

SEQUENCE LISTING

<110> GENimmune NV
 <120> HCV polyepitope construct and uses thereof
 <130> 197 PCT
 <150> EP07103582.8
 <151> 2007-03-06
 <150> EP07119517.6
 <151> 2007-10-29
 <150> US60/904,403
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 <151> 2007-10-29
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Asp Leu Met Gly Tyr Ile Pro Leu Val
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Asp Pro Arg Arg Arg Ser Arg Asn Leu
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Glu Pro Asp Val Ala Val Leu Thr Ser Met
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Gly Pro Arg Leu Gly Val Arg Ala Thr
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Gly Pro Thr Pro Leu Leu Tyr Arg Leu
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Gly Val Val Cys Ala Ala Ile Leu Arg Arg
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His Leu Ile Phe Cys His Ser Lys Lys
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His Pro Asn Ile Glu Glu Val Ala Leu
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Ile Ile Met Tyr Ala Pro Thr Leu Trp
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Leu Ile Phe Cys His Ser Lys Lys Lys
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Leu Leu Pro Arg Arg Gly Pro Arg Leu
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Leu Pro Ala Ile Leu Ser Pro Gly Ala Leu
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Leu Pro Ala Leu Ser Thr Gly Leu Ile
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<400> 46

Leu Pro Gly Cys Ser Phe Ser Ile Phe
1 5

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Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu
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Leu Pro Arg Arg Gly Pro Arg Leu Gly Val

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Leu Pro Arg Arg Gly Pro Arg Leu Gly
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Leu Pro Val Cys Gln Asp His Leu Glu Phe
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Leu Val Asn Ala Trp Lys Ser Lys Lys
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Leu Trp Ala Arg Met Ile Leu Met Thr His Phe
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Met Tyr Thr Asn Val Asp Gln Asp Leu
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Asn Ile Ile Met Tyr Ala Pro Thr Leu
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Pro Pro Val Val His Gly Cys Pro Leu
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Gln Leu Phe Thr Phe Ser Pro Arg Arg
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Gln Met Trp Lys Cys Leu Ile Arg Leu
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Gln Pro Arg Gly Arg Arg Gln Pro Ile
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Gln Tyr Leu Ala Gly Leu Ser Thr Leu
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Arg Leu Gly Ala Val Gln Asn Glu Val
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Arg Leu Gly Val Arg Ala Thr Arg Lys
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Arg Leu Leu Ala Pro Ile Thr Ala Tyr
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Arg Met Ile Leu Met Thr His Phe Phe
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Arg Pro Asp Tyr Asn Pro Pro Leu Leu
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Arg Pro Ser Gly Met Phe Asp Ser Ser Val
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Arg Val Cys Glu Lys Met Ala Leu Tyr
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Arg Val Glu Phe Leu Val Asn Ala Trp
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Arg Val Phe Thr Glu Ala Met Thr Arg
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Ser Ala Ala Cys Arg Ala Ala Lys Leu
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Ser Phe Ser Ile Phe Leu Leu Ala Leu
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Ser Met Val Gly Asn Trp Ala Lys Val
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Ser Pro Arg Gly Ser Arg Pro Ser Trp
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<400> 75

Ser Thr Asn Pro Lys Pro Gln Arg Lys
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<400> 76

Ser Val Phe Thr Gly Leu Thr His Ile
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<210> 77

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<400> 77

Thr Leu His Gly Pro Thr Pro Leu Leu
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<400> 78

Thr Leu Trp Ala Arg Met Ile Leu Met
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Thr Pro Gly Glu Arg Pro Ser Gly Met
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Thr Tyr Ser Thr Tyr Gly Lys Phe Leu
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Val Ile Lys Gly Gly Arg His Leu Ile
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<400> 83

Val Leu Val Gly Gly Val Leu Ala Ala Leu
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<400> 84

Tyr Ala Ala Gln Gly Tyr Lys Val Leu
1 5

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<400> 85

Tyr Ile Pro Leu Val Gly Ala Pro Leu
1 5

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Tyr Leu Phe Asn Trp Ala Val Arg Thr
1 5

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Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu
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Tyr Leu Asn Thr Pro Gly Leu Pro Val
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Tyr Leu Val Ala Tyr Gln Ala Thr Val
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Tyr Leu Val Thr Arg His Ala Asp Val
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<400> 91

Tyr Gln Ala Thr Val Cys Ala Arg Ala
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<400> 92

Tyr Tyr Arg Gly Leu Asp Val Ser Val
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<210> 93

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<400> 93

Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile
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<400> 94

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Ser Met Val Gly Asn Trp Ala Lys Val Gly Ala Ala Ala Tyr Leu Val
35 40 45

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

Gly Ala Ala Cys Leu Val Asp Tyr Pro Tyr Arg Leu Gly Ala Ala Ala
65 70 75 80

Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Asn Tyr Leu Val Ala Tyr
85 90 95

Gln Ala Thr Val Asn Gly Met Phe Asp Ser Ser Val Leu Cys Gly Ala
100 105 110

Ala Ala Gln Met Trp Lys Cys Leu Ile Arg Leu Asn Ala Leu Leu Phe
115 120 125

Asn Ile Leu Gly Gly Trp Val Lys Arg Leu Gly Ala Val Gln Asn Glu
130 135 140

Val Asn Ala His Met Trp Asn Phe Ile Ser Gly Ile Asn Ala Ala Ala
145 150 155 160

Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala Lys Thr Leu Trp

165

170

175

Ala Arg Met Ile Leu Met Asn Ala Tyr Leu Phe Asn Trp Ala Val Arg
 180 185 190

Thr Asn Lys Leu Gln Asp Cys Thr Met Leu Val
 195 200

<210> 95
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 gtgggagccg cagcctacct ggtgaccaga cacgcagacg tgaacagcgt gttcaccggc 180
 ctactcaca tcggcgctgc ctgcctcgtg gattaccctt atcggtctggg agccgctgct 240
 tacctgctcc ccagacgggg accccggctg aactacctgg tggcatacca ggccaccgtc 300
 aacggaatgt ttgacagcag cgtgctgtgc ggcgccgcag ccagatgtg gaaatgcctg 360
 atcaggctga acgctctgct gttcaacatt ctgggaggat gggtaagag actgggagcc 420
 gtgcaaaatg aggtgaacgc ccacatgtgg aacttcatca gcggcatcaa cgccgcagcc 480
 aagttcgtgg ccgcatggac cctgaaggcc gcagccaaga ccctgtgggc cagaatgatc 540
 ctgatgaacg cctacctgtt caactgggcc gtcagaacaa acaaactcca ggactgcacc 600
 atgctggtgt ga 612

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 <212> PRT
 <213> Artificial sequence

<220>
 <223> Polyepitope Construct

<400> 96

Met Gly Met Gln Val Gln Ile Gln Ser Leu Phe Leu Leu Leu Leu Trp
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Val Pro Gly Ser Arg Gly Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu
 20 25 30

Asn Asp Leu Met Gly Tyr Ile Pro Leu Val Asn Ala Tyr Leu Asn Thr
35 40 45

Pro Gly Leu Pro Val Gly Phe Leu Leu Leu Ala Asp Ala Arg Val Gly
50 55 60

Ala Ala Lys Val Leu Val Leu Asn Pro Ser Val Gly Ala Ala Ala Tyr
65 70 75 80

Ile Pro Leu Val Gly Ala Pro Leu Lys Phe Leu Leu Ala Leu Leu Ser
85 90 95

Cys Leu Asn Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Gly Tyr Gln
100 105 110

Ala Thr Val Cys Ala Arg Ala Lys Val Leu Val Gly Gly Val Leu Ala
115 120 125

Ala Leu Asn His Met Trp Asn Phe Ile Ser Gly Ile Asn Ala Ala Ala
130 135 140

Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala Lys Asn Ile Ile
145 150 155 160

Met Tyr Ala Pro Thr Leu Lys Ala Ala Ala Ile Leu Ala Gly Tyr Gly
165 170 175

Ala Gly Val Asn Ala Ala Leu Tyr Asp Val Val Ser Thr Leu Asn Thr
180 185 190

Leu His Gly Pro Thr Pro Leu Leu
195 200

<210> 97
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tatctgctcc ccagaagggg acctaggctg aacgacctga tgggatacat ccctctggtc 120
aatgcctacc tgaacacacc cggcctgccc gtgggcttcc tgctcctggc cgacgctaga 180
gtgggagccg ctaaggtgct ggtcctcaac cccagcgtgg gagccgcagc ctacattccc 240

ctggtgggcg caccctgaa gttcctgctc gctctgctca gctgcctgaa cggactgctc 300
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 gtcggaggcg tgctggccgc actgaaccac atgtggaact ttatctccgg catcaacgca 420
 gccgcaaagt tcgtggccgc atggaccctg aaagccgcag ccaagaacat catcatgtac 480
 gctcccaccc tgaaggccgc cgccatcctg gccggatacg gcgccggagt gaacgccgcc 540
 ctgtacgatg tggtagcac actgaacacc ctgcacggcc ccacccact gctgtga 597

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<400> 98

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Val Pro Gly Ser Arg Gly Gln Leu Phe Thr Phe Ser Pro Arg Arg Asn
 20 25 30

Ala Ala Lys Thr Ser Glu Arg Ser Gln Pro Arg Asn Leu Val Asn Ala
 35 40 45

Trp Lys Ser Lys Lys Asn Arg Val Cys Glu Lys Met Ala Leu Tyr Asn
 50 55 60

Ala Ala Ser Thr Asn Pro Lys Pro Gln Arg Lys Asn Ala Val Cys Thr
 65 70 75 80

Arg Gly Val Ala Lys Asn Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Lys
 85 90 95

Ala Lys Val Leu Val Asp Ile Leu Ala Gly Tyr Asn Ala Ser Ala Ala
 100 105 110

Cys Arg Ala Ala Lys Lys His Leu Ile Phe Cys His Ser Lys Lys Lys
 115 120 125

Lys Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala Lys Ala
 130 135 140

Ala Ala Arg Leu Gly Val Arg Ala Thr Arg Lys Asn Gly Val Val Cys
 145 150 155 160

Ala Ala Ile Leu Arg Arg Asn Arg Val Phe Thr Glu Ala Met Thr Arg
165 170 175

Asn His Leu His Ala Pro Thr Gly Ser Gly Lys Lys Arg Leu Leu Ala
180 185 190

Pro Ile Thr Ala Tyr
195

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agaggccaac tgttcacctt tagccccagg agaaatgccg caaagactag cgagcgctct 120
cagccacgca acctcgtcaa tgcttgaaa tccaagaaga accgcgtgtg tgaaaagatg 180
gcactgtaca acgcagccag cacaaacccc aaacctcaga ggaagaatgc tgtgtgcacc 240
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gtcgacatcc tggcgggata taacgccagc gctgcctgta gagctgcca gaaacacctg 360
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gctgcaaagg ccgctgctag actcgggggtg agggccaccc gcaagaacgg cgtcgtgtgc 480
gcagcaattc tccggagaaa tcgggtcttt actgaggcaa tgaccgggaa ccacctgcat 540
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Met Gly Met Gln Val Gln Ile Gln Ser Leu Phe Leu Leu Leu Leu Trp
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Val Pro Gly Ser Arg Gly Val Ile Lys Gly Gly Arg His Leu Ile Lys
20 25 30

Ala Ala Ala Cys Leu Ile Arg Leu Lys Pro Thr Leu Asn Ala Ala Ser
35 40 45

Phe Ser Ile Phe Leu Leu Ala Leu Lys Tyr Leu Asn Thr Pro Gly Leu
50 55 60

Pro Val Asn Ala Met Tyr Thr Asn Val Asp Gln Asp Leu Asn Ala Ala
65 70 75 80

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

Gly Leu Asp Val Ser Val Ile Lys Ala Ala Ala Leu Leu Pro Arg Arg
100 105 110

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

Ala Ala Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala Lys
130 135 140

Asn Ile Ile Met Tyr Ala Pro Thr Leu Trp Asn Ala Ala Ala Phe Trp
145 150 155 160

Ala Lys His Met Trp Asn Phe Ile Lys Ala Ala Ala Arg Val Glu Phe
165 170 175

Leu Val Asn Ala Trp Asn Ala Ala Leu Trp Ala Arg Met Ile Leu Met
180 185 190

Thr His Phe Phe Asn Ala Ala Ala Gln Tyr Leu Ala Gly Leu Ser Thr
195 200 205

Leu Asn Thr Leu His Gly Pro Thr Pro Leu Leu
210 215

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agaggcgtga tcaagggagg acgtcacctg atcaaggccg cagcttgccct cattcggtg 120

Phe Lys Gln Lys Ala Leu Lys Thr Ser Glu Arg Ser Gln Pro Arg Asn
130 135 140

Ala Ala Phe Pro Tyr Leu Val Ala Tyr Gln Ala Lys Ala Ala Met Tyr
145 150 155 160

Thr Asn Val Asp Gln Asp Leu Asn Thr Leu Trp Ala Arg Met Ile Leu
165 170 175

Met Asn Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Lys Ser Thr Asn
180 185 190

Pro Lys Pro Gln Arg Lys Asn Asp Tyr Pro Tyr Arg Leu Trp His Tyr
195 200 205

Lys Ala Ala Cys Leu Ile Arg Leu Lys Pro Thr Leu Asn Ile Ile Met
210 215 220

Tyr Ala Pro Thr Leu Lys Ala Ala Val Ala Thr Asp Ala Leu Met Thr
225 230 235 240

Gly Tyr Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Lys Tyr Arg Arg
245 250 255

Cys Arg Ala Ser Gly Val Leu Lys Ala Ala Val Leu Val Gly Gly Val
260 265 270

Leu Ala Ala Leu Asn Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Asn
275 280 285

Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Lys Asp Pro Arg Arg Arg Ser
290 295 300

Arg Asn Leu Lys Ala Ala Ala Tyr Leu Leu Pro Arg Arg Gly Pro Arg
305 310 315 320

Leu Asn Phe Trp Ala Lys His Met Trp Asn Phe Ile Lys Ala Ala Ala
325 330 335

Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala Lys Ala Leu Ile
340 345 350

Arg Leu Lys Pro Thr Leu His Lys Ala Ala Ala Val Cys Thr Arg Gly
355 360 365

Val Ala Lys Asn Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Lys Ala
370 375 380

Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Lys Ser Phe Ser Ile Phe
385 390 395 400

Leu Leu Ala Leu Lys Ala Ala Glu Thr Ala Gly Ala Arg Leu Val Asn
405 410 415

Ala Ala Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp
420 425 430

Gly Pro Gly Pro Gly Ser Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp
435 440 445

Val Ala Ala Gln Gly Pro Gly Pro Gly Cys Val Thr Gln Thr Val Asp
450 455 460

Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Gly Pro Gly Pro
465 470 475 480

Gly Glu Asp Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala
485 490 495

Leu Val Val Gly Pro Gly Pro Gly Gly Glu Gly Ala Val Gln Trp Met
500 505 510

Asn Arg Leu Ile Ala Phe Ala Ser Gly Pro Gly Pro Gly Met Asn Arg
515 520 525

Leu Ile Ala Phe Ala Ser Arg Gly Asn His Val Ser Pro Gly Pro Gly
530 535 540

Pro Gly Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys
545 550 555 560

Ala Gly Pro Gly Pro Gly Thr Pro Ala Glu Thr Thr Val Arg Leu Arg
565 570 575

Ala Tyr Met Asn Thr Pro Gly Leu Pro Val Gly Pro Gly Pro Gly Ala
580 585 590

Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Gly Pro
595 600 605

Gly Pro Gly Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly

610

615

620

Asn Pro Ala Gly Pro Gly Pro Gly Thr Ser Thr Trp Val Leu Val Gly
 625 630 635 640

Gly Val Leu Ala Ala Leu Ala Ala Gly Pro Gly Pro Gly Gly Tyr Lys
 645 650 655

Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Gly Pro Gly Pro Gly
 660 665 670

Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu
 675 680 685

<210> 103

<211> 2064

<212> DNA

<213> Artificial sequence

<220>

<223> Polypeptide Construct

<400> 103

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atgggcatgc aggtgcagat ccagagcctg ttctgtctgc tgctgtgggt gcccggcagc      60
cgcggcgtga tcaagggcgg caggcacctg atcaaggccg gacctcggct gggcgtgagg      120
gccacaaaag ccgctgcccc gtacctggcc ggcctgagca cactgaatgc cgctgccctt      180
accctgtggg cccgatgat cctgaatgcc gccacccca acatcgagga agtggccctg      240
aacctggtgg acatcctggc cggtacggc gccaaagcata tgtggaactt catcagcggc      300
atcaacgcct actaccgggg cctggacgtg agcgtgaagc tccaggactg caccatgctg      360
gtcaatgctg ccgctgccga gcagttcaag cagaaggccc tgaaaaccag cgagcggagc      420
cagccccgga acgcgcctt ccctacctg gtggcctacc aggccaaggc cgccatgtac      480
accaacgtgg accaggacct gaacacactg tgggccagaa tgattctgat gaacctgccc      540
atcaacgccc tgagcaacag cctgaagagc accaaccaca agccccagcg gaagaacgac      600
taccctacc ggctgtggca ctacaaggcc gcctgcctga tccggtgaa gccaccctg      660
aacatcatca tgtacgcccc aacctgaag gccgccgtgg ccaccgacgc cctgatgacc      720
ggctacaacc tgccgggctg ctcttcagc atcttcaagt accggcgggtg ccgggccagc      780
ggcgtgctca aagctgccgt cctcgtcggc ggcgtgctgg ctgctctgaa cggcctgctg      840
ggctgcatca tcaccagcct gaacgccgcc tacgccgcc agggctacaa gaaggacccc      900
aggcggcgga gccggaacct gaaggccgca gcctacctgc tgcccagaag gggccccagg      960
ctgaacttct gggccaaaca catgtggaat ttcattaagg ctgctgcaa gtttgtggcc     1020

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gcctggacac tgaagctgc cgccaaggcc ctgatcagac tgaagcctac actgcacaag 1080
gccgtgccg tgtgtacacg gggcgtggcc aagaacttca ccgacaacag cagccccct 1140
gccgtgaagg ccctgccccg cagaggcccc agactgggcg tgaagagctt ctccatcttc 1200
ctgctggccc tgaagccgc cgagaccgcc ggagcccggc tggatgaatgc cgccggacgg 1260
cacctgatct tttgccacag caagaagaag tgcgacggcc caggccctgg cagcacctg 1320
ctgttcaaca tcctgggcg atgggtggcc gccaggac ccgggccagg atgcgtgacc 1380
cagaccgtgg acttcagcct ggacccacc ttcaccatcg agaccacagg cccagggcc 1440
ggggaggacc tggatcaatct gctgcctgcc atcctgagcc ctggcgccct ggtggtgggc 1500
ccaggaccag gcggagaggg cgccgtgcag tggatgaacc ggctgatcgc cttcgccagc 1560
ggacctggcc ctggcatgaa cagactgatt gcctttgcct cccggggcaa ccacgtgagc 1620
cctggacctg gaccggggag catgagctac acctggacag gcgccctgat taccctctgc 1680
gccggacctg gaccaggcac ccctgccgag accacagtgc ggctgcgggc ctacatgaac 1740
accctggcc tggcgtggg acctgggcca ggggcccgtg gcatcttcag agccgccgtg 1800
tgtaccagag ggggtggccg accagggcc ggcggcatcc agtatctggc cgggctgtct 1860
accctgcccg gcaaccctgc cgcccagga cccggcacct ccacctgggt gctggtcggg 1920
ggagtgtctg ccgccctggc cgccggaccc ggacctggcg gctacaaggt gctggtgctg 1980
aaccacagcg tggccgccac cgggcctgga cctgggggca agcctgccat catccccgac 2040
cgggaggtgc tgtaccggga gtga 2064

<210> 104
<211> 323
<212> PRT
<213> Artificial sequence

<220>
<223> Polypeptide Construct

<400> 104

Met Gly Met Gln Val Gln Ile Gln Ser Leu Phe Leu Leu Leu Trp
1 5 10 15

Val Pro Gly Ser Arg Gly Asn Ile Ile Met Tyr Ala Pro Thr Leu Lys
20 25 30

Ala Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala Lys Cys
35 40 45

Leu Ile Arg Leu Lys Pro Thr Leu Asn Ala Ala Ala Lys Thr Ser Glu

50

55

60

Arg Ser Gln Pro Arg Asn Leu Pro Arg Arg Gly Pro Arg Leu Gly Val
65 70 75 80

Lys Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Lys Ala Val Cys Thr
85 90 95

Arg Gly Val Ala Lys Asn Ala Ala Ala Pro Thr Leu Trp Ala Arg Met
100 105 110

Ile Leu Asn Ala Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Asn Ala
115 120 125

Ala Ser Phe Ser Ile Phe Leu Leu Ala Leu Lys His Leu Ile Phe Cys
130 135 140

His Ser Lys Lys Asn Val Leu Val Gly Gly Val Leu Ala Ala Leu Asn
145 150 155 160

Ser Thr Asn Pro Lys Pro Gln Arg Lys Asn Val Ile Lys Gly Gly Arg
165 170 175

His Leu Ile Lys Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Lys Ala Ala
180 185 190

Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Lys Ala His Met Trp Asn
195 200 205

Phe Ile Ser Gly Ile Asn Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu
210 215 220

Asn Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Lys Ala Tyr Tyr Arg
225 230 235 240

Gly Leu Asp Val Ser Val Lys Ala Ala Leu Val Asp Ile Leu Ala Gly
245 250 255

Tyr Gly Ala Lys Ala Met Tyr Thr Asn Val Asp Gln Asp Leu Asn Phe
260 265 270

Trp Ala Lys His Met Trp Asn Phe Ile Lys Ala Thr Leu Trp Ala Arg
275 280 285

Met Ile Leu Met Asn Lys Leu Gln Asp Cys Thr Met Leu Val Asn Gln
290 295 300

Tyr Leu Ala Gly Leu Ser Thr Leu Asn Gly Leu Leu Gly Cys Ile Ile
 305 310 315 320

Thr Ser Leu

<210> 105
 <211> 972
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Polyepitope Construct

<400> 105
 atgggcatgc aggtgcagat ccagagcctg ttcttgctcc tgctgtgggt gccaggaagc 60
 agaggcaaca tcataatgta cgcacccaca ctgaaagcag ctaaattcgt cgccgcatgg 120
 accctgaaag ccgcagctaa atgcctgata cgtctgaagc caactctcaa tgccgctgcc 180
 aagacttccg agaggagtca acctaggaac ttgccacgcc gaggaccaag actcggagtg 240
 aagttcaccg acaacagtag ccctccggct gtcaaggccg tatgcactcg cggcgtagcc 300
 aagaacgctg ccgctccac actgtgggct aggatgatac tgaacgcggg gccacagat 360
 gcactcatga caggtataa tgccgcatcc ttctcaatct ttcttctcgc cttgaagcat 420
 ttgatcttct gccattccaa gaagaacggt cttgtcgggt gcgtgctcgc tgcactgaat 480
 agcactaacc caaagcctca gcggaagaat gtcatcaagg gaggcagaca cttgatcaag 540
 gccgcttatg ccgctcaagg gtataagaaa gctgcactgc ccataaatgc actatctaac 600
 tcgcttaagg cccacatgtg gaatttcata tctggcatta actacttact gcctagacgc 660
 ggtcccaggc taaattaccg tcgatgtaga gcctccggag tgctgaaggc atactatcgc 720
 ggactcgacg tgagcgtgaa agctgcactg gttgacattc tggctgggta cggagccaaa 780
 gctatgtaca ccaacgtgga tcaagacctg aacttctggg caaagcacat gtggaatttc 840
 attaaagcca cgctgtgggc cagaatgata ctgatgaaca agctccagga ttgtacgatg 900
 cttgttaacc agtacttggc agggctttca accctgaacg gtctattagg atgtatcatt 960
 accagcctgt ga 972

<210> 106
 <211> 332
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Polyepitope Construct

<400> 106

Met Gly Met Gln Val Gln Ile Gln Ser Leu Phe Leu Leu Leu Leu Trp
1 5 10 15

Val Pro Gly Ser Arg Gly Leu Pro Arg Arg Gly Pro Arg Leu Gly Val
20 25 30

Lys His Leu Ile Phe Cys His Ser Lys Lys Asn Val Ile Lys Gly Gly
35 40 45

Arg His Leu Ile Lys Ala Ala Ala Cys Leu Ile Arg Leu Lys Pro Thr
50 55 60

Leu Asn Ala Ala Ser Phe Ser Ile Phe Leu Leu Ala Leu Lys Leu Val
65 70 75 80

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

Ala Ser Gly Val Leu Lys Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu
100 105 110

Lys Ala Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Asn Ala Lys Leu
115 120 125

Gln Asp Cys Thr Met Leu Val Asn Ala Ala Ala Ser Thr Asn Pro Lys
130 135 140

Pro Gln Arg Lys Asn Ala Val Cys Thr Arg Gly Val Ala Lys Asn Ala
145 150 155 160

Met Tyr Thr Asn Val Asp Gln Asp Leu Asn Ala Ala Ala Lys Thr Ser
165 170 175

Glu Arg Ser Gln Pro Arg Asn Ala Tyr Tyr Arg Gly Leu Asp Val Ser
180 185 190

Val Lys Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Asn Ala Ala Phe
195 200 205

Trp Ala Lys His Met Trp Asn Phe Ile Lys Ala Ala Gln Tyr Leu Ala
210 215 220

Gly Leu Ser Thr Leu Asn Phe Thr Asp Asn Ser Ser Pro Pro Ala Val
225 230 235 240

Lys Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Lys Ala Tyr Leu Leu Pro
245 250 255

Arg Arg Gly Pro Arg Leu Asn Thr Leu Trp Ala Arg Met Ile Leu Met
260 265 270

Asn Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Asn His Met Trp Asn
275 280 285

Phe Ile Ser Gly Ile Asn Ala Ala Ala Lys Phe Val Ala Ala Trp Thr
290 295 300

Leu Lys Ala Ala Ala Lys Asn Ile Ile Met Tyr Ala Pro Thr Leu Lys
305 310 315 320

Ala Ala Val Leu Val Gly Gly Val Leu Ala Ala Leu
325 330

<210> 107
<211> 999
<212> DNA
<213> Artificial sequence

<220>
<223> Polyepitope Construct

<400> 107
atgggcatgc aggtgcagat ccagagcctg ttcctgctcc tgctgtgggt gccaggaagc 60
agaggcctcc cacggagagg ccctcggctt ggcgtaagc acttaatctt ctgtcacagt 120
aagaagaacg tgatcaaggg tgggaggcat ctaatcaaag ccgcagcttg cctgatccgg 180
ttgaagccaa ccctcaacgc cgcattcttc tcaatctttc tgctagcact gaagttggtc 240
gatataattag ccggatacgg agccaaagcc gcatacagga gatgccgtgc gaggggcgtg 300
ctcaagctgc ccatcaatgc cctgagcaac agcttgaagg ctgcacctac actgtgggct 360
aggatgatcc tgaacgctaa acttcaggac tgtactatgc tggatgaatgc agccgctagc 420
accaacccaa agcctcagcg taagaacgcc gtgtgtacta gaggcgttgc caagaatgct 480
atgtatacta atgtcgatca agacctgaac gccgctgcga agacgtctga gagatcccaa 540
cccaggaacg cctactatag aggttttagac gtttccgtca aagtcgccac agatgctctg 600
atgaccggat ataatgccgc gttctgggct aaacacatgt ggaacttcat taaggccgct 660
cagtatcttg ctggactttc aacctcaac ttacggaca actcctctcc tcccgcggtg 720
aaggctgcct acgcagctca gggatataag aaagcctacc tgctcccag acgcggacct 780

cgccttaata ccctatgggc taggatgata ctcataaatg gcttgctggg ctgcatcatt 840
 acttcgctga atcatatgtg gaacttcata agcggaatca acgccgctgc aaagttcgtg 900
 gctgcctgga cattgaaagc agctgccaag aacattatta tgtacgcgcc aacactgaag 960
 gccgcagtagc tggttggcgg tgtactggcc gcactctga 999

<210> 108
 <211> 199
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Polyepitope Construct

<400> 108

Met Gly Met Gln Val Gln Ile Gln Ser Leu Phe Leu Leu Leu Leu Trp
 1 5 10 15

Val Pro Gly Ser Arg Gly Leu Pro Arg Arg Gly Pro Arg Leu Gly Val
 20 25 30

Lys Ala Ala Ile Pro Leu Val Gly Ala Pro Leu Lys Ala Ala Ser Pro
 35 40 45

Arg Gly Ser Arg Pro Ser Trp Lys Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

Ile Lys Leu Pro Gly Cys Ser Phe Ser Ile Phe Lys His Pro Asn Ile
 65 70 75 80

Glu Glu Val Ala Leu Lys Ala Ala Lys Leu Ser Ala Leu Gly Leu Lys
 85 90 95

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

Asp His Leu Glu Phe Asn Ala Ala Ala Phe Pro Tyr Leu Val Ala Tyr
 115 120 125

Gln Ala Lys Asn Pro Ala Ile Ala Ser Leu Met Ala Phe Lys Glu Pro
 130 135 140

Glu Pro Asp Val Ala Val Leu Lys Ala Lys Phe Val Ala Ala Trp Thr
 145 150 155 160

Leu Lys Ala Ala Ala Lys Glu Pro Asp Val Ala Val Leu Thr Ser Met
 165 170 175

Asn Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Lys Ala Ala Pro Thr
 180 185 190

Leu Trp Ala Arg Met Ile Leu
 195

<210> 109
 <211> 600
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Polyepitope Construct

<400> 109
 atgggcatgc aggtgcagat ccagagcctg ttcttgctcc tgctgtgggt gccaggaagc 60
 agaggcctgc ccagaagagg cctcggctg ggagtcaagg cagccatccc tctggtggga 120
 gcacctctga aggcagccag cccaagaggc agcagaccaa gctggaaaca gccagagga 180
 agacggcagc ccatcaaact gcccggtgt agcttcagca tctttaagca tcccaacatc 240
 gaggaagtcg ctctgaaggc agccaagctg agcgccctgg gcctgaaggc tattcctacc 300
 agcggcgacg tcgtggtcaa cctcccagtg tgccaggacc acctggagtt caatgccgct 360
 gcattccctt acctggtggc ataccaggca aagaaccctg ccatcgccag cctgatggcc 420
 ttcaaggagc ccgagcctga tgtggcagtg ctcaaggcca aattcgtggc cgcttgacc 480
 ctgaaggccg ccgccaagga gcccgacgtg gccgtgctga ccagcatgaa cctgcccac 540
 aacgccctct ccaactccct gaaagccgca cccacactct gggcccggat gatcctgtga 600

<210> 110
 <211> 215
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Polyepitope Construct

<400> 110

Met Gly Met Gln Val Gln Ile Gln Ser Leu Phe Leu Leu Leu Trp
 1 5 10 15

Val Pro Gly Ser Arg Gly Asp Pro Arg Arg Arg Ser Arg Asn Leu Lys
 20 25 30

Ala Ala Gly Pro Arg Leu Gly Val Arg Ala Thr Lys Ala Pro Leu Gly
 35 40 45

Gly Ala Ala Arg Ala Leu Asn Ala Leu Pro Arg Arg Gly Pro Arg Leu
50 55 60

Gly Val Lys Leu Pro Ala Leu Ser Thr Gly Leu Ile Lys Ala Ala Thr
65 70 75 80

Pro Gly Glu Arg Pro Ser Gly Met Lys Ala Ala Tyr Ala Ala Gln Gly
85 90 95

Tyr Lys Val Leu Lys Arg Pro Ser Gly Met Phe Asp Ser Ser Val Lys
100 105 110

Ala Pro Pro Pro Ser Trp Asp Gln Met Lys Pro Thr Leu His Gly Pro
115 120 125

Thr Pro Leu Asn Ala Gly Pro Thr Pro Leu Leu Tyr Arg Leu Asn Ala
130 135 140

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

Pro Pro Leu Leu Lys Ala Ala Ala Ser Ala Ala Cys Arg Ala Ala Lys
165 170 175

Leu Lys Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala Lys
180 185 190

Ala Pro Pro Val Val His Gly Cys Pro Leu Asn Ala Ala Ala Pro Thr
195 200 205

Leu Trp Ala Arg Met Ile Leu
210 215

<210> 111
<211> 648
<212> DNA
<213> Artificial sequence

<220>
<223> Polyepitope Construct

<400> 111
atgggcatgc aggtgcagat ccagagcctg ttcctgctcc tgctgtgggt gccaggaagc 60
agaggcgacc ctagacggag gtcccgaac ctgaaggcag ccggacccag actgggcgtc 120
agagccacca aggcacctct gggaggcgcc gctcggggccc tgaacgccct gcccaggaga 180
ggacctagac tcggcgtgaa gctgcccgca ctgagcactg gactgatcaa ggccgcaaca 240

```

cccggcgaga gaccaagcgg catgaaagcc gcttacgcag cccagggcta caaggtgctg      300
aagcggccca gcggaatggt cgacagctcc gtgaaggctc cacctcccag ctgggatcag      360
atgaagccca ccctgcacgg acccacacca ctcaatgccg ggcccactcc actcctgtac      420
agactgaacg ccgcaactccc tgctatcctg agccctggcg ccctcagacc cgactacaat      480
cctccactgc tcaaggccgc tgccagcgcc gcatgccggg ccgccaaact gaaggccaag      540
ttcgtcgccg catggaccct gaaagcagcc gccaaagccc ctcccggtgt gcacggctgc      600
ccactgaacg ccgcccgtcc caccctgtgg gcccggtatga tcctgtga                  648

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<210> 112
<211> 3011
<212> PRT
<213> Hepatitis C Virus

<220>
<221> MISC_FEATURE
<222> (2414)..(2414)
<223> X is a blanc that is inserted to keep numbering of HCV genotype 1
      b consensus in line with numbering of HCV-1

```

<400> 112

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Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1          5          10          15

```

```

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
      20          25          30

```

```

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
      35          40          45

```

```

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
      50          55          60

```

```

Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly
      65          70          75          80

```

```

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp
      85          90          95

```

```

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
      100         105         110

```

```

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
      115         120         125

```

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
130 135 140

Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145 150 155 160

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

Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr
180 185 190

Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp Cys Ser
195 200 205

Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro
210 215 220

Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val
225 230 235 240

Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ser Ser Val Pro Thr Thr
245 250 255

Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys
260 265 270

Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser
275 280 285

Gln Leu Phe Thr Phe Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys
290 295 300

Asn Cys Ser Ile Tyr Pro Gly His Val Ser Gly His Arg Met Ala Trp
305 310 315 320

Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln
325 330 335

Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His
340 345 350

Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp
355 360 365

Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly Thr
370 375 380

Thr His Val Thr Gly Gly Ala Ala Ala Arg Thr Thr Ser Gly Phe Thr
385 390 395 400

Ser Leu Phe Ser Pro Gly Pro Ser Gln Lys Ile Gln Leu Val Asn Thr
405 410 415

Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser
420 425 430

Leu Gln Thr Gly Phe Leu Ala Ala Leu Phe Tyr Thr His Arg Phe Asn
435 440 445

Ala Ser Gly Cys Pro Glu Arg Met Ala Ser Cys Arg Pro Ile Asp Lys
450 455 460

Phe Ala Gln Gly Trp Gly Pro Ile Thr Tyr Ala Glu Pro Asn Ser Ser
465 470 475 480

Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile
485 490 495

Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser
500 505 510

Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Ser
515 520 525

Trp Gly Glu Asn Glu Thr Asp Val Leu Leu Leu Asn Asn Thr Arg Pro
530 535 540

Pro Gln Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Ser Thr Gly Phe
545 550 555 560

Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Val Gly Asn
565 570 575

Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala
580 585 590

Thr Tyr Thr Lys Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Leu
595 600 605

Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe

610

615

620

Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Leu
 625 630 635 640

Asn Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp
 645 650 655

Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp
 660 665 670

Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly
 675 680 685

Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly
 690 695 700

Ile Gly Ser Ala Val Val Ser Phe Ala Ile Lys Trp Glu Tyr Val Leu
 710 715 720

Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys Ala Cys Leu Trp
 725 730 735

Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val
 740 745 750

Val Leu Asn Ala Ala Ser Val Ala Gly Ala His Gly Ile Leu Ser Phe
 755 760 765

Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro
 770 775 780

Gly Ala Ala Tyr Ala Leu Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu
 785 790 795 800

Leu Ala Leu Pro Pro Arg Ala Tyr Ala Met Asp Arg Glu Met Ala Ala
 805 810 815

Ser Cys Gly Gly Ala Val Phe Val Gly Leu Ala Leu Leu Thr Leu Ser
 820 825 830

Pro Tyr Tyr Lys Val Phe Leu Ala Arg Leu Ile Trp Trp Leu Gln Tyr
 835 840 845

Phe Ile Thr Arg Ala Glu Ala His Leu Gln Val Trp Val Pro Pro Leu
 850 855 860

Asn Val Arg Gly Gly Arg Asp Ala Ile Ile Leu Leu Thr Cys Ala Val
865 870 875 880

His Pro Glu Leu Ile Phe Asp Ile Thr Lys Leu Leu Leu Ala Ile Leu
885 890 895

Gly Pro Leu Met Val Leu Gln Ala Gly Ile Thr Arg Val Pro Tyr Phe
900 905 910

Val Arg Ala Gln Gly Leu Ile Arg Ala Cys Met Leu Val Arg Lys Val
915 920 925

Ala Gly Gly His Tyr Val Gln Met Ala Phe Met Lys Leu Ala Ala Leu
930 935 940

Thr Gly Thr Tyr Val Tyr Asp His Leu Thr Pro Leu Arg Asp Trp Ala
945 950 955 960

His Ala Gly Leu Arg Asp Leu Ala Val Ala Val Glu Pro Val Val Phe
965 970 975

Ser Asp Met Glu Thr Lys Ile Ile Thr Trp Gly Ala Asp Thr Ala Ala
980 985 990

Cys Gly Asp Ile Ile Leu Gly Leu Pro Val Ser Ala Arg Arg Gly Arg
995 1000 1005

Glu Ile Leu Leu Gly Pro Ala Asp Ser Leu Glu Gly Gln Gly Trp
1010 1015 1020

Arg Leu Leu Ala Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly
1025 1030 1035

Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn
1040 1045 1050

Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser
1055 1060 1065

Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His
1070 1075 1080

Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr
1085 1090 1095

Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala
	1100					1105					1110			
Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser
	1115					1120					1125			
Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	Ile	Pro	Val	Arg
	1130					1135					1140			
Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	Arg	Pro	Val
	1145					1150					1155			
Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys	Pro	Ser
	1160					1165					1170			
Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	Gly
	1175					1180					1185			
Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr
	1190					1195					1200			
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala
	1205					1210					1215			
Val	Pro	Gln	Thr	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly
	1220					1225					1230			
Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly
	1235					1240					1245			
Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly
	1250					1255					1260			
Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Val	Asp	Pro	Asn	Ile
	1265					1270					1275			
Arg	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Ile	Thr	Tyr
	1280					1285					1290			
Ser	Thr	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly
	1295					1300					1305			
Ala	Tyr	Asp	Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser
	1310					1315					1320			

Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr
1325 1330 1335

Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly
1340 1345 1350

Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser
1355 1360 1365

Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu
1370 1375 1380

Val Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys
1385 1390 1395

Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Ala Leu Gly Leu Asn
1400 1405 1410

Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr
1415 1420 1425

Ser Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly
1430 1435 1440

Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val
1445 1450 1455

Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu
1460 1465 1470

Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg
1475 1480 1485

Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr
1490 1495 1500

Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys
1505 1510 1515

Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala
1520 1525 1530

Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu
1535 1540 1545

Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr

1550							1555								1560
Gly	Leu	Thr	His	Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	
1565						1570					1575				
Ala	Gly	Asp	Asn	Phe	Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	
1580						1585					1590				
Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp	
1595						1600					1605				
Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	Leu	His	Gly	Pro	Thr	Pro	
1610						1615					1620				
Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	Glu	Val	Thr	Leu	Thr	
1625						1630					1635				
His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser	Ala	Asp	Leu	
1640						1645					1650				
Glu	Val	Val	Thr	Ser	Thr	Trp	Val	Leu	Val	Gly	Gly	Val	Leu	Ala	
1655						1660					1665				
Ala	Leu	Ala	Ala	Tyr	Cys	Leu	Thr	Thr	Gly	Ser	Val	Val	Ile	Val	
1670						1675					1680				
Gly	Arg	Ile	Ile	Leu	Ser	Gly	Arg	Pro	Ala	Val	Ile	Pro	Asp	Arg	
1685						1690					1695				
Glu	Val	Leu	Tyr	Arg	Glu	Phe	Asp	Glu	Met	Glu	Glu	Cys	Ala	Ser	
1700						1705					1710				
His	Leu	Pro	Tyr	Ile	Glu	Gln	Gly	Met	Gln	Leu	Ala	Glu	Gln	Phe	
1715						1720					1725				
Lys	Gln	Lys	Ala	Leu	Gly	Leu	Leu	Gln	Thr	Ala	Thr	Lys	Gln	Ala	
1730						1735					1740				
Glu	Ala	Ala	Ala	Pro	Val	Val	Glu	Ser	Lys	Trp	Arg	Ala	Leu	Glu	
1745						1750					1755				
Thr	Phe	Trp	Ala	Lys	His	Met	Trp	Asn	Phe	Ile	Ser	Gly	Ile	Gln	
1760						1765					1770				
Tyr	Leu	Ala	Gly	Leu	Ser	Thr	Leu	Pro	Gly	Asn	Pro	Ala	Ile	Ala	
1775						1780					1785				

Ser Leu Met Ala Phe Thr Ala Ser Ile Thr Ser Pro Leu Thr Thr
1790 1795 1800

Gln His Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp Val Ala Ala
1805 1810 1815

Gln Leu Ala Pro Pro Ser Ala Ala Ser Ala Phe Val Gly Ala Gly
1820 1825 1830

Ile Ala Gly Ala Ala Val Gly Ser Ile Gly Leu Gly Lys Val Leu
1835 1840 1845

Val Asp Ile Leu Ala Gly Tyr Gly Ala Gly Val Ala Gly Ala Leu
1850 1855 1860

Val Ala Phe Lys Val Met Ser Gly Glu Met Pro Ser Thr Glu Asp
1865 1870 1875

Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala Leu Val
1880 1885 1890

Val Gly Val Val Cys Ala Ala Ile Leu Arg Arg His Val Gly Pro
1895 1900 1905

Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala Phe Ala
1910 1915 1920

Ser Arg Gly Asn His Val Ser Pro Thr His Tyr Val Pro Glu Ser
1925 1930 1935

Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu Thr Ile
1940 1945 1950

Thr Gln Leu Leu Lys Arg Leu His Gln Trp Ile Asn Glu Asp Cys
1955 1960 1965

Ser Thr Pro Cys Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp
1970 1975 1980

Ile Cys Thr Val Leu Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys
1985 1990 1995

Leu Leu Pro Arg Leu Pro Gly Val Pro Phe Phe Ser Cys Gln Arg
2000 2005 2010

Gly	Tyr	Lys	Gly	Val	Trp	Arg	Gly	Asp	Gly	Ile	Met	Gln	Thr	Thr
2015						2020					2025			
Cys	Pro	Cys	Gly	Ala	Gln	Ile	Thr	Gly	His	Val	Lys	Asn	Gly	Ser
2030						2035					2040			
Met	Arg	Ile	Val	Gly	Pro	Lys	Thr	Cys	Ser	Asn	Thr	Trp	His	Gly
2045						2050					2055			
Thr	Phe	Pro	Ile	Asn	Ala	Tyr	Thr	Thr	Gly	Pro	Cys	Thr	Pro	Ser
2060						2065					2070			
Pro	Ala	Pro	Asn	Tyr	Ser	Arg	Ala	Leu	Trp	Arg	Val	Ala	Ala	Glu
2075						2080					2085			
Glu	Tyr	Val	Glu	Val	Thr	Arg	Val	Gly	Asp	Phe	His	Tyr	Val	Thr
2090						2095					2100			
Gly	Met	Thr	Thr	Asp	Asn	Val	Lys	Cys	Pro	Cys	Gln	Val	Pro	Ala
2105						2110					2115			
Pro	Glu	Phe	Phe	Thr	Glu	Val	Asp	Gly	Val	Arg	Leu	His	Arg	Tyr
2120						2125					2130			
Ala	Pro	Ala	Cys	Lys	Pro	Leu	Leu	Arg	Glu	Glu	Val	Thr	Phe	Gln
2135						2140					2145			
Val	Gly	Leu	Asn	Gln	Tyr	Leu	Val	Gly	Ser	Gln	Leu	Pro	Cys	Glu
2150						2155					2160			
Pro	Glu	Pro	Asp	Val	Ala	Val	Leu	Thr	Ser	Met	Leu	Thr	Asp	Pro
2165						2170					2175			
Ser	His	Ile	Thr	Ala	Glu	Thr	Ala	Lys	Arg	Arg	Leu	Ala	Arg	Gly
2180						2185					2190			
Ser	Pro	Pro	Ser	Leu	Ala	Ser	Ser	Ser	Ala	Ser	Gln	Leu	Ser	Ala
2195						2200					2205			
Pro	Ser	Leu	Lys	Ala	Thr	Cys	Thr	Thr	His	His	Asp	Ser	Pro	Asp
2210						2215					2220			
Ala	Asp	Leu	Ile	Glu	Ala	Asn	Leu	Leu	Trp	Arg	Gln	Glu	Met	Gly
2225						2230					2235			

Gly	Asn	Ile	Thr	Arg	Val	Glu	Ser	Glu	Asn	Lys	Val	Val	Ile	Leu
2240						2245					2250			
Asp	Ser	Phe	Asp	Pro	Leu	Arg	Ala	Glu	Glu	Asp	Glu	Arg	Glu	Val
2255						2260					2265			
Ser	Val	Ala	Ala	Glu	Ile	Leu	Arg	Lys	Ser	Arg	Lys	Phe	Pro	Pro
2270						2275					2280			
Ala	Leu	Pro	Ile	Trp	Ala	Arg	Pro	Asp	Tyr	Asn	Pro	Pro	Leu	Leu
2285						2290					2295			
Glu	Ser	Trp	Lys	Asp	Pro	Asp	Tyr	Val	Pro	Pro	Val	Val	His	Gly
2300						2305					2310			
Cys	Pro	Leu	Pro	Pro	Thr	Lys	Ala	Pro	Pro	Ile	Pro	Pro	Pro	Arg
2315						2320					2325			
Arg	Lys	Arg	Thr	Val	Val	Leu	Thr	Glu	Ser	Thr	Val	Ser	Ser	Ala
2330						2335					2340			
Leu	Ala	Glu	Leu	Ala	Thr	Lys	Thr	Phe	Gly	Ser	Ser	Gly	Ser	Ser
2345						2350					2355			
Ala	Val	Asp	Ser	Gly	Thr	Ala	Thr	Ala	Pro	Pro	Asp	Gln	Ala	Ser
2360						2365					2370			
Asp	Asp	Gly	Asp	Lys	Gly	Ser	Asp	Val	Glu	Ser	Tyr	Ser	Ser	Met
2375						2380					2385			
Pro	Pro	Leu	Glu	Gly	Glu	Pro	Gly	Asp	Pro	Asp	Leu	Ser	Asp	Gly
2390						2395					2400			
Ser	Trp	Ser	Thr	Val	Ser	Glu	Glu	Ala	Ser	Xaa	Glu	Asp	Val	Val
2405						2410					2415			
Cys	Cys	Ser	Met	Ser	Tyr	Thr	Trp	Thr	Gly	Ala	Leu	Ile	Thr	Pro
2420						2425					2430			
Cys	Ala	Ala	Glu	Glu	Ser	Lys	Leu	Pro	Ile	Asn	Ala	Leu	Ser	Asn
2435						2440					2445			
Ser	Leu	Leu	Arg	His	His	Asn	Met	Val	Tyr	Ala	Thr	Thr	Ser	Arg
2450						2455					2460			
Ser	Ala	Ser	Leu	Arg	Gln	Lys	Lys	Val	Thr	Phe	Asp	Arg	Leu	Gln

2465

2470

2475

Val Leu Asp Asp His Tyr Arg Asp Val Leu Lys Glu Met Lys Ala
 2480 2485 2490

Lys Ala Ser Thr Val Lys Ala Lys Leu Leu Ser Val Glu Glu Ala
 2495 2500 2505

Cys Lys Leu Thr Pro Pro His Ser Ala Lys Ser Lys Phe Gly Tyr
 2510 2515 2520

Gly Ala Lys Asp Val Arg Asn Leu Ser Ser Lys Ala Val Asn His
 2525 2530 2535

Ile Arg Ser Val Trp Lys Asp Leu Leu Glu Asp Thr Glu Thr Pro
 2540 2545 2550

Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val Phe Cys Val Gln
 2555 2560 2565

Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg Leu Ile Val Phe Pro
 2570 2575 2580

Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr Asp Val
 2585 2590 2595

Val Ser Thr Leu Pro Gln Ala Val Met Gly Ser Ser Tyr Gly Phe
 2600 2605 2610

Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Asn Ala Trp
 2615 2620 2625

Lys Ser Lys Lys Cys Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys
 2630 2635 2640

Phe Asp Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser
 2645 2650 2655

Ile Tyr Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile
 2660 2665 2670

Arg Ser Leu Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn
 2675 2680 2685

Ser Lys Gly Gln Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly
 2690 2695 2700

Val	Leu	Thr	Thr	Ser	Cys	Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys
	2705					2710					2715			
Ala	Ser	Ala	Ala	Cys	Arg	Ala	Ala	Lys	Leu	Gln	Asp	Cys	Thr	Met
	2720					2725					2730			
Leu	Val	Asn	Gly	Asp	Asp	Leu	Val	Val	Ile	Cys	Glu	Ser	Ala	Gly
	2735					2740					2745			
Thr	Gln	Glu	Asp	Ala	Ala	Ser	Leu	Arg	Val	Phe	Thr	Glu	Ala	Met
	2750					2755					2760			
Thr	Arg	Tyr	Ser	Ala	Pro	Pro	Gly	Asp	Pro	Pro	Gln	Pro	Glu	Tyr
	2765					2770					2775			
Asp	Leu	Glu	Leu	Ile	Thr	Ser	Cys	Ser	Ser	Asn	Val	Ser	Val	Ala
	2780					2785					2790			
His	Asp	Ala	Ser	Gly	Lys	Arg	Val	Tyr	Tyr	Leu	Thr	Arg	Asp	Pro
	2795					2800					2805			
Thr	Thr	Pro	Leu	Ala	Arg	Ala	Ala	Trp	Glu	Thr	Ala	Arg	His	Thr
	2810					2815					2820			
Pro	Val	Asn	Ser	Trp	Leu	Gly	Asn	Ile	Ile	Met	Tyr	Ala	Pro	Thr
	2825					2830					2835			
Leu	Trp	Ala	Arg	Met	Ile	Leu	Met	Thr	His	Phe	Phe	Ser	Ile	Leu
	2840					2845					2850			
Leu	Ala	Gln	Glu	Gln	Leu	Glu	Lys	Ala	Leu	Asp	Cys	Gln	Ile	Tyr
	2855					2860					2865			
Gly	Ala	Cys	Tyr	Ser	Ile	Glu	Pro	Leu	Asp	Leu	Pro	Gln	Ile	Ile
	2870					2875					2880			
Glu	Arg	Leu	His	Gly	Leu	Ser	Ala	Phe	Ser	Leu	His	Ser	Tyr	Ser
	2885					2890					2895			
Pro	Gly	Glu	Ile	Asn	Arg	Val	Ala	Ser	Cys	Leu	Arg	Lys	Leu	Gly
	2900					2905					2910			
Val	Pro	Pro	Leu	Arg	Val	Trp	Arg	His	Arg	Ala	Arg	Ser	Val	Arg
	2915					2920					2925			

Ala Lys Leu Leu Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys
2930 2935 2940

Tyr Leu Phe Asn Trp Ala Val Arg Thr Lys Leu Lys Leu Thr Pro
2945 2950 2955

Ile Pro Ala Ala Ser Gln Leu Asp Leu Ser Gly Trp Phe Val Ala
2960 2965 2970

Gly Tyr Ser Gly Gly Asp Ile Tyr His Ser Leu Ser Arg Ala Arg
2975 2980 2985

Pro Arg Trp Phe Met Leu Cys Leu Leu Leu Leu Ser Val Gly Val
2990 2995 3000

Gly Ile Tyr Leu Leu Pro Asn Arg
3005 3010

<210> 113
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer Sequence

<400> 113

Gly Pro Gly Pro Gly
1 5

<210> 114
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal Sequence

<400> 114

Met Gly Met Gln Val Gln Ile Gln Ser Leu Phe Leu Leu Leu Trp
1 5 10 15

Val Pro Gly Ser Arg Gly
20

<210> 115
<211> 666
<212> PRT
<213> Artificial Sequence

<220>

<223> Polyepitope Construct

<400> 115

Met Val Ile Lys Gly Gly Arg His Leu Ile Lys Ala Gly Pro Arg Leu
1 5 10 15

Gly Val Arg Ala Thr Lys Ala Ala Ala Gln Tyr Leu Ala Gly Leu Ser
20 25 30

Thr Leu Asn Ala Ala Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Asn
35 40 45

Ala Ala His Pro Asn Ile Glu Glu Val Ala Leu Asn Leu Val Asp Ile
50 55 60

Leu Ala Gly Tyr Gly Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile
65 70 75 80

Asn Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Lys Leu Gln Asp Cys
85 90 95

Thr Met Leu Val Asn Ala Ala Ala Ala Glu Gln Phe Lys Gln Lys Ala
100 105 110

Leu Lys Thr Ser Glu Arg Ser Gln Pro Arg Asn Ala Ala Phe Pro Tyr
115 120 125

Leu Val Ala Tyr Gln Ala Lys Ala Ala Met Tyr Thr Asn Val Asp Gln
130 135 140

Asp Leu Asn Thr Leu Trp Ala Arg Met Ile Leu Met Asn Leu Pro Ile
145 150 155 160

Asn Ala Leu Ser Asn Ser Leu Lys Ser Thr Asn Pro Lys Pro Gln Arg
165 170 175

Lys Asn Asp Tyr Pro Tyr Arg Leu Trp His Tyr Lys Ala Ala Cys Leu
180 185 190

Ile Arg Leu Lys Pro Thr Leu Asn Ile Ile Met Tyr Ala Pro Thr Leu
195 200 205

Lys Ala Ala Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Asn Leu Pro
210 215 220

Gly Cys Ser Phe Ser Ile Phe Lys Tyr Arg Arg Cys Arg Ala Ser Gly
225 230 235 240

Val Leu Lys Ala Ala Val Leu Val Gly Gly Val Leu Ala Ala Leu Asn
245 250 255

Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Asn Ala Ala Tyr Ala Ala
260 265 270

Gln Gly Tyr Lys Lys Asp Pro Arg Arg Arg Ser Arg Asn Leu Lys Ala
275 280 285

Ala Ala Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Asn Phe Trp Ala
290 295 300

Lys His Met Trp Asn Phe Ile Lys Ala Ala Ala Lys Phe Val Ala Ala
305 310 315 320

Trp Thr Leu Lys Ala Ala Ala Lys Ala Leu Ile Arg Leu Lys Pro Thr
325 330 335

Leu His Lys Ala Ala Ala Val Cys Thr Arg Gly Val Ala Lys Asn Phe
340 345 350

Thr Asp Asn Ser Ser Pro Pro Ala Val Lys Ala Leu Pro Arg Arg Gly
355 360 365

Pro Arg Leu Gly Val Lys Ser Phe Ser Ile Phe Leu Leu Ala Leu Lys
370 375 380

Ala Ala Glu Thr Ala Gly Ala Arg Leu Val Asn Ala Ala Gly Arg His
385 390 395 400

Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp Gly Pro Gly Pro Gly
405 410 415

Ser Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp Val Ala Ala Gln Gly
420 425 430

Pro Gly Pro Gly Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro
435 440 445

Thr Phe Thr Ile Glu Thr Thr Gly Pro Gly Pro Gly Glu Asp Leu Val
450 455 460

Asn Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala Leu Val Val Gly Pro
465 470 475 480

Gly Pro Gly Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala
485 490 495

Phe Ala Ser Gly Pro Gly Pro Gly Met Asn Arg Leu Ile Ala Phe Ala
500 505 510

Ser Arg Gly Asn His Val Ser Pro Gly Pro Gly Pro Gly Ser Met Ser
515 520 525

Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala Gly Pro Gly Pro
530 535 540

Gly Thr Pro Ala Glu Thr Thr Val Arg Leu Arg Ala Tyr Met Asn Thr
545 550 555 560

Pro Gly Leu Pro Val Gly Pro Gly Pro Gly Ala Val Gly Ile Phe Arg
565 570 575

Ala Ala Val Cys Thr Arg Gly Val Ala Gly Pro Gly Pro Gly Gly Ile
580 585 590

Gln Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly Asn Pro Ala Gly Pro
595 600 605

Gly Pro Gly Thr Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala
610 615 620

Leu Ala Ala Gly Pro Gly Pro Gly Gly Tyr Lys Val Leu Val Leu Asn
625 630 635 640

Pro Ser Val Ala Ala Thr Gly Pro Gly Pro Gly Gly Lys Pro Ala Ile
645 650 655

Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu
660 665

<210> 116
<211> 665
<212> PRT
<213> Artificial Sequence

<220>
<223> Polyepitope Construct

<400> 116

Met	Gly	Arg	His	Leu	Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Gly	1	5	10	15
Pro	Gly	Pro	Gly	Ser	Thr	Leu	Leu	Phe	Asn	Ile	Leu	Gly	Gly	Trp	Val	20	25	30	
Ala	Ala	Gln	Gly	Pro	Gly	Pro	Gly	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	35	40	45	
Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	Gly	Pro	Gly	Pro	Gly	50	55	60	
Glu	Asp	Leu	Val	Asn	Leu	Leu	Pro	Ala	Ile	Leu	Ser	Pro	Gly	Ala	Leu	65	70	75	80
Val	Val	Gly	Pro	Gly	Pro	Gly	Gly	Glu	Gly	Ala	Val	Gln	Trp	Met	Asn	85	90	95	
Arg	Leu	Ile	Ala	Phe	Ala	Ser	Gly	Pro	Gly	Pro	Gly	Met	Asn	Arg	Leu	100	105	110	
Ile	Ala	Phe	Ala	Ser	Arg	Gly	Asn	His	Val	Ser	Pro	Gly	Pro	Gly	Pro	115	120	125	
Gly	Ser	Met	Ser	Tyr	Thr	Trp	Thr	Gly	Ala	Leu	Ile	Thr	Pro	Cys	Ala	130	135	140	
Gly	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Thr	Thr	Val	Arg	Leu	Arg	Ala	145	150	155	160
Tyr	Met	Asn	Thr	Pro	Gly	Leu	Pro	Val	Gly	Pro	Gly	Pro	Gly	Ala	Val	165	170	175	
Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	Gly	Val	Ala	Gly	Pro	Gly	180	185	190	
Pro	Gly	Gly	Ile	Gln	Tyr	Leu	Ala	Gly	Leu	Ser	Thr	Leu	Pro	Gly	Asn	195	200	205	
Pro	Ala	Gly	Pro	Gly	Pro	Gly	Thr	Ser	Thr	Trp	Val	Leu	Val	Gly	Gly	210	215	220	
Val	Leu	Ala	Ala	Leu	Ala	Ala	Gly	Pro	Gly	Pro	Gly	Gly	Tyr	Lys	Val	225	230	235	240

Leu Val Leu Asn Pro Ser Val Ala Ala Thr Gly Pro Gly Pro Gly Gly
245 250 255

Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu Lys Ala
260 265 270

Val Ile Lys Gly Gly Arg His Leu Ile Lys Ala Gly Pro Arg Leu Gly
275 280 285

Val Arg Ala Thr Lys Ala Ala Ala Gln Tyr Leu Ala Gly Leu Ser Thr
290 295 300

Leu Asn Ala Ala Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Asn Ala
305 310 315 320

Ala His Pro Asn Ile Glu Glu Val Ala Leu Asn Leu Val Asp Ile Leu
325 330 335

Ala Gly Tyr Gly Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile Asn
340 345 350

Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Lys Leu Gln Asp Cys Thr
355 360 365

Met Leu Val Asn Ala Ala Ala Ala Glu Gln Phe Lys Gln Lys Ala Leu
370 375 380

Lys Thr Ser Glu Arg Ser Gln Pro Arg Asn Ala Ala Phe Pro Tyr Leu
385 390 395 400

Val Ala Tyr Gln Ala Lys Ala Ala Met Tyr Thr Asn Val Asp Gln Asp
405 410 415

Leu Asn Thr Leu Trp Ala Arg Met Ile Leu Met Asn Leu Pro Ile Asn
420 425 430

Ala Leu Ser Asn Ser Leu Lys Ser Thr Asn Pro Lys Pro Gln Arg Lys
435 440 445

Asn Asp Tyr Pro Tyr Arg Leu Trp His Tyr Lys Ala Ala Cys Leu Ile
450 455 460

Arg Leu Lys Pro Thr Leu Asn Ile Ile Met Tyr Ala Pro Thr Leu Lys
465 470 475 480

Ala Ala Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Asn Leu Pro Gly

485

490

495

Cys Ser Phe Ser Ile Phe Lys Tyr Arg Arg Cys Arg Ala Ser Gly Val
 500 505 510

Leu Lys Ala Ala Val Leu Val Gly Gly Val Leu Ala Ala Leu Asn Gly
 515 520 525

Leu Leu Gly Cys Ile Ile Thr Ser Leu Asn Ala Ala Tyr Ala Ala Gln
 530 535 540

Gly Tyr Lys Lys Asp Pro Arg Arg Arg Ser Arg Asn Leu Lys Ala Ala
 545 550 555 560

Ala Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Asn Phe Trp Ala Lys
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His Met Trp Asn Phe Ile Lys Ala Ala Ala Lys Phe Val Ala Ala Trp
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Thr Leu Lys Ala Ala Ala Lys Ala Leu Ile Arg Leu Lys Pro Thr Leu
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His Lys Ala Ala Ala Val Cys Thr Arg Gly Val Ala Lys Asn Phe Thr
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Asp Asn Ser Ser Pro Pro Ala Val Lys Ala Leu Pro Arg Arg Gly Pro
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Arg Leu Gly Val Lys Ser Phe Ser Ile Phe Leu Leu Ala Leu Lys Ala
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<211> 18

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<213> Artificial Sequence

<220>

<223> Affinity Tag

<400> 117

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His His

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cgattcctgt ttgtaattgt ccttttaaca gcgatcgct atttcgtctc gctcaggcgc	3240
aatcacgaat gaataacggt ttggttgatg cgagtgattt tgatgacgag cgtaatggct	3300
ggcctgttga acaagtctgg aaagaaatgc ataagctttt gccattctca ccgattcag	3360
tcgtcactca tgggtgatttc tcacttgata accttatttt tgacgagggg aaattaatag	3420
gttgatttga tgttgagcga gtcggaatcg cagaccgata ccaggatctt gccatcctat	3480
ggaactgcct cggtgagttt tctccttcat tacagaaacg gctttttcaa aaatatggta	3540
ttgataatcc tgatatgaat aaattgcagt ttcatattgat gctcgatgag tttttcta	3600
cagaattggt taattggttg taacactggc agagcattac gctgacttga cgggacggcg	3660
gctttgttga ataaatcgaa cttttgctga gttgaaggat cagatcacgc atcttcccga	3720
caacgcagac cgttccgtgg caaagcaaaa gttcaaaatc accaactggg ccacctacaa	3780
caaagctctc atcaaccgtg gctccctcac tttctggctg gatgatgggg cgattcaggc	3840
ctggtatgag tcagcaacac cttcttcacg aggcagacct cagcgctcaa agatgcaggg	3900
gtaaaagcta accgcatctt taccgacaag gcatccggca gttcaacaga tcgggaagg	3960
ctggatttgc tgaggatgaa ggtggaggaa ggtgatgtca ttctggtgaa gaagctcgac	4020
cgtcttggcc gcgacacgcc gacatgatcc aactgataaa agagtttgat gctcaggggtg	4080
tagcggttcg gtttattgac gacgggatca gtaccgacgg tgatatgggg caaatggtgg	4140
tcaccatcct gtcggctgtg gcacaggctg aacgccggag ga	4182

<210> 122
<211> 10
<212> PRT
<213> Hepatitis C Virus

<400> 122

Val Ala Thr Asp Ala Leu Met Thr Gly Tyr
1 5 10

<210> 123
<211> 10
<212> PRT
<213> Hepatitis C Virus

<400> 123

Phe Thr Asp Asn Ser Ser Pro Pro Ala Val
1 5 10

<210> 124
<211> 10
<212> PRT
<213> Hepatitis C Virus

<400> 124

Leu Val Asp Ile Leu Ala Gly Tyr Gly Ala
1 5 10

<210> 125
<211> 9
<212> PRT
<213> Hepatitis C Virus

<400> 125

Ala Thr Asp Ala Leu Met Thr Gly Tyr
1 5

<210> 126
<211> 9
<212> PRT
<213> Hepatitis C Virus

<400> 126

Phe Thr Asp Asn Ser Ser Pro Pro Ala
1 5

<210> 127
<211> 9
<212> PRT
<213> Hepatitis C Virus

<400> 127

Ala Thr Asp Ala Leu Met Thr Gly Phe
1 5

<210> 128

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> Polyepitope Construct

<400> 128

Gln Ile Val Gly Gly Val Tyr Leu Leu Asn Ser Met Val Gly Asn Trp
1 5 10 15

Ala Lys Val Gly Ala Ala Ala Tyr Leu Val Thr Arg His Ala Asp Val
20 25 30

Asn Ser Val Phe Thr Gly Leu Thr His Ile Gly Ala Ala Cys Leu Val
35 40 45

Asp Tyr Pro Tyr Arg Leu Gly Ala Ala Ala Tyr Leu Leu Pro Arg Arg
50 55 60

Gly Pro Arg Leu Asn Tyr Leu Val Ala Tyr Gln Ala Thr Val Asn Gly
65 70 75 80

Met Phe Asp Ser Ser Val Leu Cys Gly Ala Ala Ala Gln Met Trp Lys
85 90 95

Cys Leu Ile Arg Leu Asn Ala Leu Leu Phe Asn Ile Leu Gly Gly Trp
100 105 110

Val Lys Arg Leu Gly Ala Val Gln Asn Glu Val Asn Ala His Met Trp
115 120 125

Asn Phe Ile Ser Gly Ile Asn Ala Ala Ala Lys Phe Val Ala Ala Trp
130 135 140

Thr Leu Lys Ala Ala Ala Lys Thr Leu Trp Ala Arg Met Ile Leu Met
145 150 155 160

Asn Ala Tyr Leu Phe Asn Trp Ala Val Arg Thr Asn Lys Leu Gln Asp
165 170 175

Cys Thr Met Leu Val
180

<210> 129
<211> 543
<212> DNA
<213> Artificial Sequence

<220>
<223> Polyepitope Construct

<400> 129
cagatcgtgg gaggcgtgta cctgctcaac tccatgggtg gcaactgggc caaggtggga 60
gccgcagcct acctggtgac cagacacgca gacgtgaaca gcgtgttcac cggcctcact 120
cacatcggcg ctgcctgcct cgtggattac ccttatcggc tgggagccgc tgcttacctg 180
ctccccagac ggggaccccg gctgaactac ctggtggcat accaggccac cgtcaacgga 240
atgtttgaca gcagcgtgct gtgcggcgcc gcagcccaga tgtggaaatg cctgatcagg 300
ctgaacgctc tgctgttcaa cattctgggc ggatgggtca agagactggg agccgtgcaa 360
aatgaggtga acgcccacat gtggaacttc atcagcggca tcaacgccgc agccaagttc 420
gtggccgcat ggaccctgaa ggccgcagcc aagaccctgt gggccagaat gatcctgatg 480
aacgcctacc tgttcaactg ggccgtcaga acaaacaaac tccaggactg caccatgctg 540
gtg 543

<210> 130
<211> 178
<212> PRT
<213> Artificial Sequence

<220>
<223> Polyepitope Construct

<400> 130

Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Asn Asp Leu Met Gly Tyr
1 5 10 15

Ile Pro Leu Val Asn Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Gly
20 25 30

Phe Leu Leu Leu Ala Asp Ala Arg Val Gly Ala Ala Lys Val Leu Val
35 40 45

Leu Asn Pro Ser Val Gly Ala Ala Ala Tyr Ile Pro Leu Val Gly Ala
50 55 60

Pro Leu Lys Phe Leu Leu Ala Leu Leu Ser Cys Leu Asn Gly Leu Leu

65		70		75		80
Gly Cys Ile Ile Thr Ser Leu Gly Tyr Gln Ala Thr Val Cys Ala Arg						
		85		90		95
Ala Lys Val Leu Val Gly Gly Val Leu Ala Ala Leu Asn His Met Trp						
	100		105		110	
Asn Phe Ile Ser Gly Ile Asn Ala Ala Lys Phe Val Ala Ala Trp						
	115		120		125	
Thr Leu Lys Ala Ala Ala Lys Asn Ile Ile Met Tyr Ala Pro Thr Leu						
	130		135		140	
Lys Ala Ala Ala Ile Leu Ala Gly Tyr Gly Ala Gly Val Asn Ala Ala						
145		150		155		160
Leu Tyr Asp Val Val Ser Thr Leu Asn Thr Leu His Gly Pro Thr Pro						
	165		170		175	
Leu Leu						

<210> 131
 <211> 534
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polyepitope Construct

<400> 131	
tatctgctcc ccagacgggg acctaggctg aacgacctga tgggatacat ccctctggtc	60
aatgcctacc tgaacacacc cggcctgccc gtgggcttcc tgcctctggc cgacgctaga	120
gtgggagccg ctaaggtgct ggtcctcaac cccagcgtgg gagccgcagc ctacattccc	180
ctgggtgggc caccctgaa gttcctgctc gctctgctca gctgcctgaa cggactgctc	240
ggctgcatca tcactagcct gggctaccag gctaccgtct gcgccagagc aaaagtgtg	300
gtcggaggcg tgcctggccgc actgaaccac atgtggaact ttatctccgg catcaacgca	360
gccgcaaagt tcgtggccgc atggaccctg aaagccgcag ccaagaacat catcatgtac	420
gctcccaccc tgaaggccgc cgccatcctg gccggatacg gcgccggagt gaacgccgcc	480
ctgtacgatg tggtagcac actgaacacc ctgcacggcc ccacccact gctg	534

<210> 132
 <211> 175

<212> PRT
<213> Artificial Sequence

<220>
<223> Polyepitope Construct

<400> 132

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

Arg Ser Gln Pro Arg Asn Leu Val Asn Ala Trp Lys Ser Lys Lys Asn
20 25 30

Arg Val Cys Glu Lys Met Ala Leu Tyr Asn Ala Ala Ser Thr Asn Pro
35 40 45

Lys Pro Gln Arg Lys Asn Ala Val Cys Thr Arg Gly Val Ala Lys Asn
50 55 60

Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Lys Ala Lys Val Leu Val Asp
65 70 75 80

Ile Leu Ala Gly Tyr Asn Ala Ser Ala Ala Cys Arg Ala Ala Lys Lys
85 90 95

His Leu Ile Phe Cys His Ser Lys Lys Lys Lys Ala Lys Phe Val Ala
100 105 110

Ala Trp Thr Leu Lys Ala Ala Ala Lys Ala Ala Ala Arg Leu Gly Val
115 120 125

Arg Ala Thr Arg Lys Asn Gly Val Val Cys Ala Ala Ile Leu Arg Arg
130 135 140

Asn Arg Val Phe Thr Glu Ala Met Thr Arg Asn His Leu His Ala Pro
145 150 155 160

Thr Gly Ser Gly Lys Lys Arg Leu Leu Ala Pro Ile Thr Ala Tyr
165 170 175

<210> 133
<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> Polyepitope Construct

<400> 133

Pro Thr Leu Trp Asn Ala Ala Ala Phe Trp Ala Lys His Met Trp Asn
130 135 140

Phe Ile Lys Ala Ala Ala Arg Val Glu Phe Leu Val Asn Ala Trp Asn
145 150 155 160

Ala Ala Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Asn Ala
165 170 175

Ala Ala Gln Tyr Leu Ala Gly Leu Ser Thr Leu Asn Thr Leu His Gly
180 185 190

Pro Thr Pro Leu Leu
195

<210> 135
<211> 591
<212> DNA
<213> Artificial Sequence

<220>
<223> Polyepitope Construct

<400> 135
gtgatcaagg gaggacgtca cctgatcaag gccgcagctt gcctcattcg gctgaagcca 60
actctgaacg ccgctagctt ctcaatcttt cttctggcac ttaagtatct gaatacgcct 120
ggctctccctg taaacgcaat gtacacaaac gttgaccagg atttgaacgc tgctgcgacc 180
tacagtacat atggaaagtt cctgaaagct gcgtactata gagggctaga cgtgtctgtc 240
atcaaggcag cagccttatt gcccaggcga gggcccagac tgggtgccgc tgtcatgggc 300
agctcctatg gctttaatgc cgcagccaag ttcgttgctg cctggactct gaaggctgcc 360
gctaagaaca tcattatgta cgctcccacc ctgtggaatg cagctgcatt ctgggctaaa 420
catatgtgga atttcatcaa agccgctgcg aggggtggagt ttctcgtgaa tgccctggaat 480
gccgcgttgt gggctcgcat gatcctcatg acccatttct tcaacgccgc agcccaatac 540
ctggcaggcc tttccaccct gaacactctg cacggaccga caccactgct c 591

<210> 136
<211> 665
<212> PRT
<213> Artificial Sequence

<220>
<223> Polyepitope Construct

<400> 136

Val Ile Lys Gly Gly Arg His Leu Ile Lys Ala Gly Pro Arg Leu Gly

1	5				10				15						
Val	Arg	Ala	Thr 20	Lys	Ala	Ala	Ala	Gln 25	Tyr	Leu	Ala	Gly	Leu 30	Ser	Thr
Leu	Asn	Ala 35	Ala	Ala	Pro	Thr	Leu 40	Trp	Ala	Arg	Met	Ile 45	Leu	Asn	Ala
Ala	His 50	Pro	Asn	Ile	Glu	Glu 55	Val	Ala	Leu	Asn	Leu 60	Val	Asp	Ile	Leu
Ala 65	Gly	Tyr	Gly	Ala	Lys 70	His	Met	Trp	Asn	Phe 75	Ile	Ser	Gly	Ile	Asn 80
Ala	Tyr	Tyr	Arg	Gly 85	Leu	Asp	Val	Ser	Val 90	Lys	Leu	Gln	Asp	Cys 95	Thr
Met	Leu	Val	Asn 100	Ala	Ala	Ala	Ala	Glu 105	Gln	Phe	Lys	Gln	Lys 110	Ala	Leu
Lys	Thr	Ser 115	Glu	Arg	Ser	Gln	Pro 120	Arg	Asn	Ala	Ala	Phe	Pro	Tyr	Leu
Val 130	Ala	Tyr	Gln	Ala	Lys	Ala 135	Ala	Met	Tyr	Thr	Asn 140	Val	Asp	Gln	Asp
Leu 145	Asn	Thr	Leu	Trp	Ala 150	Arg	Met	Ile	Leu	Met 155	Asn	Leu	Pro	Ile	Asn 160
Ala	Leu	Ser	Asn	Ser 165	Leu	Lys	Ser	Thr	Asn 170	Pro	Lys	Pro	Gln	Arg 175	Lys
Asn	Asp	Tyr	Pro 180	Tyr	Arg	Leu	Trp	His 185	Tyr	Lys	Ala	Ala	Cys 190	Leu	Ile
Arg	Leu	Lys 195	Pro	Thr	Leu	Asn	Ile 200	Ile	Met	Tyr	Ala	Pro 205	Thr	Leu	Lys
Ala	Ala	Val	Ala	Thr	Asp	Ala 215	Leu	Met	Thr	Gly	Tyr 220	Asn	Leu	Pro	Gly
Cys 225	Ser	Phe	Ser	Ile	Phe 230	Lys	Tyr	Arg	Arg	Cys 235	Arg	Ala	Ser	Gly	Val 240
Leu	Lys	Ala	Ala	Val 245	Leu	Val	Gly	Gly	Val 250	Leu	Ala	Ala	Leu	Asn 255	Gly

Leu Leu Gly Cys Ile Ile Thr Ser Leu Asn Ala Ala Tyr Ala Ala Gln
260 265 270

Gly Tyr Lys Lys Asp Pro Arg Arg Arg Ser Arg Asn Leu Lys Ala Ala
275 280 285

Ala Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Asn Phe Trp Ala Lys
290 295 300

His Met Trp Asn Phe Ile Lys Ala Ala Ala Lys Phe Val Ala Ala Trp
305 310 315 320

Thr Leu Lys Ala Ala Ala Lys Ala Leu Ile Arg Leu Lys Pro Thr Leu
325 330 335

His Lys Ala Ala Ala Val Cys Thr Arg Gly Val Ala Lys Asn Phe Thr
340 345 350

Asp Asn Ser Ser Pro Pro Ala Val Lys Ala Leu Pro Arg Arg Gly Pro
355 360 365

Arg Leu Gly Val Lys Ser Phe Ser Ile Phe Leu Leu Ala Leu Lys Ala
370 375 380

Ala Glu Thr Ala Gly Ala Arg Leu Val Asn Ala Ala Gly Arg His Leu
385 390 395 400

Ile Phe Cys His Ser Lys Lys Lys Cys Asp Gly Pro Gly Pro Gly Ser
405 410 415

Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp Val Ala Ala Gln Gly Pro
420 425 430

Gly Pro Gly Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr
435 440 445

Phe Thr Ile Glu Thr Thr Gly Pro Gly Pro Gly Glu Asp Leu Val Asn
450 455 460

Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala Leu Val Val Gly Pro Gly
465 470 475 480

Pro Gly Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala Phe
485 490 495

Ala Ser Gly Pro Gly Pro Gly Met Asn Arg Leu Ile Ala Phe Ala Ser
500 505 510

Arg Gly Asn His Val Ser Pro Gly Pro Gly Pro Gly Ser Met Ser Tyr
515 520 525

Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala Gly Pro Gly Pro Gly
530 535 540

Thr Pro Ala Glu Thr Thr Val Arg Leu Arg Ala Tyr Met Asn Thr Pro
545 550 555 560

Gly Leu Pro Val Gly Pro Gly Pro Gly Ala Val Gly Ile Phe Arg Ala
565 570 575

Ala Val Cys Thr Arg Gly Val Ala Gly Pro Gly Pro Gly Gly Ile Gln
580 585 590

Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly Asn Pro Ala Gly Pro Gly
595 600 605

Pro Gly Thr Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu
610 615 620

Ala Ala Gly Pro Gly Pro Gly Gly Tyr Lys Val Leu Val Leu Asn Pro
625 630 635 640

Ser Val Ala Ala Thr Gly Pro Gly Pro Gly Gly Lys Pro Ala Ile Ile
645 650 655

Pro Asp Arg Glu Val Leu Tyr Arg Glu
660 665

<210> 137
<211> 1995
<212> DNA
<213> Artificial Sequence

<220>
<223> Polyepitope Construct

<400> 137
gtgatcaagg gcggcaggca cctgatcaag gccggacctc ggctgggctg gagggccaca 60
aaagccgctg cccagttacct ggccggcctg agcacactga atgccgctgc ccctaccctg 120
tgggcccga tgatcctgaa tgccgcccac cccaacatcg aggaagtggc cctgaacctg 180
gtggacatcc tggccggcta cggcgccaag catatgtgga acttcatcag cggcatcaac 240

gcctactacc	ggggcctgga	cgtgagcgtg	aagctccagg	actgcaccat	gctggtcaat	300
gctgccgctg	ccgagcagtt	caagcagaag	gccctgaaaa	ccagcgagcg	gagccagccc	360
cggaacgccg	ccttccttta	cctggtggcc	taccaggcca	aggccgccat	gtacaccaac	420
gtggaccagg	acctgaacac	actgtgggcc	agaatgattc	tgatgaacct	gcccataaac	480
gccctgagca	acagcctgaa	gagcaccaac	cccaagcccc	agcggaagaa	cgactacccc	540
taccggctgt	ggcactacaa	ggccgcctgc	ctgatccggc	tgaagcccac	cctgaacatc	600
atcatgtacg	ccccaacact	gaaggccgcc	gtggccaccg	acgccctgat	gaccggctac	660
aacctgcccg	gctgctcctt	cagcatcttc	aagtaccggc	ggtgccgggc	cagcggcgtg	720
ctcaaagctg	ccgtcctcgt	cgggggcgtg	ctggctgctc	tgaacggcct	gctgggctgc	780
atcatcacca	gcctgaacgc	cgctacgcc	gccagggct	acaagaagga	ccccaggcgg	840
cggagccgga	acctgaaggc	cgcagcctac	ctgctgcca	gaaggggccc	caggctgaac	900
ttctggggcca	aacacatgtg	gaatttcatt	aaggctgctg	ccaagtttgt	ggccgcctgg	960
acactgaaag	ctgccgcaa	ggccctgatc	agactgaagc	ctacactgca	caaggccgct	1020
gccgtgtgta	cacggggcgt	ggccaagaac	ttcaccgaca	acagcagccc	ccctgccgtg	1080
aaggccctgc	cccgcagagg	cccagactg	ggcgtgaaga	gcttctccat	cttcctgctg	1140
gccctgaaag	ccgccgagac	cgccggagcc	cggttggtga	atgccgcggg	acggcacctg	1200
atcttttgcc	acagcaagaa	gaagtgcgac	ggcccaggcc	ctggcagcac	cctgctgttc	1260
aacatcctgg	gcggatgggt	ggccgcccag	ggaccggggc	caggatgcgt	gaccagacc	1320
gtggacttca	gcctggaccc	caccttcacc	atcgagacca	caggcccagg	gccaggggag	1380
gacctggtca	atctgctgcc	tgccatcctg	agccctggcg	ccctggtggt	gggcccagga	1440
ccaggcggag	agggcgccgt	gcagtggatg	aaccggctga	tcgccttcgc	cagcggacct	1500
ggccctggca	tgaacagact	gattgccttt	gcctcccggg	gcaaccacgt	gagccctgga	1560
cctggacccg	ggagcatgag	ctacacctgg	acaggcgccc	tgattacccc	ctgcgccgga	1620
cctggaccag	gcacccctgc	cgagaccaca	gtgcggctgc	gggcctacat	gaacaccctt	1680
ggcctgcccg	tgggacctgg	gccaggggcc	gtgggcatct	tcagagccgc	cgtgtgtacc	1740
agaggggtgg	ccggaccagg	gccaggcggc	atccagtatc	tggccgggct	gtctaccctg	1800
cccggcaacc	ctgccggccc	aggacccggc	acctccacct	gggtgctggt	cgggggagtg	1860
ctggccgccc	tggccgcggg	acccggacct	ggcggtctaca	aggtgctggt	gctgaacccc	1920
agcgtggccc	ccaccggggc	tggacctggg	ggcaagcctg	ccatcatccc	cgaccgggag	1980
gtgctgtacc	gggag					1995

<210> 138
<211> 301
<212> PRT
<213> Artificial Sequence

<220>
<223> Polyepitope Construct

<400> 138

Asn Ile Ile Met Tyr Ala Pro Thr Leu Lys Ala Ala Lys Phe Val Ala
1 5 10 15

Ala Trp Thr Leu Lys Ala Ala Ala Lys Cys Leu Ile Arg Leu Lys Pro
20 25 30

Thr Leu Asn Ala Ala Ala Lys Thr Ser Glu Arg Ser Gln Pro Arg Asn
35 40 45

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

Ser Pro Pro Ala Val Lys Ala Val Cys Thr Arg Gly Val Ala Lys Asn
65 70 75 80

Ala Ala Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Asn Ala Val Ala
85 90 95

Thr Asp Ala Leu Met Thr Gly Tyr Asn Ala Ala Ser Phe Ser Ile Phe
100 105 110

Leu Leu Ala Leu Lys His Leu Ile Phe Cys His Ser Lys Lys Asn Val
115 120 125

Leu Val Gly Gly Val Leu Ala Ala Leu Asn Ser Thr Asn Pro Lys Pro
130 135 140

Gln Arg Lys Asn Val Ile Lys Gly Gly Arg His Leu Ile Lys Ala Ala
145 150 155 160

Tyr Ala Ala Gln Gly Tyr Lys Lys Ala Ala Leu Pro Ile Asn Ala Leu
165 170 175

Ser Asn Ser Leu Lys Ala His Met Trp Asn Phe Ile Ser Gly Ile Asn
180 185 190

Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Asn Tyr Arg Arg Cys Arg
195 200 205

Ala Ser Gly Val Leu Lys Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val
 210 215 220

Lys Ala Ala Leu Val Asp Ile Leu Ala Gly Tyr Gly Ala Lys Ala Met
 225 230 235 240

Tyr Thr Asn Val Asp Gln Asp Leu Asn Phe Trp Ala Lys His Met Trp
 245 250 255

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

Leu Gln Asp Cys Thr Met Leu Val Asn Gln Tyr Leu Ala Gly Leu Ser
 275 280 285

Thr Leu Asn Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu
 290 295 300

<210> 139
 <211> 903
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polyepitope Construct

<400> 139
 aacatcataa tgtacgcacc cacactgaaa gcagctaaat tcgtcgccgc atggaccctg 60
 aaagccgcag ctaaattgcct gatccgtctg aagccaactc tcaatgccgc tgccaagact 120
 tccgagagga gtcaacctag gaacttgcca cgccgaggac caagactcgg agtgaagtgc 180
 accgacaaca gtagccctcc ggctgtcaag gccgtatgca ctgcgcggcgt agccaagaac 240
 gctgccgctc ccacactgtg ggctaggatg atactgaacg cgggtggccac agatgcactc 300
 atgacaggct ataatgcggc atccttctca atctttcttc tcgccttgaa gcatttgatc 360
 ttctgccatt ccaagaagaa cgttcttgtc ggtggcgtgc tcgctgcact gaatagcact 420
 aacccaaagc ctgagcggaa gaatgtcatc aagggaggca gacacttgat caaggccgct 480
 tatgccgctc aagggataaa gaaagctgca ctgcccataa atgcactatc taactcgctt 540
 aaggcccaca tgtggaattt catctctggc attaactact tactgcctag acgcggtccc 600
 aggctaaatt accgtogatg tagagcctcc ggagtgtgta aggcatacta tcgcggactc 660
 gacgtgagcg tgaaagctgc actggttgac attctggctg ggtacggagc caaagctatg 720
 tacaccaacg tggatcaaga cctgaacttc tgggcaaagc acatgtggaa tttcattaaa 780

```

gccacgctgt gggccagaat gatcctgatg aacaagctcc aggattgtac gatgcttgtt      840
aaccagtact tggcagggct ttcaaccctg aacgggtctat taggatgtat cattaccagc      900
ctg                                                                           903

```

```

<210> 140
<211> 310
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Polypeptide Construct

```

```

<400> 140

```

```

Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Lys His Leu Ile Phe Cys
1           5           10           15

```

```

His Ser Lys Lys Asn Val Ile Lys Gly Gly Arg His Leu Ile Lys Ala
          20           25           30

```

```

Ala Ala Cys Leu Ile Arg Leu Lys Pro Thr Leu Asn Ala Ala Ser Phe
          35           40           45

```

```

Ser Ile Phe Leu Leu Ala Leu Lys Leu Val Asp Ile Leu Ala Gly Tyr
          50           55           60

```

```

Gly Ala Lys Ala Ala Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Lys
65           70           75           80

```

```

Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Lys Ala Ala Pro Thr Leu
          85           90           95

```

```

Trp Ala Arg Met Ile Leu Asn Ala Lys Leu Gln Asp Cys Thr Met Leu
          100          105          110

```

```

Val Asn Ala Ala Ala Ser Thr Asn Pro Lys Pro Gln Arg Lys Asn Ala
          115          120          125

```

```

Val Cys Thr Arg Gly Val Ala Lys Asn Ala Met Tyr Thr Asn Val Asp
          130          135          140

```

```

Gln Asp Leu Asn Ala Ala Lys Thr Ser Glu Arg Ser Gln Pro Arg
145           150           155           160

```

```

Asn Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Lys Val Ala Thr Asp
          165          170          175

```

Ala Leu Met Thr Gly Tyr Asn Ala Ala Phe Trp Ala Lys His Met Trp
180 185 190

Asn Phe Ile Lys Ala Ala Gln Tyr Leu Ala Gly Leu Ser Thr Leu Asn
195 200 205

Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Lys Ala Ala Tyr Ala Ala
210 215 220

Gln Gly Tyr Lys Lys Ala Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu
225 230 235 240

Asn Thr Leu Trp Ala Arg Met Ile Leu Met Asn Gly Leu Leu Gly Cys
245 250 255

Ile Ile Thr Ser Leu Asn His Met Trp Asn Phe Ile Ser Gly Ile Asn
260 265 270

Ala Ala Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala Lys
275 280 285

Asn Ile Ile Met Tyr Ala Pro Thr Leu Lys Ala Ala Val Leu Val Gly
290 295 300

Gly Val Leu Ala Ala Leu
305 310

<210> 141
<211> 930
<212> DNA
<213> Artificial Sequence

<220>
<223> Polyepitope Construct

<400> 141
ctccacgga gaggccctcg gcttggcgtg aagcacttaa tcttctgtca cagtaagaag 60
aacgtgatca aggggtgggag gcatctaatac aaagccgcag cttgcctgat ccggttgaag 120
ccaaccctca acgcgcgcatc tttctcaatac tttctgctag cactgaagtt ggtcgatata 180
ttagccggat acggagccaa agccgcatac aggagatgcc gtgcgagtgg cgtgctcaag 240
ctgcccatac atgccttgag caacagcttg aaggctgcac ctacactgtg ggctaggatg 300
atcctgaacy ctaaaacttca ggactgtact atgctggtga atgcagccgc tagcaccaac 360
ccaaagcctc agcgtaagaa cgccgtgtgt actagaggcg ttgccaagaa tgctatgtat 420
actaatgtcg atcaagacct gaacgccgct gcgaagacgt ctgagagatc ccaaccagg 480

aacgcctact atagaggttt agacgtttcc gtcaaagtcg ccacagatgc tctgatgacc 540
 ggatataatg ccgcgttctg ggctaaacac atgtggaact tcattaaggc cgctcagtat 600
 cttgctggac tttcaaccct caactttacg gacaactcct ctctcccgc ggtgaaggct 660
 gcctacgcag ctcagggata taagaaagcc tacctgctcc cgagacgcgg acctcgcctt 720
 aataccctat gggctaggat gatcctcatg aatggcttgc tgggctgcat cattacttcg 780
 ctgaatcata tgtggaactt catcagcgga atcaacgccg ctgcaaagtt cgtggctgcc 840
 tggacattga aagcagctgc caagaacatt attatgtacg cgccaacact gaaggccgca 900
 gtactggttg gcggtgtact ggccgcactc 930

<210> 142
 <211> 177
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Polyepitope Construct

<400> 142

Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Lys Ala Ala Ile Pro Leu
 1 5 10 15

Val Gly Ala Pro Leu Lys Ala Ala Ser Pro Arg Gly Ser Arg Pro Ser
 20 25 30

Trp Lys Gln Pro Arg Gly Arg Arg Gln Pro Ile Lys Leu Pro Gly Cys
 35 40 45

Ser Phe Ser Ile Phe Lys His Pro Asn Ile Glu Glu Val Ala Leu Lys
 50 55 60

Ala Ala Lys Leu Ser Ala Leu Gly Leu Lys Ala Ile Pro Thr Ser Gly
 65 70 75 80

Asp Val Val Val Asn Leu Pro Val Cys Gln Asp His Leu Glu Phe Asn
 85 90 95

Ala Ala Ala Phe Pro Tyr Leu Val Ala Tyr Gln Ala Lys Asn Pro Ala
 100 105 110

Ile Ala Ser Leu Met Ala Phe Lys Glu Pro Glu Pro Asp Val Ala Val
 115 120 125

Leu Lys Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala Lys
 130 135 140

Glu Pro Asp Val Ala Val Leu Thr Ser Met Asn Leu Pro Ile Asn Ala
145 150 155 160

Leu Ser Asn Ser Leu Lys Ala Ala Pro Thr Leu Trp Ala Arg Met Ile
165 170 175

Leu

<210> 143
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> Polyepitope Construct

<400> 143
ctgccagaa gaggcctcg gctgggagtc aaggcagcca tccctctggt gggagcacct 60
ctgaaggcag ccagcccaag aggcagcaga ccaagctgga aacagcccag aggaagacgg 120
cagcccatca aactgcccgg ctgtagcttc agcatcttta agcatcccaa catcgaggaa 180
gtcgctctga aggcagccaa gctgagcgcc ctgggcctga aggctattcc taccagcggc 240
gacgtcgtgg tcaacctccc agtgtgccag gaccacctgg agttcaatgc cgctgcattc 300
ccttacctgg tggcatacca ggcaaagaac cctgccatcg ccagcctgat ggccttcaag 360
gagcccgagc ctgatgtggc agtgctcaag gccaaattcg tggccgcttg gaccctgaag 420
gccgccgcca aggagcccgga cgtggccgtg ctgaccagca tgaacctgcc catcaacgcc 480
ctctccaact ccctgaaagc cgcacccaca ctctgggccc ggatgatact g 531

<210> 144
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Polyepitope Construct

<400> 144

Asp Pro Arg Arg Arg Ser Arg Asn Leu Lys Ala Ala Gly Pro Arg Leu
1 5 10 15

Gly Val Arg Ala Thr Lys Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu
20 25 30

Asn Ala Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Lys Leu Pro Ala

35

40

45

Leu Ser Thr Gly Leu Ile Lys Ala Ala Thr Pro Gly Glu Arg Pro Ser
50 55 60

Gly Met Lys Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Lys Arg
65 70 75 80

Pro Ser Gly Met Phe Asp Ser Ser Val Lys Ala Pro Pro Pro Ser Trp
85 90 95

Asp Gln Met Lys Pro Thr Leu His Gly Pro Thr Pro Leu Asn Ala Gly
100 105 110

Pro Thr Pro Leu Leu Tyr Arg Leu Asn Ala Ala Leu Pro Ala Ile Leu
115 120 125

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

Ala Ala Ser Ala Ala Cys Arg Ala Ala Lys Leu Lys Ala Lys Phe Val
145 150 155 160

Ala Ala Trp Thr Leu Lys Ala Ala Ala Lys Ala Pro Pro Val Val His
165 170 175

Gly Cys Pro Leu Asn Ala Ala Ala Pro Thr Leu Trp Ala Arg Met Ile
180 185 190

Leu

<210> 145

<211> 579

<212> DNA

<213> Artificial Sequence

<220>

<223> Polyepitope Construct

<400> 145

gaccctagac ggaggtcccg gaacctgaag gcagccggac ccagactggg cgtcagagcc 60

accaaggcac ctctgggagg cgccgctcgg gccctgaacg ccctgcccag gagaggacct 120

agactcggcg tgaagctgcc cgactgagc actggactga tcaaggccgc aacacccggc 180

gagagaccaa gcggcatgaa agccgcttac gcagcccagg gctacaaggt gctgaagcgg 240

cccagcggaa tggtcgacag ctccgtgaag gctccacctc ccagctggga tcagatgaag 300

```

cccaccctgc acggaccac accactcaat gccgggccca ctccactcct gtacagactg      360
aacgccgcac tccctgctat cctgagccct ggcgccctca gacccgacta caatcctcca      420
ctgctcaagg ccgctgccag cgccgcatgc cgggccgcca aactgaaggc caagttcgtc      480
gccgcatgga ccctgaaagc agccgccaaa gcccctcccg tgggtgcacgg ctgcccactg      540
aacgccgccg ctcccaccct gtggggcccg atgatacctg      579

```

```

<210> 146
<211> 665
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Polypeptide Construct

```

```

<400> 146

```

```

Val Ile Lys Gly Gly Arg His Leu Ile Lys Ala Gly Pro Arg Leu Gly
1           5           10           15

```

```

Val Arg Ala Thr Lys Ala Ala Ala Gln Tyr Leu Ala Gly Leu Ser Thr
           20           25           30

```

```

Leu Asn Ala Ala Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Asn Ala
           35           40           45

```

```

Ala His Pro Asn Ile Glu Glu Val Ala Leu Asn Leu Val Asp Ile Leu
           50           55           60

```

```

Ala Gly Tyr Gly Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile Asn
           65           70           75           80

```

```

Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Lys Leu Gln Asp Cys Thr
           85           90           95

```

```

Met Leu Val Asn Ala Ala Ala Ala Glu Gln Phe Lys Gln Lys Ala Leu
           100          105          110

```

```

Lys Thr Ser Glu Arg Ser Gln Pro Arg Asn Ala Ala Phe Pro Tyr Leu
           115          120          125

```

```

Val Ala Tyr Gln Ala Lys Ala Ala Met Tyr Thr Asn Val Asp Gln Asp
           130          135          140

```

```

Leu Asn Thr Leu Trp Ala Arg Met Ile Leu Met Asn Leu Pro Ile Asn
           145          150          155          160

```

Ala Leu Ser Asn Ser Leu Lys Ser Thr Asn Pro Lys Pro Gln Arg Lys
165 170 175

Asn Asp Tyr Pro Tyr Arg Leu Trp His Tyr Lys Ala Ala Cys Leu Ile
180 185 190

Arg Leu Lys Pro Thr Leu Asn Ile Ile Met Tyr Ala Pro Thr Leu Lys
195 200 205

Ala Ala Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Asn Leu Pro Gly
210 215 220

Cys Ser Phe Ser Ile Phe Lys Tyr Arg Arg Cys Arg Ala Ser Gly Val
225 230 235 240

Leu Lys Ala Ala Val Leu Val Gly Gly Val Leu Ala Ala Leu Asn Gly
245 250 255

Leu Leu Gly Cys Ile Ile Thr Ser Leu Asn Ala Ala Tyr Ala Ala Gln
260 265 270

Gly Tyr Lys Lys Asp Pro Arg Arg Arg Ser Arg Asn Leu Lys Ala Ala
275 280 285

Ala Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Asn Phe Trp Ala Lys
290 295 300

His Met Trp Asn Phe Ile Lys Ala Ala Ala Lys Phe Val Ala Ala Trp
305 310 315 320

Thr Leu Lys Ala Ala Ala Lys Ala Leu Ile Arg Leu Lys Pro Thr Leu
325 330 335

His Lys Ala Ala Ala Val Cys Thr Arg Gly Val Ala Lys Asn Phe Thr
340 345 350

Asp Asn Ser Ser Pro Pro Ala Val Lys Ala Leu Pro Arg Arg Gly Pro
355 360 365

Arg Leu Gly Val Lys Ser Phe Ser Ile Phe Leu Leu Ala Leu Lys Ala
370 375 380

Ala Glu Thr Ala Gly Ala Arg Leu Val Asn Ala Ala Gly Arg His Leu
385 390 395 400

Ile Phe Cys His Ser Lys Lys Lys Cys Asp Gly Pro Gly Pro Gly Ser
405 410 415

Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp Val Ala Ala Gln Gly Pro
420 425 430

Gly Pro Gly Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr
435 440 445

Phe Thr Ile Glu Thr Thr Gly Pro Gly Pro Gly Glu Asp Leu Val Asn
450 455 460

Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala Leu Val Val Gly Pro Gly
465 470 475 480

Pro Gly Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala Phe
485 490 495

Ala Ser Gly Pro Gly Pro Gly Met Asn Arg Leu Ile Ala Phe Ala Ser
500 505 510

Arg Gly Asn His Val Ser Pro Gly Pro Gly Pro Gly Ser Met Ser Tyr
515 520 525

Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala Gly Pro Gly Pro Gly
530 535 540

Thr Pro Ala Glu Thr Thr Val Arg Leu Arg Ala Tyr Met Asn Thr Pro
545 550 555 560

Gly Leu Pro Val Gly Pro Gly Pro Gly Ala Val Gly Ile Phe Arg Ala
565 570 575

Ala Val Cys Thr Arg Gly Val Ala Gly Pro Gly Pro Gly Gly Ile Gln
580 585 590

Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly Asn Pro Ala Gly Pro Gly
595 600 605

Pro Gly Thr Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu
610 615 620

Ala Ala Gly Pro Gly Pro Gly Gly Tyr Lys Val Leu Val Leu Asn Pro
625 630 635 640

Ser Val Ala Ala Thr Gly Pro Gly Pro Gly Gly Lys Pro Ala Ile Ile

645

650

655

Pro Asp Arg Glu Val Leu Tyr Arg Glu
660 665

<210> 147

<211> 664

<212> PRT

<213> Artificial Sequence

<220>

<223> Polyepitope Construct

<400> 147

Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp Gly Pro
1 5 10 15

Gly Pro Gly Ser Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp Val Ala
20 25 30

Ala Gln Gly Pro Gly Pro Gly Cys Val Thr Gln Thr Val Asp Phe Ser
35 40 45

Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Gly Pro Gly Pro Gly Glu
50 55 60

Asp Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala Leu Val
65 70 75 80

Val Gly Pro Gly Pro Gly Gly Glu Gly Ala Val Gln Trp Met Asn Arg
85 90 95

Leu Ile Ala Phe Ala Ser Gly Pro Gly Pro Gly Met Asn Arg Leu Ile
100 105 110

Ala Phe Ala Ser Arg Gly Asn His Val Ser Pro Gly Pro Gly Pro Gly
115 120 125

Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala Gly
130 135 140

Pro Gly Pro Gly Thr Pro Ala Glu Thr Thr Val Arg Leu Arg Ala Tyr
145 150 155 160

Met Asn Thr Pro Gly Leu Pro Val Gly Pro Gly Pro Gly Ala Val Gly
165 170 175

Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Gly Pro Gly Pro
180 185 190

Gly Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly Asn Pro
195 200 205

Ala Gly Pro Gly Pro Gly Thr Ser Thr Trp Val Leu Val Gly Gly Val
210 215 220

Leu Ala Ala Leu Ala Ala Gly Pro Gly Pro Gly Gly Tyr Lys Val Leu
225 230 235 240

Val Leu Asn Pro Ser Val Ala Ala Thr Gly Pro Gly Pro Gly Gly Lys
245 250 255

Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu Lys Ala Val
260 265 270

Ile Lys Gly Gly Arg His Leu Ile Lys Ala Gly Pro Arg Leu Gly Val
275 280 285

Arg Ala Thr Lys Ala Ala Ala Gln Tyr Leu Ala Gly Leu Ser Thr Leu
290 295 300

Asn Ala Ala Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Asn Ala Ala
305 310 315 320

His Pro Asn Ile Glu Glu Val Ala Leu Asn Leu Val Asp Ile Leu Ala
325 330 335

Gly Tyr Gly Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile Asn Ala
340 345 350

Tyr Tyr Arg Gly Leu Asp Val Ser Val Lys Leu Gln Asp Cys Thr Met
355 360 365

Leu Val Asn Ala Ala Ala Ala Glu Gln Phe Lys Gln Lys Ala Leu Lys
370 375 380

Thr Ser Glu Arg Ser Gln Pro Arg Asn Ala Ala Phe Pro Tyr Leu Val
385 390 395 400

Ala Tyr Gln Ala Lys Ala Ala Met Tyr Thr Asn Val Asp Gln Asp Leu
405 410 415

Asn Thr Leu Trp Ala Arg Met Ile Leu Met Asn Leu Pro Ile Asn Ala

420		425		430
Leu Ser Asn Ser Leu Lys Ser Thr Asn Pro Lys Pro Gln Arg Lys Asn	435	440		445
Asp Tyr Pro Tyr Arg Leu Trp His Tyr Lys Ala Ala Cys Leu Ile Arg	450	455		460
Leu Lys Pro Thr Leu Asn Ile Ile Met Tyr Ala Pro Thr Leu Lys Ala	465	470		475
Ala Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Asn Leu Pro Gly Cys	485	490		495
Ser Phe Ser Ile Phe Lys Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu	500	505		510
Lys Ala Ala Val Leu Val Gly Gly Val Leu Ala Ala Leu Asn Gly Leu	515	520		525
Leu Gly Cys Ile Ile Thr Ser Leu Asn Ala Ala Tyr Ala Ala Gln Gly	530	535		540
Tyr Lys Lys Asp Pro Arg Arg Arg Ser Arg Asn Leu Lys Ala Ala Ala	545	550		555
Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Asn Phe Trp Ala Lys His	565	570		575
Met Trp Asn Phe Ile Lys Ala Ala Ala Lys Phe Val Ala Ala Trp Thr	580	585		590
Leu Lys Ala Ala Ala Lys Ala Leu Ile Arg Leu Lys Pro Thr Leu His	595	600		605
Lys Ala Ala Ala Val Cys Thr Arg Gly Val Ala Lys Asn Phe Thr Asp	610	615		620
Asn Ser Ser Pro Pro Ala Val Lys Ala Leu Pro Arg Arg Gly Pro Arg	625	630		635
Leu Gly Val Lys Ser Phe Ser Ile Phe Leu Leu Ala Leu Lys Ala Ala	645	650		655
Glu Thr Ala Gly Ala Arg Leu Val	660			

<210> 148
<211> 1995
<212> DNA
<213> Artificial Sequence

<220>
<223> Polypeptide Construct

<400> 148
gtgattaaag gcggccgtca tctgattaaa gcgggtccac gcctgggtgt tctgtcgacc 60
aaagccgcag cgcagtatct ggccggtctg agcaccctga atgcggcagc gccgacgctg 120
tgggcgcgta tgattctgaa cgcggcgcat ccgaacattg aagaagtggc gctgaacctg 180
gtggatatctc tggccggcta tggcgcaaaa catatgtgga actttatcag cggcatcaac 240
gcgtattatc gtggcctgga tgtgagcgtg aaactgcagg attgcaccat gctggtgaat 300
gcggccgcag cggaacagtt taaacagaaa gcgctgaaaa ccagcgaacg tagccagccg 360
cgtaacgcgg cgtttccgta tctggtggcg tatcaggcga aagcggcgat gtataccaac 420
gtggatcagg atctgaacac cctgtgggcc cgcattgatc tgatgaacct gccgattaac 480
gccctgagca acagcctgaa aagcaccaat ccgaaaccgc agcgtaaaaa cgattatccg 540
tatcgccctgt ggcattataa agcggcgtgc ctgattcgtc tgaaaccaac tctgaacatt 600
attatgtatg ccccgacgct gaaagcagcc gttgcgaccg atgcgctgat gaccggctat 660
aacctgccgg gctgcagctt tagcattttt aaatatcgtc gttgccgtgc gagcggcggt 720
ctgaaagctg cgggtgctggt tgggtggtgt ctggccgcgc tgaacgggtc gctgggctgc 780
attattacca gcctgaacgc ggcctatgcg gcgcagggct ataaaaaaga tccgcgtcgt 840
cgtagccgta acctgaaagc agcggcgat ctgctgccgc gccgtggccc gcgtctgaac 900
ttttgggcga aacacatgtg gaatttcatt aaagccgcgg ccaaatttgt ggcggcgtgg 960
accctgaaag ccgccgcgaa agcgtgatc cgctgaaac cgaccctgca taaagcggca 1020
gcggtgtgca cccgtggcgt ggcgaaaaac tttaccgata acagctctcc gccggcagtt 1080
aaagccctgc cgcgtcgcgg tccgcgcctg ggcgtgaaat ctttttagcat ctttctgctg 1140
gccctgaaag cggcggaac cgcggtgctg cgtctggtta atgcggcggg ccgtcatctg 1200
atTTTTTgcc acagcaaaaa aaaatgcgat gggccgggtc ctggtagcac cctgctgttt 1260
aacattctgg gcggctgggt tgcggcgcag ggtccaggtc cgggctgtgt taccagacc 1320
gtggatttta gcctggacct gaccttacc attgaaacca ctgggccagg tctggggag 1380
gacctggtga acctgctgcc ggcgattctg tctccgggtg cgctggttgt tgggtccaggt 1440
ccgggggggtg aaggtgcggt gcagtggatg aaccgtctga ttgcgtttgc gtctggtcca 1500

gggccaggta tgaaccgcct gatcgcggtc gccagccgtg gcaaccatgt ttctccgggt	1560
ccagggccag gtagcatgag ctatacctgg accggtgcgc tgattacccc gtgtgcagggt	1620
ccagggccgg gtacgccggc ggaaaccacc gttcgtctgc gtgcgtatat gaacacgccg	1680
ggctctgccg tgggtccagg tccagggtgcg gtgggcattt ttcgtgcggc ggtgtgcacc	1740
cgtggtgttg caggcccagg tccaggggggt attcagtatc tggccggcct gagcacccctg	1800
ccgggtaatc cggcgggtcc ggggtccaggc acctctacct ggggtgctggt tgggtggtgtt	1860
ctggccgcgc tggccgcagg tccgggtcca gggggctata aagtgtggt gctgaatccg	1920
agcgttgccg cgaccgggtcc ggggtccgggt ggtaaaccgg cgattattcc ggatcgtgaa	1980
gtgctgtatc gtgaa	1995

<210> 149
 <211> 1992
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polyepitope Construct

<400> 149	
ggccgtcatc tgatTTTTTg ccacagcaaa aaaaaatgcg atgggccggg tcctggtagc	60
accctgctgt ttaacattct gggcggctgg gttgcggcgc aggtccagg tccgggctgt	120
gttaccaga ccgtggattt tagcctggac ccgaccttta ccattgaaac cactgggcca	180
ggctcctggg aggaacctgt gaacctgctg ccggcgattc tgtctccggg tgcgctggtt	240
gttgggtccag gtccgggggg tgaagggtgcg gtgcagtgga tgaaccgtct gattgcgttt	300
gcgtctggtc cagggccagg tatgaaccgc ctgatcgctc tcgccagccg tggcaaccat	360
gtttctccgg gtccagggcc aggtagcatg agctatacct ggaccgggtgc gctgattacc	420
ccgtgtgcag gtccagggcc gggtagcccg gcggaaacca ccgttcgtct gcgtgcgtat	480
atgaacacgc cgggtctgcc ggtgggtcca ggtccagggt cgggtggcat ttttcgtgcg	540
gcggtgtgca cccgtggtgt tgcaggccca ggtccagggg gtattcagta tctggccggc	600
ctgagcacc tgccgggtaa tccggcgggt ccgggtccag gcacctctac ctgggtgctg	660
gttgggtggt ttctggccgc gctggccgca ggtccgggtc cagggggcta taaagtgtg	720
gtgctgaatc cgagcgttgc ggcgaccggc ccgggtccgg gtggtaaacc ggcgattatt	780
ccggatcgtg aagtgtgtg tctgaaaaa gcggtgatta aaggcggccg tcatctgatt	840
aaagcgggtc cacgcctggg tgttcgtgcg accaaagccg cagcgcagta tctggccgg	900
ctgagcacc tgaatgcggc agcgcgcacg ctgtgggcgc gtatgattct gaacgcggcg	960
catccgaaca ttgaagaagt ggcgctgaac ctggtggata ttctggccgg ctatggcgca	1020

aaacatatgt ggaactttat cagcggcatc aacgcgtatt atcgtggcct ggatgtgagc	1080
gtgaaactgc aggattgcac catgctggtg aatgcggccg cagcgaaca gtttaaacag	1140
aaagcgctga aaaccagcga acgtagccag ccgcgtaacg cggcgtttcc gtatctggtg	1200
gcgtatcagg cgaaagcggc gatgtatacc aacgtggatc aggatctgaa caccctgtgg	1260
gcccgcatga tcctgatgaa cctgccgatt aacgccctga gcaacagcct gaaaagcacc	1320
aatccgaaac cgcagcgtaa aaacgattat ccgtatcgcc tgtggcatta taaagcggcg	1380
tgcctgattc gtctgaaacc aactctgaac attattatgt atgccccgac gctgaaagca	1440
gccgttgcca ccgatgcgct gatgaccggc tataacctgc cgggctgcag ctttagcatt	1500
tttaaataatc gtcgttgccg tgcgagcggc gttctgaaag ctgcggtgct ggttggtggt	1560
gttctggccg cgctgaacgg tctgctgggc tgcattatta ccagcctgaa cgcggcctat	1620
gcggcgcagg gctataaaaa agatccgcgt cgtcgtagcc gtaacctgaa agcagcggcg	1680
tatctgctgc cgcgcgctgg cccgcgtctg aacttttggg cgaaacacat gtggaatttc	1740
attaaagccg cggccaaatt tgtggcggcg tggaccctga aagccgcgcg gaaagcgtg	1800
atccgcctga aaccgaccct gcataaagcg gcagcgggtg gcacccgtgg cgtggcgaaa	1860
aactttaccg ataacagctc tccgcggca gttaaagccc tgccgcgtcg cgggccgcgc	1920
ctgggcgtga aatcttttag catctttctg ctggccctga aagcggcgga aaccgcgggt	1980
gcgcgtctgg tt	1992

<210> 150
 <211> 9
 <212> PRT
 <213> Hepatitis C Virus

<400> 150

Leu	Ile	Arg	Leu	Lys	Pro	Thr	Leu	His
1				5				