SEQUENCE LISTING

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<120> INHIBITION OF PLATELET AGGREGATION USING ANTI-HUMAN GPVI ANTIBODIES

<130> CV - 739/PCT

<160> 27

<170> BiSSAP 1.3.6

<210> 1
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VH-CDR1

<400> 1
Gly Tyr Thr Phe Thr Ser Tyr Asn Met His
1 5 10

<210> 2
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> VH-CDR2

<400> 2
Gly Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Gln
1 5 10 15
Gly

<210> 3
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 3
Gly Thr Val Val Gly Asp Trp Tyr Phe Asp Val
1 5 10

<210> 4
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-CDR1

<400> 4
Arg Ser Ser Gln Ser Leu Glu Asn Ser Asn Gly Asn Thr Tyr Leu Asn
1 5 10 15

<210> 5
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-CDR2

<400> 5
Arg Val Ser Asn Arg Phe Ser
1 5

<210> 6
<211> 9
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<213> Artificial Sequence

<220>
<223> VL-CDR3

<400> 6
Leu Gln Leu Thr His Val Pro Trp Thr
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<210> 7
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain variable region

<400> 7
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Gly Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
    50   55   60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Thr Val Val Gly Asp Trp Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 8
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain variable region

<400> 8
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Glu Asn Ser
            20   25   30
Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
        35   40   45
Pro Lys Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro
    50   55   60
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile
65   70   75   80
Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Leu
                85   90   95
Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Thr
            100   105   110
Arg

<210> 9
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain variable region

<400> 9
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Ser Leu Glu Asn Ser
            20   25   30
Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
        35   40   45
Pro Lys Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro
    50   55   60
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65   70   75   80
Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Leu
                85   90   95
Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105   110
Arg

<210> 10
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy chain variable region

<400> 10
caggttcagc tggttcagtc aggggctgag gtgaagaagc ctggagcctc agtgaaggtg   60

tcctgcaagg cttctggcta cacatttacc agttacaata tgcactgggt aagacaggct   120

cctggacagg gcctggaatg gatgggaggt atttatccag gaaatggtga tacttcctac   180

aatcagaagt tccagggccg agttactatg actcgggaca cttccacctc tacagtgtac   240

atggagctca gcagcctgag atctgaggac accgcggtct attactgtgc aagaggcacc   300

gtggtcggcg actggtactt cgatgtgtgg ggccaaggca ccctggtcac cgtgagcagt   360

<210> 11
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain variable region

<400> 11
gacatccaga tgacccagag cccaagcagc ctgagcgcca gcgtgggtga cagagtgacc 60

atcacctgta gaagtagtca gagccttgag aacagcaacg gaaacaccta cctgaattgg 120

taccagcaga agccaggtaa ggctccaaag ctgctgatct acagagtttc caaccgattc 180

tctggtgtgc caagcagatt cagcggtagc ggtagcggta ccgacttcac cttcaccatc 240

agcagcctcc agccagagga catcgccacc tactactgcc tccagctgac tcatgtccca 300

tggaccttcg gtcagggcac caaggtggag atcacccgg 339

<210> 12
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain variable region

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atcacctgta gtgccagtca gagccttgag aacagcaacg gaaacaccta cctgaattgg 120

taccagcaga agccaggtaa ggctccaaag ctgctgatct acagagtttc caaccgattc 180

tctggtgtgc caagcagatt cagcggtagc ggtagcggta ccgacttcac cctcaccatc 240

agcagcctcc agccagagga cttcgccacc tactactgcc tccagctgac tcatgtccca 300

tggaccttcg gtcagggcac caaggtggag atcaaacgc 339

<210> 13
<211> 339
<212> PRT
<213> Homo sapiens

<400> 13
Met Ser Pro Ser Pro Thr Ala Leu Phe Cys Leu Gly Leu Cys Leu Gly
1 5 10 15
Arg Val Pro Ala Gln Ser Gly Pro Leu Pro Lys Pro Ser Leu Gln Ala
20 25 30
Leu Pro Ser Ser Leu Val Pro Leu Glu Lys Pro Val Thr Leu Arg Cys
35 40 45
Gln Gly Pro Pro Gly Val Asp Leu Tyr Arg Leu Glu Lys Leu Ser Ser
50 55 60
Ser Arg Tyr Gln Asp Gln Ala Val Leu Phe Ile Pro Ala Met Lys Arg

65 70 75 80
Ser Leu Ala Gly Arg Tyr Arg Cys Ser Tyr Gln Asn Gly Ser Leu Trp
85 90 95
Ser Leu Pro Ser Asp Gln Leu Glu Leu Val Ala Thr Gly Val Phe Ala
100 105 110
Lys Pro Ser Leu Ser Ala Gln Pro Gly Pro Ala Val Ser Ser Gly Gly
115 120 125
Asp Val Thr Leu Gln Cys Gln Thr Arg Tyr Gly Phe Asp Gln Phe Ala
130 135 140
Leu Tyr Lys Glu Gly Asp Pro Ala Pro Tyr Lys Asn Pro Glu Arg Trp
145 150 155 160
Tyr Arg Ala Ser Phe Pro Ile Ile Thr Val Thr Ala Ala His Ser Gly
165 170 175
Thr Tyr Arg Cys Tyr Ser Phe Ser Ser Arg Asp Pro Tyr Leu Trp Ser
180 185 190
Ala Pro Ser Asp Pro Leu Glu Leu Val Val Thr Gly Thr Ser Val Thr
195 200 205
Pro Ser Arg Leu Pro Thr Glu Pro Pro Ser Ser Val Ala Glu Phe Ser
210 215 220
Glu Ala Thr Ala Glu Leu Thr Val Ser Phe Thr Asn Lys Val Phe Thr
225 230 235 240
Thr Glu Thr Ser Arg Ser Ile Thr Thr Ser Pro Lys Glu Ser Asp Ser
245 250 255
Pro Ala Gly Pro Ala Arg Gln Tyr Tyr Thr Lys Gly Asn Leu Val Arg
260 265 270
Ile Cys Leu Gly Ala Val Ile Leu Ile Ile Leu Ala Gly Phe Leu Ala
275 280 285
Glu Asp Trp His Ser Arg Arg Lys Arg Leu Arg His Arg Gly Arg Ala
290 295 300
Val Gln Arg Pro Leu Pro Pro Leu Pro Pro Leu Pro Gln Thr Arg Lys
305 310 315 320
Ser His Gly Gly Gln Asp Gly Gly Arg Gln Asp Val His Ser Arg Gly
325 330 335
Leu Cys Ser

<210> 14
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy chain constant region

<400> 14
gcctccacca agggtccctc agtcttccca ctggcaccct cctccaagag cacctctggt 60

ggcacagctg ccctgggctg cctggtcaag gactacttcc cagaaccagt gactgtgtca 120

tggaactcag gcgccctgac cagcggcgtg cacaccttcc ctgctgtctt gcagtcctca 180

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 240

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agtcgagcct 300

aagtcatgcg acaagactca c 321

<210> 15
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain constant region

<400> 15
actgtggctg caccaagtgt gttcatcttc ccacctagcg atgagcagtt gaaatctgga 60

actgcctctg tcgtgtgcct cctgaacaac ttctacccac gggaggccaa ggtacagtgg 120

aaggtggata acgccctcca atccggtaac tcccaggaga gtgtcacaga gcaagatagc 180

aaggacagca cctacagcct cagcagcacc ctgactctga gcaaagcaga ctacgagaag 240

cacaaggtct acgcctgcga agtcacccat cagggcctga gttcccctgt cacaaagagc 300

ttcaaccggg gagagtgt 318

<210> 16
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Signal peptide

<400> 16
atggatatgc gtgtaccagc tcaactactt ggacttctat tgctttggct tcgtggtgct 60

agatgt 66

<210> 17
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Signal peptide

<400> 17
atggactgga cttggagaat cctattcttg gttgctgcag ctacaggtgc tcattca 57

<210> 18
<211> 762
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy chain

<400> 18
gcggccgcca ccatggactg gacttggaga atcctattct tggttgctgc agctacaggt 60

gctcattcac aggttcagct ggttcagtca ggggctgagg tgaagaagcc tggagcctca 120

gtgaaggtgt cctgcaaggc ttctggctac acatttacca gttacaatat gcactgggta 180

agacaggctc ctggacaggg cctggaatgg atgggaggta tttatccagg aaatggtgat 240

acttcctaca atcagaagtt ccagggccga gttactatga ctcgggacac ttccacctct 300

acagtgtaca tggagctcag cagcctgaga tctgaggaca ccgcggtcta ttactgtgca 360

agaggcaccg tggtcggcga ctggtacttc gatgtgtggg gccaaggcac cctggtcacc 420

gtgagcagtg cctccaccaa gggtccctca gtcttcccac tggcaccctc ctccaagagc 480

acctctggtg gcacagctgc cctgggctgc ctggtcaagg actacttccc agaaccagtg 540

actgtgtcat ggaactcagg cgccctgacc agcggcgtgc acaccttccc tgctgtcttg 600

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 660

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 720

gtcgagccta agtcatgcga caagactcac tgatgaggat cc 762

<210> 19
<211> 742
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain

<400> 19
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cgtggtgcta gatgtgacat ccagatgacc cagagcccaa gcagcctgag cgccagcgtg 120

ggtgacagag tgaccatcac ctgtagaagt agtcagagcc ttgagaacag caacggaaac 180

acctacctga attggtacca gcagaagcca ggtaaggctc caaagctgct gatctacaga 240

gtttccaacc gattctctgg tgtgccaagc agattcagcg gtagcggtag cggtaccgac 300

ttcaccttca ccatcagcag cctccagcca gaggacatcg ccacctacta ctgcctccag 360

ctgactcatg tcccatggac cttcggtcag ggcaccaagg tggagatcac ccggactgtg 420

gctgcaccaa gtgtgttcat cttcccacct agcgatgagc agttgaaatc tggaactgcc 480

tctgtcgtgt gcctcctgaa caacttctac ccacgggagg ccaaggtaca gtggaaggtg 540

gataacgccc tccaatccgg taactcccag gagagtgtca cagagcaaga tagcaaggac 600

agcacctaca gcctcagcag caccctgact ctgagcaaag cagactacga gaagcacaag 660

gtctacgcct gcgaagtcac ccatcagggc ctgagttccc ctgtcacaaa gagcttcaac 720

cggggagagt gttgatgata tc 742

<210> 20
<211> 742
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain

<400> 20
gacgtcacca tggatatgcg tgtaccagct caactacttg gacttctatt gctttggctt 60

cgtggtgcta gatgtgacat ccagatgacc cagagcccaa gcagcctgag cgccagcgtg 120

ggtgacagag tgaccatcac ctgtagtgcc agtcagagcc ttgagaacag caacggaaac 180

acctacctga attggtacca gcagaagcca ggtaaggctc caaagctgct gatctacaga 240

gtttccaacc gattctctgg tgtgccaagc agattcagcg gtagcggtag cggtaccgac 300

ttcaccctca ccatcagcag cctccagcca gaggacttcg ccacctacta ctgcctccag 360

ctgactcatg tcccatggac cttcggtcag ggcaccaagg tggagatcaa acgcactgtg 420

gctgcaccaa gtgtgttcat cttcccacct agcgatgagc agttgaaatc tggaactgcc 480

tctgtcgtgt gcctcctgaa caacttctac ccacgggagg ccaaggtaca gtggaaggtg 540

gataacgccc tccaatccgg taactcccag gagagtgtca cagagcaaga tagcaaggac 600

agcacctaca gcctcagcag caccctgact ctgagcaaag cagactacga gaagcacaag 660

gtctacgcct gcgaagtcac ccatcagggc ctgagttccc ctgtcacaaa gagcttcaac 720

cggggagagt gttgatgata tc 742

<210> 21
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L3 - Residues after

<220>
<221> SITE
<222> 3
<223> X is any amino acid

<400> 21
Phe Gly Xaa Gly
1

<210> 22
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1 - Residues before

<220>
<221> SITE
<222> 2
<223> X is any amino acid

<220>
<221> SITE
<222> 3
<223> X is any amino acid

<220>
<221> SITE
<222> 4
<223> X is any amino acid

<400> 22
Cys Xaa Xaa Xaa
1

<210> 23
<211> 5
<212> PRT

<213> Artificial Sequence

<220>
<223> CDR-H2 - Residues before

<400> 23
Leu Glu Trp Ile Gly
1   5

<210> 24
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3 - Residues after

<220>
<221> SITE
<222> 3
<223> X is any amino acid

<400> 24
Trp Gly Xaa Gly
1

<210> 25
<211> 527
<212> PRT
<213> Homo sapiens

<400> 25
Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln
1   5   10   15
Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
            20   25   30
Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
        35   40   45
Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
    50   55   60
Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
65   70   75   80
Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln
                85   90   95
Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu
            100   105   110
Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly
        115   120   125
Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys
    130   135   140
Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala

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145                 150                 155                 160
Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly
                165                 170                 175
Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His
            180                 185                 190
Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile
        195                 200                 205
Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu
    210                 215                 220
Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
225                 230                 235                 240
Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
                245                 250                 255
Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
            260                 265                 270
Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro
        275                 280                 285
Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro Gly Glu Arg
    290                 295                 300
Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala
305                 310                 315                 320
Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile
                325                 330                 335
Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe
            340                 345                 350
Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr
        355                 360                 365
Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys
    370                 375                 380
Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp
385                 390                 395                 400
Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys
                405                 410                 415
His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys Glu Ala His
            420                 425                 430
Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
        435                 440                 445
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly
    450                 455                 460
Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly
465                 470                 475                 480
Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile
                485                 490                 495
Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr
            500                 505                 510
Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro
        515                 520                 525
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<210> 26
<211> 275
<212> PRT
<213> Homo sapiens

<400> 26
Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln
1   5   10   15
Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
            20   25   30
Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
        35   40   45
Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
    50   55   60
Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
65   70   75   80
Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln
                85   90   95
Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu
            100   105   110
Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly
        115   120   125
Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys
    130   135   140
Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala
145   150   155   160
Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly
                165   170   175
Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His
            180   185   190
Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile
        195   200   205
Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu
    210   215   220
Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
225   230   235   240
Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
                245   250   255
Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
            260   265   270
Gln Phe Arg
        275

<210> 27
<211> 252
<212> PRT
<213> Homo sapiens

<400> 27
Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro Trp Gln Ala
1   5   10   15
Ala Ile Phe Ala Lys His Arg Arg Ser Pro Gly Glu Arg Phe Leu Cys
            20   25   30
Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala Ala His Cys
        35   40   45
Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly Arg
    50   55   60
Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu

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65                  70                  75                  80
Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp
                85                  90                  95
Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu
            100                 105                 110
Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu
        115                 120                 125
Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys His Glu Ala
    130                 135                 140
Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys Glu Ala His Val Arg Leu
145                 150                 155                 160
Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn Arg Thr Val
                165                 170                 175
Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro Gln
            180                 185                 190
Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
        195                 200                 205
Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly
    210                 215                 220
Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr
225                 230                 235                 240
Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro
                245                 250
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