

UPVG0037WO2_SequenceListing
SEQUENCE LISTING

<110> THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
Weiner, David B.
Yan, Jian
Obeng-Adjei, Nyamakye

<120> NUCLEIC ACID MOLECULES ENCODING HEPATITIS B VIRUS CORE PROTEIN
AND SURFACE ANTIGEN PROTEIN AND VACCINE COMPRISING THE SAME

<130> UPVG0037 WO2

<140> PCT/US13/60618

<141> 2013-09-19

<150> US 13/622,965

<151> 2012-09-19

<160> 21

<170> PatentIn version 3.5

<210> 1

<211> 552

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleic acid sequence M-core

<220>

<221> misc_feature

<222> (1)..(3)

<223> n is a, c, g, or t

<400> 1

nnngacatcg acccctacaa agaattcggc gccaccgtgg aactgctgag cttcctgccc 60

agcgacttct tcccctccgt gcggggacctg ctggataccg ccagcgcctt gtacagagag 120

gccctggaaa gccccgagca ctgcagccct caccacacag ccctgcggca ggccatcctg 180

tgctggggcg agctgatgac cctggccacc tgggtcggaa gcaacctgga agatcccgcc 240

agccggggacc tgggtgtgtc ctacgtgaac accaacaatgg gcctgaagat ccggcagctg 300

ctgtggttcc acatctcctg cctgaccttc ggccgggaaa ccgtgctgga atacctggtg 360

tccttcggcg tgtggatcag aacccccct gcctacagac cccccaacgc ccctatcctg 420

agcacctgc ccgagacaac cgtggtccgc agacggggca gaagccccag aagaagaacc 480

cccagcccta gacggcggag atctcagagc cccaggcgga gaagatccca gagccgcgag 540

agccagtgtc ga 552

<210> 2

<211> 183

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<212> PRT

<213> Artificial Sequence

<220>

<223> Amino Acid Sequence of M-Core

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa can be any naturally occurring amino acid

<400> 2

Xaa Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

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<210> 3

<211> 603

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleic acid sequence IgE leader - M-Core

<400> 3

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ttccctccg tgcgggacct gctggatacc gccagcgccc tgtacagaga ggccttgaa    180
agccccgagc actgcagccc tcaccacaca gccctgcggc aggccatcct gtgctggggc    240
gagctgatga ccctggccac ctgggtcgga agcaacctgg aagatccgc cagccgggac    300
ctggtggtgt cctacgtgaa caccaacatg ggcctgaaga tccggcagct gctgtggttc    360
cacatctct gctgacctt cggccgggaa accgtgctgg aatactggt gtcctcggc    420
gtgtggatca gaaccccccc tgcctacaga ccccccaacg cccctatcct gagcacctg    480
cccagacaaa ccgtggtccg cagacggggc agaagcccca gaagaagaac cccagccct    540
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tga                                     603
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<210> 4

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino Acid Sequence of IgE leader - M-Core

<400> 4

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Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Thr Arg Val
1      5      10     15

His Ser Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu
      20     25     30

Leu Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu
      35     40     45

Asp Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His
      50     55     60

Cys Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly
      65     70     75     80
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Glu Leu Met Thr Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro
85 90 95

Ala Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu
100 105 110

Lys Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly
115 120 125

Arg Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg
130 135 140

Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu
145 150 155 160

Pro Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg
165 170 175

Thr Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg
180 185 190

Ser Gln Ser Arg Glu Ser Gln Cys
195 200

<210> 5

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleic acid sequence IgE leader - M-Core + HA Tag

<400> 5

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ttccctccg tgcgggacct gctggatacc gccagcgccc tgtacagaga ggccctggaa 180

agccccgagc actgcagccc tcaccacaca gccctgcggc aggccatcct gtgctggggc 240

gagctgatga ccctggccac ctgggtcgga agcaacctgg aagatccgc cagccgggac 300

ctggtggtgt cctacgtgaa caccaacatg ggctgaaga tccggcagct gctgtggtc 360

cacatctcct gcctgacctt cggccgggaa accgtgctgg aatactggt gtcctcggc 420

gtgtggatca gaaccccc tgcctacaga cccccaacg cccctatcct gagcaccctg 480

cccagacaa ccgtgtccg cagacggggc agaagcccca gaagaagaac cccagccct 540

UPVG0037WO2_SequenceListing

agacggcgga gatctcagag cccagggcgg agaagatccc agagccgcga gagccagtgc 600

taccctacg acgtgcccga ctacgcctga 630

<210> 6

<211> 209

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino Acid Sequence of IgE leader - M-Core + HA Tag

<400> 6

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu
20 25 30

Leu Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu
35 40 45

Asp Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His
50 55 60

Cys Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly
65 70 75 80

Glu Leu Met Thr Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro
85 90 95

Ala Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu
100 105 110

Lys Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly
115 120 125

Arg Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg
130 135 140

Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu
145 150 155 160

Pro Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg
165 170 175

Thr Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg
180 185 190

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Ser Gln Ser Arg Glu Ser Gln Cys Tyr Pro Tyr Asp Val Pro Asp Tyr
 195 200 205

Ala

<210> 7
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgE leader amino acid sequence

<400> 7

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1 5 10 15

His Ser

<210> 8
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HA Tag amino acid sequence

<400> 8

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1 5

<210> 9
 <211> 1317
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic (LHBs-A)

<400> 9
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 aatcctctgg ggttctttcc agaccaccag ctggaccccg ctttcggcgc aaactccaac 180
 aatcctgact gggacttcaa cccaatcaaa gaccactggc cagcagctaa ccaagtggga 240
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agaggcagga aacggagatc tatgcagtgg aatagtacag ccttccatca ggctctgcag    480
gacccccggg tgcggggact gtactttcca gccggaggca gtcctctgg cactgtcaac    540
cctgcaccaa atatcgctc ccacatcagt tcaatttctg ctggaactgg agaccccggtg    600
accaaccggg gcagaaagag ggcagtatg gagaatatta cctcaggggt cctgggacct    660
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tacagatgga tgtgcctgcg acggttcac atttcctgt ttatcctgt gctgtgcctg    900
atthtctgc tgggtctgct ggactatcag ggcagtctgc cagtctgcc cctgattcct    960
gggtccacta ccacatctac aggaccctgt aagacttga ctaccctgc ccagggggaac   1020
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tggtgagcc tgctggtgcc ctctgtccag tggttgtgg gactgagccc taccgtctgg   1200
ctgtccgcca tctggatgat gtgtactgg gggcccagcc tgtattcaat cgtgtctcca   1260
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<210> 10

<211> 431

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic (LHBs-A)

<400> 10

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Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1       5       10      15

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His Ser Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn
20      25      30

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Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp
35      40      45

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Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro
50      55      60

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UPVG0037WO2_SequenceListing

Ile Lys Asp His Trp Pro Ala Ala Asn Gln Val Gly Val Gly Ala Phe
65 70 75 80

Gly Pro Gly Leu Thr Pro Pro His Gly Gly Ile Leu Gly Trp Ser Pro
85 90 95

Gln Ala Gln Gly Ile Leu Thr Thr Val Ser Thr Ile Pro Pro Pro Ala
100 105 110

Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro
115 120 125

Leu Arg Asp Ser His Pro Gln Ala Arg Gly Arg Lys Arg Arg Ser Met
130 135 140

Gln Trp Asn Ser Thr Ala Phe His Gln Ala Leu Gln Asp Pro Arg Val
145 150 155 160

Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val Asn
165 170 175

Pro Ala Pro Asn Ile Ala Ser His Ile Ser Ser Ile Ser Ala Arg Thr
180 185 190

Gly Asp Pro Val Thr Asn Arg Gly Arg Lys Arg Arg Ser Met Glu Asn
195 200 205

Ile Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
210 215 220

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
225 230 235 240

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ser Pro Val Cys Leu Gly Gln
245 250 255

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
260 265 270

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
275 280 285

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
290 295 300

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Thr Thr
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305 310 315 320

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Thr Pro Ala Gln Gly Asn
 325 330 335

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Thr Asp Gly Asn Cys
 340 345 350

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Lys Tyr Leu Trp
 355 360 365

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
 370 375 380

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Ala Ile
 385 390 395 400

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Ser Ile Val Ser Pro
 405 410 415

Phe Ile Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
 420 425 430

<210> 11
 <211> 1319
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic (LHBs-C)

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 aatcctctgg ggttctttcc cgaccaccag ctggatcctg ccttcggcgc taactctaac 180
 aatccagact gggactcaa cccaataag gaccactggc ctgaggcaaa tcaagtggga 240
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 cagtcaggac gccagccaac cccatttct ccaccctga gggacagtca ccctcaggcc 420
 agaggcagga agcggagaag catgcagtgg aacagcacta cttccatca ggcactgctg 480
 gatccacgcg tcgaggact gtactttcca gccggaggca gtcctctgg aaccgtgaac 540
 cctgtcccaa caactgctc ccaatcagt tcaatttct ctggagagg agaccccgct 600
 cctaatcggg gcagaaaaag gcgctcaatg gaaagcacca catccgggtt tctgggacca 660

UPVG0037WO2_SequenceListing

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aactctcaga gtccaacatc aaatcatagc cccacttct gtcctccaat ctgccctggc 840
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<210> 12
<211> 431
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic (LHBs-C)

<400> 12

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn
20 25 30

Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp
35 40 45

Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro
50 55 60

Asn Lys Asp His Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe
65 70 75 80

Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro
85 90 95

Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala
100 105 110

UPVG0037WO2_SequenceListing

Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro
115 120 125

Leu Arg Asp Ser His Pro Gln Ala Arg Gly Arg Lys Arg Arg Ser Met
130 135 140

Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu Asp Pro Arg Val
145 150 155 160

Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val Asn
165 170 175

Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr
180 185 190

Gly Asp Pro Ala Pro Asn Arg Gly Arg Lys Arg Arg Ser Met Glu Ser
195 200 205

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
210 215 220

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
225 230 235 240

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
245 250 255

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
260 265 270

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
275 280 285

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
290 295 300

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
305 310 315 320

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr
325 330 335

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys
340 345 350

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Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
355 360 365

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
370 375 380

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
385 390 395 400

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
405 410 415

Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
420 425 430

<210> 13
<211> 753
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic (SHBs-A)

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<210> 14
<211> 243
<212> PRT
<213> Artificial Sequence

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<220>

<223> Synthetic (SHBs-A)

<400> 14

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
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His Ser Glu Asn Ile Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
20 25 30

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
35 40 45

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ser Pro Val
50 55 60

Cys Leu Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
65 70 75 80

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
85 90 95

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
100 105 110

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro
115 120 125

Gly Ser Thr Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Thr Pro
130 135 140

Ala Gln Gly Asn Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Thr
145 150 155 160

Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
165 170 175

Lys Tyr Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
180 185 190

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
195 200 205

Leu Ser Ala Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Ser
210 215 220

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Ile Val Ser Pro Phe Ile Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
225 230 235 240

Val Tyr Ile

<210> 15
<211> 755
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic (SHBs-C)

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tttctgtga cacgaatctt gactattcca cagtcaactg acagctgggtg gaccagcctg 180
aacttcttgg gcggggcccc tacatgtcca ggacagaact ctgagagtc cacttccaat 240
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<210> 16
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic (SHBs-C)

<400> 16

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Thr Arg Val
1 5 10 15

His Ser Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
20 25 30

UPVG0037WO2_SequenceListing

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
35 40 45

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
50 55 60

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
65 70 75 80

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
85 90 95

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
100 105 110

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
115 120 125

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
130 135 140

Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
145 150 155 160

Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
165 170 175

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195 200 205

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
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UPVG0037WO2_SequenceListing

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