01 SQ listing ST25 11-FEB-2010
SEQUENCE LISTING

11 FEB 2014

<110> Novozymes Biopharma UK Ltd
Novozymes A/S

<120> Albumin variants and conjugates

<130> 11527.400-EP

<150> EP09152625.1
<151> 2009-02-11

<150> EP09152686.3
<151> 2009-02-12

<160> 108

<170> PatentIn version 3.5

<210> 1
<211> 585
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(585)
<223> Human serum albumin (mature protein)

<400> 1

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Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
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Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
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Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225                 230                 235                 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
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Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
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Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
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Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
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Ala Ala Ser Gln Ala Ala Leu Gly Leu
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<211> 1758
<212> DNA
<213> Artificial Sequence

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gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900

gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960

gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020

tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080

tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140

gtggaagagc ctcagaattt aatcaaacaa aattgtgagc tttttgagca gcttggagag 1200

tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtacccca agtgtcaact 1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gcagcaaatg ttgtaaacat 1320

cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440

ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg atgaaacata cgttcccaaa 1500

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aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttataa 1758

<210> 3
<211> 1758
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide coding sequence (codon optimised for expression in yeast) for human serum albumin

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aagttggtca acgaagttac cgaattcgct aagacttgtg ttgctgacga atctgctgaa 180

aactgtgaca agtccttgca caccttgttc ggtgataagt tgtgtactgt tgctaccttg 240

agagaaacct acggtgaaat ggctgactgt tgtgctaagc aagaaccaga aagaaacgaa 300

tgtttcttgc aacacaagga cgacaaccca aacttgccaa gattggttag accagaagtt 360

gacgtcatgt gtactgcttt ccacgacaac gaagaaacct tcttgaagaa gtacttgtac 420

gaaattgcta gaagacaccc atacttctac gctccagaat tgttgttctt cgctaagaga 480

tacaaggctg ctttcaccga atgttgtcaa gctgctgata aggctgcttg tttgttgcca 540

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gcttccttgc aaaagttcgg tgaaagagct ttcaaggctt gggctgtcgc tagattgtct 660

caaagattcc caaaggctga attcgctgaa gtttctaagt tggttactga cttgactaag 720

gttcacactg aatgttgtca cggtgacttg ttggaatgtg ctgatgacag agctgacttg 780

gctaagtaca tctgtgaaaa ccaagactct atctcttcca agttgaagga atgttgtgaa 840

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gacttgccat ctttggctgc tgacttcgtt gaatctaagg acgtttgtaa gaactacgct 960

gaagctaagg acgtcttctt gggtatgttc ttgtacgaat acgctagaag acacccagac 1020

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tgtgctgctg ctgacccaca cgaatgttac gctaaggttt tcgatgaatt caagccattg 1140

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tgtgttttgc acgaaaagac cccagtctct gatagagtca ccaagtgttg tactgaatct 1440

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gaattcaacg ctgaaacttt caccttccac gctgatatct gtaccttgtc cgaaaaggaa 1560

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aaggaacaat tgaaggctgt catggatgat ttcgctgctt tcgttgaaaa gtgttgtaag 1680

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gctgctttgg gtttgtaa 1758

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<212> DNA
<213> Artificial Sequence

<220>
<223> HA mutated to introduce restriction enzyme sites

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca taccctttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

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gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960

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cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440

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gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

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aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

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gctgccttag gcttataa 1758

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<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA1: HA with A2C

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

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gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

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gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

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tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtacccca agtgtcaact 1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gatccaaatg ttgtaaacat 1320

cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440

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gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

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aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttataa 1758

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<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA2: HA with D1C

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

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gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

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gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

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cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

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gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

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gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttataa 1758

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<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA3: HA with C75S

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

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cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900

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cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

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agacaaatca agaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca 1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttataa 1758

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<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA4: HA with T79C

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cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300
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<210> 9
<211> 1758
<212> DNA
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<223> TA5: HA with E82C

<400> 9

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gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgttgtacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

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gctgccttag gcttataa 1758

<210> 10
<211> 1758
<212> DNA
<213> Artificial sequence

<220>

<223> TA6: HA with E86C

<400> 10

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

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tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

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cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

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gctgccttag gcttataa 1758

<210> 11
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA7: HA with C124S

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gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

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gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

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cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

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agacaaatca agaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca 1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

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gctgccttag gcttataa 1758

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<211> 1758

<212> DNA
<213> Artificial sequence

<220>
<223> TA8: HA with C168S

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gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atcttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

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gctgccttag gcttataa 1758

<210> 13
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA9: HA with C169S

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttctcaa gctgctgata aagctgcctg cctgttgcca 540

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gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

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gctgccttag gcttataa 1758

<210> 14
<211> 1758
<212> DNA
<213> Artificial sequence

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<223> TA10: HA with C91S

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gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

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<210> 15
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<212> DNA
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<223> TA11: HA with D121C

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

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ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gatccaaatg ttgtaaacat 1320

cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440

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gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

agacaaatca agaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca 1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcattgtaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

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cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

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gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

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cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440

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gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

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gctgccttag gcttataa 1758

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<211> 1758
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<223> TA14:HA with C316A

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

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gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

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cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

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gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

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aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

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gctgccttag gcttataa 1758

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<211> 1758
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<213> Artificial sequence

<220>
<223> TA16: HA with C360S

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gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

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tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

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gctgccttag gcttataa 1758

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<211> 1758
<212> DNA
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<220>
<223> TA17: HA with C361A

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

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aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

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gctgccttag gcttataa 1758

<210> 21
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA18: HA with C361S

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

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<210> 22
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA19: HA with A364C

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

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gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttataa 1758

<210> 23
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA20: HA with Q397C

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

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<223> TA21: HA with A504C

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

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<223> TA22: HA with A578C

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

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<211> 1758
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<223> TA23: HA with A581C

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

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gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

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gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

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<211> 1758
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<223> TA24: HA with C558S

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

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<223> TA25: HA with C567S

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

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<211> 1758
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<223> TA26: HA with D549C

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

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<211> 1758
<212> DNA
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<223> TA27: HA with D562C

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

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cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

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gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

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gctgccttag gcttataa 1758

<210> 31
<211> 1758
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<213> Artificial sequence

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<223> TA28: HA with E505C

<400> 31
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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

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gagtttaatg cttgtacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

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aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttataa 1758

<210> 32
<211> 1758
<212> DNA
<213> Artificial sequence

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<223> TA29: HA with L585C

<400> 32
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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

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gctgccttag gctgttaa 1758

<210> 33
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA33: HA with A2C and L585C

<400> 33
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gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

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cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

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aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

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gctgccttag gctgttaa 1758

<210> 34
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA34: HA with A2C and A504C

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gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

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aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttataa 1758

<210> 35
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA35: HA with A2C, A364C and D562C

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

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cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

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gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

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gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

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aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gcttgtgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttataa 1758

<210> 36
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA36: HA with A2C, C34A, A364C and D562C

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gccttggtgt tgattgcctt tgctcagtat cttcagcagg ctccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

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gcttgtgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttataa 1758

<210> 37
<211> 1758
<212> DNA
<213> Artificial sequence

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<223> TA38: HA withA2C, A364C, D562C and L585C

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gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

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aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

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agacaaatca agaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca 1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gcttgtgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gctgttaa 1758

<210> 38
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA39: HA with C34A, A504C and E505C.

<400> 38
gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60

gccttggtgt tgattgcctt tgctcagtat cttcagcagg ctccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900

gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960

gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020

tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080

tgtgccgctg ctgatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140

gtggaagagc ctcagaattt aatcaaacaa aattgtgagc tttttgagca gcttggagag 1200

tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtacccca agtgtcaact 1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gatccaaatg ttgtaaacat 1320

cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440

ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg acgaaacata cgttcccaaa 1500

gagtttaatt gttgtacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

agacaaatca agaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca 1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttataa 1758

<210> 39
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA41: HA with S270C and A581C

<400> 39
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gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattgt atctccagta aactgaagga atgctgtgaa 840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900

gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960

gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020

tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080

tgtgccgctg ctgatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140

gtggaagagc ctcagaattt aatcaaacaa aattgtgagc tttttgagca gcttggagag 1200

tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtacccca agtgtcaact 1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gatccaaatg ttgtaaacat 1320

cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440

ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg acgaaacata cgttcccaaa 1500

gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

agacaaatca agaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca 1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

tgtgccttag gcttataa 1758

<210> 40
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA43: HA with D129C, S270C and A581C

<400> 40
gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60

gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcattgtaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattgt atctccagta aactgaagga atgctgtgaa 840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900

gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960

gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020

tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080

tgtgccgctg ctgatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140

gtggaagagc ctcagaattt aatcaaacaa aattgtgagc tttttgagca gcttggagag 1200

tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtacccca agtgtcaact 1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gatccaaatg ttgtaaacat 1320

cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440

ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg acgaaacata cgttcccaaa 1500

gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

agacaaatca agaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca 1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

tgtgccttag gcttataa 1758

<210> 41
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA46: HA with C169S

<400> 41
gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60

gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttctcaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900

gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgttgctaa aaactatgct 960

gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020

tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080

tgtgccgctg ctgatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140

gtggaagagc ctcagaattt aatcaaacaa aattgtgagc tttttgagca gcttggagag 1200

tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtacccca agtgtcaact 1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gatccaaatg ttgtaaacat 1320

cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440

ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg acgaaacata cgttcccaaa 1500

gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

agacaaatca agaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca 1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttataa 1758

<210> 42
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA47: HA with D129C, C360S and L585C

<400> 42
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gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120
aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180
aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300
tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360
gatgtgatgt gcactgcttt tcattgtaat gaagagacat ttttgaaaaa atacttatat 420
gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540
aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660
cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720
gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900
gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960
gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020
tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtct 1080
tgtgccgctg ctgatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140
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tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtacccca agtgtcaact 1260
ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gatccaaatg ttgtaaacat 1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440
ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg acgaaacata cgttcccaaa 1500
gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560
agacaaatca agaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca 1620
aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680
gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740
gctgccttag gctgttaa 1758

<210> 43
<211> 1761
<212> DNA
<213> Artificial sequence

<220>
<223> TA51: HA with A2C and a cysteine immediately before the stop codon

<400> 43
gattgtcaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60

gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900

gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960

gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020

tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080

tgtgccgctg ctgatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140

gtggaagagc ctcagaattt aatcaaacaa aattgtgagc tttttgagca gcttggagag 1200

tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtacccca agtgtcaact 1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gatccaaatg ttgtaaacat 1320

cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440

ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg acgaaacata cgttcccaaa 1500

gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

agacaaatca agaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca 1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttatgtta a 1761

<210> 44
<211> 1761
<212> DNA
<213> Artificial sequence

<220>
<223> TA57: HA with A2C and a Cys insertion between G584 and L585

<400> 44
gattgtcaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60

gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900

gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960

gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020

tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080

tgtgccgctg ctgatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140

gtggaagagc ctcagaattt aatcaaacaa aattgtgagc tttttgagca gcttggagag 1200

tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtacccca agtgtcaact 1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gatccaaatg ttgtaaacat 1320

cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440

ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg acgaaacata cgttcccaaa 1500

gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

agacaaatca agaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca 1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gctgtttata a 1761

<210> 45
<211> 1755
<212> DNA

<213> Artificial sequence

<220>
<223> TA60: HA with A2C deltion of C316

<400> 45
gattgtcaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60

gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900

gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgttaaaaa ctatgctgag 960

gcaaaggatg tcttcctggg catgtttttg tatgaatatg caagaaggca tcctgattac 1020

tctgtcgtgc tgctgctgag acttgccaag acatatgaaa ccactctaga gaagtgctgt 1080

gccgctgctg atcctcatga atgctatgcc aaagtgttcg atgaatttaa acctcttgtg 1140

gaagagcctc agaatttaat caaacaaaat tgtgagcttt ttgagcagct tggagagtac 1200

aaattccaga atgcgctatt agttcgttac accaagaaag taccccaagt gtcaactcca 1260

actcttgtag aggtctcaag aaacctagga aaagtgggat ccaaatgttg taaacatcct 1320

gaagcaaaaa gaatgccctg tgcagaagac tatctatccg tggtcctgaa ccagttatgt 1380

gtgttgcatg agaaaacgcc agtaagtgac agagtcacca aatgctgcac agaatccttg 1440

gtgaacaggc gaccatgctt ttcagctctg gaagtcgacg aaacatacgt tcccaaagag 1500

tttaatgctg aaacattcac cttccatgca gatatatgca cactttctga gaaggagaga 1560

caaatcaaga aacaaactgc acttgttgag ctcgtgaaac acaagcccaa ggcaacaaaa 1620

gagcaactga aagctgttat ggatgatttc gcagcttttg tagagaagtg ctgcaaggct 1680

gacgataagg agacctgctt tgccgaggag ggtaaaaaac ttgttgctgc aagtcaagct 1740

gccttaggct tataa 1755

<210> 46

<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA63: HA with H39C and C253P

<400> 46
gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60

gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agattgtgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagccag ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900

gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960

gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020

tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080

tgtgccgctg ctgatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140

gtggaagagc ctcagaattt aatcaaacaa aattgtgagc tttttgagca gcttggagag 1200

tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtacccca agtgtcaact 1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gatccaaatg ttgtaaacat 1320

cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440

ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg acgaaacata cgttcccaaa 1500

gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

agacaaatca agaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca 1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttataa 1758

<210> 47
<211> 1758
<212> DNA
<213> Artificial sequence

<220>
<223> TA64: HA with C177F

<400> 47
gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60

gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtccgcggaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctt tctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gctagctctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg ctcgagtgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900

gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960

gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020

tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080

tgtgccgctg ctgatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140

gtggaagagc ctcagaattt aatcaaacaa aattgtgagc tttttgagca gcttggagag 1200

tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtacccca agtgtcaact 1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gatccaaatg ttgtaaacat 1320

cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440

ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg acgaaacata cgttcccaaa 1500

gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560

agacaaatca agaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca 1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740

gctgccttag gcttataa 1758

<210> 48
<211> 1767
<212> DNA
<213> Artificial sequence

<220>
<223> TA65: HA with a Cys at the N-terminus and an Ala-Cys extension at the C-terminus

<400> 48
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aaagccttgg tgttgattgc ctttgctcag tatcttcagc agtgtccatt tgaagatcat 120

gtaaaattag tgaatgaagt aactgaattt gcaaaaacat gtgttgctga tgagtccgcg 180

gaaaattgtg acaaatcact tcataccctt tttggagaca aattatgcac agttgcaact 240

cttcgtgaaa cctatggtga aatggctgac tgctgtgcaa aacaagaacc tgagagaaat 300

gaatgcttct tgcaacacaa agatgacaac ccaaacctcc cccgattggt gagaccagag 360

gttgatgtga tgtgcactgc ttttcatgac aatgaagaga cattttgaa aaaatactta 420

tatgaaattg ccagaagaca tccttacttt tatgccccgg aactcctttt ctttgctaaa 480

aggtataaag ctgcttttac agaatgttgc caagctgctg ataaagctgc ctgcctgttg 540

ccaaagctcg atgaacttcg ggatgaaggg aaggctagct ctgccaaaca gagactcaag 600

tgtgccagtc tccaaaaatt tggagaaaga gctttcaaag catgggcagt agctcgcctg 660

agccagagat ttcccaaagc tgagtttgca gaagtttcca agttagtgac agatcttacc 720

aaagtccaca cggaatgctg ccatggagat ctgctcgagt gtgctgatga cagggcggac 780

cttgccaagt atatctgtga aaatcaagat tcgatctcca gtaaactgaa ggaatgctgt 840

gaaaaacctc tgttggaaaa atcccactgc attgccgaag tggaaaatga tgagatgcct 900

gctgacttgc cttcattagc tgctgatttt gttgaaagta aggatgtttg caaaaactat 960

gctgaggcaa aggatgtctt cctgggcatg tttttgtatg aatatgcaag aaggcatcct 1020

gattactctg tcgtgctgct gctgagactt gccaagacat atgaaaccac tctagagaag 1080

tgctgtgccg ctgctgatcc tcatgaatgc tatgccaaag tgttcgatga atttaaacct 1140

cttgtggaag agcctcagaa tttaatcaaa caaaattgtg agcttttga gcagcttgga 1200

gagtacaaat tccagaatgc gctattagtt cgttacacca agaaagtacc ccaagtgtca 1260

actccaactc ttgtagaggt ctcaagaaac ctaggaaaag tgggatccaa atgttgtaaa 1320

catcctgaag caaaaagaat gccctgtgca gaagactatc tatccgtggt cctgaaccag 1380

ttatgtgtgt tgcatgagaa aacgccagta agtgacagag tcaccaaatg ctgcacagaa 1440

tccttggtga acaggcgacc atgcttttca gctctggaag tcgacgaaac atacgttccc 1500

aaagagttta atgctgaaac attcaccttc catgcagata tatgcacact ttctgagaag 1560

gagagacaaa tcaagaaaca aactgcactt gttgagctcg tgaaacacaa gcccaaggca 1620

acaaaagagc aactgaaagc tgttatggat gatttcgcag cttttgtaga gaagtgctgc 1680

aaggctgacg ataaggagac ctgctttgcc gaggagggta aaaaacttgt tgctgcaagt 1740

caagctgcct taggcttagc ttgttaa 1767

<210> 49
<211> 609
<212> PRT
<213> Artificial Sequence

<220>
<223> HA with fusion leader sequence

<400> 49

Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Arg Ser Leu Asp Lys Arg Asp Ala His Lys Ser Glu Val Ala
20 25 30

His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu
35 40 45

Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
50 55 60

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
65 70 75 80

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
85 90 95

Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
100 105 110

Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
115 120 125

His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
130 135 140

Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
145 150 155 160

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
165 170 175

Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
180 185 190

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
195 200 205

```
Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys
    210                 215                 220

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
225                 230                 235                 240

Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
                245                 250                 255

Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
            260                 265                 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
        275                 280                 285

Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
    290                 295                 300

Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
305                 310                 315                 320

Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
                325                 330                 335

Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
            340                 345                 350

Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
        355                 360                 365

Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
    370                 375                 380

Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
385                 390                 395                 400

Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
                405                 410                 415

Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
            420                 425                 430

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

Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
    450                 455                 460

Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val
465                 470                 475                 480
```

```
Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
                485                 490                 495

Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
            500                 505                 510

Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
        515                 520                 525

Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu
    530                 535                 540

Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
545                 550                 555                 560

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala
                565                 570                 575

Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe
            580                 585                 590

Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly
        595                 600                 605

Leu
```

<210> 50
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA1: HA with A2C

<400> 50

```
Asp Cys His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95
```

```
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365
```

```
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 51
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA2: HA with D1C

<400> 51

```
Cys Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                  10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270
```

```
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540
```

```
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 52
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA3: HA with C75S

<400> 52

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Ser Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190
```

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

```
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 53
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA4: HA with T79C

<400> 53

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Cys Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95
```

```
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365
```

```
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585


<210>  54
<211>  585
<212>  PRT
<213>  Artificial sequence

<220>
<223>  TA5: HA with E82C

<400>  54

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15
```

```
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Cys Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285
```

```
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560
```

```
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 55
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA6: HA with E86C

<400> 55

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Cys Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190
```

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

```
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 56
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA7: HA with C124S

<400> 56

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110
```

```
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Ser Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380
```

```
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585


<210>  57
<211>  585
<212>  PRT
<213>  Artificial sequence

<220>
<223>  TA8: HA with C168S

<400>  57

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15
```

```
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Ser Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285
```

```
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560
```

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 58
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA9: HA with C169S

<400> 58

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Ser Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

```
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210                 215                 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480
```

```
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 59
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA10: HA with C91S

<400> 59

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

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

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110
```

```
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380
```

```
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585


<210>  60
<211>  585
<212>  PRT
<213>  Artificial sequence

<220>
<223>  TA11: HA with D121C

<400>  60

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30
```

```
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Cys Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300
```

```
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575
```

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 61
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA12: HA with D129C

<400> 61

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Cys Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

```
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210                 215                 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480
```

```
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 62
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA13: HA with S270C

<400> 62

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125
```

```
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Cys Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400
```

```
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 63
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA14: HA with C316A

<400> 63

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30
```

```
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300
```

```
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Ala Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575
```

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 64
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA16: HA with C360S

<400> 64

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Ser Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

```
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 65
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA17: HA with C361A

<400> 65

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125
```

```
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Ala Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400
```

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 66
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA18: HA with C361S

<400> 66

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

```
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320
```

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Ser Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 67
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA19: HA with A364C

<400> 67

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                  10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210                 215                 220
```

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Cys Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495
```

```
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 68
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA20: HA with Q397C

<400> 68

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140
```

```
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Cys Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415
```

```
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 69
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA21: HA with A504C

<400> 69

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45
```

```
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320
```

```
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Cys Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 70
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA22: HA with A578C

<400> 70

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                  10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

```
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510
```

```
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Cys Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 71
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA23: HA with A581C

<400> 71

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140
```

```
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415
```

```
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Cys Ala Leu Gly Leu
            580                 585
```

<210> 72
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA24: HA with C558S

<400> 72

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60
```

```
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335
```

```
Arg His Pro Asp Tyr Ser Val Val Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Ser Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 73
<211> 585

<212> PRT
<213> Artificial sequence

<220>
<223> TA25: HA with C567S

<400> 73

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                  10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

```
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510
```

```
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Ser Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585


<210>  74
<211>  585
<212>  PRT
<213>  Artificial sequence

<220>
<223>  TA26: HA with D549C

<400>  74

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160
```

```
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430
```

```
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Cys Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 75
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA27: HA with D562C

<400> 75

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60
```

```
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335
```

```
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Cys Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 76
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA28: HA with E505C

<400> 76

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                  10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255
```

```
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Cys Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525
```

```
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 77
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA29: HA with L585C

<400> 77

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160
```

```
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430
```

```
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Cys
            580                 585
```

<210> 78
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA33: HA with A2C and L585C

<400> 78

```
Asp Cys His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80
```

```
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350
```

```
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Cys
            580                 585
```

<210> 79
<211> 585
<212> PRT
<213> Artificial sequence

<220>

<223> TA34: HA with A2C and A504C

<400> 79

```
Asp Cys His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                  10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255
```

```
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Cys Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525
```

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 80
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA35: HA with A2C, A364C and D562C

<400> 80

Asp Cys His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

```
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Cys Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445
```

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Cys Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 81
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA36: HA with A2C, A364C and D562C

<400> 81

Asp Cys His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

```
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350
```

```
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Cys Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Cys Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 82
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA38: HA with A2C, A364C, D562C and L585C

<400> 82

Asp Cys His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

```
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Cys Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540
```

```
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Cys Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Cys
            580                 585
```

<210> 83
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA39: HA with C34A, A504C and E505C.

<400> 83

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175
```

```
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445
```

```
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Cys Cys Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 84
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA41: HA with S270C and A581C

<400> 84

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95
```

```
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Cys Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365
```

```
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Cys Ala Leu Gly Leu
            580                 585
```

<210> 85
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA43: HA with D129C, S270C and A581C

<400> 85

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                  10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Cys Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Cys Ile Ser
            260                 265                 270
```

```
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540
```

```
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Cys Ala Leu Gly Leu
            580                 585
```

<210> 86
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA46: HA with C169S

<400> 86

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Ser Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190
```

```
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Ala Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460
```

```
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 87
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA47: HA with D129C and L585C

<400> 87

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95
```

```
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Cys Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Ser Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365
```

```
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Cys
            580                 585
```

<210> 88
<211> 586
<212> PRT
<213> Artificial sequence

<220>
<223> TA51: HA with A2C and a cysteine immediately before the stop codon

<400> 88

```
Asp Cys His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
```

```
1               5                  10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
```

```
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
```

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Cys
580 585

<210> 89
<211> 586
<212> PRT
<213> Artificial sequence

<220>
<223> TA57: HA with A2C and an insertion between G584 and L585

<400> 89

Asp Cys His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

```
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460
```

```
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Cys Leu
            580                 585
```

<210> 90
<211> 584
<212> PRT
<213> Artificial sequence

<220>
<223> TA60: HA with A2C and deletion of C316

<400> 90

```
Asp Cys His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
```

```
          100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Lys Asn Tyr Ala Glu
305                 310                 315                 320

Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg
                325                 330                 335

His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr
            340                 345                 350

Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys
        355                 360                 365

Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln
```

370 375 380

Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr
385 390 395 400

Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln
405 410 415

Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys Val
420 425 430

Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala
435 440 445

Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu
450 455 460

Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu
465 470 475 480

Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr
485 490 495

Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile
500 505 510

Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu
515 520 525

Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys
530 535 540

Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala
545 550 555 560

Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala
565 570 575

Ala Ser Gln Ala Ala Leu Gly Leu
580

<210> 91
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA63: HA with H39C and C253P

<400> 91

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

```
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp Cys Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Pro Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285
```

```
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560
```

```
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 92
<211> 585
<212> PRT
<213> Artificial sequence

<220>
<223> TA64: HA with C177F

<400> 92

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Phe Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
```

```
        195                 200                 205

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

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
```

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 93
<211> 588
<212> PRT
<213> Artificial sequence

<220>
<223> TA65: HA with a Cys at the N-terminus and an Ala-Cys extension at the C-terminus of HA

<400> 93

Cys Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly
1 5 10 15

Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu
20 25 30

Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr
35 40 45

Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp
50 55 60

Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr
65 70 75 80

Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu
85 90 95

Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn
100 105 110

```
Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe
        115                 120                 125

His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala
    130                 135                 140

Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys
145                 150                 155                 160

Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala
                165                 170                 175

Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala
            180                 185                 190

Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly
        195                 200                 205

Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe
    210                 215                 220

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

Lys Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp
                245                 250                 255

Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile
            260                 265                 270

Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser
        275                 280                 285

His Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro
    290                 295                 300

Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr
305                 310                 315                 320

Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala
                325                 330                 335

Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys
            340                 345                 350

Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His
        355                 360                 365

Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu
    370                 375                 380
```

```
Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly
385                 390                 395                 400

Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val
                405                 410                 415

Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly
            420                 425                 430

Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro
        435                 440                 445

Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu
    450                 455                 460

His Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu
465                 470                 475                 480

Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu
                485                 490                 495

Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala
            500                 505                 510

Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr
        515                 520                 525

Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln
    530                 535                 540

Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys
545                 550                 555                 560

Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu
                565                 570                 575

Val Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Cys
            580                 585
```

<210> 94
<211> 607
<212> PRT
<213> Bos taurus

<400> 94

```
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Leu Leu Phe Ser Ser Ala
1               5                   10                  15

Tyr Ser Arg Gly Val Phe Arg Arg Asp Thr His Lys Ser Glu Ile Ala
            20                  25                  30
```

```
His Arg Phe Lys Asp Leu Gly Glu Glu His Phe Lys Gly Leu Val Leu
        35                  40                  45

Ile Ala Phe Ser Gln Tyr Leu Gln Gln Cys Pro Phe Asp Glu His Val
    50                  55                  60

Lys Leu Val Asn Glu Leu Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
65                  70                  75                  80

Glu Ser His Ala Gly Cys Glu Lys Ser Leu His Thr Leu Phe Gly Asp
                85                  90                  95

Glu Leu Cys Lys Val Ala Ser Leu Arg Glu Thr Tyr Gly Asp Met Ala
            100                 105                 110

Asp Cys Cys Glu Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Ser
        115                 120                 125

His Lys Asp Asp Ser Pro Asp Leu Pro Lys Leu Lys Pro Asp Pro Asn
    130                 135                 140

Thr Leu Cys Asp Glu Phe Lys Ala Asp Glu Lys Lys Phe Trp Gly Lys
145                 150                 155                 160

Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu
                165                 170                 175

Leu Leu Tyr Tyr Ala Asn Lys Tyr Asn Gly Val Phe Gln Glu Cys Cys
            180                 185                 190

Gln Ala Glu Asp Lys Gly Ala Cys Leu Leu Pro Lys Ile Glu Thr Met
        195                 200                 205

Arg Glu Lys Val Leu Ala Ser Ser Ala Arg Gln Arg Leu Arg Cys Ala
    210                 215                 220

Ser Ile Gln Lys Phe Gly Glu Arg Ala Leu Lys Ala Trp Ser Val Ala
225                 230                 235                 240

Arg Leu Ser Gln Lys Phe Pro Lys Ala Glu Phe Val Glu Val Thr Lys
                245                 250                 255

Leu Val Thr Asp Leu Thr Lys Val His Lys Glu Cys Cys His Gly Asp
            260                 265                 270

Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys
        275                 280                 285

Asp Asn Gln Asp Thr Ile Ser Ser Lys Leu Lys Glu Cys Cys Asp Lys
    290                 295                 300
```

```
Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Lys Asp Ala
305                 310                 315                 320

Ile Pro Glu Asn Leu Pro Pro Leu Thr Ala Asp Phe Ala Glu Asp Lys
                325                 330                 335

Asp Val Cys Lys Asn Tyr Gln Glu Ala Lys Asp Ala Phe Leu Gly Ser
            340                 345                 350

Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Glu Tyr Ala Val Ser Val
        355                 360                 365

Leu Leu Arg Leu Ala Lys Glu Tyr Glu Ala Thr Leu Glu Glu Cys Cys
    370                 375                 380

Ala Lys Asp Asp Pro His Ala Cys Tyr Ser Thr Val Phe Asp Lys Leu
385                 390                 395                 400

Lys His Leu Val Asp Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Asp
                405                 410                 415

Gln Phe Glu Lys Leu Gly Glu Tyr Gly Phe Gln Asn Ala Leu Ile Val
            420                 425                 430

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

Val Ser Arg Ser Leu Gly Lys Val Gly Thr Arg Cys Cys Thr Lys Pro
    450                 455                 460

Glu Ser Glu Arg Met Pro Cys Thr Glu Asp Tyr Leu Ser Leu Ile Leu
465                 470                 475                 480

Asn Arg Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Glu Lys Val
                485                 490                 495

Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser
            500                 505                 510

Ala Leu Thr Pro Asp Glu Thr Tyr Val Pro Lys Ala Phe Asp Glu Lys
        515                 520                 525

Leu Phe Thr Phe His Ala Asp Ile Cys Thr Leu Pro Asp Thr Glu Lys
    530                 535                 540

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Leu Lys His Lys Pro
545                 550                 555                 560

Lys Ala Thr Glu Glu Gln Leu Lys Thr Val Met Glu Asn Phe Val Ala
                565                 570                 575
```

```
Phe Val Asp Lys Cys Cys Ala Ala Asp Asp Lys Glu Ala Cys Phe Ala
            580                 585                 590

Val Glu Gly Pro Lys Leu Val Val Ser Thr Gln Thr Ala Leu Ala
        595                 600                 605
```

<210> 95
<211> 608
<212> PRT
<213> Felis catus

<400> 95

```
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Leu Leu Phe Ser Ser Ala
1               5                   10                  15

Tyr Ser Arg Gly Val Thr Arg Arg Glu Ala His Gln Ser Glu Ile Ala
            20                  25                  30

His Arg Phe Asn Asp Leu Gly Glu Glu His Phe Arg Gly Leu Val Leu
        35                  40                  45

Val Ala Phe Ser Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
    50                  55                  60

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Gly Cys Val Ala Asp
65                  70                  75                  80

Gln Ser Ala Ala Asn Cys Glu Lys Ser Leu His Glu Leu Leu Gly Asp
                85                  90                  95

Lys Leu Cys Thr Val Ala Ser Leu Arg Asp Lys Tyr Gly Glu Met Ala
            100                 105                 110

Asp Cys Cys Glu Lys Lys Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
        115                 120                 125

His Lys Asp Asp Asn Pro Gly Phe Gly Gln Leu Val Thr Pro Glu Ala
    130                 135                 140

Asp Ala Met Cys Thr Ala Phe His Glu Asn Glu Gln Arg Phe Leu Gly
145                 150                 155                 160

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
                165                 170                 175

Glu Leu Leu Tyr Tyr Ala Glu Glu Tyr Lys Gly Val Phe Thr Glu Cys
            180                 185                 190

Cys Glu Ala Ala Asp Lys Ala Ala Cys Leu Thr Pro Lys Val Asp Ala
        195                 200                 205
```

```
Leu Arg Glu Lys Val Leu Ala Ser Ser Ala Lys Glu Arg Leu Lys Cys
    210                 215                 220

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ser Val
225                 230                 235                 240

Ala Arg Leu Ser Gln Lys Phe Pro Lys Ala Glu Phe Ala Glu Ile Ser
                245                 250                 255

Lys Leu Val Thr Asp Leu Ala Lys Ile His Lys Glu Cys Cys His Gly
            260                 265                 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
        275                 280                 285

Cys Glu Asn Gln Asp Ser Ile Ser Thr Lys Leu Lys Glu Cys Cys Gly
    290                 295                 300

Lys Pro Val Leu Glu Lys Ser His Cys Ile Ser Glu Val Glu Arg Asp
305                 310                 315                 320

Glu Leu Pro Ala Asp Leu Pro Pro Leu Ala Val Asp Phe Val Glu Asp
                325                 330                 335

Lys Glu Val Cys Lys Asn Tyr Gln Glu Ala Lys Asp Val Phe Leu Gly
            340                 345                 350

Thr Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Glu Tyr Ser Val Ser
        355                 360                 365

Leu Leu Leu Arg Leu Ala Lys Glu Tyr Glu Ala Thr Leu Glu Lys Cys
    370                 375                 380

Cys Ala Thr Asp Asp Pro Pro Ala Cys Tyr Ala His Val Phe Asp Glu
385                 390                 395                 400

Phe Lys Pro Leu Val Glu Glu Pro His Asn Leu Val Lys Thr Asn Cys
                405                 410                 415

Glu Leu Phe Glu Lys Leu Gly Glu Tyr Gly Phe Gln Asn Ala Leu Leu
            420                 425                 430

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

Glu Val Ser Arg Ser Leu Gly Lys Val Gly Ser Lys Cys Cys Thr His
    450                 455                 460

Pro Glu Ala Glu Arg Leu Ser Cys Ala Glu Asp Tyr Leu Ser Val Val
465                 470                 475                 480
```

```
Leu Asn Arg Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Glu Arg
                485                 490                 495

Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
            500                 505                 510

Ser Ala Leu Gln Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Ser Ala
        515                 520                 525

Glu Thr Phe Thr Phe His Ala Asp Leu Cys Thr Leu Pro Glu Ala Glu
    530                 535                 540

Lys Gln Ile Lys Lys Gln Ser Ala Leu Val Glu Leu Leu Lys His Lys
545                 550                 555                 560

Pro Lys Ala Thr Glu Glu Gln Leu Lys Thr Val Met Gly Asp Phe Gly
                565                 570                 575

Ser Phe Val Asp Lys Cys Cys Ala Ala Glu Asp Lys Glu Ala Cys Phe
            580                 585                 590

Ala Glu Glu Gly Pro Lys Leu Val Ala Ala Ala Gln Ala Ala Leu Ala
        595                 600                 605
```

<210> 96
<211> 608
<212> PRT
<213> Canis lupus familaris

<400> 96

```
Met Lys Trp Val Thr Phe Ile Ser Leu Phe Phe Leu Phe Ser Ser Ala
1               5                   10                  15

Tyr Ser Arg Gly Leu Val Arg Arg Glu Ala Tyr Lys Ser Glu Ile Ala
            20                  25                  30

His Arg Tyr Asn Asp Leu Gly Glu Glu His Phe Arg Gly Leu Val Leu
        35                  40                  45

Val Ala Phe Ser Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
    50                  55                  60

Lys Leu Ala Lys Glu Val Thr Glu Phe Ala Lys Ala Cys Ala Ala Glu
65                  70                  75                  80

Glu Ser Gly Ala Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
                85                  90                  95

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

Asp Cys Cys Glu Lys Gln Glu Pro Asp Arg Asn Glu Cys Phe Leu Ala
```

115 120 125

His Lys Asp Asp Asn Pro Gly Phe Pro Pro Leu Val Ala Pro Glu Pro
130 135 140

Asp Ala Leu Cys Ala Ala Phe Gln Asp Asn Glu Gln Leu Phe Leu Gly
145 150 155 160

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
165 170 175

Glu Leu Leu Tyr Tyr Ala Gln Gln Tyr Lys Gly Val Phe Ala Glu Cys
180 185 190

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Gly Pro Lys Ile Glu Ala
195 200 205

Leu Arg Glu Lys Val Leu Leu Ser Ser Ala Lys Glu Arg Phe Lys Cys
210 215 220

Ala Ser Leu Gln Lys Phe Gly Asp Arg Ala Phe Lys Ala Trp Ser Val
225 230 235 240

Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Asp Phe Ala Glu Ile Ser
245 250 255

Lys Val Val Thr Asp Leu Thr Lys Val His Lys Glu Cys Cys His Gly
260 265 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Met
275 280 285

Cys Glu Asn Gln Asp Ser Ile Ser Thr Lys Leu Lys Glu Cys Cys Asp
290 295 300

Lys Pro Val Leu Glu Lys Ser Gln Cys Leu Ala Glu Val Glu Arg Asp
305 310 315 320

Glu Leu Pro Gly Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Asp
325 330 335

Lys Glu Val Cys Lys Asn Tyr Gln Glu Ala Lys Asp Val Phe Leu Gly
340 345 350

Thr Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Glu Tyr Ser Val Ser
355 360 365

Leu Leu Leu Arg Leu Ala Lys Glu Tyr Glu Ala Thr Leu Glu Lys Cys
370 375 380

Cys Ala Thr Asp Asp Pro Pro Thr Cys Tyr Ala Lys Val Leu Asp Glu

385 390 395 400

Phe Lys Pro Leu Val Asp Glu Pro Gln Asn Leu Val Lys Thr Asn Cys
405 410 415

Glu Leu Phe Glu Lys Leu Gly Glu Tyr Gly Phe Gln Asn Ala Leu Leu
420 425 430

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

Glu Val Ser Arg Lys Leu Gly Lys Val Gly Thr Lys Cys Cys Lys Lys
450 455 460

Pro Glu Ser Glu Arg Met Ser Cys Ala Glu Asp Phe Leu Ser Val Val
465 470 475 480

Leu Asn Arg Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Glu Arg
485 490 495

Val Thr Lys Cys Cys Ser Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
500 505 510

Ser Gly Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
515 520 525

Glu Thr Phe Thr Phe His Ala Asp Leu Cys Thr Leu Pro Glu Ala Glu
530 535 540

Lys Gln Val Lys Lys Gln Thr Ala Leu Val Glu Leu Leu Lys His Lys
545 550 555 560

Pro Lys Ala Thr Asp Glu Gln Leu Lys Thr Val Met Gly Asp Phe Gly
565 570 575

Ala Phe Val Glu Lys Cys Cys Ala Ala Glu Asn Lys Glu Gly Cys Phe
580 585 590

Ser Glu Glu Gly Pro Lys Leu Val Ala Ala Ala Gln Ala Ala Leu Val
595 600 605

<210> 97
<211> 607
<212> PRT
<213> Equus asinus

<400> 97

Met Lys Trp Val Thr Phe Val Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

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

```
His Arg Phe Asn Asp Leu Gly Glu Lys His Phe Lys Gly Leu Val Leu
        35                  40                  45

Val Ala Phe Ser Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
    50                  55                  60

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Lys Cys Ala Ala Asp
65                  70                  75                  80

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
                85                  90                  95

Lys Leu Cys Thr Val Ala Thr Leu Arg Ala Thr Tyr Gly Glu Leu Ala
            100                 105                 110

Asp Cys Cys Glu Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Thr
        115                 120                 125

His Lys Asp Asp His Pro Asn Leu Pro Lys Leu Lys Pro Glu Pro Asp
    130                 135                 140

Ala Gln Cys Ala Ala Phe Gln Glu Asp Pro Asp Lys Phe Leu Gly Lys
145                 150                 155                 160

Tyr Leu Tyr Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Gly Pro Glu
                165                 170                 175

Leu Leu Phe His Ala Glu Glu Tyr Lys Ala Asp Phe Thr Glu Cys Cys
            180                 185                 190

Pro Ala Asp Asp Lys Ala Gly Cys Leu Ile Pro Lys Leu Asp Ala Leu
        195                 200                 205

Lys Glu Arg Ile Leu Leu Ser Ser Ala Lys Glu Arg Leu Lys Cys Ser
    210                 215                 220

Ser Phe Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ser Val Ala
225                 230                 235                 240

Arg Leu Ser Gln Lys Phe Pro Lys Ala Asp Phe Ala Glu Val Ser Lys
                245                 250                 255

Ile Val Thr Asp Leu Thr Lys Val His Lys Glu Cys Cys His Gly Asp
            260                 265                 270

Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Thr Lys Tyr Ile Cys
        275                 280                 285

Glu His Gln Asp Ser Ile Ser Gly Lys Leu Lys Ala Cys Cys Asp Lys
    290                 295                 300
```

```
Pro Leu Leu Gln Lys Ser His Cys Ile Ala Glu Val Lys Glu Asp Asp
305                 310                 315                 320

Leu Pro Ser Asp Leu Pro Ala Leu Ala Ala Asp Phe Ala Glu Asp Lys
                325                 330                 335

Glu Ile Cys Lys His Tyr Lys Asp Ala Lys Asp Val Phe Leu Gly Thr
            340                 345                 350

Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Asp Tyr Ser Val Ser Leu
        355                 360                 365

Leu Leu Arg Ile Ala Lys Thr Tyr Glu Ala Thr Leu Glu Lys Cys Cys
    370                 375                 380

Ala Glu Ala Asp Pro Pro Ala Cys Tyr Ala Thr Val Phe Asp Gln Phe
385                 390                 395                 400

Thr Pro Leu Val Glu Glu Pro Lys Ser Leu Val Lys Lys Asn Cys Asp
                405                 410                 415

Leu Phe Glu Glu Val Gly Glu Tyr Asp Phe Gln Asn Ala Leu Ile Val
            420                 425                 430

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

Ile Gly Arg Thr Leu Gly Lys Val Gly Ser Arg Cys Cys Lys Leu Pro
    450                 455                 460

Glu Ser Glu Arg Leu Pro Cys Ser Glu Asn His Leu Ala Leu Ala Leu
465                 470                 475                 480

Asn Arg Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Glu Lys Ile
                485                 490                 495

Thr Lys Cys Cys Thr Asp Ser Leu Ala Glu Arg Arg Pro Cys Phe Ser
            500                 505                 510

Ala Leu Glu Leu Asp Glu Gly Tyr Ile Pro Lys Glu Phe Lys Ala Glu
        515                 520                 525

Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Pro Glu Asp Glu Lys
    530                 535                 540

Gln Ile Lys Lys Gln Ser Ala Leu Ala Glu Leu Val Lys His Lys Pro
545                 550                 555                 560

Lys Ala Thr Lys Glu Gln Leu Lys Thr Val Leu Gly Asn Phe Ser Ala
                565                 570                 575
```

```
Phe Val Ala Lys Cys Cys Gly Ala Glu Asp Lys Glu Ala Cys Phe Ala
            580                 585                 590

Glu Glu Gly Pro Lys Leu Val Ala Ser Ser Gln Leu Ala Leu Ala
        595                 600                 605
```

<210> 98
<211> 609
<212> PRT
<213> Meriones unguiculatus

<400> 98

```
Met Lys Trp Val Thr Phe Leu Leu Leu Leu Phe Val Ser Gly Ser Ala
1               5                   10                  15

Phe Ser Arg Gly Val Phe Arg Arg Asp Ala Ala His Lys Ser Glu Ile
            20                  25                  30

Ala His Arg Tyr Lys Asp Leu Gly Glu Lys Tyr Phe Lys Gly Leu Val
        35                  40                  45

Leu Tyr Thr Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Glu Glu His
    50                  55                  60

Val Lys Leu Val Arg Glu Val Thr Asp Phe Ala Ser Asn Cys Ala Lys
65                  70                  75                  80

Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly
                85                  90                  95

Asp Lys Leu Cys Ser Leu Pro Asn Phe Gly Glu Lys Tyr Ala Glu Met
            100                 105                 110

Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu
        115                 120                 125

Gln His Lys Asp Asp Asn Pro Gln Leu Pro Pro Phe Lys Arg Ala Glu
    130                 135                 140

Pro Asp Ala Met Cys Thr Ala Phe Gln Glu Asn Ala Glu Ala Phe Met
145                 150                 155                 160

Gly His Tyr Leu His Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Gly
                165                 170                 175

Pro Glu Leu Leu Tyr Leu Ala Asp Lys Tyr Thr Ala Val Leu Thr Glu
            180                 185                 190

Cys Cys Ala Ala Asp Asp Lys Gly Ala Cys Leu Thr Pro Lys Leu Asp
        195                 200                 205
```

```
Ala Leu Lys Glu Lys Ala Leu Val Ser Ala Val Arg Gln Arg Leu Lys
    210                 215                 220

Cys Ser Ser Met Lys Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala
225                 230                 235                 240

Val Ala Arg Met Ser Gln Thr Phe Pro Asn Ala Asp Phe Ala Glu Ile
                245                 250                 255

Thr Lys Leu Ala Thr Asp Leu Thr Lys Val Thr Gln Glu Cys Cys His
            260                 265                 270

Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Glu Leu Ala Lys Tyr
        275                 280                 285

Met Cys Glu Asn Gln Ala Ser Ile Ser Ser Lys Leu Gln Ala Cys Cys
    290                 295                 300

Asp Lys Glu Met Leu Gln Lys Ser Gln Cys Leu Ala Glu Val Glu His
305                 310                 315                 320

Asp Asp Met Pro Ala Asp Leu Pro Ala Leu Thr Ala Asp Phe Val Glu
                325                 330                 335

Asp Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu
            340                 345                 350

Gly Thr Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Glu Tyr Ser Val
        355                 360                 365

Ser Leu Leu Leu Arg Leu Ala Lys Lys Tyr Glu Ala Thr Leu Glu Lys
    370                 375                 380

Cys Cys Ala Glu Ala Asp Pro His Ala Cys Tyr Gly His Val Phe Asp
385                 390                 395                 400

Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Val Lys Ser Asn
                405                 410                 415

Cys Glu Leu Tyr Glu Lys Leu Gly Glu Tyr Gly Phe Gln Asn Ala Val
            420                 425                 430

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

Val Glu Ala Ala Arg Ser Leu Gly Arg Val Gly Thr His Cys Cys Ala
    450                 455                 460

Leu Pro Glu Lys Lys Arg Leu Pro Cys Val Glu Asp Tyr Leu Ser Ala
465                 470                 475                 480
```

```
Ile Leu Asn Arg Val Cys Leu Leu His Glu Lys Thr Pro Val Ser Glu
                485                 490                 495

Gln Val Thr Lys Cys Cys Ser Gly Ser Leu Val Glu Arg Arg Pro Cys
            500                 505                 510

Phe Ser Ala Leu Pro Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Lys
        515                 520                 525

Ala Glu Thr Phe Thr Phe His Ala Asn Ile Cys Thr Leu Pro Glu Lys
    530                 535                 540

Glu Lys Gln Met Glu Lys Gln Thr Ala Leu Ala Glu Leu Val Lys His
545                 550                 555                 560

Lys Pro Gln Ala Thr Glu Glu Gln Leu Lys Lys Val Met Gly Asp Phe
                565                 570                 575

Ala Glu Phe Leu Glu Lys Cys Cys Lys Gln Glu Asp Lys Glu Ala Cys
            580                 585                 590

Phe Ser Thr Glu Gly Pro Lys Leu Val Ala Glu Ser Gln Lys Ala Leu
        595                 600                 605

Ala
```

<210> 99
<211> 583
<212> PRT
<213> Capra hircus

<400> 99

```
Asp Thr His Lys Ser Glu Ile Ala His Arg Phe Asn Asp Leu Gly Glu
1               5                   10                  15

Glu Asn Phe Gln Gly Leu Val Leu Ile Ala Phe Ser Gln Tyr Leu Gln
            20                  25                  30

Gln Cys Pro Phe Asp Glu His Val Lys Leu Val Lys Glu Leu Thr Glu
        35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser His Ala Gly Cys Asp Lys
    50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Glu Leu Cys Lys Val Ala Thr Leu
65                  70                  75                  80

Arg Glu Thr Tyr Gly Asp Met Ala Asp Cys Cys Glu Lys Gln Glu Pro
                85                  90                  95
```

```
Glu Arg Asn Glu Cys Phe Leu Lys His Lys Asp Asp Ser Pro Asp Leu
            100                 105                 110

Pro Lys Leu Lys Pro Glu Pro Asp Thr Leu Cys Ala Glu Phe Lys Ala
        115                 120                 125

Asp Glu Lys Lys Phe Trp Gly Lys Tyr Leu Tyr Glu Val Ala Arg Arg
    130                 135                 140

His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Tyr Tyr Ala Asn Lys Tyr
145                 150                 155                 160

Asn Gly Val Phe Gln Glu Cys Cys Gln Ala Glu Asp Lys Gly Ala Cys
                165                 170                 175

Leu Leu Pro Lys Ile Glu Thr Met Arg Glu Lys Val Leu Ala Ser Ser
            180                 185                 190

Ala Arg Gln Arg Leu Arg Cys Ala Ser Ile Gln Lys Phe Gly Glu Arg
        195                 200                 205

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

Ala Asp Phe Thr Asp Val Thr Lys Ile Val Thr Asp Leu Thr Lys Val
225                 230                 235                 240

His Lys Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg
                245                 250                 255

Ala Asp Leu Ala Lys Tyr Ile Cys Asp His Gln Asp Thr Leu Ser Ser
            260                 265                 270

Lys Leu Lys Glu Cys Cys Asp Lys Pro Val Leu Glu Lys Ser His Cys
        275                 280                 285

Ile Ala Glu Ile Asp Lys Asp Ala Val Pro Glu Asn Leu Pro Pro Leu
    290                 295                 300

Thr Ala Asp Phe Ala Glu Asp Lys Glu Val Cys Lys Asn Tyr Gln Glu
305                 310                 315                 320

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

His Pro Glu Tyr Ala Val Ser Val Leu Leu Arg Leu Ala Lys Glu Tyr
            340                 345                 350

Glu Ala Thr Leu Glu Asp Cys Cys Ala Lys Glu Asp Pro His Ala Cys
        355                 360                 365
```

```
Tyr Ala Thr Val Phe Asp Lys Leu Lys His Leu Val Asp Glu Pro Gln
    370                 375                 380

Asn Leu Ile Lys Lys Asn Cys Glu Leu Phe Glu Lys His Gly Glu Tyr
385                 390                 395                 400

Gly Phe Gln Asn Ala Leu Ile Val Arg Tyr Thr Arg Lys Ala Pro Gln
                405                 410                 415

Val Ser Thr Pro Thr Leu Val Glu Ile Ser Arg Ser Leu Gly Lys Val
            420                 425                 430

Gly Thr Lys Cys Cys Ala Lys Pro Glu Ser Glu Arg Met Pro Cys Thr
        435                 440                 445

Glu Asp Tyr Leu Ser Leu Ile Leu Asn Arg Leu Cys Val Leu His Glu
    450                 455                 460

Lys Thr Pro Val Ser Glu Lys Val Thr Lys Cys Cys Thr Glu Ser Leu
465                 470                 475                 480

Val Asn Arg Arg Pro Cys Phe Ser Asp Leu Thr Leu Asp Glu Thr Tyr
                485                 490                 495

Val Pro Lys Pro Phe Asp Gly Glu Ser Phe Thr Phe His Ala Asp Ile
            500                 505                 510

Cys Thr Leu Pro Asp Thr Glu Lys Gln Ile Lys Lys Gln Thr Ala Leu
        515                 520                 525

Val Glu Leu Leu Lys His Lys Pro Lys Ala Thr Asp Glu Gln Leu Lys
    530                 535                 540

Thr Val Met Glu Asn Phe Val Ala Phe Val Asp Lys Cys Cys Ala Ala
545                 550                 555                 560

Asp Asp Lys Glu Gly Cys Phe Leu Leu Glu Gly Pro Lys Leu Val Ala
                565                 570                 575

Ser Thr Gln Ala Ala Leu Ala
            580


<210>  100
<211>  608
<212>  PRT
<213>  Cavia porcellus

<400>  100

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Val
1               5                   10                  15

Tyr Ser Arg Gly Val Phe Arg Arg Glu Ala His Lys Ser Glu Ile Ala
```

```
            20                  25                  30

His Arg Phe Asn Asp Leu Gly Glu Gly His Phe Lys Gly Leu Val Leu
        35                  40                  45

Ile Thr Leu Ser Gln His Leu Gln Lys Ser Pro Phe Glu Glu His Val
    50                  55                  60

Lys Leu Val Asn Glu Val Thr Asp Phe Ala Lys Ala Cys Val Ala Asp
65                  70                  75                  80

Glu Ser Ala Gln Asn Cys Gly Lys Ala Ile Ala Thr Leu Phe Gly Asp
                85                  90                  95

Lys Val Cys Ala Ile Pro Ser Leu Arg Glu Thr Tyr Gly Glu Leu Ala
            100                 105                 110

Asp Cys Cys Ala Lys Glu Asp Pro Asp Arg Val Glu Cys Phe Leu Gln
        115                 120                 125

His Lys Asp Asp Asn Pro Asn Leu Pro Pro Phe Glu Arg Pro Glu Pro
    130                 135                 140

Glu Ala Leu Cys Thr Ala Phe Lys Glu Asn Asn Asp Arg Phe Ile Gly
145                 150                 155                 160

His Tyr Leu Tyr Glu Val Ser Arg Arg His Pro Tyr Phe Tyr Ala Pro
                165                 170                 175

Glu Leu Leu Tyr Tyr Ala Glu Lys Tyr Lys Asn Ala Leu Thr Glu Cys
            180                 185                 190

Cys Glu Ala Ala Asp Lys Ala Ala Cys Leu Thr Pro Lys Leu Asp Ala
        195                 200                 205

Ile Lys Glu Lys Ala Leu Val Ser Ser Ala Gln Gln Arg Leu Lys Cys
    210                 215                 220

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ser Val
225                 230                 235                 240

Ala Arg Leu Ser Gln Lys Phe Pro Lys Ala Glu Phe Ala Glu Ile Ser
                245                 250                 255

Thr Ile Val Thr Ser Leu Thr Lys Val Thr Lys Glu Cys Cys His Gly
            260                 265                 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Gln Glu Leu Ala Lys Tyr Met
        275                 280                 285

Cys Glu His Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Val
```

290 295 300

Lys Pro Thr Leu Gln Lys Ala His Cys Ile Leu Glu Ile Gln Arg Asp
305 310 315 320

Glu Leu Pro Thr Glu Leu Pro Asp Leu Ala Val Asp Phe Val Glu Asp
325 330 335

Lys Glu Val Cys Lys Asn Phe Ala Glu Ala Lys Asp Val Phe Leu Gly
340 345 350

Thr Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Glu Tyr Ser Ile Gly
355 360 365

Met Leu Leu Arg Ile Ala Lys Gly Tyr Glu Ala Lys Leu Glu Lys Cys
370 375 380

Cys Ala Glu Ala Asp Pro His Ala Cys Tyr Ala Lys Val Phe Asp Glu
385 390 395 400

Leu Gln Pro Leu Ile Asp Glu Pro Lys Lys Leu Val Gln Gln Asn Cys
405 410 415

Glu Leu Phe Asp Lys Leu Gly Glu Tyr Gly Phe Gln Asn Ala Leu Ala
420 425 430

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

Glu Tyr Ala Arg Lys Leu Gly Ser Val Gly Thr Lys Cys Cys Ser Leu
450 455 460

Pro Glu Thr Glu Arg Leu Ser Cys Thr Glu Asn Tyr Leu Ala Leu Ile
465 470 475 480

Leu Asn Arg Leu Cys Ile Leu His Glu Lys Thr Pro Val Ser Glu Arg
485 490 495

Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
500 505 510

Ser Ala Leu His Val Asp Glu Thr Tyr Val Pro Lys Pro Phe His Ala
515 520 525

Asp Ser Phe Thr Phe His Ala Asp Ile Cys Thr Leu Pro Glu Lys Glu
530 535 540

Lys Gln Val Lys Lys Gln Met Ala Leu Val Glu Leu Val Lys His Lys
545 550 555 560

Pro Lys Ala Ser Glu Glu Gln Met Lys Thr Val Met Gly Asp Phe Ala

565 570 575

Ala Phe Leu Lys Lys Cys Cys Asp Ala Asp Asn Lys Glu Ala Cys Phe
580 585 590

Thr Glu Asp Gly Pro Lys Leu Val Ala Lys Cys Gln Ala Thr Leu Ala
595 600 605

<210> 101
<211> 607
<212> PRT
<213> Equus caballus

<400> 101

Met Lys Trp Val Thr Phe Val Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

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

His Arg Phe Asn Asp Leu Gly Glu Lys His Phe Lys Gly Leu Val Leu
35 40 45

Val Ala Phe Ser Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
50 55 60

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Lys Cys Ala Ala Asp
65 70 75 80

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
85 90 95

Lys Leu Cys Thr Val Ala Thr Leu Arg Ala Thr Tyr Gly Glu Leu Ala
100 105 110

Asp Cys Cys Glu Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Thr
115 120 125

His Lys Asp Asp His Pro Asn Leu Pro Lys Leu Lys Pro Glu Pro Asp
130 135 140

Ala Gln Cys Ala Ala Phe Gln Glu Asp Pro Asp Lys Phe Leu Gly Lys
145 150 155 160

Tyr Leu Tyr Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Gly Pro Glu
165 170 175

Leu Leu Phe His Ala Glu Glu Tyr Lys Ala Asp Phe Thr Glu Cys Cys
180 185 190

Pro Ala Asp Asp Lys Leu Ala Cys Leu Ile Pro Lys Leu Asp Ala Leu
195 200 205

```
Lys Glu Arg Ile Leu Leu Ser Ser Ala Lys Glu Arg Leu Lys Cys Ser
    210                 215                 220

Ser Phe Gln Asn Phe Gly Glu Arg Ala Val Lys Ala Trp Ser Val Ala
225                 230                 235                 240

Arg Leu Ser Gln Lys Phe Pro Lys Ala Asp Phe Ala Glu Val Ser Lys
                245                 250                 255

Ile Val Thr Asp Leu Thr Lys Val His Lys Glu Cys Cys His Gly Asp
            260                 265                 270

Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys
        275                 280                 285

Glu His Gln Asp Ser Ile Ser Gly Lys Leu Lys Ala Cys Cys Asp Lys
    290                 295                 300

Pro Leu Leu Gln Lys Ser His Cys Ile Ala Glu Val Lys Glu Asp Asp
305                 310                 315                 320

Leu Pro Ser Asp Leu Pro Ala Leu Ala Ala Asp Phe Ala Glu Asp Lys
                325                 330                 335

Glu Ile Cys Lys His Tyr Lys Asp Ala Lys Asp Val Phe Leu Gly Thr
            340                 345                 350

Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Asp Tyr Ser Val Ser Leu
        355                 360                 365

Leu Leu Arg Ile Ala Lys Thr Tyr Glu Ala Thr Leu Glu Lys Cys Cys
    370                 375                 380

Ala Glu Ala Asp Pro Pro Ala Cys Tyr Arg Thr Val Phe Asp Gln Phe
385                 390                 395                 400

Thr Pro Leu Val Glu Glu Pro Lys Ser Leu Val Lys Lys Asn Cys Asp
                405                 410                 415

Leu Phe Glu Glu Val Gly Glu Tyr Asp Phe Gln Asn Ala Leu Ile Val
            420                 425                 430

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

Ile Gly Arg Thr Leu Gly Lys Val Gly Ser Arg Cys Cys Lys Leu Pro
    450                 455                 460

Glu Ser Glu Arg Leu Pro Cys Ser Glu Asn His Leu Ala Leu Ala Leu
465                 470                 475                 480
```

```
Asn Arg Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Glu Lys Ile
                485                 490                 495

Thr Lys Cys Cys Thr Asp Ser Leu Ala Glu Arg Arg Pro Cys Phe Ser
            500                 505                 510

Ala Leu Glu Leu Asp Glu Gly Tyr Val Pro Lys Glu Phe Lys Ala Glu
        515                 520                 525

Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Pro Glu Asp Glu Lys
    530                 535                 540

Gln Ile Lys Lys Gln Ser Ala Leu Ala Glu Leu Val Lys His Lys Pro
545                 550                 555                 560

Lys Ala Thr Lys Glu Gln Leu Lys Thr Val Leu Gly Asn Phe Ser Ala
                565                 570                 575

Phe Val Ala Lys Cys Cys Gly Arg Glu Asp Lys Glu Ala Cys Phe Ala
            580                 585                 590

Glu Glu Gly Pro Lys Leu Val Ala Ser Ser Gln Leu Ala Leu Ala
        595                 600                 605
```

<210> 102
<211> 609
<212> PRT
<213> Homo sapiens

<400> 102

```
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1               5                   10                  15

Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala
            20                  25                  30

His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu
        35                  40                  45

Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
    50                  55                  60

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
65                  70                  75                  80

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
                85                  90                  95

Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
            100                 105                 110
```

```
Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
        115                 120                 125

His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
    130                 135                 140

Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
145                 150                 155                 160

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
                165                 170                 175

Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
            180                 185                 190

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
        195                 200                 205

Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys
    210                 215                 220

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
225                 230                 235                 240

Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
                245                 250                 255

Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
            260                 265                 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
        275                 280                 285

Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
    290                 295                 300

Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
305                 310                 315                 320

Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
                325                 330                 335

Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
            340                 345                 350

Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
        355                 360                 365

Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
    370                 375                 380
```

```
Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
385                 390                 395                 400

Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
                405                 410                 415

Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
            420                 425                 430

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

Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
    450                 455                 460

Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val
465                 470                 475                 480

Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
                485                 490                 495

Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
            500                 505                 510

Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
        515                 520                 525

Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu
    530                 535                 540

Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
545                 550                 555                 560

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala
                565                 570                 575

Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe
            580                 585                 590

Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly
        595                 600                 605

Leu
```

<210> 103
<211> 600
<212> PRT
<213> Macca mulatta

<400> 103

```
Leu Leu Phe Leu Phe Ser Ser Ala Tyr Ser Arg Gly Val Phe Arg Arg
1               5                  10                  15

Asp Thr His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
            20                  25                  30

Glu His Phe Lys Gly Leu Val Leu Val Ala Phe Ser Gln Tyr Leu Gln
        35                  40                  45

Gln Cys Pro Phe Glu Glu His Val Lys Leu Val Asn Glu Val Thr Glu
    50                  55                  60

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
65                  70                  75                  80

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
                85                  90                  95

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
            100                 105                 110

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
        115                 120                 125

Pro Pro Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
    130                 135                 140

Asp Asn Glu Ala Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Val Ala Arg
145                 150                 155                 160

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Ala Arg
                165                 170                 175

Tyr Lys Ala Ala Phe Ala Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
            180                 185                 190

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
        195                 200                 205

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Asp
    210                 215                 220

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Lys Phe Pro
225                 230                 235                 240

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
                245                 250                 255

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
            260                 265                 270
```

```
Arg Ala Asp Leu Ala Lys Tyr Met Cys Glu Asn Gln Asp Ser Ile Ser
        275                 280                 285

Ser Lys Leu Lys Glu Cys Cys Asp Lys Pro Leu Leu Glu Lys Ser His
    290                 295                 300

Cys Leu Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
305                 310                 315                 320

Leu Ala Ala Asp Tyr Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
                325                 330                 335

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
            340                 345                 350

Arg His Pro Asp Tyr Ser Val Met Leu Leu Leu Arg Leu Ala Lys Ala
        355                 360                 365

Tyr Glu Ala Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
    370                 375                 380

Cys Tyr Ala Lys Val Phe Asp Glu Phe Gln Pro Leu Val Glu Glu Pro
385                 390                 395                 400

Gln Asn Leu Val Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
                405                 410                 415

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
            420                 425                 430

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
        435                 440                 445

Val Gly Ala Lys Cys Cys Lys Leu Pro Glu Ala Lys Arg Met Pro Cys
    450                 455                 460

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Arg Leu Cys Val Leu His
465                 470                 475                 480

Glu Lys Thr Pro Val Ser Glu Lys Val Thr Lys Cys Cys Thr Glu Ser
                485                 490                 495

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Leu Asp Glu Ala
            500                 505                 510

Tyr Val Pro Lys Ala Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
        515                 520                 525

Met Cys Thr Leu Ser Glu Lys Glu Lys Gln Val Lys Lys Gln Thr Ala
    530                 535                 540
```

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
545 550 555 560

Lys Gly Val Met Asp Asn Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
565 570 575

Ala Asp Asp Lys Glu Ala Cys Phe Ala Glu Glu Gly Pro Lys Phe Val
580 585 590

Ala Ala Ser Gln Ala Ala Leu Ala
595 600

<210> 104
<211> 608
<212> PRT
<213> Mus musculus

<400> 104

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

Phe Ser Arg Gly Val Phe Arg Arg Glu Ala His Lys Ser Glu Ile Ala
20 25 30

His Arg Tyr Asn Asp Leu Gly Glu Gln His Phe Lys Gly Leu Val Leu
35 40 45

Ile Ala Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp Glu His Ala
50 55 60

Lys Leu Val Gln Glu Val Thr Asp Phe Ala Lys Thr Cys Val Ala Asp
65 70 75 80

Glu Ser Ala Ala Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
85 90 95

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

Asp Cys Cys Thr Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
115 120 125

His Lys Asp Asp Asn Pro Ser Leu Pro Pro Phe Glu Arg Pro Glu Ala
130 135 140

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

His Tyr Leu His Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
165 170 175

Glu Leu Leu Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu Thr Gln Cys

```
            180                 185                 190

Cys Ala Glu Ala Asp Lys Glu Ser Cys Leu Thr Pro Lys Leu Asp Gly
        195                 200                 205

Val Lys Glu Lys Ala Leu Val Ser Ser Val Arg Gln Arg Met Lys Cys
    210                 215                 220

Ser Ser Met Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
225                 230                 235                 240

Ala Arg Leu Ser Gln Thr Phe Pro Asn Ala Asp Phe Ala Glu Ile Thr
                245                 250                 255

Lys Leu Ala Thr Asp Leu Thr Lys Val Asn Lys Glu Cys Cys His Gly
            260                 265                 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Glu Leu Ala Lys Tyr Met
        275                 280                 285

Cys Glu Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr Cys Cys Asp
    290                 295                 300

Lys Pro Leu Leu Lys Lys Ala His Cys Leu Ser Glu Val Glu His Asp
305                 310                 315                 320

Thr Met Pro Ala Asp Leu Pro Ala Ile Ala Ala Asp Phe Val Glu Asp
                325                 330                 335

Gln Glu Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
            340                 345                 350

Thr Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Asp Tyr Ser Val Ser
        355                 360                 365

Leu Leu Leu Arg Leu Ala Lys Lys Tyr Glu Ala Thr Leu Glu Lys Cys
    370                 375                 380

Cys Ala Glu Ala Asn Pro Pro Ala Cys Tyr Gly Thr Val Leu Ala Glu
385                 390                 395                 400

Phe Gln Pro Leu Val Glu Glu Pro Lys Asn Leu Val Lys Thr Asn Cys
                405                 410                 415

Asp Leu Tyr Glu Lys Leu Gly Glu Tyr Gly Phe Gln Asn Ala Ile Leu
            420                 425                 430

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

Glu Ala Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys Cys Thr Leu
```

```
450                 455                 460

Pro Glu Asp Gln Arg Leu Pro Cys Val Glu Asp Tyr Leu Ser Ala Ile
465                 470                 475                 480

Leu Asn Arg Val Cys Leu Leu His Glu Lys Thr Pro Val Ser Glu His
                485                 490                 495

Val Thr Lys Cys Cys Ser Gly Ser Leu Val Glu Arg Arg Pro Cys Phe
            500                 505                 510

Ser Ala Leu Thr Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Lys Ala
        515                 520                 525

Glu Thr Phe Thr Phe His Ser Asp Ile Cys Thr Leu Pro Glu Lys Glu
    530                 535                 540

Lys Gln Ile Lys Lys Gln Thr Ala Leu Ala Glu Leu Val Lys His Lys
545                 550                 555                 560

Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr Val Met Asp Asp Phe Ala
                565                 570                 575

Gln Phe Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp Thr Cys Phe
            580                 585                 590

Ser Thr Glu Gly Pro Asn Leu Val Thr Arg Cys Lys Asp Ala Leu Ala
        595                 600                 605

<210>  105
<211>  607
<212>  PRT
<213>  Sus scrofa

<400>  105

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

Tyr Ser Arg Gly Val Phe Arg Arg Asp Thr Tyr Lys Ser Glu Ile Ala
            20                  25                  30

His Arg Phe Lys Asp Leu Gly Glu Gln Tyr Phe Lys Gly Leu Val Leu
        35                  40                  45

Ile Ala Phe Ser Gln His Leu Gln Gln Cys Pro Tyr Glu Glu His Val
    50                  55                  60

Lys Leu Val Arg Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
65                  70                  75                  80

Glu Ser Ala Glu Asn Cys Asp Lys Ser Ile His Thr Leu Phe Gly Asp
                85                  90                  95
```

```
Lys Leu Cys Ala Ile Pro Ser Leu Arg Glu His Tyr Gly Asp Leu Ala
            100                 105                 110

Asp Cys Cys Glu Lys Glu Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
        115                 120                 125

His Lys Asn Asp Asn Pro Asp Ile Pro Lys Leu Lys Pro Asp Pro Val
    130                 135                 140

Ala Leu Cys Ala Asp Phe Gln Glu Asp Glu Gln Lys Phe Trp Gly Lys
145                 150                 155                 160

Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu
                165                 170                 175

Leu Leu Tyr Tyr Ala Ile Ile Tyr Lys Asp Val Phe Ser Glu Cys Cys
            180                 185                 190

Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Ile Glu His Leu
        195                 200                 205

Arg Glu Lys Val Leu Thr Ser Ala Ala Lys Gln Arg Leu Lys Cys Ala
    210                 215                 220

Ser Ile Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ser Leu Ala
225                 230                 235                 240

Arg Leu Ser Gln Arg Phe Pro Lys Ala Asp Phe Thr Glu Ile Ser Lys
                245                 250                 255

Ile Val Thr Asp Leu Ala Lys Val His Lys Glu Cys Cys His Gly Asp
            260                 265                 270

Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys
        275                 280                 285

Glu Asn Gln Asp Thr Ile Ser Thr Lys Leu Lys Glu Cys Cys Asp Lys
    290                 295                 300

Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Ala Lys Arg Asp Glu
305                 310                 315                 320

Leu Pro Ala Asp Leu Asn Pro Leu Glu His Asp Phe Val Glu Asp Lys
                325                 330                 335

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

Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Asp Tyr Ser Val Ser Leu
        355                 360                 365
```

```
Leu Leu Arg Ile Ala Lys Ile Tyr Glu Ala Thr Leu Glu Asp Cys Cys
    370                 375                 380

Ala Lys Glu Asp Pro Pro Ala Cys Tyr Ala Thr Val Phe Asp Lys Phe
385                 390                 395                 400

Gln Pro Leu Val Asp Glu Pro Lys Asn Leu Ile Lys Gln Asn Cys Glu
                405                 410                 415

Leu Phe Glu Lys Leu Gly Glu Tyr Gly Phe Gln Asn Ala Leu Ile Val
            420                 425                 430

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

Val Ala Arg Lys Leu Gly Leu Val Gly Ser Arg Cys Cys Lys Arg Pro
    450                 455                 460

Glu Glu Glu Arg Leu Ser Cys Ala Glu Asp Tyr Leu Ser Leu Val Leu
465                 470                 475                 480

Asn Arg Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Glu Lys Val
                485                 490                 495

Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser
            500                 505                 510

Ala Leu Thr Pro Asp Glu Thr Tyr Lys Pro Lys Glu Phe Val Glu Gly
        515                 520                 525

Thr Phe Thr Phe His Ala Asp Leu Cys Thr Leu Pro Glu Asp Glu Lys
    530                 535                 540

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Leu Lys His Lys Pro
545                 550                 555                 560

His Ala Thr Glu Glu Gln Leu Arg Thr Val Leu Gly Asn Phe Ala Ala
                565                 570                 575

Phe Val Gln Lys Cys Cys Ala Ala Pro Asp His Glu Ala Cys Phe Ala
            580                 585                 590

Val Glu Gly Pro Lys Phe Val Ile Glu Ile Arg Gly Ile Leu Ala
        595                 600                 605
```

<210> 106
<211> 608
<212> PRT
<213> Oryctolagus cuniculus

<400> 106

```
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1               5                  10                  15

Tyr Ser Arg Gly Val Phe Arg Arg Glu Ala His Lys Ser Glu Ile Ala
            20                  25                  30

His Arg Phe Asn Asp Val Gly Glu Glu His Phe Ile Gly Leu Val Leu
        35                  40                  45

Ile Thr Phe Ser Gln Tyr Leu Gln Lys Cys Pro Tyr Glu Glu His Ala
    50                  55                  60

Lys Leu Val Lys Glu Val Thr Asp Leu Ala Lys Ala Cys Val Ala Asp
65                  70                  75                  80

Glu Ser Ala Ala Asn Cys Asp Lys Ser Leu His Asp Ile Phe Gly Asp
                85                  90                  95

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

Asp Cys Cys Glu Lys Lys Glu Pro Glu Arg Asn Glu Cys Phe Leu His
        115                 120                 125

His Lys Asp Asp Lys Pro Asp Leu Pro Pro Phe Ala Arg Pro Glu Ala
    130                 135                 140

Asp Val Leu Cys Lys Ala Phe His Asp Asp Glu Lys Ala Phe Phe Gly
145                 150                 155                 160

His Tyr Leu Tyr Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
                165                 170                 175

Glu Leu Leu Tyr Tyr Ala Gln Lys Tyr Lys Ala Ile Leu Thr Glu Cys
            180                 185                 190

Cys Glu Ala Ala Asp Lys Gly Ala Cys Leu Thr Pro Lys Leu Asp Ala
        195                 200                 205

Leu Glu Gly Lys Ser Leu Ile Ser Ala Ala Gln Glu Arg Leu Arg Cys
    210                 215                 220

Ala Ser Ile Gln Lys Phe Gly Asp Arg Ala Tyr Lys Ala Trp Ala Leu
225                 230                 235                 240

Val Arg Leu Ser Gln Arg Phe Pro Lys Ala Asp Phe Thr Asp Ile Ser
                245                 250                 255

Lys Ile Val Thr Asp Leu Thr Lys Val His Lys Glu Cys Cys His Gly
            260                 265                 270
```

```
Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Met
        275                 280                 285

Cys Glu His Gln Glu Thr Ile Ser Ser His Leu Lys Glu Cys Cys Asp
    290                 295                 300

Lys Pro Ile Leu Glu Lys Ala His Cys Ile Tyr Gly Leu His Asn Asp
305                 310                 315                 320

Glu Thr Pro Ala Gly Leu Pro Ala Val Ala Glu Glu Phe Val Glu Asp
                325                 330                 335

Lys Asp Val Cys Lys Asn Tyr Glu Glu Ala Lys Asp Leu Phe Leu Gly
            340                 345                 350

Lys Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Asp Tyr Ser Val Val
        355                 360                 365

Leu Leu Leu Arg Leu Gly Lys Ala Tyr Glu Ala Thr Leu Lys Lys Cys
    370                 375                 380

Cys Ala Thr Asp Asp Pro His Ala Cys Tyr Ala Lys Val Leu Asp Glu
385                 390                 395                 400

Phe Gln Pro Leu Val Asp Glu Pro Lys Asn Leu Val Lys Gln Asn Cys
                405                 410                 415

Glu Leu Tyr Glu Gln Leu Gly Asp Tyr Asn Phe Gln Asn Ala Leu Leu
            420                 425                 430

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

Glu Ile Ser Arg Ser Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
    450                 455                 460

Pro Glu Ala Glu Arg Leu Pro Cys Val Glu Asp Tyr Leu Ser Val Val
465                 470                 475                 480

Leu Asn Arg Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Glu Lys
                485                 490                 495

Val Thr Lys Cys Cys Ser Glu Ser Leu Val Asp Arg Arg Pro Cys Phe
            500                 505                 510

Ser Ala Leu Gly Pro Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
        515                 520                 525

Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Pro Glu Thr Glu
    530                 535                 540
```

```
Arg Lys Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
545                 550                 555                 560

Pro His Ala Thr Asn Asp Gln Leu Lys Thr Val Val Gly Glu Phe Thr
                565                 570                 575

Ala Leu Leu Asp Lys Cys Cys Ser Ala Glu Asp Lys Glu Ala Cys Phe
            580                 585                 590

Ala Val Glu Gly Pro Lys Leu Val Glu Ser Ser Lys Ala Thr Leu Gly
        595                 600                 605
```

<210> 107
<211> 608
<212> PRT
<213> Rattus norvegicus

<400> 107

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

Phe Ser Arg Gly Val Phe Arg Arg Glu Ala His Lys Ser Glu Ile Ala
            20                  25                  30

His Arg Phe Lys Asp Leu Gly Glu Gln His Phe Lys Gly Leu Val Leu
        35                  40                  45

Ile Ala Phe Ser Gln Tyr Leu Gln Lys Cys Pro Tyr Glu Glu His Ile
    50                  55                  60

Lys Leu Val Gln Glu Val Thr Asp Phe Ala Lys Thr Cys Val Ala Asp
65                  70                  75                  80

Glu Asn Ala Glu Asn Cys Asp Lys Ser Ile His Thr Leu Phe Gly Asp
                85                  90                  95

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

Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
        115                 120                 125

His Lys Asp Asp Asn Pro Asn Leu Pro Pro Phe Gln Arg Pro Glu Ala
    130                 135                 140

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

His Tyr Leu His Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
                165                 170                 175
```

```
Glu Leu Leu Tyr Tyr Ala Glu Lys Tyr Asn Glu Val Leu Thr Gln Cys
            180                 185                 190

Cys Thr Glu Ser Asp Lys Ala Ala Cys Leu Thr Pro Lys Leu Asp Ala
        195                 200                 205

Val Lys Glu Lys Ala Leu Val Ala Ala Val Arg Gln Arg Met Lys Cys
    210                 215                 220

Ser Ser Met Gln Arg Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
225                 230                 235                 240

Ala Arg Met Ser Gln Arg Phe Pro Asn Ala Glu Phe Ala Glu Ile Thr
                245                 250                 255

Lys Leu Ala Thr Asp Val Thr Lys Ile Asn Lys Glu Cys Cys His Gly
            260                 265                 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Glu Leu Ala Lys Tyr Met
        275                 280                 285

Cys Glu Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Ala Cys Cys Asp
    290                 295                 300

Lys Pro Val Leu Gln Lys Ser Gln Cys Leu Ala Glu Ile Glu His Asp
305                 310                 315                 320

Asn Ile Pro Ala Asp Leu Pro Ser Ile Ala Ala Asp Phe Val Glu Asp
                325                 330                 335

Lys Glu Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
            340                 345                 350

Thr Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Asp Tyr Ser Val Ser
        355                 360                 365

Leu Leu Leu Arg Leu Ala Lys Lys Tyr Glu Ala Thr Leu Glu Lys Cys
    370                 375                 380

Cys Ala Glu Gly Asp Pro Pro Ala Cys Tyr Gly Thr Val Leu Ala Glu
385                 390                 395                 400

Phe Gln Pro Leu Val Glu Glu Pro Lys Asn Leu Val Lys Thr Asn Cys
                405                 410                 415

Glu Leu Tyr Glu Lys Leu Gly Glu Tyr Gly Phe Gln Asn Ala Val Leu
            420                 425                 430

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

```
Glu Ala Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys Cys Thr Leu
    450                 455                 460

Pro Glu Ala Gln Arg Leu Pro Cys Val Glu Asp Tyr Leu Ser Ala Ile
465                 470                 475                 480

Leu Asn Arg Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Glu Lys
                485                 490                 495

Val Thr Lys Cys Cys Ser Gly Ser Leu Val Glu Arg Arg Pro Cys Phe
            500                 505                 510

Ser Ala Leu Thr Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Lys Ala
        515                 520                 525

Glu Thr Phe Thr Phe His Ser Asp Ile Cys Thr Leu Pro Asp Lys Glu
    530                 535                 540

Lys Gln Ile Lys Lys Gln Thr Ala Leu Ala Glu Leu Val Lys His Lys
545                 550                 555                 560

Pro Lys Ala Thr Glu Asp Gln Leu Lys Thr Val Met Gly Asp Phe Ala
                565                 570                 575

Gln Phe Val Asp Lys Cys Cys Lys Ala Ala Asp Lys Asp Asn Cys Phe
            580                 585                 590

Ala Thr Glu Gly Pro Asn Leu Val Ala Arg Ser Lys Glu Ala Leu Ala
        595                 600                 605
```

<210> 108
<211> 607
<212> PRT
<213> Ovis aries

<400> 108

```
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Leu Leu Phe Ser Ser Ala
1               5                   10                  15

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

His Arg Phe Asn Asp Leu Gly Glu Glu Asn Phe Gln Gly Leu Val Leu
        35                  40                  45

Ile Ala Phe Ser Gln Tyr Leu Gln Gln Cys Pro Phe Asp Glu His Val
    50                  55                  60

Lys Leu Val Lys Glu Leu Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
65                  70                  75                  80

Glu Ser His Ala Gly Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
```

85 90 95

Glu Leu Cys Lys Val Ala Thr Leu Arg Glu Thr Tyr Gly Asp Met Ala
100 105 110

Asp Cys Cys Glu Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Asn
115 120 125

His Lys Asp Asp Ser Pro Asp Leu Pro Lys Leu Lys Pro Glu Pro Asp
130 135 140

Thr Leu Cys Ala Glu Phe Lys Ala Asp Glu Lys Lys Phe Trp Gly Lys
145 150 155 160

Tyr Leu Tyr Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu
165 170 175

Leu Leu Tyr Tyr Ala Asn Lys Tyr Asn Gly Val Phe Gln Glu Cys Cys
180 185 190

Gln Ala Glu Asp Lys Gly Ala Cys Leu Leu Pro Lys Ile Asp Ala Met
195 200 205

Arg Glu Lys Val Leu Ala Ser Ser Ala Arg Gln Arg Leu Arg Cys Ala
210 215 220

Ser Ile Gln Lys Phe Gly Glu Arg Ala Leu Lys Ala Trp Ser Val Ala
225 230 235 240

Arg Leu Ser Gln Lys Phe Pro Lys Ala Asp Phe Thr Asp Val Thr Lys
245 250 255

Ile Val Thr Asp Leu Thr Lys Val His Lys Glu Cys Cys His Gly Asp
260 265 270

Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys
275 280 285

Asp His Gln Asp Ala Leu Ser Ser Lys Leu Lys Glu Cys Cys Asp Lys
290 295 300

Pro Val Leu Glu Lys Ser His Cys Ile Ala Glu Val Asp Lys Asp Ala
305 310 315 320

Val Pro Glu Asn Leu Pro Pro Leu Thr Ala Asp Phe Ala Glu Asp Lys
325 330 335

Glu Val Cys Lys Asn Tyr Gln Glu Ala Lys Asp Val Phe Leu Gly Ser
340 345 350

Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Glu Tyr Ala Val Ser Val

355 360 365

Leu Leu Arg Leu Ala Lys Glu Tyr Glu Ala Thr Leu Glu Asp Cys Cys
370 375 380

Ala Lys Glu Asp Pro His Ala Cys Tyr Ala Thr Val Phe Asp Lys Leu
385 390 395 400

Lys His Leu Val Asp Glu Pro Gln Asn Leu Ile Lys Lys Asn Cys Glu
405 410 415

Leu Phe Glu Lys His Gly Glu Tyr Gly Phe Gln Asn Ala Leu Ile Val
420 425 430

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

Ile Ser Arg Ser Leu Gly Lys Val Gly Thr Lys Cys Cys Ala Lys Pro
450 455 460

Glu Ser Glu Arg Met Pro Cys Thr Glu Asp Tyr Leu Ser Leu Ile Leu
465 470 475 480

Asn Arg Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Glu Lys Val
485 490 495

Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser
500 505 510

Asp Leu Thr Leu Asp Glu Thr Tyr Val Pro Lys Pro Phe Asp Glu Lys
515 520 525

Phe Phe Thr Phe His Ala Asp Ile Cys Thr Leu Pro Asp Thr Glu Lys
530 535 540

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Leu Lys His Lys Pro
545 550 555 560

Lys Ala Thr Asp Glu Gln Leu Lys Thr Val Met Glu Asn Phe Val Ala
565 570 575

Phe Val Asp Lys Cys Cys Ala Ala Asp Asp Lys Glu Gly Cys Phe Val
580 585 590

Leu Glu Gly Pro Lys Leu Val Ala Ser Thr Gln Ala Ala Leu Ala
595 600 605