60	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0107	60	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0401	55	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0106	53	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0102	48	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0104	43	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*1501	25	„	„	„
375	389	WGPSLYSIVSPFIPL	1456	*0701	85	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0401	20	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*1501	18	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0104	88	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0102	85	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0101	83	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0105	83	„	„	„

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
375	389	WGPSLYSIVSPFIPL	„	*0106	83	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0107	83	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0103	15	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*1101	15	„	„	„
376	390	GPSLYSIVSPFIPLL	1457	*0701	83	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0401	43	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*1501	43	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0101	33	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0104	100	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0102	98	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0105	93	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0107	93	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0106	90	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0103	50	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*1101	35	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*1301	15	„	„	„
377	391	PSLYSIVSPFIPLL	1458	*0701	63	„	„	„
377	391	PSLYSIVSPFIPLL	„	*1501	33	„	„	„
377	391	PSLYSIVSPFIPLL	„	*0101	10	„	„	„
377	391	PSLYSIVSPFIPLL	„	*0401	5	„	„	„
377	391	PSLYSIVSPFIPLL	„	*0104	93	„	„	„
377	391	PSLYSIVSPFIPLL	„	*0102	90	„	„	„
377	391	PSLYSIVSPFIPLL	„	*0106	85	„	„	„
377	391	PSLYSIVSPFIPLL	„	*0105	80	„	„	„
377	391	PSLYSIVSPFIPLL	„	*0107	80	„	„	„
377	391	PSLYSIVSPFIPLL	„	*0103	20	„	„	„
377	391	PSLYSIVSPFIPLL	„	*1101	20	„	„	„
377	391	PSLYSIVSPFIPLL	„	*1301	10	„	„	„
378	392	SLYSIVSPFIPLLPI	1459	*0701	43	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0104	83	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0102	78	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0106	73	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0101	63	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0105	63	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0107	63	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*1501	35	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0401	20	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0103	5	„	„	„
379	393	LYSIVSPFIPLLPIF	1460	*0701	33	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0106	63	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0102	55	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0104	55	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0101	53	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0105	53	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0107	53	„	„	„
380	394	YSIVSPFIPLLPIFF	1461	*1101	35	„	„	„
380	394	YSIVSPFIPLLPIFF	„	*0101	8	„	„	„
380	394	YSIVSPFIPLLPIFF	„	*0104	23	„	„	„
380	394	YSIVSPFIPLLPIFF	„	*0106	18	„	„	„
380	394	YSIVSPFIPLLPIFF	„	*0105	5	„	„	„

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
380	394	YSIVSPFIPLLPPIFF	„	*0107	5	„	„	„
381	395	SIVSPFIPLLPPIFFC	1462	*1101	33	„	„	„
381	395	SIVSPFIPLLPPIFFC	„	*0101	5	„	„	„
382	396	IVSPFIPLLPPIFFCL	1463	*1101	30	„	„	„
382	396	IVSPFIPLLPPIFFCL	„	*0101	3	„	„	„
382	396	IVSPFIPLLPPIFFCL	„	*0104	18	„	„	„
382	396	IVSPFIPLLPPIFFCL	„	*0105	15	„	„	„
382	396	IVSPFIPLLPPIFFCL	„	*0107	15	„	„	„
382	396	IVSPFIPLLPPIFFCL	„	*0102	3	„	„	„
383	397	VSPFIPLLPPIFFCLW	1464	*1101	28	„	„	„
383	397	VSPFIPLLPPIFFCLW	„	*0101	13	„	„	„
383	397	VSPFIPLLPPIFFCLW	„	*0105	13	„	„	„
383	397	VSPFIPLLPPIFFCLW	„	*0107	13	„	„	„
383	397	VSPFIPLLPPIFFCLW	„	*0104	10	„	„	„
384	398	SPFIPLLPPIFFCLWV	1465	*1101	25	„	„	„
384	398	SPFIPLLPPIFFCLWV	„	*1501	5	„	„	„
386	400	FIPLLPPIFFCLWVYI	1466	*1101	23	„	„	„
Cumulative Class II-B score:					4035			

370	384	WMMWYWGPSLYSIVS	1452	*1501	28	37	370	400
370	384	WMMWYWGPSLYSIVS	„	*0101	33	„	„	„
370	384	WMMWYWGPSLYSIVS	„	*0105	33	„	„	„
370	384	WMMWYWGPSLYSIVS	„	*0107	33	„	„	„
371	385	MMWYWGPSLYSIVSP	1453	*1501	8	„	„	„
373	387	WYWGPSLYSIVSPFI	1454	*0701	90	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0401	40	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0106	45	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0101	43	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0105	43	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0107	43	„	„	„
373	387	WYWGPSLYSIVSPFI	„	*0102	18	„	„	„
374	388	YWGPSLYSIVSPFIP	1455	*0701	65	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0101	60	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0105	60	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0107	60	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0401	55	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0106	53	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0102	48	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*0104	43	„	„	„
374	388	YWGPSLYSIVSPFIP	„	*1501	25	„	„	„
375	389	WGPSLYSIVSPFIPL	1456	*0701	85	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0401	20	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*1501	18	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0104	88	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0102	85	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0101	83	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0105	83	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0106	83	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*0107	83	„	„	„

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
375	389	WGPSLYSIVSPFIPL	„	*0103	15	„	„	„
375	389	WGPSLYSIVSPFIPL	„	*1101	15	„	„	„
376	390	GPSLYSIVSPFIPLL	1457	*0701	83	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0401	43	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*1501	43	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0101	33	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0104	100	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0102	98	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0105	93	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0107	93	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0106	90	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*0103	50	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*1101	35	„	„	„
376	390	GPSLYSIVSPFIPLL	„	*1301	15	„	„	„
377	391	PSLYSIVSPFIPLLP	1458	*0701	63	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*1501	33	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0101	10	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0401	5	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0104	93	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0102	90	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0106	85	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0105	80	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0107	80	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*0103	20	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*1101	20	„	„	„
377	391	PSLYSIVSPFIPLLP	„	*1301	10	„	„	„
378	392	SLYSIVSPFIPLLPI	1459	*0701	43	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0104	83	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0102	78	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0106	73	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0101	63	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0105	63	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0107	63	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*1501	35	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0401	20	„	„	„
378	392	SLYSIVSPFIPLLPI	„	*0103	5	„	„	„
379	393	LYSIVSPFIPLLPIF	1460	*0701	33	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0106	63	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0102	55	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0104	55	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0101	53	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0105	53	„	„	„
379	393	LYSIVSPFIPLLPIF	„	*0107	53	„	„	„
380	394	YSIVSPFIPLLPIFF	1461	*1101	35	„	„	„
380	394	YSIVSPFIPLLPIFF	„	*0101	8	„	„	„
380	394	YSIVSPFIPLLPIFF	„	*0104	23	„	„	„
380	394	YSIVSPFIPLLPIFF	„	*0106	18	„	„	„
380	394	YSIVSPFIPLLPIFF	„	*0105	5	„	„	„
380	394	YSIVSPFIPLLPIFF	„	*0107	5	„	„	„
381	395	SIVSPFIPLLPIFFC	1462	*1101	33	„	„	„

HLA class II binding peptides in SLP derived from HBV Surface antigen						Peptide of invention (SLP)		
Start	End	Sequence ^A	SEQ ID NO:	HLA-DRB1 molecule	Class II-B score ^B	SLP#	SLP Start	SLP End
381	395	SIVSPFIPLLPIFFC	„	*0101	5	„	„	„
382	396	IVSPFIPLLPIFFCL	1463	*1101	30	„	„	„
382	396	IVSPFIPLLPIFFCL	„	*0101	3	„	„	„
382	396	IVSPFIPLLPIFFCL	„	*0104	18	„	„	„
382	396	IVSPFIPLLPIFFCL	„	*0105	15	„	„	„
382	396	IVSPFIPLLPIFFCL	„	*0107	15	„	„	„
382	396	IVSPFIPLLPIFFCL	„	*0102	3	„	„	„
383	397	VSPFIPLLPIFFCLW	1464	*1101	28	„	„	„
383	397	VSPFIPLLPIFFCLW	„	*0101	13	„	„	„
383	397	VSPFIPLLPIFFCLW	„	*0105	13	„	„	„
383	397	VSPFIPLLPIFFCLW	„	*0107	13	„	„	„
383	397	VSPFIPLLPIFFCLW	„	*0104	10	„	„	„
384	398	SPFIPLLPIFFCLWV	1465	*1101	25	„	„	„
384	398	SPFIPLLPIFFCLWV	„	*1501	5	„	„	„
386	400	FIPLLPIFFCLWVYI	1466	*1101	23	„	„	„
Cumulative Class II-B score:					4160			

“Start” and “End” are relative to the amino acid sequence of human HBV large surface protein as depicted in SEQ ID NO: 1141

^A Peptide amino acid sequence. Each HLA-DRB1 binding peptide of HBV large surface protein is listed separately for each HLA class II molecule to which it is predicted to bind, and each peptide can be listed multiple times for that reason.

^B B-score. See *Material and Methods* (Examples section).

^C Cumulative B-score. See *Material and Methods* (Examples section).

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CLAIMS

1. A peptide comprising at least 70 predicted T-cell epitopes, and at least 3 proteasomal cleavage sites, wherein said peptide is derived from an HBV protein and wherein said peptide is from 15 to 100 amino acids in length.
5
2. A peptide according to claim 1, wherein said peptide comprises or consists of an amino acid sequence of any of the proteins selected from the group consisting of HBV polymerase, HBV core protein, HBV X-protein and HBV large surface protein.
10
3. A peptide according to claim 1 or 2, wherein said peptide comprises at least 70 predicted HLA class I-restricted CD8⁺ cytotoxic T-cell epitopes and at least 1 predicted HLA class II-restricted CD4⁺ T-helper epitopes, preferably said peptide comprises a peptide selected from the group consisting of SEQ ID NO: 75, 51-74, 76-79, 1142-
15 1145 and 1468-1471.
4. A peptide according to any of the claims 1-3, wherein said peptide comprises at least 70 predicted HLA class I-restricted CD8⁺ cytotoxic T-cell epitopes and at least 15 predicted HLA class II-restricted CD4⁺ T-helper epitopes, preferably said peptide
20 comprises a peptide selected from the group consisting of SEQ ID NO: 75, 51-53, 55, 57, 60, 63, 64, 66, 68, 71, 72, 74, 76-78, 1142, 1145, 1468-1471.
5. A peptide according to any of the claims 1 – 4, wherein said peptide comprises at least 95 predicted HLA class I-restricted CD8⁺ cytotoxic T-cell epitopes and at least 25 predicted HLA class II-restricted CD4⁺ T-helper epitopes, preferably said peptide
25 comprises a peptide selected from the group consisting of SEQ ID NO: 75, 55, 60, 63, 64, 68, 71, 77, 1142 and 1469.
6. A peptide selected from the group consisting of SEQ ID NO: 75, 55, 60, 63, 64, 68,
30 71, 77, 1142 and 1469.

7. A peptide according to any one of claims 1 to 6, comprising a modified amino acid, a non-naturally occurring amino acid and/or a covalently linked functional group such as a fluorinated group, a human toll-like receptor ligand and/or agonist, an oligonucleotide conjugate, PSA, a sugar chain or glycan, a pam3cys and/or derivative thereof,
- 5 preferably a pam3cys lipopeptide or variant or derivative thereof, CpG oligodeoxynucleotides (CpG-ODNs), Cyclic dinucleotides (CDNs), 2-aminoisobutyric acid (Abu), Muramyl dipeptide (MDP), a DC pulse cassette, a tetanus toxin derived peptide.
- 10 8. A polynucleotide encoding a peptide according to any one of claims 1 to 7.
9. A composition comprising a peptide according to any one of claims 1 to 7 and/or a polynucleotide according to claim 8, and a pharmaceutically acceptable carrier.
- 15 10. A composition comprising at least two different peptides according to any one of claims 1 to 7 and/or at least two different polynucleotides according to claim 8, and a pharmaceutically acceptable carrier.
11. A composition according to claim 9 or 10, further comprising at least one adjuvant.
- 20 12. A peptide according to any one of claims 1 to 7 and/or a polynucleotide according to claim 8 and/or a composition according to any one of claims 9-11, for use as a medicament.
- 25 13. A method for the prevention and/or treatment of an HBV related disease comprising administering to a subject an effective amount of a peptide according to any one of claims 1 to 7 and/or a polynucleotide according to claim 8 and/or a composition according to any one of claims 9-11.
- 30 14. A peptide according to any one of claims 1 to 7 and/or a polynucleotide according to claim 8 and/or a composition according to any one of claims 9-11, for the treatment and/or prevention of an HBV related disease or condition.

15. Use of a peptide according to any one of claims 1 to 7 and/or a polynucleotide according to claim 8 and/or a composition according to any one of claims 9-11, for the manufacturing of a medicament for the treatment and/or prevention of an HBV related disease or condition.

1/6

1	W	1	+	1,08	→	2	P	2	0,09	3	T	3	0,99	4	S	4	0,27	5	A	5	+	1,87	6	O	6	0,88	7	H	7	0,70	8	F	8	+	1,42	9	R	9	1,83	→	10	X	10	1,21	11	T	11	+	1,89	12	T	12	1,82	13	T	13	1,71	14	T	14	1,85	15	O	15	0,80	→	16	D	16	0,57	17	G	17	0,07	18	I	18	0,12	19	E	19	0,52	20	V	20	1,41	21	G	21	0,62	22	P	22	0,06	23	T	23	0,79	24	E	24	0,44	25	E	25	0,97	26	E	26	0,33	→	27	T	27	1,36	28	P	28	0,07	29	R	29	0,94	30	T	30	1,77
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1	N	419	0,83	
2	T	420	+ 1,42	←
3	T	421	1,64	
4	S	422	0,84	
5	S	423	0,60	←
6	N	424	0,13	
7	T	425	+ 1,79	→
8	S	426	0,30	
9	M	427	1,77	
10	T	428	+ 1,54	→
11	S	429	0,55	
12	T	430	+ 1,74	←
13	D	431	0,11	→
14	K	432	+ 1,41	←
15	S	433	0,37	
16	V	434	1,33	
17	V	435	0,74	
18	F	436	1,90	
19	K	437	+ 1,81	→
20	H	438	0,61	
21	-	439	+ 1,79	→
22	D	440	0,16	
23	T	441	1,00	
24	H	442	0,25	←
25	D	443	0,27	←
26	V	444	0,89	
27	V	445	0,62	
28	M	446	+ 1,63	→
29	D	447	0,32	
30	H	448	0,52	
31	T	449	+ 1,61	←
32	T	450	+ 1,81	→
33	-	451	0,84	→
34	G	452	0,32	
35	S	453	0,77	←
36	S	454	0,26	
37	G	455	0,11	
38	T	456	1,81	

1	H	481	0,31
2	D	482	0,87
3	S	483	0,13
4	C	484	0,18
5	S	485	0,30
6	B	486	1,12
7	D	487	0,56
8	T	488	+ 1,49
9	K	489	0,96
10	K	490	+ 1,20
11	S	491	0,58
12	T	492	+ 1,59
13	M	493	1,55
14	T	494	+ 1,55
15	T	495	1,34
16	K	496	+ 1,80
17	K	497	1,07
18	L	498	0,21
19	K	499	1,86
20	G	500	0,13
21	M	501	+ 1,93
22	K	502	0,71
23	T	503	+ 1,95
24	H	504	0,88
25	T	505	+ 1,71
26	K	506	+ 1,90
27	S	507	0,29
28	H	508	0,84
29	D	509	0,08
30	-	510	0,99
31	K	511	0,55
32	T	512	+ 1,95
33	G	513	0,48
34	F	514	1,62

Fig. 1b

SLP no.14. HBV Polymerase aa 524 - 559 (SEQ ID NO: 64)																																																																																																																																															
1	S	524	0.42	2	P	525	0.57	3	F	526	0.96	4	L	527	0.99	5	L	528	+ 1.72	6	A	529	+ 1.51	7	Q	530	1.00	8	F	531	+ 1.59	9	T	532	0.30	10	S	533	0.76	11	A	534	0.92	12	I	535	0.94	13	C	536	0.65	14	S	537	0.41	15	V	538	+ 1.40	16	V	539	+ 1.34	17	R	540	+ 1.19	18	R	541	+ 1.69	19	A	542	0.50	20	F	543	+ 1.06	21	P	544	0.13	22	H	545	0.14	23	C	546	0.21	24	L	547	+ 1.96	25	A	548	+ 1.06	26	F	549	+ 1.82	27	S	550	0.25	28	Y	551	+ 1.93	29	M	552	1.02	30	D	553	0.88	31	D	554	0.76	32	V	555	0.60	33	V	556	0.34	34	L	557	+ 1.21	35	G	558	0.31	36	A	559	1.49

SLP no.18. HBV Polymerase aa 653 - 691 (SEQ ID NO: 68)																																																																																																																																																											
1	Y	653	+ 1.69	2	P	654	0.20	3	A	655	0.11	4	L	656	0.95	5	M	657	+ 1.18	6	P	658	0.13	7	L	659	1.00	8	Y	660	+ 1.81	9	A	661	+ 1.43	10	C	662	0.21	11	I	663	1.19	12	Q	664	0.20	13	A	665	+ 1.41	14	K	666	1.01	15	Q	667	1.04	16	A	668	0.96	17	F	669	1.07	18	T	670	0.07	19	F	671	+ 1.58	20	S	672	0.78	21	D	673	0.16	22	T	674	0.07	23	Y	675	+ 1.81	24	K	676	1.78	25	A	677	+ 1.62	26	F	678	0.94	27	L	679	0.51	28	S	680	0.71	29	K	681	+ 1.52	30	Q	682	0.56	31	Y	683	+ 1.56	32	M	684	+ 1.51	33	N	685	0.39	34	L	686	+ 1.83	35	Y	687	+ 1.58	36	P	688	0.10	37	V	689	0.93	38	A	690	1.25	39	R	691	1.78

SLP no.21. HBV Polymerase aa 754 - 791 (SEQ ID NO: 71)																																																																																																																																																							
1	V	754	0.55	2	L	755	+ 1.83	3	S	756	0.42	4	R	757	+ 1.59	5	K	758	0.82	6	Y	759	+ 1.71	7	T	760	0.92	8	S	761	0.13	9	F	762	+ 1.77	10	P	763	0.18	11	W	764	0.99	12	L	765	1.24	13	L	766	+ 1.92	14	G	767	0.64	15	C	768	0.66	16	T	769	0.19	17	A	770	+ 1.76	18	N	771	0.39	19	M	772	+ 1.72	20	I	773	0.22	21	L	774	+ 1.41	22	R	775	+ 1.01	23	G	776	0.55	24	T	777	0.80	25	S	778	0.39	26	F	779	+ 1.20	27	V	780	1.19	28	Y	781	+ 1.69	29	V	782	+ 1.67	30	P	783	0.23	31	S	784	0.55	32	A	785	+ 1.35	33	L	786	+ 1.57	34	N	787	0.25	35	P	788	0.38	36	A	789	0.68	37	D	790	0.18	38	D	791	0.43

Fig. 1c

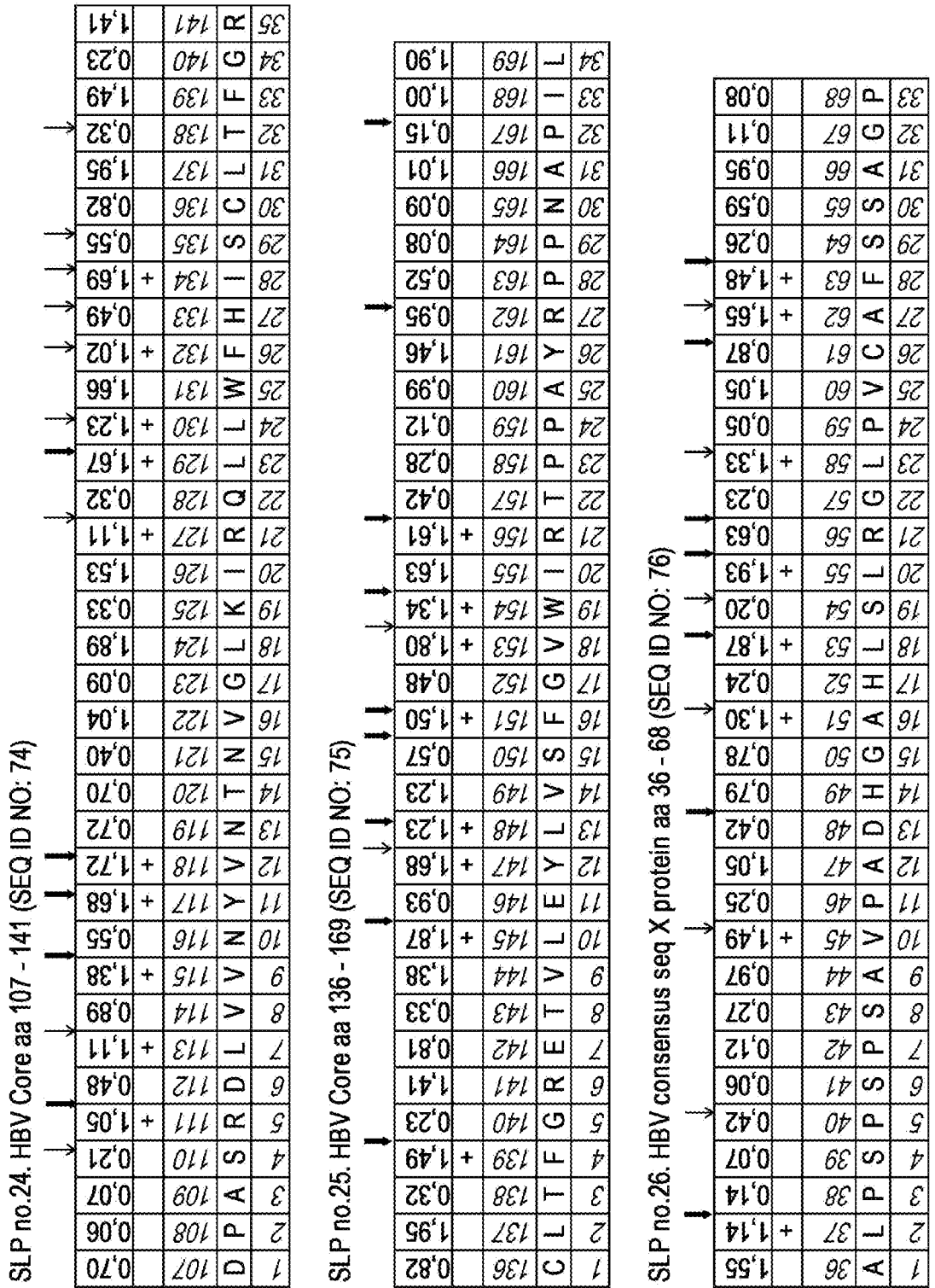
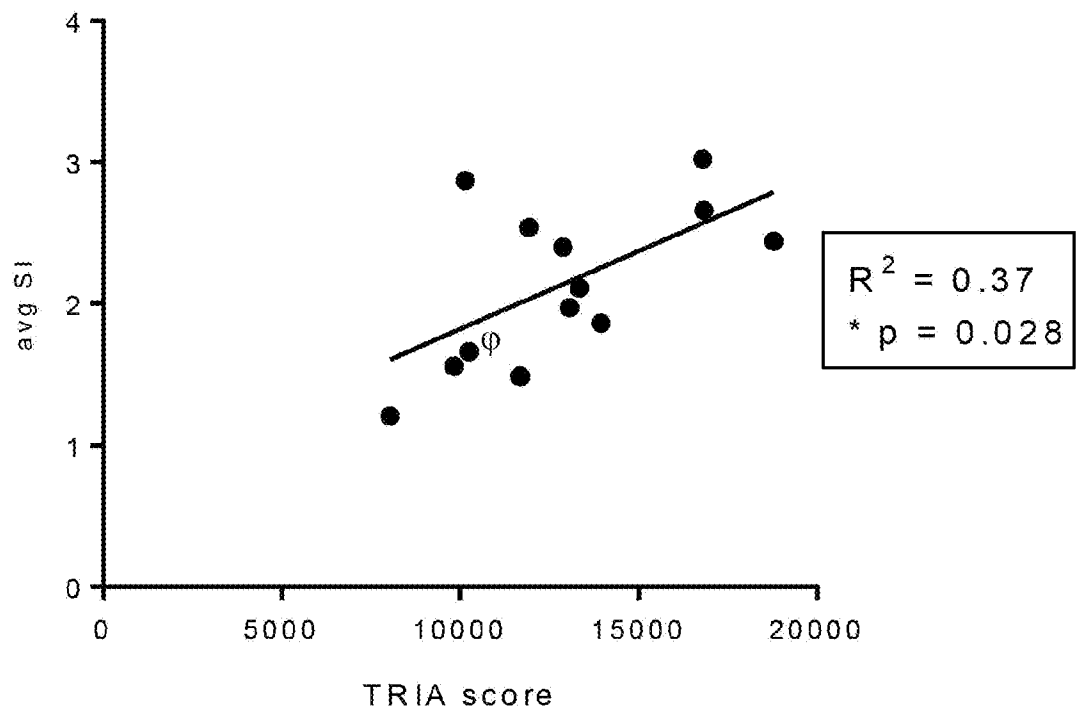


Fig. 4



INTERNATIONAL SEARCH REPORT

International application No
PCT/NL2015/050390

A. CLASSIFICATION OF SUBJECT MATTER
INV. A61K38/16 C12N15/00
ADD.

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
A61K C12N

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

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

EP0-Internal, BIOSIS, Sequence Search, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

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X	----- US 2012/149120 A1 (LEE JEE WON [KR] ET AL) 14 June 2012 (2012-06-14) sequence 15	1-15
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☒ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

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"&" document member of the same patent family

Date of the actual completion of the international search

22 July 2015

Date of mailing of the international search report

03/08/2015

Name and mailing address of the ISA/

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040,
Fax: (+31-70) 340-3016

Authorized officer

Scheffzyk, Irmgard

INTERNATIONAL SEARCH REPORT

International application No
PCT/NL2015/050390

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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