<110> HANMI PHARM. CO., LTD.

<120> Novel therapeutic enzyme fusion protein and use thereof

<130> OPA18228

<150> KR 10-2017-0086594
<151> 2017-07-07

<160> 26

<170> KoPatentIn 3.0

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cgcctgtacg acttcaactc ctactggagg gtgcacgctg gaaacttctc caccatcccc 360

cagtacttca aggagaatgg ctatgtgacc atgtcggtgg gaaaagtctt tcaccctggg 420

atatcttcta accataccga tgattctccg tatagctggt cttttccacc ttatcatcct 480

tcctctgaga agtatgaaaa cactaagaca tgtcgagggc cagatggaga actccatgcc 540

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Thr Thr Asp Ala Leu Asn Val Leu Leu Ile Ile Val Asp Asp Leu Arg
         35                  40                  45

Pro Ser Leu Gly Cys Tyr Gly Asp Lys Leu Val Arg Ser Pro Asn Ile
     50                  55                  60

Asp Gln Leu Ala Ser His Ser Leu Leu Phe Gln Asn Ala Phe Ala Gln
 65                  70                  75                  80

Gln Ala Val Cys Ala Pro Ser Arg Val Ser Phe Leu Thr Gly Arg Arg
                 85                  90                  95

Pro Asp Thr Thr Arg Leu Tyr Asp Phe Asn Ser Tyr Trp Arg Val His
            100                 105                 110

Ala Gly Asn Phe Ser Thr Ile Pro Gln Tyr Phe Lys Glu Asn Gly Tyr
        115                 120                 125

Val Thr Met Ser Val Gly Lys Val Phe His Pro Gly Ile Ser Ser Asn
    130                 135                 140

His Thr Asp Asp Ser Pro Tyr Ser Trp Ser Phe Pro Pro Tyr His Pro
145                 150                 155                 160

Ser Ser Glu Lys Tyr Glu Asn Thr Lys Thr Cys Arg Gly Pro Asp Gly
                165                 170                 175

Glu Leu His Ala Asn Leu Leu Cys Pro Val Asp Val Leu Asp Val Pro
            180                 185                 190

Glu Gly Thr Leu Pro Asp Lys Gln Ser Thr Glu Gln Ala Ile Gln Leu
        195                 200                 205

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

Leu Tyr Pro Leu Glu Asn Ile Thr Leu Ala Pro Asp Pro Glu Val Pro
                245                 250                 255

Asp Gly Leu Pro Pro Val Ala Tyr Asn Pro Trp Met Asp Ile Arg Gln
            260                 265                 270

Arg Glu Asp Val Gln Ala Leu Asn Ile Ser Val Pro Tyr Gly Pro Ile
        275                 280                 285
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Pro Val Asp Phe Gln Arg Lys Ile Arg Gln Ser Tyr Phe Ala Ser Val
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Ser Tyr Leu Asp Thr Gln Val Gly Arg Leu Leu Ser Ala Leu Asp Asp
305                 310                 315                 320

Leu Gln Leu Ala Asn Ser Thr Ile Ile Ala Phe Thr Ser Asp His Gly
                325                 330                 335

Trp Ala Leu Gly Glu His Gly Glu Trp Ala Lys Tyr Ser Asn Phe Asp
            340                 345                 350

Val Ala Thr His Val Pro Leu Ile Phe Tyr Val Pro Gly Arg Thr Ala
        355                 360                 365

Ser Leu Pro Glu Ala Gly Glu Lys Leu Phe Pro Tyr Leu Asp Pro Phe
    370                 375                 380

Asp Ser Ala Ser Gln Leu Met Glu Pro Gly Arg Gln Ser Met Asp Leu
385                 390                 395                 400

Val Glu Leu Val Ser Leu Phe Pro Thr Leu Ala Gly Leu Ala Gly Leu
                405                 410                 415

Gln Val Pro Pro Arg Cys Pro Val Pro Ser Phe His Val Glu Leu Cys
            420                 425                 430

Arg Glu Gly Lys Asn Leu Leu Lys His Phe Arg Phe Arg Asp Leu Glu
        435                 440                 445

Glu Asp Pro Tyr Leu Pro Gly Asn Pro Arg Glu Leu Ile Ala Tyr Ser
    450                 455                 460

Gln Tyr Pro Arg Pro Ser Asp Ile Pro Gln Trp Asn Ser Asp Lys Pro
465                 470                 475                 480

Ser Leu Lys Asp Ile Lys Ile Met Gly Tyr Ser Ile Arg Thr Ile Asp
                485                 490                 495

Tyr Arg Tyr Thr Val Trp Val Gly Phe Asn Pro Asp Glu Phe Leu Ala
            500                 505                 510

Asn Phe Ser Asp Ile His Ala Gly Glu Leu Tyr Phe Val Asp Ser Asp
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Pro Leu Gln Asp His Asn Met Tyr Asn Asp Ser Gln Gly Gly Asp Leu
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Phe Gln Leu Leu Met Pro
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gccagccggc cgccccacct ggtcttcttg ctggcagacg acctaggctg gaacgacgtc       180

ggcttccacg gctcccgcat ccgcacgccg cacctggacg cgctggcggc cggcggggtg       240

ctcctggaca actactacac gcagccgctg tgcacgccgt cgcggagcca gctgctcact       300
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catatggtcg gaaaatggca cctgggaatg taccggaaag aatgccttcc aacccgccga 480

ggatttgata cctactttgg atatctcctg ggtagtgaag attattattc ccatgaacgc 540

tgtacattaa ttgacgctct gaatgtcaca cgatgtgctc ttgattttcg agatggcgaa 600

gaagttgcaa caggatataa aaatatgtat tcaacaaaca tattcaccaa aagggctata 660

gccctcataa ctaaccatcc accagagaag cctctgtttc tctaccttgc tctccagtct 720

gtgcatgagc cccttcaggt ccctgaggaa tacttgaagc catatgactt tatccaagac 780

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<213> Homo Sapiens

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             20                  25                  30

Ala Pro Pro Gly Ser Gly Ala Gly Ala Ser Arg Pro Pro His Leu Val
         35                  40                  45

Phe Leu Leu Ala Asp Asp Leu Gly Trp Asn Asp Val Gly Phe His Gly
     50                  55                  60

Ser Arg Ile Arg Thr Pro His Leu Asp Ala Leu Ala Ala Gly Gly Val
 65                  70                  75                  80

Leu Leu Asp Asn Tyr Tyr Thr Gln Pro Leu Cys Thr Pro Ser Arg Ser
                 85                  90                  95
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Gln Leu Leu Thr Gly Arg Tyr Gln Ile Arg Thr Gly Leu Gln His Gln
            100                 105                 110

Ile Ile Trp Pro Cys Gln Pro Ser Cys Val Pro Leu Asp Glu Lys Leu
        115                 120                 125

Leu Pro Gln Leu Leu Lys Glu Ala Gly Tyr Thr Thr His Met Val Gly
    130                 135                 140

Lys Trp His Leu Gly Met Tyr Arg Lys Glu Cys Leu Pro Thr Arg Arg
145                 150                 155                 160

Gly Phe Asp Thr Tyr Phe Gly Tyr Leu Leu Gly Ser Glu Asp Tyr Tyr
                165                 170                 175

Ser His Glu Arg Cys Thr Leu Ile Asp Ala Leu Asn Val Thr Arg Cys
            180                 185                 190

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

Met Tyr Ser Thr Asn Ile Phe Thr Lys Arg Ala Ile Ala Leu Ile Thr
    210                 215                 220

Asn His Pro Pro Glu Lys Pro Leu Phe Leu Tyr Leu Ala Leu Gln Ser
225                 230                 235                 240

Val His Glu Pro Leu Gln Val Pro Glu Glu Tyr Leu Lys Pro Tyr Asp
                245                 250                 255

Phe Ile Gln Asp Lys Asn Arg His His Tyr Ala Gly Met Val Ser Leu
            260                 265                 270

Met Asp Glu Ala Val Gly Asn Val Thr Ala Ala Leu Lys Ser Ser Gly
        275                 280                 285

Leu Trp Asn Asn Thr Val Phe Ile Phe Ser Thr Asp Asn Gly Gly Gln
    290                 295                 300

Thr Leu Ala Gly Gly Asn Asn Trp Pro Leu Arg Gly Arg Lys Trp Ser
305                 310                 315                 320

Leu Trp Glu Gly Gly Val Arg Gly Val Gly Phe Val Ala Ser Pro Leu
                325                 330                 335

Leu Lys Gln Lys Gly Val Lys Asn Arg Glu Leu Ile His Ile Ser Asp
            340                 345                 350

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

Lys Pro Leu Asp Gly Phe Asp Val Trp Lys Thr Ile Ser Glu Gly Ser
    370                 375                 380

Pro Ser Pro Arg Ile Glu Leu Leu His Asn Ile Asp Pro Asn Phe Val
385                 390                 395                 400

Asp Ser Ser Pro Cys Pro Arg Asn Ser Met Ala Pro Ala Lys Asp Asp
                405                 410                 415

Ser Ser Leu Pro Glu Tyr Ser Ala Phe Asn Thr Ser Val His Ala Ala
            420                 425                 430

Ile Arg His Gly Asn Trp Lys Leu Leu Thr Gly Tyr Pro Gly Cys Gly
        435                 440                 445

Tyr Trp Phe Pro Pro Pro Ser Gln Tyr Asn Val Ser Glu Ile Pro Ser
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450 455 460

Ser Asp Pro Pro Thr Lys Thr Leu Trp Leu Phe Asp Ile Asp Arg Asp
465 470 475 480

Pro Glu Glu Arg His Asp Leu Ser Arg Glu Tyr Pro His Ile Val Thr
485 490 495

Lys Leu Leu Ser Arg Leu Gln Phe Tyr His Lys His Ser Val Pro Val
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Tyr Phe Pro Ala Gln Asp Pro Arg Cys Asp Pro Lys Ala Thr Gly Val
515 520 525

Trp Gly Pro Trp Met
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<213> Artificial Sequence

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<223> Peptide Linker

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<210> 6
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide Linker

<400> 6
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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<210> 7
<211> 666
<212> DNA
<213> Artificial Sequence

<220>
<223> Immunoglobulin Fc variant

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agccaggaag accctgaggt ccagttcaac tggtacgtgg acggcgtgga ggtgcataat 180

gccaagacaa agccgcggga ggagcagttc aacagcacgt accgtgtggt cagcgtcctc 240

accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 300

ggcctcccat cctccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 360

caggtgtaca ccctgccccc atcccaggag gagatgacca agaaccaggt cagcctgacc 420

tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 480

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 540

tacagcaggc taaccgtgga caagagcagg tggcaggagg ggaacgtctt ctcatgctcc 600

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aaatga 666

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<211> 221
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<213> Artificial Sequence

<220>
<223> IgG4 Fc

<400> 8

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Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
            20                  25                  30

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
        35                  40                  45

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
    50                  55                  60

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
65                  70                  75                  80

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
                85                  90                  95

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
            100                 105                 110

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
        115                 120                 125

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
    130                 135                 140

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
145                 150                 155                 160

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
                165                 170                 175

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
            180                 185                 190

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
        195                 200                 205

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
    210                 215                 220
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<210> 9
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<213> Artificial Sequence

<220>
<223> Immunoglobulin Fc variant

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Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
             20                  25                  30

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
         35                  40                  45

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
     50                  55                  60

Pro Arg Glu Glu Gln Phe Gln Ser Thr Tyr Arg Val Val Ser Val Leu
 65                  70                  75                  80

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
                 85                  90                  95

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
            100                 105                 110

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
        115                 120                 125

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
    130                 135                 140

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
145                 150                 155                 160

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
                165                 170                 175

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
            180                 185                 190

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
        195                 200                 205

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
    210                 215                 220
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<210> 10
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<212> DNA
<213> Artificial Sequence

<220>
<223> IDS-F (KpnI)

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<210> 11
<211> 44
<212> DNA

<213> Artificial Sequence

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<223> IDS-R (overlap)

<400> 11
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<210> 12
<211> 34
<212> DNA
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<223> L15Fc(IDS)-F

<400> 12
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<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> L15Fc-R (XhoI)

<400> 13
gactcgagtc atttacccag agacagggag agg 33

<210> 14
<211> 26
<212> DNA
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<223> ARSB-F (KpnI)

<400> 14
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<210> 15
<211> 35
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<400> 15
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<210> 16
<211> 34
<212> DNA
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<223> L15Fc(ARSB)-F

<400> 16
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<210> 17
<211> 33
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<223> L15Fc-R (XhoI)

<400> 17
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<210> 18
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<212> DNA
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<223> Fc(S2P)_F

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<210> 19
<211> 43
<212> DNA
<213> Artificial Sequence

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<223> Fc(S2P)_R

<400> 19
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<220>
<223> Fc(N71Q)_F

<400> 20
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<210> 21
<211> 43
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<220>
<223> Fc(N71Q)_R

<400> 21
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<223> IDS-Fc

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ctcatcatcg tggatgacct gcgcccctcc ctgggctgtt atggggataa gctggtgagg 180

tccccaaata ttgaccaact ggcatcccac agcctcctct tccagaatgc ctttgcgcag 240

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ctggccgttg ggtatcataa gccacacatc cccttcagat accccaagga atttcagaag 720

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caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 2160

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 2220

ggctccttct tcctctacag caggctaacc gtggacaaga gcaggtggca ggaggggaac 2280

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 2340

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<212> PRT
<213> Artificial Sequence

<220>
<223> IDS-Fc

<400> 23

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Leu Ser Ser Val Cys Val Ala Leu Gly Ser Glu Thr Gln Ala Asn Ser
20 25 30

Thr Thr Asp Ala Leu Asn Val Leu Leu Ile Ile Val Asp Asp Leu Arg
35 40 45

Pro Ser Leu Gly Cys Tyr Gly Asp Lys Leu Val Arg Ser Pro Asn Ile
50 55 60

Asp Gln Leu Ala Ser His Ser Leu Leu Phe Gln Asn Ala Phe Ala Gln
65 70 75 80

Gln Ala Val Cys Ala Pro Ser Arg Val Ser Phe Leu Thr Gly Arg Arg
85 90 95

Pro Asp Thr Thr Arg Leu Tyr Asp Phe Asn Ser Tyr Trp Arg Val His
100 105 110

Ala Gly Asn Phe Ser Thr Ile Pro Gln Tyr Phe Lys Glu Asn Gly Tyr
115 120 125

Val Thr Met Ser Val Gly Lys Val Phe His Pro Gly Ile Ser Ser Asn
130 135 140

His Thr Asp Asp Ser Pro Tyr Ser Trp Ser Phe Pro Pro Tyr His Pro
145 150 155 160

Ser Ser Glu Lys Tyr Glu Asn Thr Lys Thr Cys Arg Gly Pro Asp Gly

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                165                 170                 175

Glu Leu His Ala Asn Leu Leu Cys Pro Val Asp Val Leu Asp Val Pro
            180                 185                 190

Glu Gly Thr Leu Pro Asp Lys Gln Ser Thr Glu Gln Ala Ile Gln Leu
        195                 200                 205

Leu Glu Lys Met Lys Thr Ser Ala Ser Pro Phe Phe Leu Ala Val Gly
    210                 215                 220

Tyr His Lys Pro His Ile Pro Phe Arg Tyr Pro Lys Glu Phe Gln Lys
225                 230                 235                 240

Leu Tyr Pro Leu Glu Asn Ile Thr Leu Ala Pro Asp Pro Glu Val Pro
                245                 250                 255

Asp Gly Leu Pro Pro Val Ala Tyr Asn Pro Trp Met Asp Ile Arg Gln
            260                 265                 270

Arg Glu Asp Val Gln Ala Leu Asn Ile Ser Val Pro Tyr Gly Pro Ile
        275                 280                 285

Pro Val Asp Phe Gln Arg Lys Ile Arg Gln Ser Tyr Phe Ala Ser Val
    290                 295                 300

Ser Tyr Leu Asp Thr Gln Val Gly Arg Leu Leu Ser Ala Leu Asp Asp
305                 310                 315                 320

Leu Gln Leu Ala Asn Ser Thr Ile Ile Ala Phe Thr Ser Asp His Gly
                325                 330                 335

Trp Ala Leu Gly Glu His Gly Glu Trp Ala Lys Tyr Ser Asn Phe Asp
            340                 345                 350

Val Ala Thr His Val Pro Leu Ile Phe Tyr Val Pro Gly Arg Thr Ala
        355                 360                 365

Ser Leu Pro Glu Ala Gly Glu Lys Leu Phe Pro Tyr Leu Asp Pro Phe
    370                 375                 380

Asp Ser Ala Ser Gln Leu Met Glu Pro Gly Arg Gln Ser Met Asp Leu
385                 390                 395                 400

Val Glu Leu Val Ser Leu Phe Pro Thr Leu Ala Gly Leu Ala Gly Leu
                405                 410                 415

Gln Val Pro Pro Arg Cys Pro Val Pro Ser Phe His Val Glu Leu Cys
            420                 425                 430

Arg Glu Gly Lys Asn Leu Leu Lys His Phe Arg Phe Arg Asp Leu Glu
        435                 440                 445

Glu Asp Pro Tyr Leu Pro Gly Asn Pro Arg Glu Leu Ile Ala Tyr Ser
    450                 455                 460

Gln Tyr Pro Arg Pro Ser Asp Ile Pro Gln Trp Asn Ser Asp Lys Pro
465                 470                 475                 480

Ser Leu Lys Asp Ile Lys Ile Met Gly Tyr Ser Ile Arg Thr Ile Asp
                485                 490                 495

Tyr Arg Tyr Thr Val Trp Val Gly Phe Asn Pro Asp Glu Phe Leu Ala
            500                 505                 510

Asn Phe Ser Asp Ile His Ala Gly Glu Leu Tyr Phe Val Asp Ser Asp
        515                 520                 525
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Pro Leu Gln Asp His Asn Met Tyr Asn Asp Ser Gln Gly Gly Asp Leu
530 535 540

Phe Gln Leu Leu Met Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
545 550 555 560

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

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
580 585 590

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
595 600 605

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
610 615 620

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Gln Ser Thr Tyr Arg
625 630 635 640

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
645 650 655

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
660 665 670

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
675 680 685

Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
690 695 700

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
705 710 715 720

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
725 730 735

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
740 745 750

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
755 760 765

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
770 775 780

Gly Lys
785

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<211> 2310
<212> DNA
<213> Artificial Sequence

<220>
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gccagccggc cgccccacct ggtcttcttg ctggcagacg acctaggctg gaacgacgtc 180

ggcttccacg gctcccgcat ccgcacgccg cacctggacg cgctggcggc cggcggggtg 240

ctcctggaca actactacac gcagccgctg tgcacgccgt cgcggagcca gctgctcact 300

ggccgctacc agatccgtac aggtttacag caccaaataa tctggccctg tcagcccagc 360

tgtgttcctc tggatgaaaa actcctgccc cagctcctaa aagaagcagg ttatactacc 420

catatggtcg gaaaatggca cctgggaatg taccggaaag aatgccttcc aacccgccga 480

ggatttgata cctactttgg atatctcctg ggtagtgaag attattattc ccatgaacgc 540

tgtacattaa ttgacgctct gaatgtcaca cgatgtgctc ttgattttcg agatggcgaa 600

gaagttgcaa caggatataa aaatatgtat tcaacaaaca tattcaccaa aagggctata 660

gccctcataa ctaaccatcc accagagaag cctctgtttc tctaccttgc tctccagtct 720

gtgcatgagc cccttcaggt ccctgaggaa tacttgaagc catatgactt tatccaagac 780

aagaacaggc atcactatgc aggaatggtg tcccttatgg atgaagcagt aggaaatgtc 840

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aacggagggc agactttggc agggggtaat aactggcccc ttcgaggaag aaaatggagc 960

ctgtgggaag gaggcgtccg aggggtgggc tttgtggcaa gccccttgct gaagcagaag 1020

ggcgtgaaga accgggagct catccacatc tctgactggc tgccaacact cgtgaagctg 1080

gccaggggac acaccaatgg cacaaagcct ctggatggct tcgacgtgtg gaaaaccatc 1140

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gactcttcac cgtgtcccag gaacagcatg gctccagcaa aggatgactc ttctcttcca 1260

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tgtgatccca aggccactgg ggtgtggggc ccttggatgg gtggaggcgg ttcaggcgga 1620

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tacaagtgca aggtctccaa caaaggcctc ccatcctcca tcgagaaaac catctccaaa 1980

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatccca ggaggagatg 2040

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 2100

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 2160

gactccgacg gctccttctt cctctacagc aggctaaccg tggacaagag caggtggcag 2220

gaggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 2280

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<210> 25
<211> 769
<212> PRT
<213> Artificial Sequence

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<223> ARSB-Fc

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Arg Leu Leu Leu Pro Val Val Leu Pro Leu Leu Leu Leu Leu Leu Leu
            20                  25                  30

Ala Pro Pro Gly Ser Gly Ala Gly Ala Ser Arg Pro Pro His Leu Val
         35                  40                  45

Phe Leu Leu Ala Asp Asp Leu Gly Trp Asn Asp Val Gly Phe His Gly
     50                  55                  60

Ser Arg Ile Arg Thr Pro His Leu Asp Ala Leu Ala Ala Gly Gly Val
 65                  70                  75                  80

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

Gln Leu Leu Thr Gly Arg Tyr Gln Ile Arg Thr Gly Leu Gln His Gln
            100                 105                 110

Ile Ile Trp Pro Cys Gln Pro Ser Cys Val Pro Leu Asp Glu Lys Leu
        115                 120                 125

Leu Pro Gln Leu Leu Lys Glu Ala Gly Tyr Thr Thr His Met Val Gly
    130                 135                 140

Lys Trp His Leu Gly Met Tyr Arg Lys Glu Cys Leu Pro Thr Arg Arg
145                 150                 155                 160

Gly Phe Asp Thr Tyr Phe Gly Tyr Leu Leu Gly Ser Glu Asp Tyr Tyr
                165                 170                 175

Ser His Glu Arg Cys Thr Leu Ile Asp Ala Leu Asn Val Thr Arg Cys
            180                 185                 190

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

Met Tyr Ser Thr Asn Ile Phe Thr Lys Arg Ala Ile Ala Leu Ile Thr
    210                 215                 220

Asn His Pro Pro Glu Lys Pro Leu Phe Leu Tyr Leu Ala Leu Gln Ser
225                 230                 235                 240

Val His Glu Pro Leu Gln Val Pro Glu Glu Tyr Leu Lys Pro Tyr Asp
                245                 250                 255

Phe Ile Gln Asp Lys Asn Arg His His Tyr Ala Gly Met Val Ser Leu
            260                 265                 270

Met Asp Glu Ala Val Gly Asn Val Thr Ala Ala Leu Lys Ser Ser Gly
        275                 280                 285
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Leu Trp Asn Asn Thr Val Phe Ile Phe Ser Thr Asp Asn Gly Gly Gln
    290                 295                 300

Thr Leu Ala Gly Gly Asn Asn Trp Pro Leu Arg Gly Arg Lys Trp Ser
305                 310                 315                 320

Leu Trp Glu Gly Gly Val Arg Gly Val Gly Phe Val Ala Ser Pro Leu
                325                 330                 335

Leu Lys Gln Lys Gly Val Lys Asn Arg Glu Leu Ile His Ile Ser Asp
            340                 345                 350

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

Lys Pro Leu Asp Gly Phe Asp Val Trp Lys Thr Ile Ser Glu Gly Ser
    370                 375                 380

Pro Ser Pro Arg Ile Glu Leu Leu His Asn Ile Asp Pro Asn Phe Val
385                 390                 395                 400

Asp Ser Ser Pro Cys Pro Arg Asn Ser Met Ala Pro Ala Lys Asp Asp
                405                 410                 415

Ser Ser Leu Pro Glu Tyr Ser Ala Phe Asn Thr Ser Val His Ala Ala
            420                 425                 430

Ile Arg His Gly Asn Trp Lys Leu Leu Thr Gly Tyr Pro Gly Cys Gly
        435                 440                 445

Tyr Trp Phe Pro Pro Pro Ser Gln Tyr Asn Val Ser Glu Ile Pro Ser
    450                 455                 460

Ser Asp Pro Pro Thr Lys Thr Leu Trp Leu Phe Asp Ile Asp Arg Asp
465                 470                 475                 480

Pro Glu Glu Arg His Asp Leu Ser Arg Glu Tyr Pro His Ile Val Thr
                485                 490                 495

Lys Leu Leu Ser Arg Leu Gln Phe Tyr His Lys His Ser Val Pro Val
            500                 505                 510

Tyr Phe Pro Ala Gln Asp Pro Arg Cys Asp Pro Lys Ala Thr Gly Val
        515                 520                 525

Trp Gly Pro Trp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    530                 535                 540

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

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                565                 570                 575

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
            580                 585                 590

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        595                 600                 605

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Gln Ser Thr Tyr Arg Val
    610                 615                 620

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
625                 630                 635                 640

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
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645 650 655

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
660 665 670

Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
675 680 685

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
690 695 700

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
705 710 715 720

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
725 730 735

Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
740 745 750

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
755 760 765

Lys

<210> 26
<211> 12
<212> PRT
<213> Homo Sapiens

<400> 26
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
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