

2014004579
SEQUENCE LISTING

<110> Humabs BioMed SA

<120> Human Cytomegalovirus vaccine compositions and method of producing the same

<130> HB01P010W01

<160> 55

<170> PatentIn version 3.5

<210> 1

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> signal peptide

<400> 1

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<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> signal sequence

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<211> 151

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<213> Artificial Sequence

<220>

<223> UL128

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<400> 3

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Pro Pro Glu Arg Cys Tyr Asp Phe Lys Met Cys Asn Arg Phe Thr Val
20 25 30

Ala Tyr Val Leu Arg Cys Pro Asp Gly Glu Val Cys Tyr Ser Pro Glu
35 40 45

Lys Thr Ala Glu Ile Arg Gly Ile Val Thr Thr Met Thr His Ser Leu
50 55 60

Thr Arg Gln Val Val His Asn Lys Leu Thr Ser Cys Asn Tyr Asn Pro
65 70 75 80

Leu Tyr Leu Glu Ala Asp Gly Arg Ile Arg Cys Gly Lys Val Asn Asp
85 90 95

Lys Ala Gln Tyr Leu Leu Gly Ala Ala Gly Ser Val Pro Tyr Arg Trp
100 105 110

Ile Asn Leu Glu Tyr Asp Lys Ile Thr Arg Ile Val Gly Leu Asp Gln
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Tyr Leu Glu Ser Val Lys Lys His Lys Arg Leu Asp Val Cys Arg Ala
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Lys Met Gly Tyr Met Leu Gln
145 150

<210> 4

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<223> UL128

<400> 4

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<223> UL130v1

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Leu Thr Tyr Ser Lys Pro His Asp Ala Ala Thr Phe Tyr Cys Pro Phe
20 25 30

Leu Tyr Pro Ser Pro Pro Arg Ser Pro Ser Gln Phe Ser Gly Phe Gln
35 40 45

Arg Val Ser Thr Gly Pro Glu Cys Arg Asn Glu Thr Leu Tyr Leu Leu
50 55 60

Tyr Asn Arg Glu Gly Gln Thr Leu Val Glu Arg Ser Ser Thr Trp Val
65 70 75 80

Lys Lys Val Ile Trp Tyr Leu Ser Gly Arg Asn Gln Thr Ile Leu Gln
85 90 95

Arg Met Pro Arg Thr Ala Ser Lys Pro Ser Asp Gly Asn Val Gln Ile
100 105 110

Ser Val Glu Asp Ala Lys Ile Phe Gly Ala His Met Val Pro Lys Gln
115 120 125

Thr Lys Leu Leu Arg Phe Val Val Asn Asp Gly Thr Arg Tyr Gln Met
130 135 140

Cys Val Met Lys Leu Glu Ser Trp Ala His Val Phe Arg Asp Tyr Ser
145 150 155 160

Val Ser Phe Gln Val Arg Leu Thr Phe Thr Glu Ala Asn Asn Gln Thr
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Tyr Thr Phe Cys Thr His Pro Asn Leu Ile
180 185

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<220>
<223> Nucleotide sequence encoding UL130_v1

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ccaagtcagt tcagcggatt tcagcgagtg tctactgggc ccgagtgtcg taatgaaacc 180
ctgtacctgc tgtataacag ggagggacag accctgggtg aacgggtccag cacatgggtg 240
aagaaagtca tctgggtatct gtctgggcgg aatcagacaa ttctgcagag gatgccccgg 300
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ggggcacata tgggtgccccaa gcagacaaaa ctgctgagat ttgtgggtcaa tgacggcact 420
cgctaccaga tgtgcgtgat gaagctggag agctgggccc acgtctttcg agattattca 480
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actcatccta atctgatc 558

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<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> F2A

<400> 9

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
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Glu Ser Asn Pro Gly Pro
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<210> 10
<211> 66
<212> DNA

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<213> Artificial Sequence

<220>

<223> F2A

<400> 10

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ggacca 66

<210> 11

<211> 111

<212> PRT

<213> Artificial Sequence

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<223> UL131Av1

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Gln Cys Gln Arg Glu Thr Ala Glu Lys Asn Asp Tyr Tyr Arg Val Pro
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His Tyr Trp Asp Ala Cys Ser Arg Ala Leu Pro Asp Gln Thr Arg Tyr
20 25 30

Lys Tyr Val Glu Gln Leu Val Asp Leu Thr Leu Asn Tyr His Tyr Asp
35 40 45

Ala Ser His Gly Leu Asp Asn Phe Asp Val Leu Lys Arg Ile Asn Val
50 55 60

Thr Glu Val Ser Leu Leu Ile Ser Asp Phe Arg Arg Gln Asn Arg Arg
65 70 75 80

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

Pro His Ala Arg Ser Leu Glu Phe Ser Val Arg Leu Phe Ala Asn
100 105 110

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<211> 333

<212> DNA

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<213> Artificial Sequence

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<223> Nucleotide sequence encoding UL131_v1

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ctgacactga actaccacta tgatgcctcc catggcctgg acaatttcga tgtgctgaag 180

agaatcaacg tgactgaagt ctctctgctg attagtgatt tcaggcggca gaacagacgc 240

ggcggaaacca ataagcgcac tacctttaac gctgcaggct ccctggcccc acatgctagg 300

tcactggagt tctccgtgcg gctgtttgct aac 333

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<212> PRT

<213> Artificial Sequence

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<223> TEV site

<400> 13

Glu Asn Leu Tyr Phe Gln Gly

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<211> 21

<212> DNA

<213> Artificial Sequence

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<223> TEV site

<400> 14

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<212> PRT

<213> Artificial Sequence

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<223> GS linker

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<400> 15

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<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> GS linker

<400> 16

agcggttctg gc

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<223> tandem Strep-tag_v1

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Gln Phe Glu Lys
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<212> DNA

<213> Artificial Sequence

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<223> tandem Strep-tag_v1

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<210> 19

<211> 19

<212> PRT

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<213> Artificial Sequence

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<223> Mouse IgG signal peptide

<400> 19

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
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Val His Ser

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<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse IgG signal peptide nt seq

<400> 20

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<210> 21

<211> 688

<212> PRT

<213> Artificial Sequence

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<223> Amino acid sequence of gH_v1

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Gly Ala Asp Ala Ala Ser Glu Ala Leu Asp Pro His Ala Phe His Leu
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20 25 30

Thr Gln Cys Thr Tyr Asn Ser Ser Leu Arg Asn Ser Thr Val Val Arg
35 40 45

Glu Asn Ala Ile Ser Phe Asn Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr
50 55 60

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Val Phe His Met Pro Arg Cys Leu Phe Ala Gly Pro Leu Ala Glu Gln
65 70 75 80

Phe Leu Asn Gln Val Asp Leu Thr Glu Thr Leu Glu Arg Tyr Gln Gln
85 90 95

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

Ser Phe Pro Gln Gln Leu Lys Ala Gln Asp Ser Leu Gly Gln Gln Pro
115 120 125

Thr Thr Val Pro Pro Pro Ile Asp Leu Ser Ile Pro His Val Trp Met
130 135 140

Pro Pro Gln Thr Thr Pro His Asp Trp Lys Gly Ser His Thr Thr Ser
145 150 155 160

Gly Leu His Arg Pro His Phe Asn Gln Thr Cys Ile Leu Phe Asp Gly
165 170 175

His Asp Leu Leu Phe Ser Thr Val Thr Pro Cys Leu His Gln Gly Phe
180 185 190

Tyr Leu Met Asp Glu Leu Arg Tyr Val Lys Ile Thr Leu Thr Glu Asp
195 200 205

Phe Phe Val Val Thr Val Ser Ile Asp Asp Asp Thr Pro Met Leu Leu
210 215 220

Ile Phe Gly His Leu Pro Arg Val Leu Phe Lys Ala Pro Tyr Gln Arg
225 230 235 240

Asp Asn Phe Ile Leu Arg Gln Thr Glu Lys His Glu Leu Leu Val Leu
245 250 255

Val Lys Lys Thr Gln Leu Asn Arg His Ser Tyr Leu Lys Asp Ser Asp
260 265 270

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Phe Leu Asp Ala Ala Leu Asp Phe Asn Tyr Leu Asp Leu Ser Ala Leu
275 280 285

Leu Arg Asn Ser Phe His Arg Tyr Ala Val Asp Val Leu Lys Ser Gly
290 295 300

Arg Cys Gln Met Leu Asp Arg Arg Thr Val Glu Met Ala Phe Ala Tyr
305 310 315 320

Ala Leu Ala Leu Phe Ala Ala Ala Arg Gln Glu Glu Ala Gly Thr Glu
325 330 335

Ile Ser Ile Pro Arg Ala Leu Asp Arg Gln Ala Ala Leu Leu Gln Ile
340 345 350

Gln Glu Phe Met Ile Thr Cys Leu Ser Gln Thr Pro Pro Arg Thr Thr
355 360 365

Leu Leu Leu Tyr Pro Thr Ala Val Asp Leu Ala Lys Arg Ala Leu Trp
370 375 380

Thr Pro Asp Gln Ile Thr Asp Ile Thr Ser Leu Val Arg Leu Val Tyr
385 390 395 400

Ile Leu Ser Lys Gln Asn Gln Gln His Leu Ile Pro Gln Trp Ala Leu
405 410 415

Arg Gln Ile Ala Asp Phe Ala Leu Gln Leu His Lys Thr His Leu Ala
420 425 430

Ser Phe Leu Ser Ala Phe Ala Arg Gln Glu Leu Tyr Leu Met Gly Ser
435 440 445

Leu Val His Ser Met Leu Val His Thr Thr Glu Arg Arg Glu Ile Phe
450 455 460

Ile Val Glu Thr Gly Leu Cys Ser Leu Ala Glu Leu Ser His Phe Thr
465 470 475 480

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Gln Leu Leu Ala His Pro His His Glu Tyr Leu Ser Asp Leu Tyr Thr
485 490 495

Pro Cys Ser Ser Ser Gly Arg Arg Asp His Ser Leu Glu Arg Leu Thr
500 505 510

Arg Leu Phe Pro Asp Ala Thr Val Pro Ala Thr Val Pro Ala Ala Leu
515 520 525

Ser Ile Leu Ser Thr Met Gln Pro Ser Thr Leu Glu Thr Phe Pro Asp
530 535 540

Leu Phe Cys Leu Pro Leu Gly Glu Ser Phe Ser Ala Leu Thr Val Ser
545 550 555 560

Glu His Val Ser Tyr Val Val Thr Asn Gln Tyr Leu Ile Lys Gly Ile
565 570 575

Ser Tyr Pro Val Ser Thr Thr Val Val Gly Gln Ser Leu Ile Ile Thr
580 585 590

Gln Thr Asp Ser Gln Ser Lys Cys Glu Leu Thr Arg Asn Met His Thr
595 600 605

Thr His Ser Ile Thr Ala Ala Leu Asn Ile Ser Leu Glu Asn Cys Ala
610 615 620

Phe Cys Gln Ser Ala Leu Leu Glu Tyr Asp Asp Thr Gln Gly Val Ile
625 630 635 640

Asn Ile Met Tyr Met His Asp Ser Asp Asp Val Leu Phe Ala Leu Asp
645 650 655

Pro Tyr Asn Glu Val Val Val Ser Ser Pro Arg Thr His Tyr Leu Met
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Leu Leu Lys Asn Gly Thr Val Leu Glu Val Thr Asp Val Val Val Asp
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<210> 22
<211> 2064
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide Sequence encoding gH_v1

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aaccagtact atgtgttcca catgccaaga tgtctgtttg ctggaccctt ggcagagcag 240
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aacattatgt atatgcacga tagcgatgac gtgctgttcg ctctggaccc atacaacgag	1980
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<210> 23
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 <223> P2A

<400> 23

Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn
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Pro Gly Pro

<210> 24
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 <212> DNA
 <213> Artificial Sequence

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<220>

<223> P2A nt seq

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<210> 25

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of gL_v1

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Pro Glu Leu Thr Arg Arg Cys Leu Leu Gly Glu Val Phe Gln Gly Asp
20 25 30

Lys Tyr Glu Ser Trp Leu Arg Pro Leu Val Asn Val Thr Gly Arg Asn
35 40 45

Gly Pro Leu Ser Gln Leu Ile Arg Tyr Arg Pro Val Thr Pro Glu Ala
50 55 60

Ala Asn Ser Val Leu Leu Asp Asp Ala Phe Leu Asp Thr Leu Ala Leu
65 70 75 80

Leu Tyr Asn Asn Pro Asp Gln Leu Arg Ala Leu Leu Thr Leu Leu Ser
85 90 95

Ser Asp Thr Ala Pro Arg Trp Met Thr Val Met Arg Gly Tyr Ser Glu
100 105 110

Cys Gly Asp Gly Ser Pro Ala Val Tyr Thr Cys Val Asp Asp Leu Cys
115 120 125

Arg Gly Tyr Asp Leu Thr Arg Leu Ser Tyr Gly Arg Ser Ile Phe Thr
130 135 140

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Glu His Val Leu Gly Phe Glu Leu Val Pro Pro Ser Leu Phe Asn Val
145 150 155 160

Val Val Ala Ile Arg Asn Glu Ala Thr Arg Thr Asn Arg Ala Val Arg
165 170 175

Leu Pro Val Ser Thr Ala Ala Ala Pro Glu Gly Ile Thr Leu Phe Tyr
180 185 190

Gly Leu Tyr Asn Ala Val Lys Glu Phe Cys Leu Arg His Gln Leu Asp
195 200 205

Pro Pro Leu Leu Arg His Leu Asp Lys Tyr Tyr Ala Gly Leu Pro Pro
210 215 220

Glu Leu Lys Gln Thr Arg Val Asn Leu Pro Ala His Ser Arg Tyr Gly
225 230 235 240

Pro Gln Ala Val Asp Ala Arg
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<210> 26
<211> 741
<212> DNA
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<223> Nucleotide sequence encoding gL_v1

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tatacctgcg tggatgacct gtgtcgaggc tacgacctga caaggctgtc ttatggacgg 420

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<210> 27
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of P2A_v2

<400> 27

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
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<210> 28
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding P2A_v2

<400> 28
ggaagcggag caacaaactt ttactgctg aaacaggccg gggatgtgga ggaaaaatcct 60
ggtcca 66

<210> 29
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of P2A_v3

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<400> 29

Arg Lys Arg Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln
1 5 10 15

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
20 25

<210> 30

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding P2A_v3

<400> 30

cgcaaacgcc gcggaagcgg agcaacaaac ttttcactgc tgaaacaggc cggggatgtg 60

gaggaaaatc ctggtcca 78

<210> 31

<211> 189

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence encoding UL130_v2

<400> 31

Ser Ser Trp Ser Thr Leu Thr Ala Asn Gln Asn Pro Ser Pro Pro Trp
1 5 10 15

Ser Lys Leu Thr Tyr Ser Lys Pro His Asp Ala Ala Thr Phe Tyr Cys
20 25 30

Pro Phe Leu Tyr Pro Ser Pro Pro Arg Ser Pro Ser Gln Phe Ser Gly
35 40 45

Phe Gln Arg Val Ser Thr Gly Pro Glu Cys Arg Asn Glu Thr Leu Tyr
50 55 60

Leu Leu Tyr Asn Arg Glu Gly Gln Thr Leu Val Glu Arg Ser Ser Thr

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65		70		75		80
Trp Val Lys Lys Val Ile Trp Tyr Leu Ser Gly Arg Asn Gln Thr Ile						
		85		90		95
Leu Gln Arg Met Pro Arg Thr Ala Ser Lys Pro Ser Asp Gly Asn Val						
		100		105		110
Gln Ile Ser Val Glu Asp Ala Lys Ile Phe Gly Ala His Met Val Pro						
		115		120		125
Lys Gln Thr Lys Leu Leu Arg Phe Val Val Asn Asp Gly Thr Arg Tyr						
		130		135		140
Gln Met Cys Val Met Lys Leu Glu Ser Trp Ala His Val Phe Arg Asp						
		145		150		155
Tyr Ser Val Ser Phe Gln Val Arg Leu Thr Phe Thr Glu Ala Asn Asn						
		165		170		175
Gln Thr Tyr Thr Phe Cys Thr His Pro Asn Leu Ile Val						
		180		185		

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 <223> Nucleotide sequence encoding UL130_v2

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aggtctccaa gtcagttcag cggatttcag cgagtgtcta ctgggcccga gtgtcgtaat	180
gaaaccctgt acctgctgta taacagggag ggacagaccc tgggtggaacg gtccagcaca	240
tgggtgaaga aagtcattctg gtatctgtct gggcggaatc agacaattct gcagaggatg	300
ccccggactg ccagtaagcc ttcagacgga aacgtgcaga tcagtgtcga ggatgctaaa	360

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attttcgggg cacatatggt gcccaagcag acaaaactgc tgagatttgt ggtcaatgac 420
 ggcaactcgct accagatgtg cgtgatgaag ctggagagct gggcccacgt ctttcgagat 480
 tattcagtgt ccttccaggt ccgtctgacc ttacagaag ctaacaatca gacttacacc 540
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<210> 33
 <211> 110
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of UL131_v2

<400> 33

Cys Gln Arg Glu Thr Ala Glu Lys Asn Asp Tyr Tyr Arg Val Pro His
 1 5 10 15

Tyr Trp Asp Ala Cys Ser Arg Ala Leu Pro Asp Gln Thr Arg Tyr Lys
 20 25 30

Tyr Val Glu Gln Leu Val Asp Leu Thr Leu Asn Tyr His Tyr Asp Ala
 35 40 45

Ser His Gly Leu Asp Asn Phe Asp Val Leu Lys Arg Ile Asn Val Thr
 50 55 60

Glu Val Ser Leu Leu Ile Ser Asp Phe Arg Arg Gln Asn Arg Arg Gly
 65 70 75 80

Gly Thr Asn Lys Arg Thr Thr Phe Asn Ala Ala Gly Ser Leu Ala Pro
 85 90 95

His Ala Arg Ser Leu Glu Phe Ser Val Arg Leu Phe Ala Asn
 100 105 110

<210> 34
 <211> 330
 <212> DNA
 <213> Artificial Sequence

2014004579

<220>

<223> Nucleotide sequence encoding UL131_v2

<400> 34

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tgccagcgag agaccgcaga aaagaacgac tactatcggg tgcctcacta ttgggacgca      60
tgttctcgag ccctgccaga tcagaccgtg tacaatatg tggagcagct ggtcgacctg      120
aactgaact accactatga tgcctcccat ggcctggaca atttcgatgt gctgaagaga      180
atcaacgtga ctgaagtctc tctgctgatt agtgatttca ggcggcagaa cagacgcggc      240
ggaaccaata agcgactac ctttaacgct gcaggctccc tggccccaca tgctagggtca      300
ctggagttct ccgtgcggct gtttgctaac      330
```

<210> 35

<211> 690

<212> PRT

<213> Artificial Sequence

<220>

<223> gHv2

<400> 35

```
Arg Tyr Gly Ala Asp Ala Ala Ser Glu Ala Leu Asp Pro His Ala Phe
1              5              10              15
```

```
His Leu Leu Leu Asn Thr Tyr Gly Arg Pro Ile Arg Phe Leu Arg Glu
20              25              30
```

```
Asn Thr Thr Gln Cys Thr Tyr Asn Ser Ser Leu Arg Asn Ser Thr Val
35              40              45
```

```
Val Arg Glu Asn Ala Ile Ser Phe Asn Phe Phe Gln Ser Tyr Asn Gln
50              55              60
```

```
Tyr Tyr Val Phe His Met Pro Arg Cys Leu Phe Ala Gly Pro Leu Ala
65              70              75              80
```

```
Glu Gln Phe Leu Asn Gln Val Asp Leu Thr Glu Thr Leu Glu Arg Tyr
85              90              95
```

```
Gln Gln Arg Leu Asn Thr Tyr Ala Leu Val Ser Lys Asp Leu Ala Ser
```

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100

105

110

Tyr Arg Ser Phe Pro Gln Gln Leu Lys Ala Gln Asp Ser Leu Gly Gln
115 120 125

Gln Pro Thr Thr Val Pro Pro Pro Ile Asp Leu Ser Ile Pro His Val
130 135 140

Trp Met Pro Pro Gln Thr Thr Pro His Asp Trp Lys Gly Ser His Thr
145 150 155 160

Thr Ser Gly Leu His Arg Pro His Phe Asn Gln Thr Cys Ile Leu Phe
165 170 175

Asp Gly His Asp Leu Leu Phe Ser Thr Val Thr Pro Cys Leu His Gln
180 185 190

Gly Phe Tyr Leu Met Asp Glu Leu Arg Tyr Val Lys Ile Thr Leu Thr
195 200 205

Glu Asp Phe Phe Val Val Thr Val Ser Ile Asp Asp Asp Thr Pro Met
210 215 220

Leu Leu Ile Phe Gly His Leu Pro Arg Val Leu Phe Lys Ala Pro Tyr
225 230 235 240

Gln Arg Asp Asn Phe Ile Leu Arg Gln Thr Glu Lys His Glu Leu Leu
245 250 255

Val Leu Val Lys Lys Thr Gln Leu Asn Arg His Ser Tyr Leu Lys Asp
260 265 270

Ser Asp Phe Leu Asp Ala Ala Leu Asp Phe Asn Tyr Leu Asp Leu Ser
275 280 285

Ala Leu Leu Arg Asn Ser Phe His Arg Tyr Ala Val Asp Val Leu Lys
290 295 300

Ser Gly Arg Cys Gln Met Leu Asp Arg Arg Thr Val Glu Met Ala Phe

305		310		315		320
Ala Tyr Ala Leu	Ala Leu Phe Ala Ala	Ala Arg Gln Glu Glu	Ala Gly			
	325	330	335			
Thr Glu Ile Ser	Ile Pro Arg Ala Leu	Asp Arg Gln Ala	Ala Leu Leu			
	340	345	350			
Gln Ile Gln Glu	Phe Met Ile Thr Cys Leu	Ser Gln Thr Pro	Pro Arg			
	355	360	365			
Thr Thr Leu Leu	Leu Tyr Pro Thr	Ala Val Asp Leu	Ala Lys Arg Ala			
	370	375	380			
Leu Trp Thr Pro	Asp Gln Ile Thr	Asp Ile Thr Ser	Leu Val Arg Leu			
385	390	395	400			
Val Tyr Ile Leu	Ser Lys Gln Asn Gln	Gln His Leu Ile	Pro Gln Trp			
	405	410	415			
Ala Leu Arg Gln	Ile Ala Asp Phe Ala	Leu Gln Leu His	Lys Thr His			
	420	425	430			
Leu Ala Ser Phe	Leu Ser Ala Phe	Ala Arg Gln Glu	Leu Tyr Leu Met			
	435	440	445			
Gly Ser Leu Val	His Ser Met Leu	Val His Thr Thr	Glu Arg Arg Glu			
	450	455	460			
Ile Phe Ile Val	Glu Thr Gly Leu	Cys Ser Leu Ala	Glu Leu Ser His			
465	470	475	480			
Phe Thr Gln Leu	Leu Ala His Pro	His His Glu Tyr	Leu Ser Asp Leu			
	485	490	495			
Tyr Thr Pro Cys	Ser Ser Ser Gly	Arg Arg Asp His	Ser Leu Glu Arg			
	500	505	510			
Leu Thr Arg Leu	Phe Pro Asp Ala	Thr Val Pro Ala	Thr Val Pro Ala			

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515

520

525

Ala Leu Ser Ile Leu Ser Thr Met Gln Pro Ser Thr Leu Glu Thr Phe
530 535 540

Pro Asp Leu Phe Cys Leu Pro Leu Gly Glu Ser Phe Ser Ala Leu Thr
545 550 555 560

Val Ser Glu His Val Ser Tyr Val Val Thr Asn Gln Tyr Leu Ile Lys
565 570 575

Gly Ile Ser Tyr Pro Val Ser Thr Thr Val Val Gly Gln Ser Leu Ile
580 585 590

Ile Thr Gln Thr Asp Ser Gln Ser Lys Cys Glu Leu Thr Arg Asn Met
595 600 605

His Thr Thr His Ser Ile Thr Ala Ala Leu Asn Ile Ser Leu Glu Asn
610 615 620

Cys Ala Phe Cys Gln Ser Ala Leu Leu Glu Tyr Asp Asp Thr Gln Gly
625 630 635 640

Val Ile Asn Ile Met Tyr Met His Asp Ser Asp Asp Val Leu Phe Ala
645 650 655

Leu Asp Pro Tyr Asn Glu Val Val Val Ser Ser Pro Arg Thr His Tyr
660 665 670

Leu Met Leu Leu Lys Asn Gly Thr Val Leu Glu Val Thr Asp Val Val
675 680 685

Val Asp
690

<210> 36
<211> 2070
<212> DNA
<213> Artificial Sequence

2014004579

<220>

<223> gHv2

<400> 36

cgctatggag cagacgcagc atcagaggcc ctggaccctc acgcttttca tctgctgctg	60
aacacctacg gccgaccaat ccgtttcctg agggagaata ccacacagtg cacatataac	120
tccagcctga gaaatagcac tgtgggtccgc gaaaacgccca ttagtttttaa tttctttcag	180
tcatacaacc agtactatgt gttccacatg ccaagatgtc tgtttgctgg acccctggca	240
gagcagttcc tgaaccaggt ggatctgaca gagactctgg aaaggtagca gcagcggctg	300
aatacctatg ctctgggtgc taaggacctg gcaagttatc gctcatttcc ccagcagctg	360
aaagctcagg acagtctggg acagcagcct actaccgtcc cacctccaat cgatctgtca	420
attcctcatg tgtggatgcc ccctcagaca actccacacg actggaaggg gtcacatacc	480
acatccgggtc tgcacagacc acatttcaac cagacatgca tcctgtttga tggccacgac	540
ctgctgttct ccaccgtgac accctgtctg catcagggat tctacctgat ggatgagctg	600
agatatgtga agattactct gaccgaagac ttctttgtgg tcaccgtgag catcgacgat	660
gacacaccaa tgctgctgat ttttggacac ctgcctcgcg tgctgttcaa ggccccatac	720
cagcgagata actttatcct gcgtcagact gagaaacacg aactgctggg cctgggtgaag	780
aaaaccagc tgaatcgcca ttcatatctg aaagattccg actttctgga tgccgctctg	840
gacttcaact acctggacct gtccgctctg ctgcgaaata gcttccatcg ttatgcagtc	900
gatgtgctga agagcggcag gtgccagatg ctggacaggc ggacagtgga gatggccttt	960
gcttacgcac tggcactgtt cgcagccgct cgacaggagg aagcaggaac tgagatctct	1020
attcctagag ctctggatcg ccaggcagcc ctgctgcaga tccaggagtt catgattact	1080
tgtctgtccc agaccccacc acgaactacc ctgctgctgt acccaaccgc cgtggacctg	1140
gccaagagag ctctgtggac acccgatcag atcactgaca ttaccagcct ggtccgcctg	1200
gtgtatatcc tgtctaaaca gaaccagcag cacctgatcc cacagtgggc cctgcgacag	1260
attgcagact tcgccctgca gctgcacaag acccatctgg cttccttcct gagcgctttt	1320
gcacggcagg agctgtacct gatggggagc ctgggtccact ctatgctggg gcatacaact	1380
gagagacgcg aaatctttat tgtggagaca ggtctgtgca gcctggccga actgtctcac	1440

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ttcactcagc tgctggctca tccacacccat gactacctgt ccgatctgta tactccctgt	1500
tctagttcag ggcgacgtga ccacagcctg gaacggctga ccagactgtt tcccgatgcc	1560
accgtcccag ctacagtgcc cgctgcactg tctatcctga gtaccatgca gccttctaca	1620
ctggagactt tccccgatct gttttgcctg cctctgggcg agtcattctc cgccctgacc	1680
gtcagtgaac atgtgtcata cgtggtcaca aaccagtatc tgatcaaagg gatttcctac	1740
cccgtgagca ccacagtggg cggccagtcc ctgatcatta cacagactga cagccagtct	1800
aagtgtgagc tgactaggaa tatgcacact acccattcaa tcaccgccgc tctgaacatt	1860
tccctggaga attgcgcttt ttgtcagagt gcactgctgg aatacgaatga caccagggc	1920
gtgatcaaca ttatgtatat gcacgatagc gatgacgtgc tgttcgctct ggaccatac	1980
aacgaggtgg tcgtgtccag cccacgaacc cattatctga tgctgctgaa gaatggtaca	2040
gtcctggaag tgactgatgt cgtggtcgac	2070

<210> 37
 <211> 248
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> gLv2

<400> 37

Val	Ala	Val	Ser	Val	Ala	Pro	Thr	Ala	Ala	Glu	Lys	Val	Pro	Ala	Glu
1				5				10						15	

Cys	Pro	Glu	Leu	Thr	Arg	Arg	Cys	Leu	Leu	Gly	Glu	Val	Phe	Gln	Gly
			20					25					30		

Asp	Lys	Tyr	Glu	Ser	Trp	Leu	Arg	Pro	Leu	Val	Asn	Val	Thr	Gly	Arg
		35					40					45			

Asn	Gly	Pro	Leu	Ser	Gln	Leu	Ile	Arg	Tyr	Arg	Pro	Val	Thr	Pro	Glu
	50					55					60				

Ala	Ala	Asn	Ser	Val	Leu	Leu	Asp	Asp	Ala	Phe	Leu	Asp	Thr	Leu	Ala
65					70					75				80	

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Leu Leu Tyr Asn Asn Pro Asp Gln Leu Arg Ala Leu Leu Thr Leu Leu
85 90 95

Ser Ser Asp Thr Ala Pro Arg Trp Met Thr Val Met Arg Gly Tyr Ser
100 105 110

Glu Cys Gly Asp Gly Ser Pro Ala Val Tyr Thr Cys Val Asp Asp Leu
115 120 125

Cys Arg Gly Tyr Asp Leu Thr Arg Leu Ser Tyr Gly Arg Ser Ile Phe
130 135 140

Thr Glu His Val Leu Gly Phe Glu Leu Val Pro Pro Ser Leu Phe Asn
145 150 155 160

Val Val Val Ala Ile Arg Asn Glu Ala Thr Arg Thr Asn Arg Ala Val
165 170 175

Arg Leu Pro Val Ser Thr Ala Ala Ala Pro Glu Gly Ile Thr Leu Phe
180 185 190

Tyr Gly Leu Tyr Asn Ala Val Lys Glu Phe Cys Leu Arg His Gln Leu
195 200 205

Asp Pro Pro Leu Leu Arg His Leu Asp Lys Tyr Tyr Ala Gly Leu Pro
210 215 220

Pro Glu Leu Lys Gln Thr Arg Val Asn Leu Pro Ala His Ser Arg Tyr
225 230 235 240

Gly Pro Gln Ala Val Asp Ala Arg
245

<210> 38

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<223> gLv2 nt seq

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<400> 38
gtggcagtct ctgtggcacc aaccgcagca gagaagggtgc ctgcagagtg cccagaactg 60
acaaggcgggt gtctgctggg cgagggtgttc caggagagaca aatacgaatc ctggctgaga 120
cccctgggtca acgtgacagg gcgcaatggg cctctgtctc agctgatcag atatcgcccc 180
gtcactcctg aggctgcaaa cagtgtgctg ctggatgacg catttctgga taccctggcc 240
ctgctgtaca acaatcctga ccagctgagg gcactgctga ccctgctgtc tagtgacaca 300
gctccaagggt ggatgactgt gatgcggggc tactctgaat gcggcgatgg aagtcctgcc 360
gtctatacct gcgtggatga cctgtgtcga ggctacgacc tgacaaggct gtcttatgga 420
cggagtatct ttactgagca cgtcctggga ttcgaactgg tgcctccaag cctgttcaat 480
gtggtcgtgg ccattcggaa cgaggctacc cgcacaaatc gagccgtccg tctgcccgtg 540
tctactgccg ctgcacctga gggcatcacc ctgttttacg gactgtataa cgctgtgaag 600
gagttctgtc tgcgacacca gctggatccc cctctgctgc gtcactctgga caagtactat 660
gccggcctgc caccgagct gaaacagaca agagtcaacc tgcccgcaca cagccgctat 720
ggaccccagg ccgtggatgc tcgt 744

<210> 39
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> tandem strep-tag_v2

<400> 39

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly
1 5 10 15

Gly Ser Gly Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu Lys
20 25 30

<210> 40
<211> 93
<212> DNA
<213> Artificial Sequence

2014004579

<220>

<223> tandem strep-tag_v2 nt seq

<400> 40

agcgcacatggt cacacccaca gtttgaaaaa ggtgggtggta gcggtgggtg ttccggtggt 60

agcagcgcacat ggtcacaccc acagtttgaa aaa 93

<210> 41

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 6xHis tag

<400> 41

His His His His His His

1 5

<210> 42

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> 6xHis tag nt seq

<400> 42

catcatcacc atcaccac 18

<210> 43

<211> 523

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of pentamer_UL128-130-131A_v1

<400> 43

Met Ser Pro Lys Asp Leu Thr Pro Phe Leu Thr Ala Leu Trp Leu Leu

1 5 10 15

Leu Gly His Ser Arg Val Pro Arg Val Arg Ala Glu Glu Cys Cys Glu

20 25 30

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Phe Ile Asn Val Asn His Pro Pro Glu Arg Cys Tyr Asp Phe Lys Met
35 40 45

Cys Asn Arg Phe Thr Val Ala Tyr Val Leu Arg Cys Pro Asp Gly Glu
50 55 60

Val Cys Tyr Ser Pro Glu Lys Thr Ala Glu Ile Arg Gly Ile Val Thr
65 70 75 80

Thr Met Thr His Ser Leu Thr Arg Gln Val Val His Asn Lys Leu Thr
85 90 95

Ser Cys Asn Tyr Asn Pro Leu Tyr Leu Glu Ala Asp Gly Arg Ile Arg
100 105 110

Cys Gly Lys Val Asn Asp Lys Ala Gln Tyr Leu Leu Gly Ala Ala Gly
115 120 125

Ser Val Pro Tyr Arg Trp Ile Asn Leu Glu Tyr Asp Lys Ile Thr Arg
130 135 140

Ile Val Gly Leu Asp Gln Tyr Leu Glu Ser Val Lys Lys His Lys Arg
145 150 155 160

Leu Asp Val Cys Arg Ala Lys Met Gly Tyr Met Leu Gln Trp Ser Thr
165 170 175

Leu Thr Ala Asn Gln Asn Pro Ser Pro Pro Trp Ser Lys Leu Thr Tyr
180 185 190

Ser Lys Pro His Asp Ala Ala Thr Phe Tyr Cys Pro Phe Leu Tyr Pro
195 200 205

Ser Pro Pro Arg Ser Pro Ser Gln Phe Ser Gly Phe Gln Arg Val Ser
210 215 220

Thr Gly Pro Glu Cys Arg Asn Glu Thr Leu Tyr Leu Leu Tyr Asn Arg
225 230 235 240

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Glu Gly Gln Thr Leu Val Glu Arg Ser Ser Thr Trp Val Lys Lys Val
245 250 255

Ile Trp Tyr Leu Ser Gly Arg Asn Gln Thr Ile Leu Gln Arg Met Pro
260 265 270

Arg Thr Ala Ser Lys Pro Ser Asp Gly Asn Val Gln Ile Ser Val Glu
275 280 285

Asp Ala Lys Ile Phe Gly Ala His Met Val Pro Lys Gln Thr Lys Leu
290 295 300

Leu Arg Phe Val Val Asn Asp Gly Thr Arg Tyr Gln Met Cys Val Met
305 310 315 320

Lys Leu Glu Ser Trp Ala His Val Phe Arg Asp Tyr Ser Val Ser Phe
325 330 335

Gln Val Arg Leu Thr Phe Thr Glu Ala Asn Asn Gln Thr Tyr Thr Phe
340 345 350

Cys Thr His Pro Asn Leu Ile Val Lys Gln Thr Leu Asn Phe Asp Leu
355 360 365

Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Gln Cys Gln
370 375 380

Arg Glu Thr Ala Glu Lys Asn Asp Tyr Tyr Arg Val Pro His Tyr Trp
385 390 395 400

Asp Ala Cys Ser Arg Ala Leu Pro Asp Gln Thr Arg Tyr Lys Tyr Val
405 410 415

Glu Gln Leu Val Asp Leu Thr Leu Asn Tyr His Tyr Asp Ala Ser His
420 425 430

Gly Leu Asp Asn Phe Asp Val Leu Lys Arg Ile Asn Val Thr Glu Val
435 440 445

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Ser Leu Leu Ile Ser Asp Phe Arg Arg Gln Asn Arg Arg Gly Gly Thr
450 455 460

Asn Lys Arg Thr Thr Phe Asn Ala Ala Gly Ser Leu Ala Pro His Ala
465 470 475 480

Arg Ser Leu Glu Phe Ser Val Arg Leu Phe Ala Asn Glu Asn Leu Tyr
485 490 495

Phe Gln Gly Ser Gly Ser Gly Trp Ser His Pro Gln Phe Glu Lys Gly
500 505 510

Ser Gly Ser Trp Ser His Pro Gln Phe Glu Lys
515 520

<210> 44
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding pentamer_UL128-130-131A_v1

<400> 44
atgtctccta aagacctgac tccattcctg accgccctgt ggctgctgct ggggcattcc 60
cgtgtccctc gtgtccgtgc tgaagagtgc tgtgagttca tcaacgtgaa tcacccccct 120
gaaagggtgct acgacttcaa gatgtgtaat aggttcaccg tggcttacgt cctgcgctgc 180
ccagatggcg aagtgtgtta ttcccccgag aagactgcag aaatcagggg cattgtcacc 240
acaatgacac acagtctgac tcggcagggtg gtccataaca aactgacctc atgcaactac 300
aatcctctgt atctggaagc cgacggtcga atccgttgtg gcaagggtcaa tgataaagct 360
cagtacctgc tgggagccgc tggctcagtc ccatacagat ggattaacct ggagtatgac 420
aagatcacc cgcattgtggg actggatcag tacctggaaa gcgtaagaa acacaagaga 480
ctggacgtct gccgcgcaaa aatgggatat atgctgcagg aggggagagg gtccctgctg 540
acatgtggcg acgtggagga aaaccccggc ccttgagca cactgactgc taaccagaat 600
ccctccccac cctggagcaa gctgacctac tctaaacctc atgacgcagc cacattctac 660

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tgcccttttc tgtatccaag tcctccaagg tctccaagtc agttcagcgg atttcagcga	720
gtgtctactg ggcccagagtg tcgtaatgaa accctgtacc tgctgtataa cagggagggga	780
cagaccctgg tggaacgggtc cagcacatgg gtgaagaaag tcatctggta tctgtctggg	840
cggaatcaga caattctgca gaggatgccc cggactgccca gtaagccttc agacggaaac	900
gtgcagatca gtgtcgagga tgctaaaatt ttcggggcac atatggtgcc caagcagaca	960
aaactgctga gatttgtggt caatgacggc actcgctacc agatgtgcgt gatgaagctg	1020
gagagctggg cccacgtctt tcgagattat tcagtgtcct tccaggtccg tctgaccttt	1080
acagaagcta acaatcagac ttacaccttc tgtactcatc ctaatctgat cgtgaagcag	1140
accctgaact ttgacctgct gaaactggca ggcgacgtgg agagcaatcc aggaccacag	1200
tgccagcgag agaccgcaga aaagaacgac tactatcggg tgcctcacta ttgggacgca	1260
tgttctcgag ccctgccaga tcagaccctg tacaatatg tggagcagct ggtcgacctg	1320
acactgaact accactatga tgcctcccat ggcctggaca atttcgatgt gctgaagaga	1380
atcaacgtga ctgaagtctc tctgctgatt agtgatttca ggcggcagaa cagacgcggc	1440
ggaaccaata agcgactac ctttaacgct gcaggctccc tggccccaca tgctaggtca	1500
ctggagttct ccgtgcggct gtttgctaac gaaaatctgt actttcaggg gagcggttct	1560
ggctgggtcac acccacagtt tgaaaaaggt agcggttcct ggtcacaccc acagtttgaa	1620
aaa	1623

<210> 45
 <211> 973
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of pentamer_gH-gL_v1

<400> 45

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5				10						15	

Val	His	Ser	Gly	Ala	Asp	Ala	Ala	Ser	Glu	Ala	Leu	Asp	Pro	His	Ala
			20					25					30		

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Phe His Leu Leu Leu Asn Thr Tyr Gly Arg Pro Ile Arg Phe Leu Arg
35 40 45

Glu Asn Thr Thr Gln Cys Thr Tyr Asn Ser Ser Leu Arg Asn Ser Thr
50 55 60

Val Val Arg Glu Asn Ala Ile Ser Phe Asn Phe Phe Gln Ser Tyr Asn
65 70 75 80

Gln Tyr Tyr Val Phe His Met Pro Arg Cys Leu Phe Ala Gly Pro Leu
85 90 95

Ala Glu Gln Phe Leu Asn Gln Val Asp Leu Thr Glu Thr Leu Glu Arg
100 105 110

Tyr Gln Gln Arg Leu Asn Thr Tyr Ala Leu Val Ser Lys Asp Leu Ala
115 120 125

Ser Tyr Arg Ser Phe Pro Gln Gln Leu Lys Ala Gln Asp Ser Leu Gly
130 135 140

Gln Gln Pro Thr Thr Val Pro Pro Pro Ile Asp Leu Ser Ile Pro His
145 150 155 160

Val Trp Met Pro Pro Gln Thr Thr Pro His Asp Trp Lys Gly Ser His
165 170 175

Thr Thr Ser Gly Leu His Arg Pro His Phe Asn Gln Thr Cys Ile Leu
180 185 190

Phe Asp Gly His Asp Leu Leu Phe Ser Thr Val Thr Pro Cys Leu His
195 200 205

Gln Gly Phe Tyr Leu Met Asp Glu Leu Arg Tyr Val Lys Ile Thr Leu
210 215 220

Thr Glu Asp Phe Phe Val Val Thr Val Ser Ile Asp Asp Asp Thr Pro
225 230 235 240

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Met Leu Leu Ile Phe Gly His Leu Pro Arg Val Leu Phe Lys Ala Pro
245 250 255

Tyr Gln Arg Asp Asn Phe Ile Leu Arg Gln Thr Glu Lys His Glu Leu
260 265 270

Leu Val Leu Val Lys Lys Thr Gln Leu Asn Arg His Ser Tyr Leu Lys
275 280 285

Asp Ser Asp Phe Leu Asp Ala Ala Leu Asp Phe Asn Tyr Leu Asp Leu
290 295 300

Ser Ala Leu Leu Arg Asn Ser Phe His Arg Tyr Ala Val Asp Val Leu
305 310 315 320

Lys Ser Gly Arg Cys Gln Met Leu Asp Arg Arg Thr Val Glu Met Ala
325 330 335

Phe Ala Tyr Ala Leu Ala Leu Phe Ala Ala Ala Arg Gln Glu Glu Ala
340 345 350

Gly Thr Glu Ile Ser Ile Pro Arg Ala Leu Asp Arg Gln Ala Ala Leu
355 360 365

Leu Gln Ile Gln Glu Phe Met Ile Thr Cys Leu Ser Gln Thr Pro Pro
370 375 380

Arg Thr Thr Leu Leu Leu Tyr Pro Thr Ala Val Asp Leu Ala Lys Arg
385 390 395 400

Ala Leu Trp Thr Pro Asp Gln Ile Thr Asp Ile Thr Ser Leu Val Arg
405 410 415

Leu Val Tyr Ile Leu Ser Lys Gln Asn Gln Gln His Leu Ile Pro Gln
420 425 430

Trp Ala Leu Arg Gln Ile Ala Asp Phe Ala Leu Gln Leu His Lys Thr
435 440 445

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His Leu Ala Ser Phe Leu Ser Ala Phe Ala Arg Gln Glu Leu Tyr Leu
450 455 460

Met Gly Ser Leu Val His Ser Met Leu Val His Thr Thr Glu Arg Arg
465 470 475 480

Glu Ile Phe Ile Val Glu Thr Gly Leu Cys Ser Leu Ala Glu Leu Ser
485 490 495

His Phe Thr Gln Leu Leu Ala His Pro His His Glu Tyr Leu Ser Asp
500 505 510

Leu Tyr Thr Pro Cys Ser Ser Ser Gly Arg Arg Asp His Ser Leu Glu
515 520 525

Arg Leu Thr Arg Leu Phe Pro Asp Ala Thr Val Pro Ala Thr Val Pro
530 535 540

Ala Ala Leu Ser Ile Leu Ser Thr Met Gln Pro Ser Thr Leu Glu Thr
545 550 555 560

Phe Pro Asp Leu Phe Cys Leu Pro Leu Gly Glu Ser Phe Ser Ala Leu
565 570 575

Thr Val Ser Glu His Val Ser Tyr Val Val Thr Asn Gln Tyr Leu Ile
580 585 590

Lys Gly Ile Ser Tyr Pro Val Ser Thr Thr Val Val Gly Gln Ser Leu
595 600 605

Ile Ile Thr Gln Thr Asp Ser Gln Ser Lys Cys Glu Leu Thr Arg Asn
610 615 620

Met His Thr Thr His Ser Ile Thr Ala Ala Leu Asn Ile Ser Leu Glu
625 630 635 640

Asn Cys Ala Phe Cys Gln Ser Ala Leu Leu Glu Tyr Asp Asp Thr Gln
645 650 655

2014004579

Gly Val Ile Asn Ile Met Tyr Met His Asp Ser Asp Asp Val Leu Phe
660 665 670

Ala Leu Asp Pro Tyr Asn Glu Val Val Val Ser Ser Pro Arg Thr His
675 680 685

Tyr Leu Met Leu Leu Lys Asn Gly Thr Val Leu Glu Val Thr Asp Val
690 695 700

Val Val Asp Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
705 710 715 720

Glu Glu Asn Pro Gly Pro Ala Val Ser Val Ala Pro Thr Ala Ala Glu
725 730 735

Lys Val Pro Ala Glu Cys Pro Glu Leu Thr Arg Arg Cys Leu Leu Gly
740 745 750

Glu Val Phe Gln Gly Asp Lys Tyr Glu Ser Trp Leu Arg Pro Leu Val
755 760 765

Asn Val Thr Gly Arg Asn Gly Pro Leu Ser Gln Leu Ile Arg Tyr Arg
770 775 780

Pro Val Thr Pro Glu Ala Ala Asn Ser Val Leu Leu Asp Asp Ala Phe
785 790 795 800

Leu Asp Thr Leu Ala Leu Leu Tyr Asn Asn Pro Asp Gln Leu Arg Ala
805 810 815

Leu Leu Thr Leu Leu Ser Ser Asp Thr Ala Pro Arg Trp Met Thr Val
820 825 830

Met Arg Gly Tyr Ser Glu Cys Gly Asp Gly Ser Pro Ala Val Tyr Thr
835 840 845

Cys Val Asp Asp Leu Cys Arg Gly Tyr Asp Leu Thr Arg Leu Ser Tyr
850 855 860

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Gly Arg Ser Ile Phe Thr Glu His Val Leu Gly Phe Glu Leu Val Pro
865 870 875 880

Pro Ser Leu Phe Asn Val Val Val Ala Ile Arg Asn Glu Ala Thr Arg
885 890 895

Thr Asn Arg Ala Val Arg Leu Pro Val Ser Thr Ala Ala Ala Pro Glu
900 905 910

Gly Ile Thr Leu Phe Tyr Gly Leu Tyr Asn Ala Val Lys Glu Phe Cys
915 920 925

Leu Arg His Gln Leu Asp Pro Pro Leu Leu Arg His Leu Asp Lys Tyr
930 935 940

Tyr Ala Gly Leu Pro Pro Glu Leu Lys Gln Thr Arg Val Asn Leu Pro
945 950 955 960

Ala His Ser Arg Tyr Gly Pro Gln Ala Val Asp Ala Arg
965 970

<210> 46
<211> 2919
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding pentamer_gH-gL_v1

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cagtactatg tgttccacat gccaaagtgt ctgtttgctg gaccctggc agagcagttc 300
ctgaaccagg tggatctgac agagactctg gaaaggtacc agcagcggct gaatacctat 360
gctctggtgt ctaaggacct ggcaagttat cgctcatttc cccagcagct gaaagctcag 420

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tccaccgtga caccctgtct gcatcaggga ttctacctga tggatgagct gagatatgtg	660
aagattactc tgaccgaaga cttctttgtg gtcaccgtga gcatcgacga tgacacacca	720
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<210> 47

<211> 521

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of Pentamer_UL128-130-131A_v3

<400> 47

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
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			20				25						30		

Val	Asn	His	Pro	Pro	Glu	Arg	Cys	Tyr	Asp	Phe	Lys	Met	Cys	Asn	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

Phe Thr Val Ala Tyr Val Leu Arg Cys Pro Asp Gly Glu Val Cys Tyr
 50 55 60

Ser Pro Glu Lys Thr Ala Glu Ile Arg Gly Ile Val Thr Thr Met Thr
 65 70 75 80

His Ser Leu Thr Arg Gln Val Val His Asn Lys Leu Thr Ser Cys Asn
 85 90 95

Tyr Asn Pro Leu Tyr Leu Glu Ala Asp Gly Arg Ile Arg Cys Gly Lys
 100 105 110

Val Asn Asp Lys Ala Gln Tyr Leu Leu Gly Ala Ala Gly Ser Val Pro
 115 120 125

Tyr Arg Trp Ile Asn Leu Glu Tyr Asp Lys Ile Thr Arg Ile Val Gly
 130 135 140

Leu Asp Gln Tyr Leu Glu Ser Val Lys Lys His Lys Arg Leu Asp Val
 145 150 155 160

Cys Arg Ala Lys Met Gly Tyr Met Leu Gln Arg Lys Arg Arg Gly Ser
 165 170 175

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
 180 185 190

Asn Pro Gly Pro Ser Ser Trp Ser Thr Leu Thr Ala Asn Gln Asn Pro
 195 200 205

Ser Pro Pro Trp Ser Lys Leu Thr Tyr Ser Lys Pro His Asp Ala Ala
 210 215 220

Thr Phe Tyr Cys Pro Phe Leu Tyr Pro Ser Pro Pro Arg Ser Pro Ser
 225 230 235 240

Gln Phe Ser Gly Phe Gln Arg Val Ser Thr Gly Pro Glu Cys Arg Asn

245

250

255

Glu Thr Leu Tyr Leu Leu Tyr Asn Arg Glu Gly Gln Thr Leu Val Glu
 260 265 270

Arg Ser Ser Thr Trp Val Lys Lys Val Ile Trp Tyr Leu Ser Gly Arg
 275 280 285

Asn Gln Thr Ile Leu Gln Arg Met Pro Arg Thr Ala Ser Lys Pro Ser
 290 295 300

Asp Gly Asn Val Gln Ile Ser Val Glu Asp Ala Lys Ile Phe Gly Ala
 305 310 315 320

His Met Val Pro Lys Gln Thr Lys Leu Leu Arg Phe Val Val Asn Asp
 325 330 335

Gly Thr Arg Tyr Gln Met Cys Val Met Lys Leu Glu Ser Trp Ala His
 340 345 350

Val Phe Arg Asp Tyr Ser Val Ser Phe Gln Val Arg Leu Thr Phe Thr
 355 360 365

Glu Ala Asn Asn Gln Thr Tyr Thr Phe Cys Thr His Pro Asn Leu Ile
 370 375 380

Val Arg Lys Arg Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
 385 390 395 400

Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Cys Gln Arg Glu Thr
 405 410 415

Ala Glu Lys Asn Asp Tyr Tyr Arg Val Pro His Tyr Trp Asp Ala Cys
 420 425 430

Ser Arg Ala Leu Pro Asp Gln Thr Arg Tyr Lys Tyr Val Glu Gln Leu
 435 440 445

Val Asp Leu Thr Leu Asn Tyr His Tyr Asp Ala Ser His Gly Leu Asp

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450

455

460

Asn Phe Asp Val Leu Lys Arg Ile Asn Val Thr Glu Val Ser Leu Leu
465 470 475 480

Ile Ser Asp Phe Arg Arg Gln Asn Arg Arg Gly Gly Thr Asn Lys Arg
485 490 495

Thr Thr Phe Asn Ala Ala Gly Ser Leu Ala Pro His Ala Arg Ser Leu
500 505 510

Glu Phe Ser Val Arg Leu Phe Ala Asn
515 520

<210> 48

<211> 1563

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding Pentamer_UL128-130-131A_v3

<400> 48

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tacgacttca agatgtgtaa taggttcacc gtggcttacg tcctgcgctg cccagatggc	180
gaagtgtgtt attccccga gaagactgca gaaatcaggg gcattgtcac cacaatgaca	240
cacagtctga ctggcaggt ggtccataac aaactgacct catgcaacta caatcctctg	300
tatctggaag ccgacggctg aatccgttgt ggcaagggtca atgataaagc tcagtacctg	360
ctgggagccg ctggctcagt cccatacaga tggattaacc tggagtatga caagatcacc	420
cgcattgtgg gactggatca gtacctggaa agcgtgaaga aacacaagag actggacgtc	480
tgccgcgcaa aaatgggata tatgctgcag cgcaaacgcc gcggaagcgg agcaacaaac	540
ttttcactgc tgaaacaggc cggggatgtg gaggaaaatc ctggtccatc ttcgtggagc	600
aaactgactg ctaaccagaa tccctcccca cctggagca agctgacct ctctaaacct	660
catgacgcag ccacattcta ctgccctttt ctgtatccaa gtcctccaag gtctccaagt	720

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cagttcagcg gatttcagcg agtgtctact gggcccaggt gtcgtaatga aaccctgtac      780
ctgctgtata acagggaggg acagaccctg gtggaacggt ccagcacatg ggtgaagaaa      840
gtcatctggg atctgtctgg gcggaatcag acaattctgc agaggatgcc ccggactgcc      900
agtaagcctt cagacggaaa cgtgcagatc agtgtcgagg atgctaaaat tttcggggca      960
catatgggtgc ccaagcagac aaaactgctg agatttgtgg tcaatgacgg cactcgctac     1020
cagatgtgcg tgatgaagct ggagagctgg gcccacgtct ttcgagatta ttcagtgtcc     1080
ttccagggtcc gtctgacctt tacagaagct aacaatcaga cttacacctt ctgtactcat     1140
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caggccgggg atgtggagga aaatcctggg ccatgccagc gagagaccgc agaaaagaac     1260
gactactatc ggggtgcctca ctattgggac gcatgttctc gagccctgcc agatcagacc     1320
cgttacaaat atgtggagca gctggtcgac ctgacactga actaccacta tgatgcctcc     1380
catggcctgg acaatttcga tgtgctgaag agaatcaacg tgactgaagt ctctctgctg     1440
attagtgatt tcaggcggca gaacagacgc ggcggaacca ataagcgac tacctttaac     1500
gctgcaggct ccctggcccc acatgctagg tctactggagt tctccgtgcg gctgtttgct     1560
aac                                                                    1563

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<210> 49
 <211> 983
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of pentamer_gH-gL_v3

<400> 49

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

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His Ala Phe His Leu Leu Leu Asn Thr Tyr Gly Arg Pro Ile Arg Phe
          35          40          45

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Leu Arg Glu Asn Thr Thr Gln Cys Thr Tyr Asn Ser Ser Leu Arg Asn
50 55 60

Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe Asn Phe Phe Gln Ser
65 70 75 80

Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg Cys Leu Phe Ala Gly
85 90 95

Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp Leu Thr Glu Thr Leu
100 105 110

Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala Leu Val Ser Lys Asp
115 120 125

Leu Ala Ser Tyr Arg Ser Phe Pro Gln Gln Leu Lys Ala Gln Asp Ser
130 135 140

Leu Gly Gln Gln Pro Thr Thr Val Pro Pro Pro Ile Asp Leu Ser Ile
145 150 155 160

Pro His Val Trp Met Pro Pro Gln Thr Thr Pro His Asp Trp Lys Gly
165 170 175

Ser His Thr Thr Ser Gly Leu His Arg Pro His Phe Asn Gln Thr Cys
180 185 190

Ile Leu Phe Asp Gly His Asp Leu Leu Phe Ser Thr Val Thr Pro Cys
195 200 205

Leu His Gln Gly Phe Tyr Leu Met Asp Glu Leu Arg Tyr Val Lys Ile
210 215 220

Thr Leu Thr Glu Asp Phe Phe Val Val Thr Val Ser Ile Asp Asp Asp
225 230 235 240

Thr Pro Met Leu Leu Ile Phe Gly His Leu Pro Arg Val Leu Phe Lys
245 250 255

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Ala Pro Tyr Gln Arg Asp Asn Phe Ile Leu Arg Gln Thr Glu Lys His
260 265 270

Glu Leu Leu Val Leu Val Lys Lys Thr Gln Leu Asn Arg His Ser Tyr
275 280 285

Leu Lys Asp Ser Asp Phe Leu Asp Ala Ala Leu Asp Phe Asn Tyr Leu
290 295 300

Asp Leu Ser Ala Leu Leu Arg Asn Ser Phe His Arg Tyr Ala Val Asp
305 310 315 320

Val Leu Lys Ser Gly Arg Cys Gln Met Leu Asp Arg Arg Thr Val Glu
325 330 335

Met Ala Phe Ala Tyr Ala Leu Ala Leu Phe Ala Ala Ala Arg Gln Glu
340 345 350

Glu Ala Gly Thr Glu Ile Ser Ile Pro Arg Ala Leu Asp Arg Gln Ala
355 360 365

Ala Leu Leu Gln Ile Gln Glu Phe Met Ile Thr Cys Leu Ser Gln Thr
370 375 380

Pro Pro Arg Thr Thr Leu Leu Leu Tyr Pro Thr Ala Val Asp Leu Ala
385 390 395 400

Lys Arg Ala Leu Trp Thr Pro Asp Gln Ile Thr Asp Ile Thr Ser Leu
405 410 415

Val Arg Leu Val Tyr Ile Leu Ser Lys Gln Asn Gln Gln His Leu Ile
420 425 430

Pro Gln Trp Ala Leu Arg Gln Ile Ala Asp Phe Ala Leu Gln Leu His
435 440 445

Lys Thr His Leu Ala Ser Phe Leu Ser Ala Phe Ala Arg Gln Glu Leu
450 455 460

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Tyr Leu Met Gly Ser Leu Val His Ser Met Leu Val His Thr Thr Glu
465 470 475 480

Arg Arg Glu Ile Phe Ile Val Glu Thr Gly Leu Cys Ser Leu Ala Glu
485 490 495

Leu Ser His Phe Thr Gln Leu Leu Ala His Pro His His Glu Tyr Leu
500 505 510

Ser Asp Leu Tyr Thr Pro Cys Ser Ser Ser Gly Arg Arg Asp His Ser
515 520 525

Leu Glu Arg Leu Thr Arg Leu Phe Pro Asp Ala Thr Val Pro Ala Thr
530 535 540

Val Pro Ala Ala Leu Ser Ile Leu Ser Thr Met Gln Pro Ser Thr Leu
545 550 555 560

Glu Thr Phe Pro Asp Leu Phe Cys Leu Pro Leu Gly Glu Ser Phe Ser
565 570 575

Ala Leu Thr Val Ser Glu His Val Ser Tyr Val Val Thr Asn Gln Tyr
580 585 590

Leu Ile Lys Gly Ile Ser Tyr Pro Val Ser Thr Thr Val Val Gly Gln
595 600 605

Ser Leu Ile Ile Thr Gln Thr Asp Ser Gln Ser Lys Cys Glu Leu Thr
610 615 620

Arg Asn Met His Thr Thr His Ser Ile Thr Ala Ala Leu Asn Ile Ser
625 630 635 640

Leu Glu Asn Cys Ala Phe Cys Gln Ser Ala Leu Leu Glu Tyr Asp Asp
645 650 655

Thr Gln Gly Val Ile Asn Ile Met Tyr Met His Asp Ser Asp Asp Val
660 665 670

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Leu Phe Ala Leu Asp Pro Tyr Asn Glu Val Val Val Ser Ser Pro Arg
675 680 685

Thr His Tyr Leu Met Leu Leu Lys Asn Gly Thr Val Leu Glu Val Thr
690 695 700

Asp Val Val Val Asp Arg Lys Arg Arg Gly Ser Gly Ala Thr Asn Phe
705 710 715 720

Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Val
725 730 735

Ala Val Ser Val Ala Pro Thr Ala Ala Glu Lys Val Pro Ala Glu Cys
740 745 750

Pro Glu Leu Thr Arg Arg Cys Leu Leu Gly Glu Val Phe Gln Gly Asp
755 760 765

Lys Tyr Glu Ser Trp Leu Arg Pro Leu Val Asn Val Thr Gly Arg Asn
770 775 780

Gly Pro Leu Ser Gln Leu Ile Arg Tyr Arg Pro Val Thr Pro Glu Ala
785 790 795 800

Ala Asn Ser Val Leu Leu Asp Asp Ala Phe Leu Asp Thr Leu Ala Leu
805 810 815

Leu Tyr Asn Asn Pro Asp Gln Leu Arg Ala Leu Leu Thr Leu Leu Ser
820 825 830

Ser Asp Thr Ala Pro Arg Trp Met Thr Val Met Arg Gly Tyr Ser Glu
835 840 845

Cys Gly Asp Gly Ser Pro Ala Val Tyr Thr Cys Val Asp Asp Leu Cys
850 855 860

Arg Gly Tyr Asp Leu Thr Arg Leu Ser Tyr Gly Arg Ser Ile Phe Thr
865 870 875 880

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Glu His Val Leu Gly Phe Glu Leu Val Pro Pro Ser Leu Phe Asn Val
885 890 895

Val Val Ala Ile Arg Asn Glu Ala Thr Arg Thr Asn Arg Ala Val Arg
900 905 910

Leu Pro Val Ser Thr Ala Ala Ala Pro Glu Gly Ile Thr Leu Phe Tyr
915 920 925

Gly Leu Tyr Asn Ala Val Lys Glu Phe Cys Leu Arg His Gln Leu Asp
930 935 940

Pro Pro Leu Leu Arg His Leu Asp Lys Tyr Tyr Ala Gly Leu Pro Pro
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Glu Leu Lys Gln Thr Arg Val Asn Leu Pro Ala His Ser Arg Tyr Gly
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Pro Gln Ala Val Asp Ala Arg
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<210> 50
<211> 2949
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding pentamer_gH-gL_v3

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cagttcctga accaggtgga tctgacagag actctggaaa ggtaccagca gcggctgaat 360
acctatgctc tgggtgtctaa ggacctggca agttatcgct catttcccca gcagctgaaa 420

2014004579

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Gly Ser Thr Ser Gly Ser Gly Xaa Pro Gly Ser Gly Glu Gly Ser Thr

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