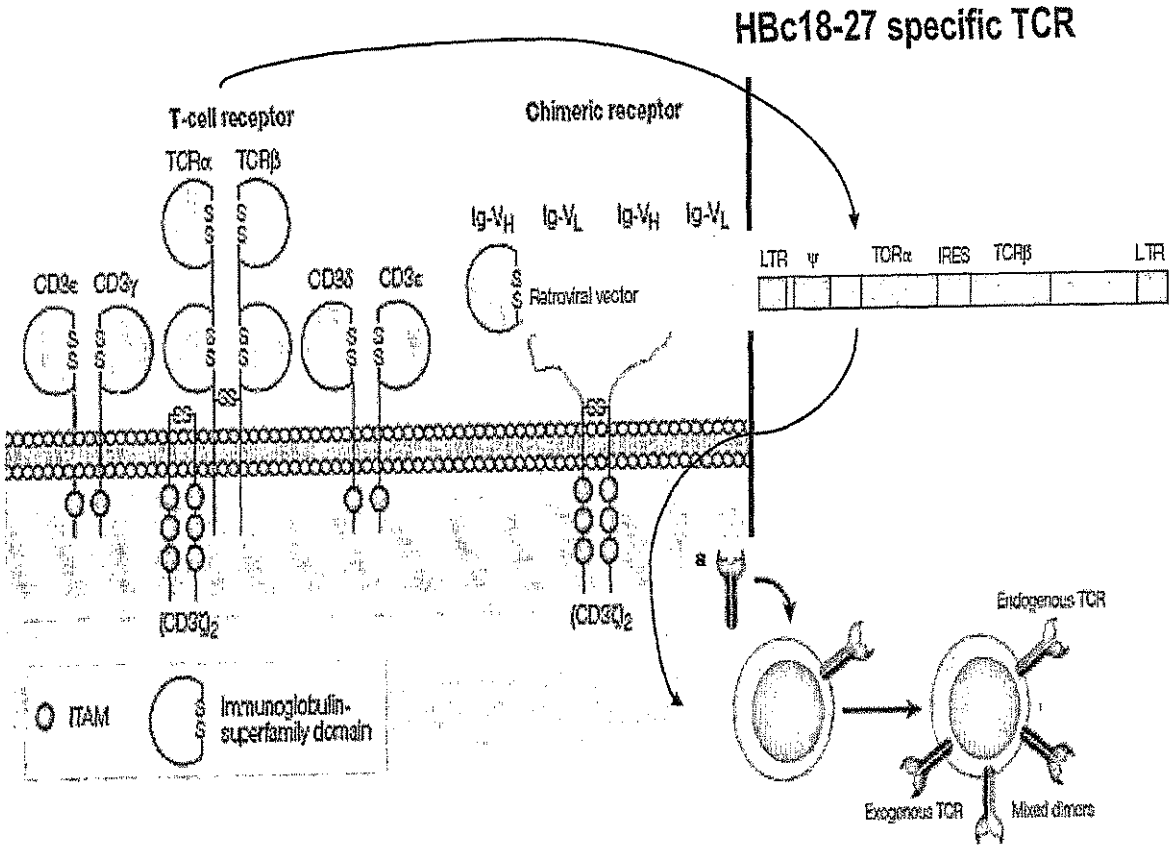
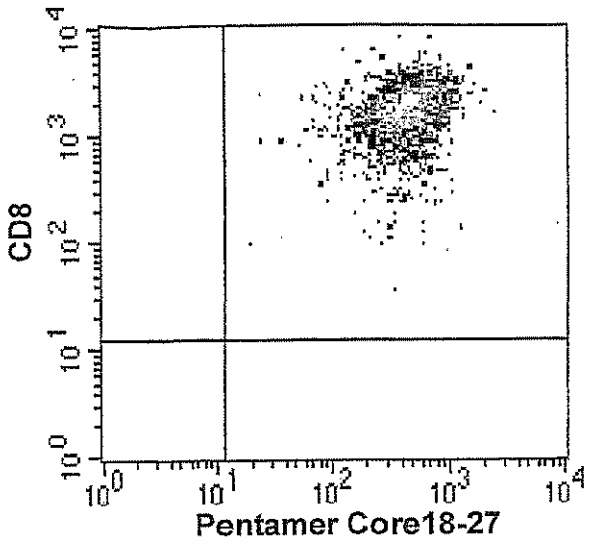


T cell clone from resolved HLA-A2+ HBV patient

Schumacher et. al., 2002, Nat Rev. Immunol, Vol 2: 512

Figure 1

A


CD8
Pentamer Core18-27

B

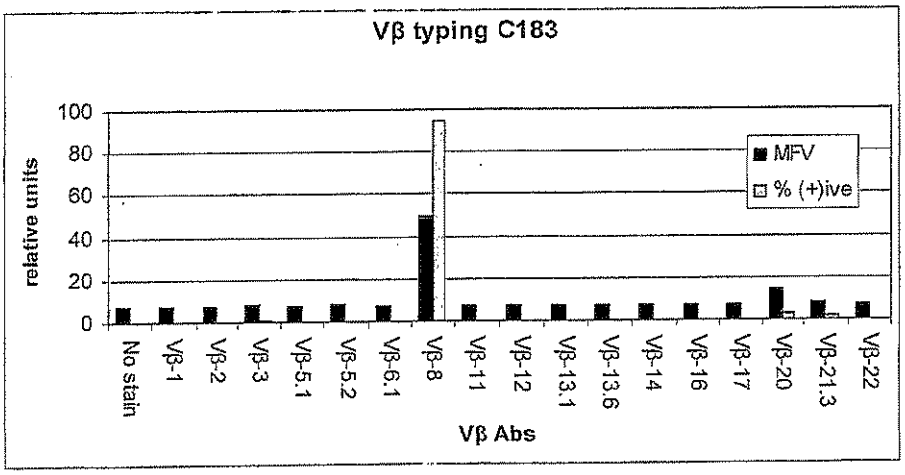

Vβ typing C183
relative units
MFV
% (+)ive
No stain
Vβ-1
Vβ-2
Vβ-3
Vβ-5.1
Vβ-5.2
Vβ-6.1
Vβ-8
Vβ-11
Vβ-12
Vβ-13.1
Vβ-13.6
Vβ-14
Vβ-16
Vβ-17
Vβ-20
Vβ-21.3
Vβ-22
Vβ Abs

Figure 2

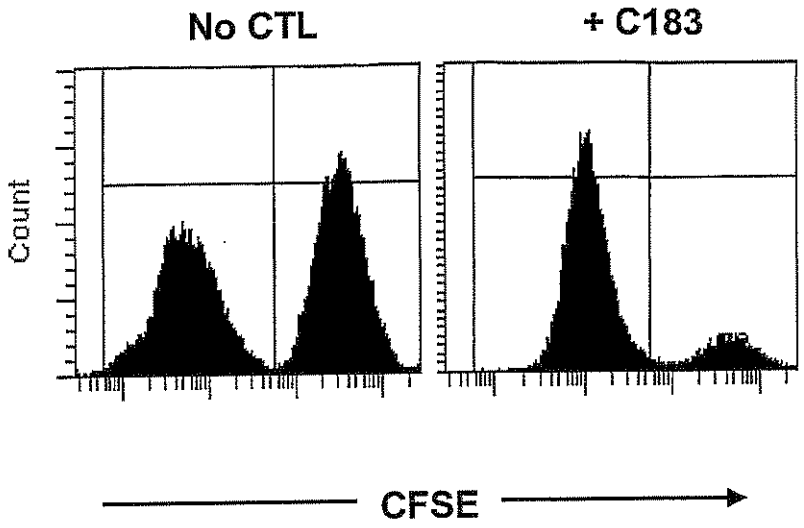


Figure 3

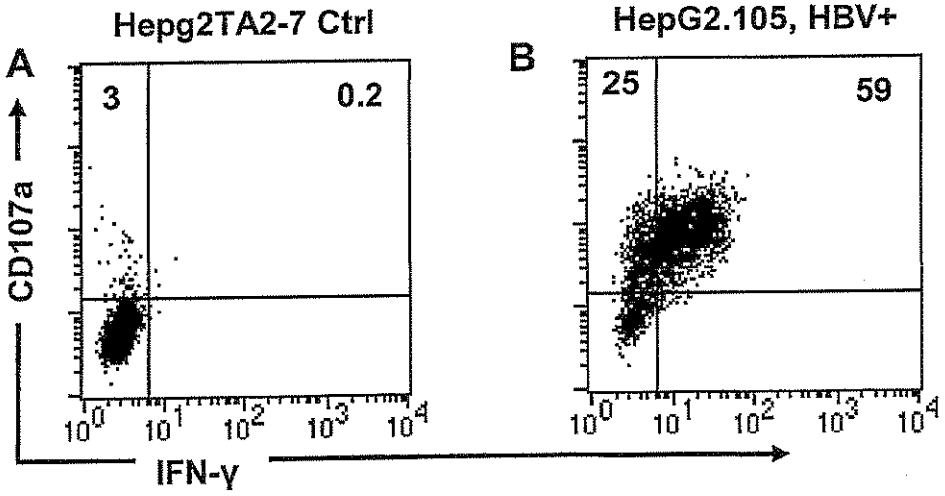


Figure 4

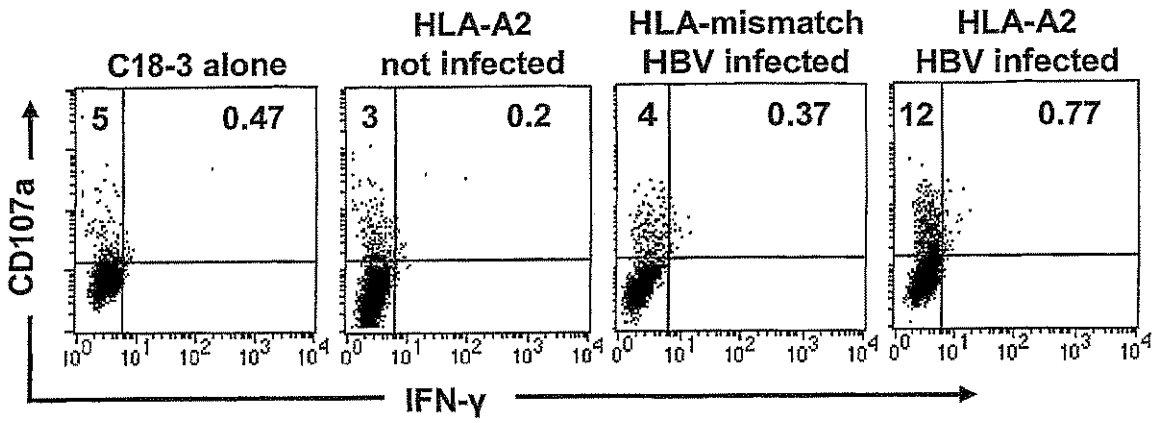


Figure 5

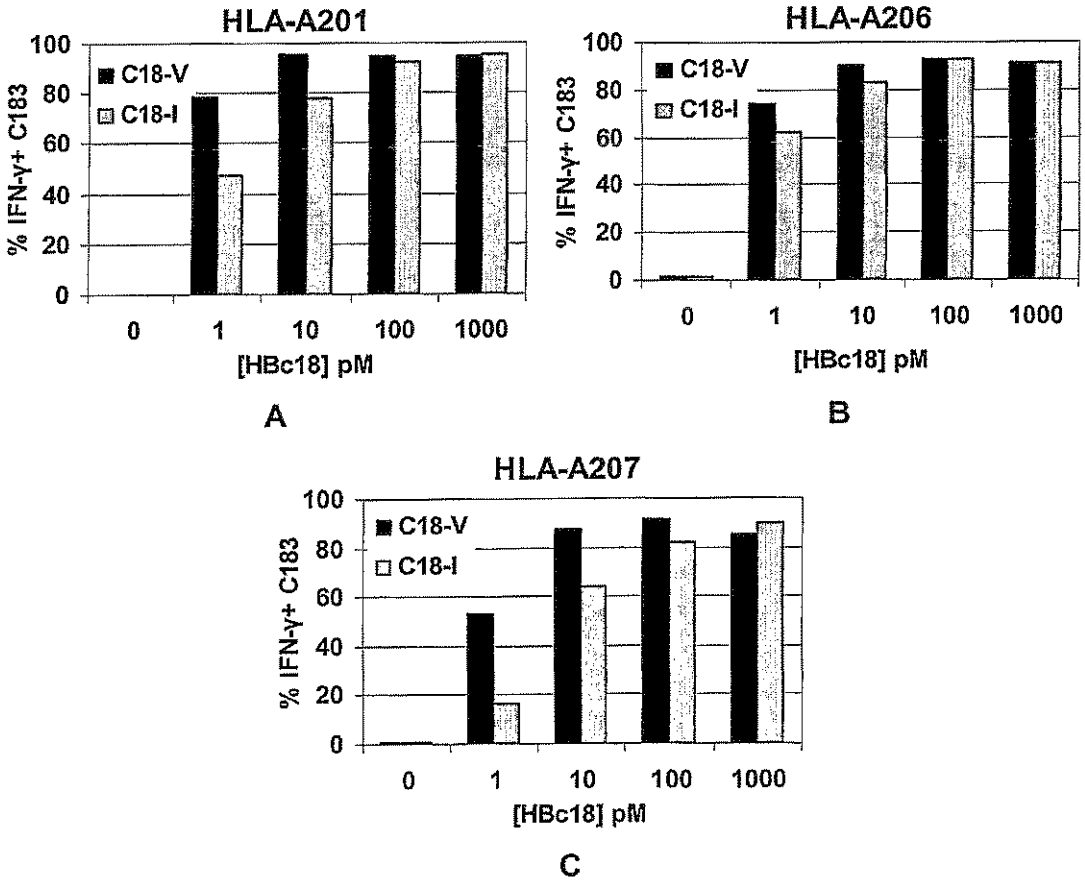


Figure 6

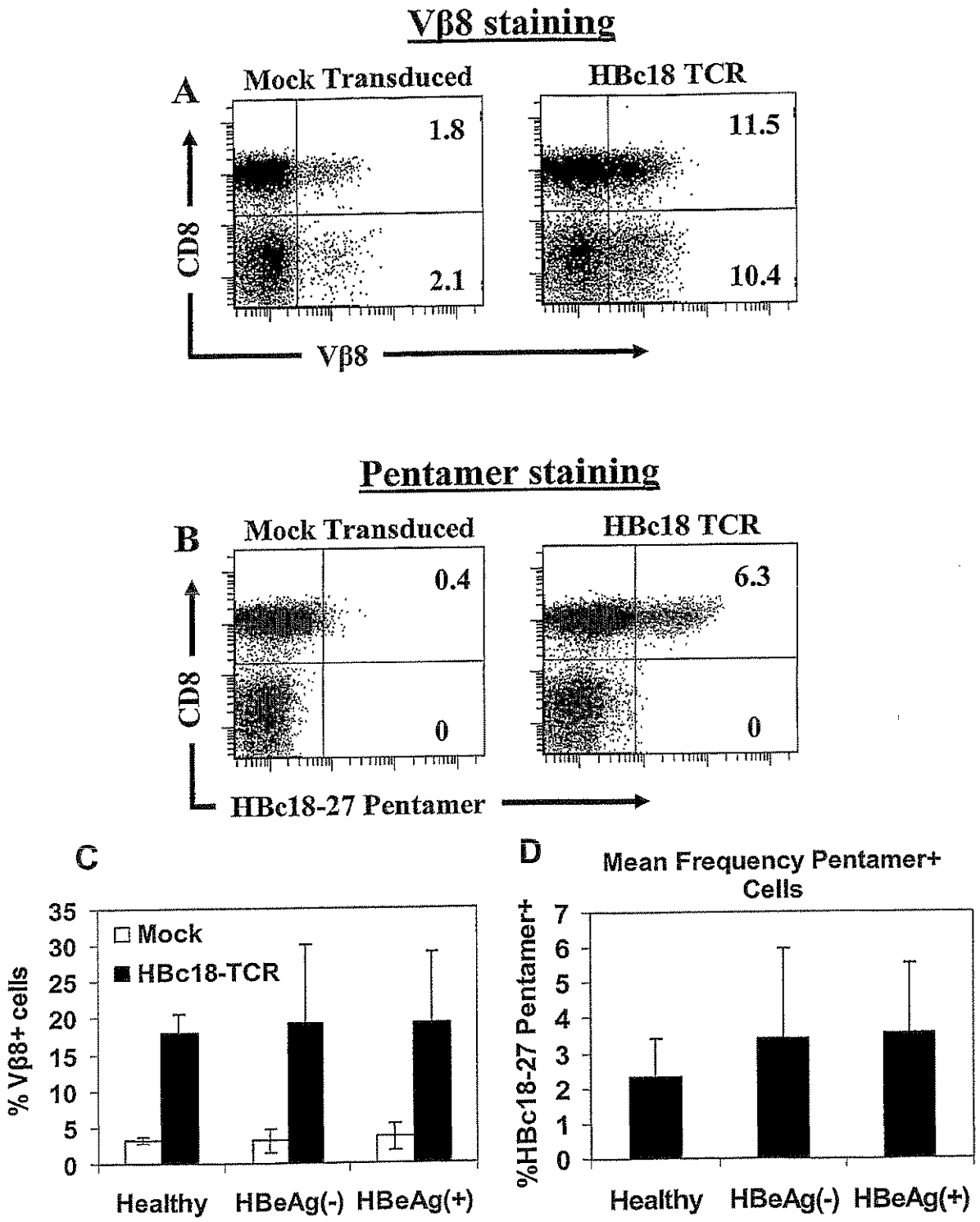
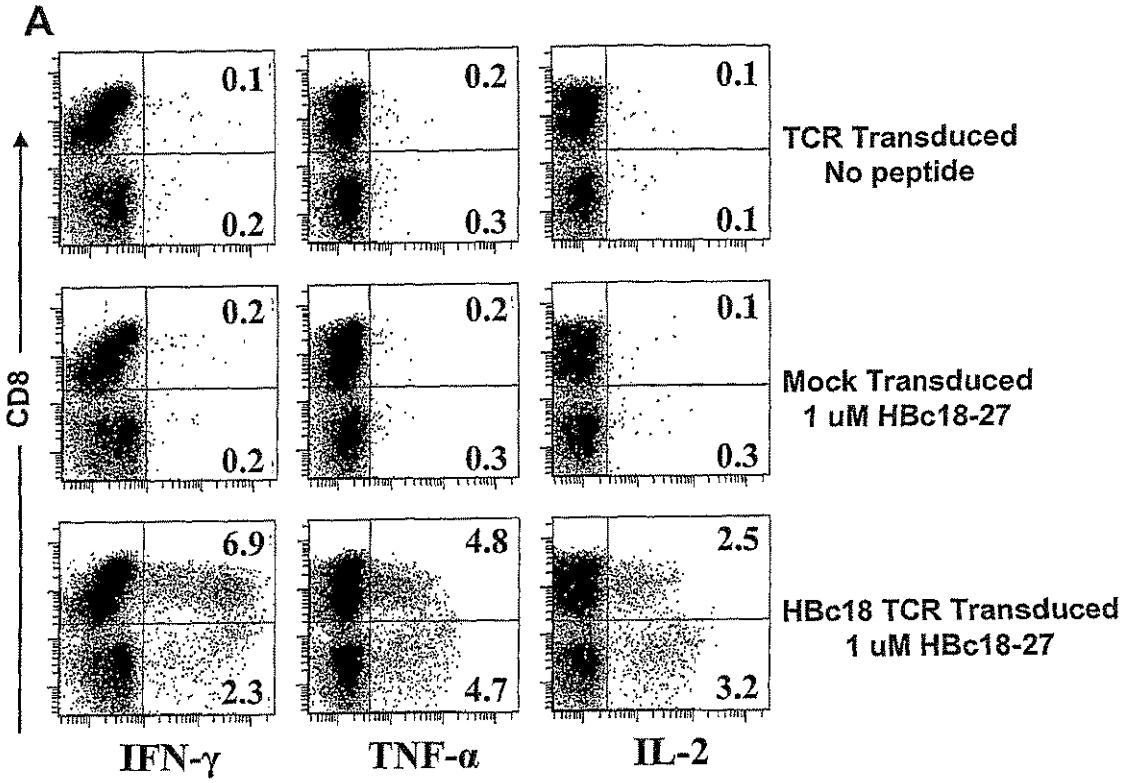

Vβ8 staining
A
Mock Transduced
HBc18 TCR
1.8
2.1
11.5
10.4
CD8
Vβ8
Pentamer staining
B
Mock Transduced
HBc18 TCR
0.4
0
6.3
0
CD8
HBc18-27 Pentamer
C
% Vβ8+ cells
Mock
HBc18-TCR
Healthy
HBeAg(-)
HBeAg(+)
D
Mean Frequency Pentamer+ Cells
%HBc18-27 Pentamer+
Healthy
HBeAg(-)
HBeAg(+)

Figure 7


A
CD8
0.1
0.2
0.2
0.3
0.1
0.1
TCR Transduced
No peptide
0.2
0.2
0.2
0.3
0.1
0.3
Mock Transduced
1 uM HBc18-27
6.9
2.3
4.8
4.7
2.5
3.2
HBc18 TCR Transduced
1 uM HBc18-27
IFN-γ
TNF-α
IL-2

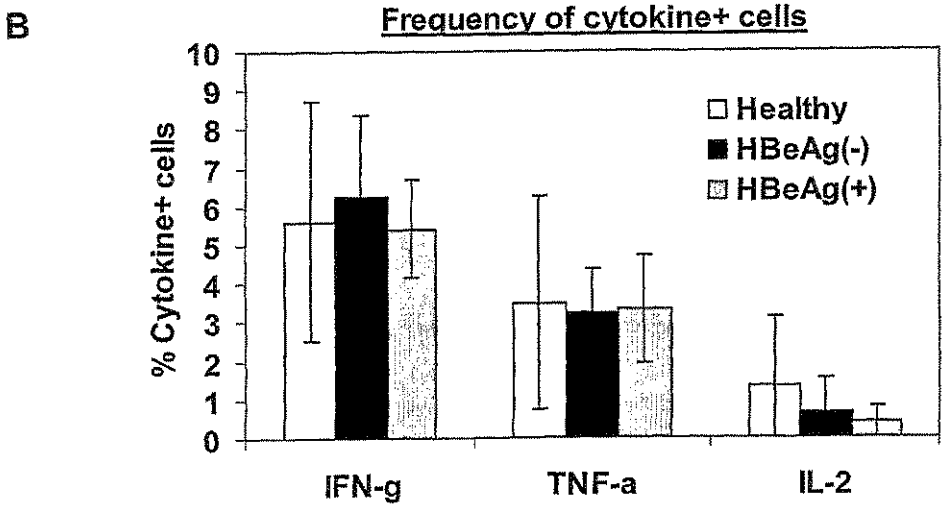
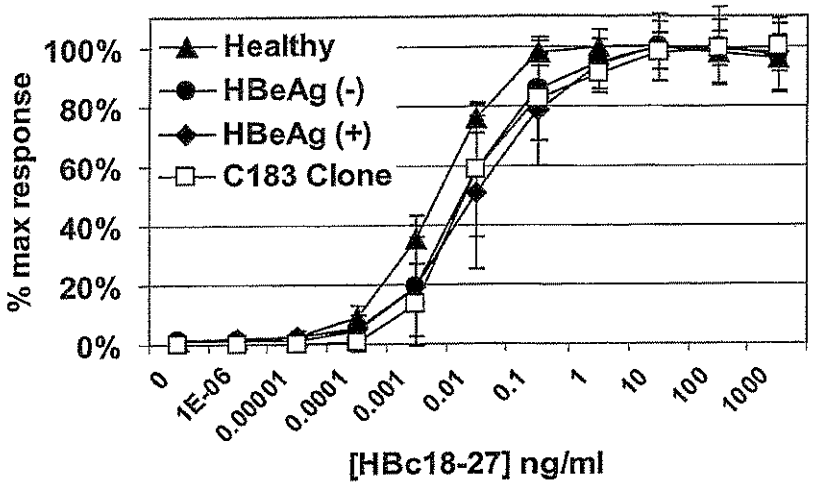

B
Frequency of cytokine+ cells
% Cytokine+ cells
10
9
8
7
6
5
4
3
2
1
0
Healthy
HBeAg(-)
HBeAg(+)
IFN-g
TNF-a
IL-2

Figure 8

A


CD8+ T cell Sensitivity
Healthy
HBeAg (-)
HBeAg (+)
C183 Clone
% max response
100%
80%
60%
40%
20%
0%
0
1E-06
0.00001
0.0001
0.001
0.01
0.1
1
10
100
1000
[HBc18-27] ng/ml

B

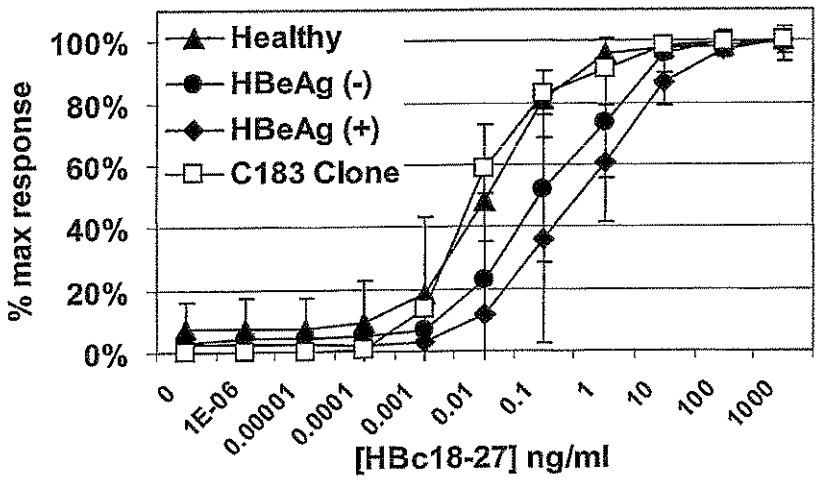

CD4+ T cell Sensitivity
Healthy
HBeAg (-)
HBeAg (+)
C183 Clone
% max response
100%
80%
60%
40%
20%
0%
0
1E-06
0.00001
0.0001
0.001
0.01
0.1
1
10
100
1000
[HBc18-27] ng/ml

Figure 9

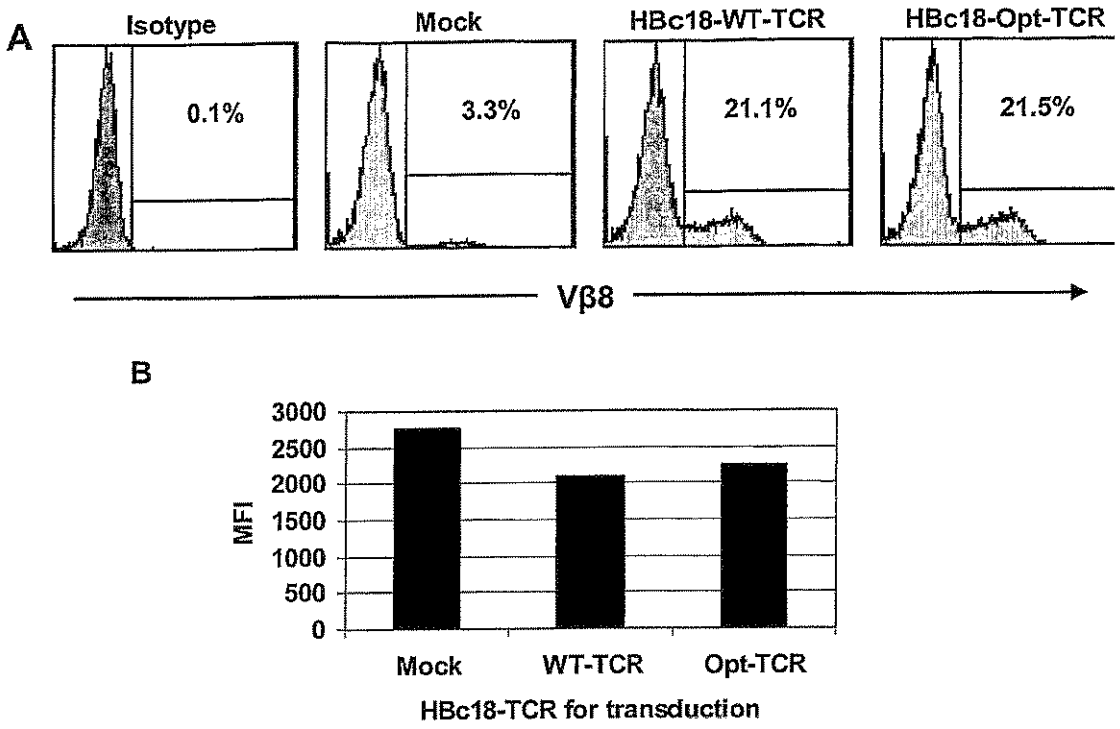

A
Isotype
Mock
HBc18-WT-TCR
HBc18-Opt-TCR
0.1%
3.3%
21.1%
21.5%
Vβ8
B
MFI
3000
2500
2000
1500
1000
500
0
Mock
WT-TCR
Opt-TCR
HBc18-TCR for transduction
C
Mock
HBc18-WT-TCR
HBc18-Opt-TCR
0.4
1.4
2.6

Figure 10

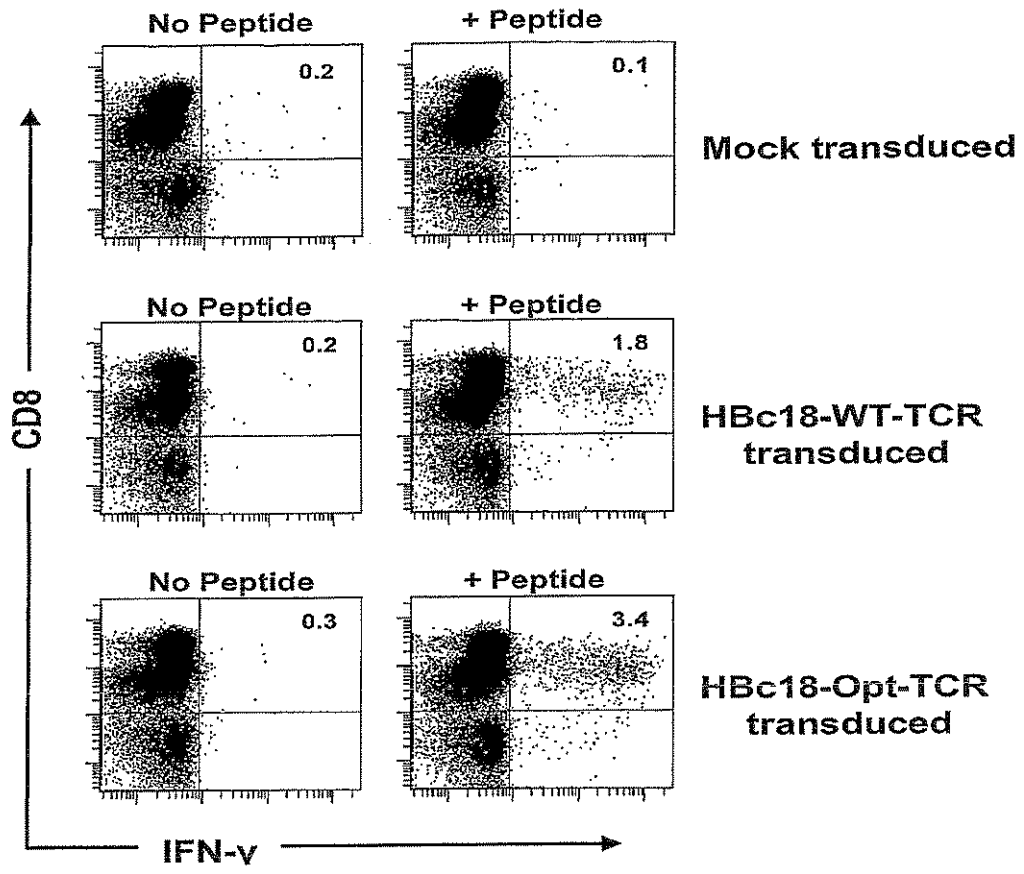

No Peptide
+ Peptide
0.2
0.1
Mock transduced
No Peptide
+ Peptide
0.2
1.8
HBc18-WT-TCR transduced
No Peptide
+ Peptide
0.3
3.4
HBc18-Opt-TCR transduced
CD8
IFN-γ

Figure 11

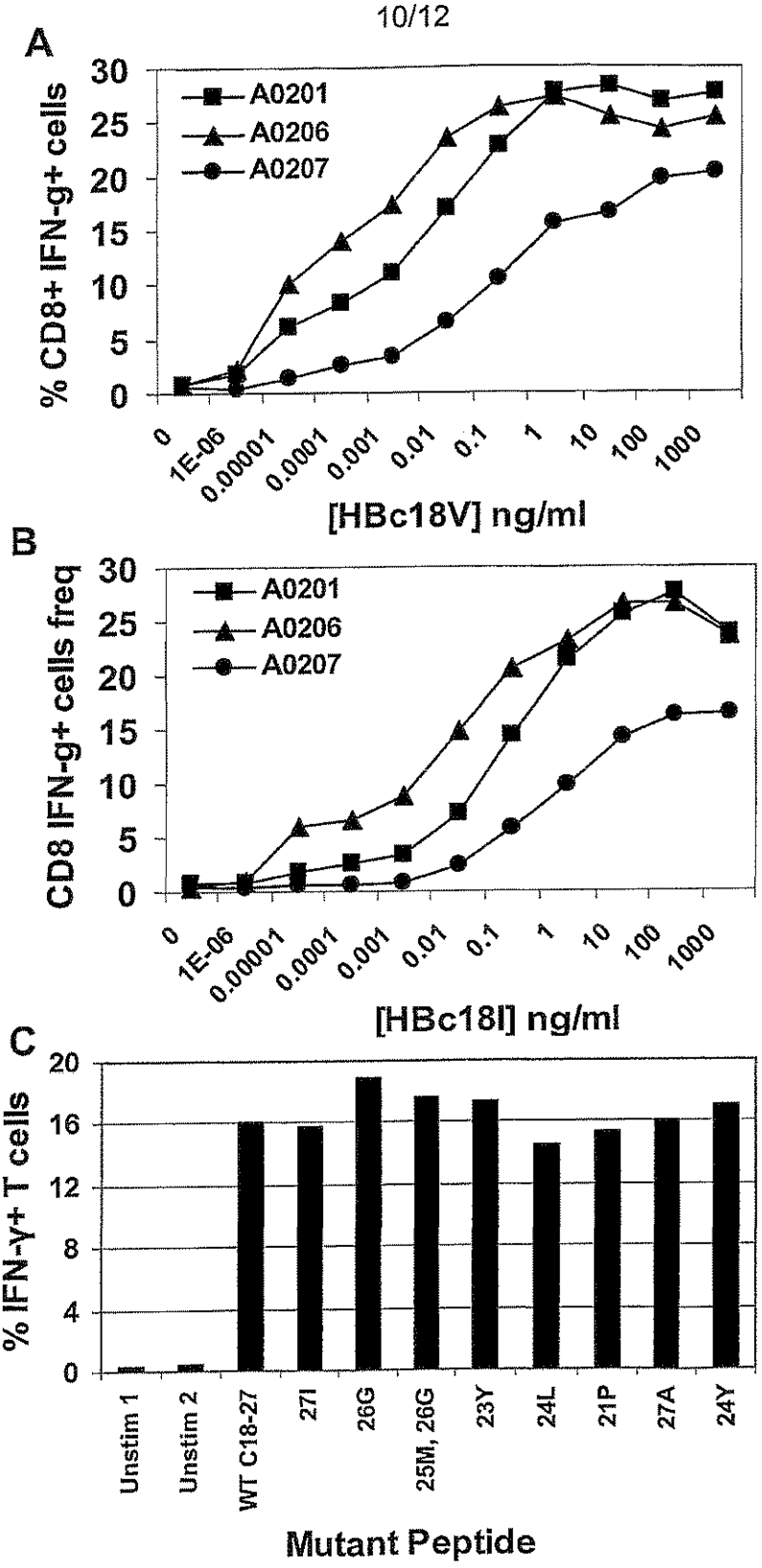

A
% CD8+ IFN-g+ cells
30
25
20
15
10
5
0
A0201
A0206
A0207
0
1E-06
0.00001
0.0001
0.001
0.01
0.1
1
10
100
1000
[HBc18V] ng/ml
B
CD8 IFN-g+ cells freq
30
25
20
15
10
5
0
A0201
A0206
A0207
0
1E-06
0.00001
0.0001
0.001
0.01
0.1
1
10
100
1000
[HBc18I] ng/ml
C
% IFN-γ+ T cells
20
16
12
8
4
0
Unstim 1
Unstim 2
WT C18-27
27I
26G
25M, 26G
23Y
24L
21P
27A
24Y
Mutant Peptide

Figure 12

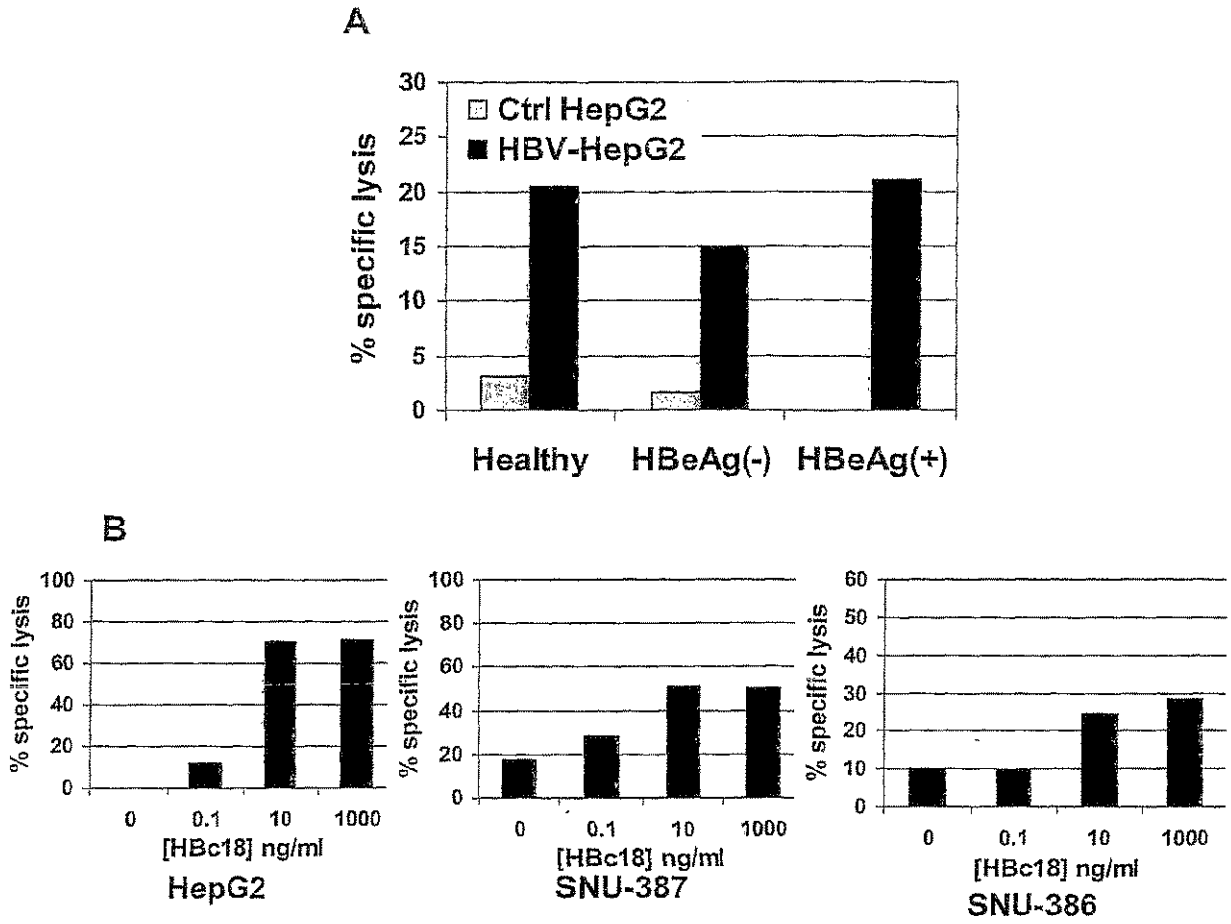

A
% specific lysis
30
25
20
15
10
5
0
Ctrl HepG2
HBV-HepG2
Healthy
HBeAg(-)
HBeAg(+)
B
% specific lysis
100
80
60
40
20
0
0
0.1
10
1000
[HBc18] ng/ml
HepG2
% specific lysis
100
80
60
40
20
0
0
0.1
10
1000
[HBc18] ng/ml
SNU-387
% specific lysis
60
50
40
30
20
10
0
0
0.1
10
1000
[HBc18] ng/ml
SNU-386

Figure 13

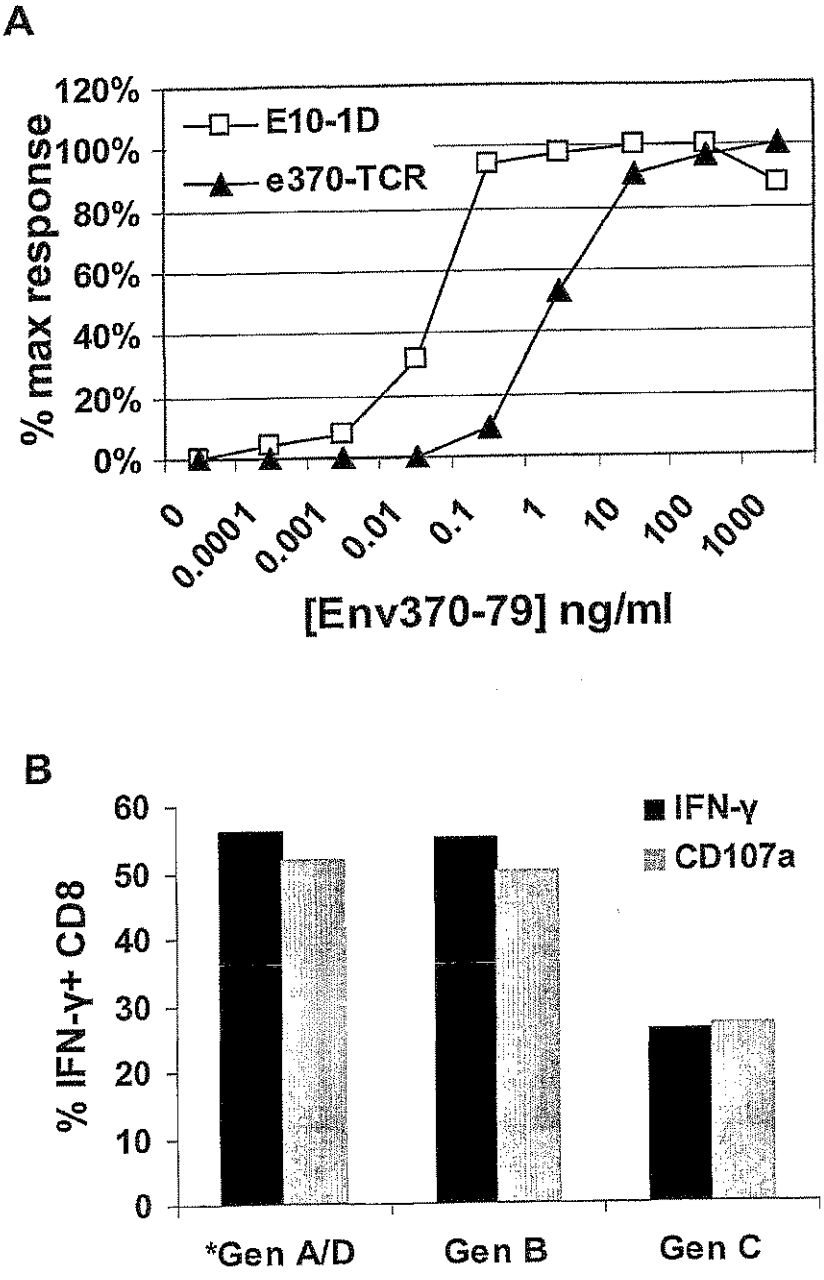

A
120%
100%
80%
60%
40%
20%
0%
% max response
E10-1D
e370-TCR
0
0.0001
0.001
0.01
0.1
1
10
100
1000
[Env370-79] ng/ml
B
60
50
40
30
20
10
0
% IFN-γ+ CD8
IFN-γ
CD107a
*Gen A/D
Gen B
Gen C

Figure 14

SEQUENCE LISTING

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Agency for Science Technology and Research

<120> HBV Epitope-Reactive Exogenous T Cell Receptor and Uses Thereof

<130> FP4671

<160> 58

<170> PatentIn version 3.4

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<210> 2
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<212> DNA
<213> Homo sapiens

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<211> 42
<212> DNA
<213> Homo sapiens

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wild type TCR

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42

<210> 4
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<223> Alpha chain of wild type TCR

<220>
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<223> Alpha 3 chain of wild type TCR

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60

agtcaacagg gagaagagga tcctcaggcc ttgagcatcc aggagggtga aaatgccacc
120

atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt
180

agaggccttg tccacctaat tttaatacgt tcaaatgaaa gagagaaaca cagtggaaga
240

ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg
300

gcagcagaca ctgcttctta cttctgtgct acgtggctct ctggttctgc aaggcaactg
360

acctttggat ctgggacaca attgactgtt ttacctgata tccagaaccc tgaccctgcc
420

gtgtaccagc tgagagactc taaatccagt gacaagtctg tctgcctatt caccgatttt
480

gattctcaaa caaatgtgtc acaaagtaag gattctgatg tgtatatcac agacaaaact
540

gtgctagaca tgaggtctat ggacttcaag agcaacagtg ctgtggcctg gagcaacaaa
600

tctgactttg catgtgcaaa cgccttcaac aacagcatta ttccagaaga caccttcttc
660

cccagcccag aaagttcctg tgatgtcaag ctggtcgaga aaagctttga aacagatacg
720

aacctaaact ttcaaaacct gtcagtgatt gggttccgaa tcctcctcct gaaagtggcc
780

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822

<210> 5
<211> 21
<212> DNA
<213> Homo sapiens

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of
optimised TCR

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21

<210> 6
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<213> Homo sapiens

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of
optimised TCR

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24

<210> 7
<211> 42
<212> DNA
<213> Homo sapiens

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optimised TCR

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42

<210> 8
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60

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120

atgaattgct catacaagac atcaatcaac aacttgcagt ggtaccgtca gaactctggg
180

agaggactcg tgcacctgat cctgattcgg agtaatgagc gggaaaaaca ctctggaagg
240

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300

gccgccgaca ccgcttccta cttctgtgct acatggctga gtggcagcgc acggcaattg
360

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420

gtgtatcagc tgagagactc aaagtcaagt gacaagagtg tgtgcctgtt cactgatttt
480

gactctcaga ccaacgtctc tcagtctaag gacagcgacg tttacatcac tgacaaaact
540

gtgctggaca tgcgcagtat ggactttaaa tcaaattccg ccgtggcttg gagcaataag
600

tctgacttcg cctgtgctaa tgcttttaat aactccatca ttccggagga tacatttttc
660

cctagccccg agtcatcctg cgacgtgaag ctggtggaga agtcattcga gaccgacacc
720

aatcttaact ttcagaacct gtccgttatc gggtttagaa tcctgctgct gaaggttgcc
780

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822

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<212> PRT
<213> Homo sapiens

<220>
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TCR

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Lys Thr Ser Ile Asn Asn Leu
1 5

<210> 10
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<220>
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TCR

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1 5

<210> 11
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<220>
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TCR

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1 5 10

<210> 12
<211> 273
<212> PRT
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<220>
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<400> 12

```
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1               5                  10                  15

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
            20                  25                  30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
        35                  40                  45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
    50                  55                  60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65                  70                  75                  80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
                85                  90                  95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Trp
            100                 105                 110

Leu Ser Gly Ser Ala Arg Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu
        115                 120                 125

Thr Val Leu Pro Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu
    130                 135                 140

Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe
145                 150                 155                 160

Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile
                165                 170                 175

Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn
            180                 185                 190

Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala
        195                 200                 205
```

Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu
210 215 220

Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr
225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu
245 250 255

Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser
260 265 270

Ser

<210> 13
<211> 21
<212> DNA
<213> Homo sapiens

<220>
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21

<210> 14
<211> 24
<212> DNA
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24

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<211> 45
<212> DNA

<213> Homo sapiens

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120

agatgtaaac caatttcagg acacgactac cttttctggt acagacagac catgatgcgg
180

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360

aatgagcagt tcttcgggcc agggacacgg ctcaccgtgc tagaggacct gaaaaacgtg
420

ttcccacccg aggtcgctgt gtttgagcca tcagaagcag agatctccca cacccaaaag
480

gccacactgg tgtgcctggc cacaggcttc taccccgacc acgtggagct gagctggtgg
540

gtgaatggga aggaggtgca cagtggggtc agcacagacc cgcagccccc caaggagcag
600

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840

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942

<210> 17
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21

<210> 18
<211> 24
<212> DNA
<213> Homo sapiens

<220>
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24

<210> 19
<211> 45
<212> DNA
<213> Homo sapiens

<220>
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optimised TCR

<400> 19
tgtgcctcct ccaaccgggc ctcctcttat aacgagcagt tcttc
45

<210> 20
<211> 942
<212> DNA
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Beta 8 chain of optimised TCR

<400> 20
atggacagct ggacactgtg ctgcgtgagc ctgtgcattc tggtggccaa gcacaccgac
60

gccggcgtga tccagagccc tcgccacgag gtgaccgaaa tgggccagga ggtgacactg
120

cgctgcaagc caatctctgg gcacgactac ctgttctggt acaggcagac catgatgagg
180

ggcctggaac tgctgatcta ttttaataac aatgtgccta tcgatgactc tggcatgccc
240

gaggacaggt tctccgccaa gatgcccaac gccagcttct ccaccctgaa gatccagccc
300

tccgaaccta gggactccgc cgtgtacttc tgtgcctcct ccaaccgggc ctcctcttat
360

aacgagcagt tcttcggccc tggaacccgc ctgaccgtgc tggaggacct gaaaaatgtg
420

tttccccccg aggtggccgt gtttgaacca agcgaggccg agatcagcca cacacagaag
480

gccaccctgg tgtgtctggc caccggattc tatcccgatc acgtggagct gagctggtgg
540

gtgaacggga aggaggtgca ctctggcgtg agcaccgacc ctcagccact gaaagagcag
600

cccgccctga atgattctcg gtactgcctg tccagccgcc tgcgcgtgtc tgccaccttc
660

tggcagaacc ccagaaatca cttcaggtgc caggtgcagt tctatgggct gagcgagaac
720

gacgaatgga cccaggacag agccaagcct gtgacacaga tcgtgtctgc cgaagcctgg
780

ggcagagccg actgcggctt taccagcgag agctaccagc agggcgtgct gtccgccaca
840

attctgtacg agatcctgct gggaaaggcc acactgtacg ccgtgctggt gagcgccctg
900

gtgctgatgg ccatggtgaa gcggaaagac tcccggggct ga
942

<210> 21
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 1 (CDR1) for beta 8 chain of TCR

<400> 21

Ile Ser Gly His Asp Tyr Leu
1 5

<210> 22
<211> 8
<212> PRT
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 2 (CDR2) for beta 8 chain of TCR

<400> 22

Tyr Phe Asn Asn Asn Val Pro Ile
1 5

<210> 23
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 3 (CDR3) for beta 8 chain of TCR

<400> 23

```
Cys Ala Ser Ser Asn Arg Ala Ser Ser Tyr Asn Glu Gln Phe Phe
1               5                  10                  15
```

<210> 24
<211> 313
<212> PRT
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Beta 8 chain of TCR

<400> 24

```
Met Asp Ser Trp Thr Leu Cys Cys Val Ser Leu Cys Ile Leu Val Ala
1               5                  10                  15

Lys His Thr Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr
            20                  25                  30

Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Ser Gly His
        35                  40                  45

Asp Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu
    50                  55                  60

Leu Ile Tyr Phe Asn Asn Asn Val Pro Ile Asp Asp Ser Gly Met Pro
65                  70                  75                  80

Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu
                85                  90                  95

Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala
            100                 105                 110

Ser Ser Asn Arg Ala Ser Ser Tyr Asn Glu Gln Phe Phe Gly Pro Gly
        115                 120                 125

Thr Arg Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu
    130                 135                 140

Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys
145                 150                 155                 160

Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu
```

165 170 175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
180 185 190

Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
195 200 205

Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
210 215 220

Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
225 230 235 240

Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
245 250 255

Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr
260 265 270

Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
275 280 285

Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
290 295 300

Met Val Lys Arg Lys Asp Ser Arg Gly
305 310

<210> 25
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> HBc18-27 epitope (Genotype A/D/E/F); (WT C18-27)

<400> 25

Phe Leu Pro Ser Asp Phe Phe Pro Ser Val
1 5 10

<210> 26
<211> 10

<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> HBc18-27 epitope (Genotype B/C); 27I

<400> 26

Phe Leu Pro Ser Asp Phe Phe Pro Ser Ile
1 5 10

<210> 27
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> Natural Variant 1 of HBc18-27 epitope

<400> 27

Phe Leu Pro Asn Asp Phe Phe Pro Ser Val
1 5 10

<210> 28
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> Natural Variant 2 of HBc18-27 epitope

<400> 28

Phe Leu Pro Asn Asp Phe Phe Pro Ser Ala
1 5 10

<210> 29
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> Natural Variant 3 of HBc18-27 epitope

<400> 29

Phe Leu Pro Ala Asp Phe Phe Pro Ser Ile
1 5 10

<210> 30
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> Natural Variant 4 of HBc18-27 epitope

<400> 30

Phe Leu Pro Val Asp Phe Phe Pro Ser Ile
1 5 10

<210> 31
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> Natural Variant 5 of HBc18-27 epitope

<400> 31

Phe Leu Pro Thr Asp Tyr Phe Pro Ser Val
1 5 10

<210> 32
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> Natural Variant 6 of HBc18-27 epitope

<400> 32

Phe Leu Pro Ser Asp Phe Tyr Pro Pro Val
1 5 10

<210> 33
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> Natural Variant 7 of HBc18-27 epitope; 26G

<400> 33

Phe Leu Pro Ser Asp Phe Phe Pro Gly Val
1 5 10

<210> 34
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> Natural Variant 8 of HBc18-27 epitope; 25M, 26G

<400> 34

Phe Leu Pro Ser Asp Phe Phe Met Gly Val
1 5 10

<210> 35
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> Natural Variant 9 of HBc18-27 epitope; 23Y

<400> 35

Phe Leu Pro Ser Asp Tyr Phe Pro Ser Val
1 5 10

<210> 36
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> Natural Variant 10 of HBc18-27 epitope; 24L

<400> 36

Phe Leu Pro Ser Asp Phe Leu Pro Ser Val

1 5 10

<210> 37
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> Natural Variant 11 of HBc18-27 epitope; 21P

<400> 37

Phe Leu Pro Pro Asp Phe Phe Pro Ser Val
1 5 10

<210> 38
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> Natural Variant 12 of HBc18-27 epitope; 27A

<400> 38

Phe Leu Pro Ser Asp Phe Phe Pro Ser Ala
1 5 10

<210> 39
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> Natural Variant 13 of HBc18-27 epitope; 24Y

<400> 39

Phe Leu Pro Ser Asp Phe Tyr Pro Ser Val
1 5 10

<210> 40
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 1 (CDR1) for alpha 12 chain of
wild type TCR

<400> 40
gaccgaggtt cccagtcc
18

<210> 41
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 2 (CDR2) for alpha 12 chain of
wild type TCR

<400> 41
atatactcca atggt
15

<210> 42
<211> 39
<212> DNA
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 3 (CDR3) for alpha 12 chain of
wild type TCR

<400> 42
tgtgccgtga acctctatgc aggcaacatg ctcaccttt
39

<210> 43
<211> 825
<212> DNA
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Alpha 12 chain of wild type TCR

<400> 43

atgatgaaat ccttgagagt tttactagtg atcctgtggc ttcagttgag ctgggtttgg
60

agccaacaga aggaggtgga gcagaattct ggacccctca gtgttccaga gggagccatt
120

gcctctctca actgcactta cagtgaccga ggttcccagt ccttcttctg gtacagacaa
180

tattctggga aaagccctga gttgataatg ttcatatact ccaatggtga caaagaagat
240

ggaaggttta cagcacagct caataaagcc agccagtatg tttctctgct catcagagac
300

tcccagccca gtgattcagc cacctacctc tgtgccgtga acctctatgc aggcaacatg
360

ctcacctttg gaggggggaac aaggttaatg gtcaaacccc atatccagaa ccctgaccct
420

gccgtgtacc agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat
480

tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa
540

actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac
600

aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc
660

ttccccagcc cagaaagttc ctgtgatgtc aagctggtcg agaaaagctt tgaaacagat
720

acgaacctaa actttcaaaa cctgtcagtg attgggttcc gaatcctcct cctgaaagtg
780

gccgggttta atctgctcat gacgctgcgg ctgtggtcca gctga
825

<210> 44
<211> 6
<212> PRT
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 1 (CDR1) for alpha 12 chain
of
TCR

<400> 44

Asp Arg Gly Ser Gln Ser
1 5

<210> 45
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 2 (CDR2) for alpha 12 chain of
TCR

<400> 45

Ile Tyr Ser Asn Gly
1 5

<210> 46
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 3 (CDR3) for alpha 12 chain of
TCR

<400> 46

Cys Ala Val Asn Leu Tyr Ala Gly Asn Met Leu Thr Phe
1 5 10

<210> 47
<211> 274
<212> PRT
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Alpha 12 chain of TCR

<400> 47

Met Met Lys Ser Leu Arg Val Leu Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15

Ser Trp Val Trp Ser Gln Gln Lys Glu Val Glu Gln Asn Ser Gly Pro

```
            20                  25                  30

Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser
        35                  40                  45

Asp Arg Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys
    50                  55                  60

Ser Pro Glu Leu Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp
65                  70                  75                  80

Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu
                85                  90                  95

Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala
            100                 105                 110

Val Asn Leu Tyr Ala Gly Asn Met Leu Thr Phe Gly Gly Gly Thr Arg
        115                 120                 125

Leu Met Val Lys Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
    130                 135                 140

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
145                 150                 155                 160

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
                165                 170                 175

Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
            180                 185                 190

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
        195                 200                 205

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
    210                 215                 220

Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp
225                 230                 235                 240

Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu
                245                 250                 255
```

Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp
260 265 270

Ser Ser

<210> 48
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 1 (CDR1) for beta 7.8 chain of
wild type TCR

<400> 48
tcgggtcatg tatcc
15

<210> 49
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 2 (CDR2) for beta 7.8 chain of
wild type TCR

<400> 49
ttccagaatg aagctcaa
18

<210> 50
<211> 42
<212> DNA
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 3 (CDR3) for beta 7.8 chain of
wild type TCR

<400> 50

tgtgccagca gctcggactt tggcaatcag ccccagcatt tt
42

<210> 51
<211> 933
<212> DNA
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Beta 7.8 chain of wild type TCR

<400> 51
atgggcacca ggctcctctg ctgggtggtc ctgggtttcc tagggacaga tcacacaggt
60

gctggagtct cccagtcccc taggtacaaa gtcgcaaaga gaggacagga tgtagctctc
120

aggtgtgatc caatttcggg tcatgtatcc ctttttggt accaacaggc cctggggcag
180

gggccagagt ttctgactta tttccagaat gaagctcaac tagacaaatc ggggctgccc
240

agtgatcgct tctttgcaga aaggcctgag ggatccgtct ccactctgaa gatccagcgc
300

acacagcagg aggactccgc cgtgtatctc tgtgccagca gctcggactt tggcaatcag
360

ccccagcatt ttggtgatgg gactcgactc tccatcctag aggacctgaa caaggtgttc
420

ccacccgagg tcgctgtgtt tgagccatca gaagcagaga tctcccacac ccaaaaggcc
480

acactggtgt gcctggccac aggcttcttc cctgaccacg tggagctgag ctggtgggtg
540

aatgggaagg aggtgcacag tggggtcagc acggacccgc agccccтcaa ggagcagccc
600

gccctcaatg actccagata ctgcctgagc agccgcctga gggtctcggc caccttctgg
660

cagaaccccc gcaaccactt ccgctgtcaa gtccagttct acgggctctc ggagaatgac
720

gagtggaccc aggatagggc caaacccgtc acccagatcg tcagcgccga ggcctggggt
780

agagcagact gtggctttac ctcggtgtcc taccagcaag gggtcctgtc tgccaccatc
840

ctctatgaga tcctgctagg gaaggccacc ctgtatgctg tgctggtcag cgcccttgtg
900

ttgatggcca tggtcaagag aaaggatttc tga
933

<210> 52
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 1 (CDR1) for beta 7.8 chain
of
TCR

<400> 52

Ser Gly His Val Ser
1 5

<210> 53
<211> 6
<212> PRT
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 2 (CDR2) for beta 7.8 chain
of
TCR

<400> 53

Phe Gln Asn Glu Ala Gln
1 5

<210> 54
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Complementarity Determining Region 3 (CDR3) for beta 7.8 chain
of
TCR

<400> 54

```
Cys Ala Ser Ser Ser Asp Phe Gly Asn Gln Pro Gln His Phe
1               5                   10
```

<210> 55
<211> 310
<212> PRT
<213> Homo sapiens

<220>
<221> Misc_feature
<223> Beta 7.8 chain of TCR

<400> 55

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Met Gly Thr Arg Leu Leu Cys Trp Val Val Leu Gly Phe Leu Gly Thr
1               5                   10                  15

Asp His Thr Gly Ala Gly Val Ser Gln Ser Pro Arg Tyr Lys Val Ala
            20                  25                  30

Lys Arg Gly Gln Asp Val Ala Leu Arg Cys Asp Pro Ile Ser Gly His
        35                  40                  45

Val Ser Leu Phe Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Glu Phe
    50                  55                  60

Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Asp Lys Ser Gly Leu Pro
65                  70                  75                  80

Ser Asp Arg Phe Phe Ala Glu Arg Pro Glu Gly Ser Val Ser Thr Leu
                85                  90                  95

Lys Ile Gln Arg Thr Gln Gln Glu Asp Ser Ala Val Tyr Leu Cys Ala
            100                 105                 110

Ser Ser Ser Asp Phe Gly Asn Gln Pro Gln His Phe Gly Asp Gly Thr
        115                 120                 125

Arg Leu Ser Ile Leu Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val
    130                 135                 140

Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala
145                 150                 155                 160

Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu
```

165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys
195 200 205

Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg
210 215 220

Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp
225 230 235 240

Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala
245 250 255

Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln
260 265 270

Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys
275 280 285

Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met
290 295 300

Val Lys Arg Lys Asp Phe
305 310

<210> 56
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> HBe370-79 epitope (Genotype A/D)

<400> 56

Ser Ile Val Ser Pro Phe Ile Pro Leu Leu
1 5 10

<210> 57
<211> 10

<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> HBc18-27 epitope (Genotype B)

<220>
<221> Misc_feature
<223> HBe370-79 epitope (Genotype B)

<400> 57

Asn Ile Leu Ser Pro Phe Met Pro Leu Leu
1 5 10

<210> 58
<211> 10
<212> PRT
<213> Hepatitis B virus

<220>
<221> Misc_feature
<223> HBe370-79 epitope (Genotype C)

<400> 58

Asn Ile Leu Asn Pro Phe Leu Pro Leu Leu
1 5 10