SEQUENCE LISTING

<110> Eli Lilly and Company

<120> Variants of Human GDNF

<130> X19073

<150> 61/474024
<151> 2011-04-11

<160> 44

<170> PatentIn version 3.5

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

<400> 1

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Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1               5                  10                  15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
            20                  25                  30

Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
        35                  40                  45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
    50                  55                  60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
65                  70                  75                  80

Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
                85                  90                  95

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
            100                 105                 110

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
        115                 120                 125

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

Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu
145                 150                 155                 160

Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln
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165 170 175

Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
180 185 190

Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
195 200 205

Gly Cys Ile
210

<210> 2
<211> 633
<212> DNA
<213> Homo sapiens

<400> 2
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ccactgccag ccggcaagag acccccagag gccccagccg aggacagaag cctgggcagg 120

cggagggccc cattcgccct gagcagcgac agcaacatgc cagaggacta ccccgaccag 180

ttcgacgacg tcatggactt catccaggcc accatcaaga ggctgaagag gtcacccgac 240

aagcagatgg ccgtgctgcc caggcgggag aggaacaggc aggccgccgc cgccaaccca 300

gagaattcca ggggcaaggg cagaaggggt caacggggca agaacagggg ctgcgtgctg 360

accgccatcc acctgaacgt gaccgacctg ggcctgggct acgagaccaa ggaggagctg 420

atcttcaggt actgcagcgg cagctgcgac gccgccgaga ccacctacga caagatcctg 480

aagaacctga gcaggaacag gcggctggtc tccgacaagg tgggccaggc ctgctgcagg 540

cccatcgcct tcgacgacga cctgagcttc ctggacgaca acctggtgta ccacatcctg 600

aggaagcaca gcgccaagag atgcggctgc atc 633

<210> 3
<211> 134
<212> PRT
<213> Homo sapiens

<400> 3

Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg
1 5 10 15

Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
20 25 30

Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
35 40 45

Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
50 55 60

Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp
65 70 75 80

Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys
85 90 95

Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser
100 105 110

Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
115 120 125

Lys Arg Cys Gly Cys Ile
130

<210> 4
<211> 19
<212> PRT
<213> Homo sapiens

<400> 4

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15

Ala Ser Ala

<210> 5
<211> 58
<212> PRT
<213> Homo sapiens

<400> 5

Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro Ala Glu Asp
1 5 10 15

Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser Ser Asp Ser
20 25 30

Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp Phe
35 40 45

Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg
50 55

<210> 6

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

<220>
<223> Synthetic Construct

<400> 6
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<210> 7
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 7
ggtgctcgag ttattaaatg cagccgcaac gtttcgcgct 40

<210> 8
<211> 103
<212> PRT
<213> Homo sapiens

<400> 8

Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His
1 5 10 15

Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu
20 25 30

Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr
35 40 45

Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp
50 55 60

Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu
65 70 75 80

Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser
85 90 95

Ala Lys Arg Cys Gly Cys Ile
100

<210> 9
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 9

Arg Gly Gln Arg Gly Lys Gln Arg Gly Cys Val Leu Thr Ala Ile His
1 5 10 15

Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu
20 25 30

Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr
35 40 45

Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Glu
50 55 60

Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu
65 70 75 80

Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser
85 90 95

Ala Lys Arg Cys Gly Cys Ile
100

<210> 10
<211> 309
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 10
aggggtcaac ggggcaagca gaggggctgc gtgctgaccg ccatccacct gaacgtgacc 60

gacctgggcc tgggctacga gaccaaggag gagctgatct tcaggtactg cagcggcagc 120

tgcgacgccg ccgagaccac ctacgacaag atcctgaaga acctgagcag gaacaggcgg 180

ctggtctccg agaaggtggg ccaggcctgc tgcaggccca tcgccttcga cgacgacctg 240

agcttcctgg acgacaacct ggtgtaccac atcctgagga agcacagcgc caagagatgc 300

ggctgcatc 309

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

<220>
<223> Synthetic Construct

<400> 11

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
20 25 30

Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
35 40 45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
50 55 60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
65 70 75 80

Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
85 90 95

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
100 105 110

Gly Lys Gln Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
115 120 125

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

Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu
145 150 155 160

Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Glu Lys Val Gly Gln
165 170 175

Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
180 185 190

Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
195 200 205

Gly Cys Ile
210

<210> 12
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12

Arg Gly Gln Arg Gly Lys Gln Arg Gly Cys Val Leu Thr Ala Ile His
1 5 10 15

Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu
20 25 30

Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr
35 40 45

Asp Lys Ile Leu Ala Asn Leu Ser Lys Asn Lys Arg Leu Val Ser Glu
50 55 60

Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu
65 70 75 80

Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser
85 90 95

Ala Lys Arg Cys Gly Cys Ile
100

<210> 13
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 13
atgaagctgt gggacgtggt ggccgtgtgc ctggtgctgc tgcacaccgc cagcgctttc 60

ccactgccag ccggcaagag acccccagag gccccagccg aggacagaag cctgggcagg 120

cggagggccc cattcgccct gagcagcgac agcaacatgc cagaggacta ccccgaccag 180

ttcgacgacg tcatggactt catccaggcc accatcaaga ggctgaagag gtcacccgac 240

aagcagatgg ccgtgctgcc caggcgggag aggaacaggc aggccgccgc cgccaaccca 300

gagaattcca ggggcaaggg cagaaggggt caacggggca agcagagggg ctgcgtgctg 360

accgccatcc acctgaacgt gaccgacctg ggcctgggct acgagaccaa ggaggagctg 420

atcttcaggt actgcagcgg cagctgcgac gccgccgaga ccacctacga caagatcctg 480

gccaacctga gcaagaacaa gcggctggtc tccgagaagg tgggccaggc ctgctgcagg 540

cccatcgcct tcgacgacga cctgagcttc ctggacgaca acctggtgta ccacatcctg 600

aggaagcaca gcgccaagag atgcggctgc atc 633

<210> 14
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
20 25 30

Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
35 40 45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
50 55 60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
65 70 75 80

Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
85 90 95

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
100 105 110

Gly Lys Gln Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
115 120 125

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

Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu
145 150 155 160

Ala Asn Leu Ser Lys Asn Lys Arg Leu Val Ser Glu Lys Val Gly Gln
165 170 175

Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
180 185 190

Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
195 200 205

Gly Cys Ile
210

<210> 15
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 15

Arg Gly Gln Arg Gly Lys Gln Arg Gly Cys Val Leu Thr Ala Ile His
1 5 10 15

Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu
20 25 30

Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr
35 40 45

Asp Lys Ile Leu Ala Asn Leu Ser Lys Asn Lys Arg Leu Val Ser Glu
50 55 60

Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu
65 70 75 80

Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Glu His Ser
85 90 95

Ala Lys Glu Cys Gly Cys Ile
100

<210> 16
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16
atgaagctgt gggacgtggt ggccgtgtgc ctggtgctgc tgcacaccgc cagcgctttc 60

ccactgccag ccggcaagag acccccagag gccccagccg aggacagaag cctgggcagg 120

cggagggccc cattcgccct gagcagcgac agcaacatgc cagaggacta ccccgaccag 180

ttcgacgacg tcatggactt catccaggcc accatcaaga ggctgaagag gtcacccgac 240

aagcagatgg ccgtgctgcc caggcgggag aggaacaggc aggccgccgc cgccaaccca 300

gagaattcca ggggcaaggg cagaaggggt caacggggca agcagagggg ctgcgtgctg 360

accgccatcc acctgaacgt gaccgacctg ggcctgggct acgagaccaa ggaggagctg 420

atcttcaggt actgcagcgg cagctgcgac gccgccgaga ccacctacga caagatcctg 480

gccaacctga gcaagaacaa gcggctggtc tccgagaagg tgggccaggc ctgctgcagg 540

cccatcgcct tcgacgacga cctgagcttc ctggacgaca acctggtgta ccacatcctg 600

agggagcaca gcgccaagga gtgcggctgc atc 633

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

<220>
<223> Synthetic Construct

<400> 17

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
20 25 30

Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
35 40 45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
50 55 60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
65 70 75 80

Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
85 90 95

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
100 105 110

Gly Lys Gln Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
115 120 125

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

Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu
145 150 155 160

Ala Asn Leu Ser Lys Asn Lys Arg Leu Val Ser Glu Lys Val Gly Gln

165 170 175

Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
180 185 190

Asp Asn Leu Val Tyr His Ile Leu Arg Glu His Ser Ala Lys Glu Cys
195 200 205

Gly Cys Ile
210

<210> 18
<211> 57
<212> DNA
<213> Homo sapiens

<400> 18
atgaagctgt gggacgtggt ggccgtgtgc ctggtgctgc tgcacaccgc cagcgct 57

<210> 19
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 19
atgaagctgt gggacgtggt ggccgtgtgc ctggtgctgc tgcacaccgc cagcgctagg 60

ggtcaacggg gcaagcagag gggctgcgtg ctgaccgcca tccacctgaa cgtgaccgac 120

ctgggcctgg gctacgagac caaggaggag ctgatcttca ggtactgcag cggcagctgc 180

gacgccgccg agaccaccta cgacaagatc ctgaagaacc tgagcaggaa caggcggctg 240

gtctccgaga aggtgggcca ggcctgctgc aggcccatcg ccttcgacga cgacctgagc 300

ttcctggacg acaacctggt gtaccacatc ctgaggaagc acagcgccaa gagatgcggc 360

tgcatc 366

<210> 20
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 20

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15

Ala Ser Ala Arg Gly Gln Arg Gly Lys Gln Arg Gly Cys Val Leu Thr

20 25 30

Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys
35 40 45

Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu
50 55 60

Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu
65 70 75 80

Val Ser Glu Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp
85 90 95

Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg
100 105 110

Lys His Ser Ala Lys Arg Cys Gly Cys Ile
115 120

<210> 21
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 21
atgaagctgt gggacgtggt ggccgtgtgc ctggtgctgc tgcacaccgc cagcgctagg 60

ggtcaacggg gcaagcagag gggctgcgtg ctgaccgcca tccacctgaa cgtgaccgac 120

ctgggcctgg gctacgagac caaggaggag ctgatcttca ggtactgcag cggcagctgc 180

gacgccgccg agaccaccta cgacaagatc ctggccaacc tgagcaagaa caagcggctg 240

gtctccgaga aggtgggcca ggcctgctgc aggcccatcg ccttcgacga cgacctgagc 300

ttcctggacg acaacctggt gtaccacatc ctgaggaagc acagcgccaa gagatgcggc 360

tgcatc 366

<210> 22
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15

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

Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys
35 40 45

Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu
50 55 60

Thr Thr Tyr Asp Lys Ile Leu Ala Asn Leu Ser Lys Asn Lys Arg Leu
65 70 75 80

Val Ser Glu Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp
85 90 95

Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg
100 105 110

Lys His Ser Ala Lys Arg Cys Gly Cys Ile
115 120

<210> 23
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (53)..(53)
<223> Xaa at position 53 is Lys or Ala

<220>
<221> MISC_FEATURE
<222> (57)..(57)
<223> Xaa at position 57 is Arg or Lys

<220>
<221> MISC_FEATURE
<222> (59)..(59)
<223> Xaa at position 59 is Arg or Lys

<220>
<221> MISC_FEATURE
<222> (94)..(94)
<223> Xaa at position 94 is Lys or Glu

<220>
<221> MISC_FEATURE
<222> (99)..(99)
<223> Xaa at position 99 is Arg or Glu

<400> 23

Arg Gly Gln Arg Gly Lys Gln Arg Gly Cys Val Leu Thr Ala Ile His
1 5 10 15

Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu
20 25 30

Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr
35 40 45

Asp Lys Ile Leu Xaa Asn Leu Ser Xaa Asn Xaa Arg Leu Val Ser Glu
50 55 60

Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu
65 70 75 80

Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Xaa His Ser
85 90 95

Ala Lys Xaa Cys Gly Cys Ile
100

<210> 24
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (72)..(72)
<223> Xaa at position 72 is Lys or Ala

<220>
<221> MISC_FEATURE
<222> (76)..(76)
<223> Xaa at position 76 is arg or Lys

<220>
<221> MISC_FEATURE
<222> (78)..(78)
<223> Xaa at position 78 is Arg or Lys

<220>
<221> MISC_FEATURE
<222> (113)..(113)
<223> Xaa at position 113 is Lys or Glu

<220>
<221> MISC_FEATURE
<222> (118)..(118)

<223> Xaa at position 118 is Arg or Glu

<400> 24

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Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1               5                   10                  15

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

Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys
        35                  40                  45

Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu
    50                  55                  60

Thr Thr Tyr Asp Lys Ile Leu Xaa Asn Leu Ser Xaa Asn Xaa Arg Leu
65                  70                  75                  80

Val Ser Glu Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp
                85                  90                  95

Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg
            100                 105                 110

Xaa His Ser Ala Lys Xaa Cys Gly Cys Ile
        115                 120
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<210> 25
<211> 20
<212> PRT
<213> Mus musculus

<400> 25

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Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                   10                  15

Gly Ser Thr Gly
            20
```

<210> 26
<211> 60
<212> DNA
<213> Mus musculus

<400> 26
atggagacag acacactcct gctatgggta ctgctgctct gggttccagg atctaccggt 60

<210> 27
<211> 369
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 27
atggagacag acacactcct gctatgggta ctgctgctct gggttccagg atctaccggt 60

aggggtcaac ggggcaagca gaggggctgc gtgctgaccg ccatccacct gaacgtgacc 120

gacctgggcc tgggctacga gaccaaggag gagctgatct tcaggtactg cagcggcagc 180

tgcgacgccg ccgagaccac ctacgacaag atcctgaaga acctgagcag gaacaggcgg 240

ctggtctccg agaaggtggg ccaggcctgc tgcaggccca tcgccttcga cgacgacctg 300

agcttcctgg acgacaacct ggtgtaccac atcctgagga agcacagcgc caagagatgc 360

ggctgcatc 369

<210> 28
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Arg Gly Gln Arg Gly Lys Gln Arg Gly Cys Val Leu
20 25 30

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

Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala
50 55 60

Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg
65 70 75 80

Leu Val Ser Glu Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe
85 90 95

Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu
100 105 110

Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile
115 120

<210> 29
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 29
atggagacag acacactcct gctatgggta ctgctgctct gggttccagg atctaccggt 60

aggggtcaac ggggcaagca gaggggctgc gtgctgaccg ccatccacct gaacgtgacc 120

gacctgggcc tgggctacga gaccaaggag gagctgatct tcaggtactg cagcggcagc 180

tgcgacgccg ccgagaccac ctacgacaag atcctggcca acctgagcaa gaacaagcgg 240

ctggtctccg agaaggtggg ccaggcctgc tgcaggccca tcgccttcga cgacgacctg 300

agcttcctgg acgacaacct ggtgtaccac atcctgagga agcacagcgc caagagatgc 360

ggctgcatc 369

<210> 30
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 30

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Arg Gly Gln Arg Gly Lys Gln Arg Gly Cys Val Leu
20 25 30

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

Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala
50 55 60

Glu Thr Thr Tyr Asp Lys Ile Leu Ala Asn Leu Ser Lys Asn Lys Arg
65 70 75 80

Leu Val Ser Glu Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe
85 90 95

Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu
100 105 110

Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile

115 120

<210> 31
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (73)..(73)
<223> Xaa at position 73 is Lys or Ala

<220>
<221> MISC_FEATURE
<222> (77)..(77)
<223> Xaa at position 77 is Arg or Lys

<220>
<221> MISC_FEATURE
<222> (79)..(79)
<223> Xaa at position 79 is Arg or Lys

<220>
<221> MISC_FEATURE
<222> (114)..(114)
<223> Xaa at position 114 is Lys or Glu

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa at position 119 is Arg or Glu

<400> 31

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Arg Gly Gln Arg Gly Lys Gln Arg Gly Cys Val Leu
20 25 30

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

Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala
50 55 60

Glu Thr Thr Tyr Asp Lys Ile Leu Xaa Asn Leu Ser Xaa Asn Xaa Arg
65 70 75 80

Leu Val Ser Glu Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe
85 90 95

Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu
100 105 110

Arg Xaa His Ser Ala Lys Xaa Cys Gly Cys Ile
115 120

<210> 32
<211> 26
<212> PRT
<213> Homo sapiens

<400> 32

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
20 25

<210> 33
<211> 78
<212> DNA
<213> Homo sapiens

<400> 33
atggctaccg gcagcaggac ctctctgctg ctggccttcg gcctgctgtg cctgccctgg 60

ctgcaggaag gcagcgcc 78

<210> 34
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34
atggctaccg gcagcaggac ctctctgctg ctggccttcg gcctgctgtg cctgccctgg 60

ctgcaggaag gcagcgccag gggtcaacgg ggcaagcaga ggggctgcgt gctgaccgcc 120

atccacctga acgtgaccga cctgggcctg ggctacgaga ccaaggagga gctgatcttc 180

aggtactgca gcggcagctg cgacgccgcc gagaccacct acgacaagat cctgaagaac 240

ctgagcagga acaggcggct ggtctccgag aaggtgggcc aggcctgctg caggcccatc 300

gccttcgacg acgacctgag cttcctggac gacaacctgg tgtaccacat cctgaggaag 360

cacagcgcca agagatgcgg ctgcatc 387

<210> 35
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 35

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Arg Gly Gln Arg Gly Lys
20 25 30

Gln Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu
35 40 45

Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser
50 55 60

Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn
65 70 75 80

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

Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn
100 105 110

Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
115 120 125

Ile

<210> 36
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 36
atggctaccg gcagcaggac ctctctgctg ctggccttcg gcctgctgtg cctgccctgg 60

ctgcaggaag gcagcgccag gggtcaacgg ggcaagcaga ggggctgcgt gctgaccgcc 120

atccacctga acgtgaccga cctgggcctg ggctacgaga ccaaggagga gctgatcttc 180

aggtactgca gcggcagctg cgacgccgcc gagaccacct acgacaagat cctggccaac 240

ctgagcaaga acaagcggct ggtctccgag aaggtgggcc aggcctgctg caggcccatc 300

gccttcgacg acgacctgag cttcctggac gacaacctgg tgtaccacat cctgaggaag 360

cacagcgcca agagatgcgg ctgcatc 387

<210> 37
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 37

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Arg Gly Gln Arg Gly Lys
20 25 30

Gln Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu
35 40 45

Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser
50 55 60

Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Ala Asn
65 70 75 80

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

Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn
100 105 110

Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
115 120 125

Ile

<210> 38
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (79)..(79)
<223> Xaa at position 79 is Lys or Ala

<220>

<221> MISC_FEATURE
<222> (83)..(83)
<223> Xaa at position 83 is Arg or Lys

<220>
<221> MISC_FEATURE
<222> (85)..(85)
<223> Xaa at position 85 is Arg or Lys

<220>
<221> MISC_FEATURE
<222> (120)..(120)
<223> Xaa at position 120 is Lys or Glu

<220>
<221> MISC_FEATURE
<222> (125)..(125)
<223> Xaa at position 125 is Arg or Glu

<400> 38

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Arg Gly Gln Arg Gly Lys
20 25 30

Gln Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu
35 40 45

Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser
50 55 60

Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Xaa Asn
65 70 75 80

Leu Ser Xaa Asn Xaa Arg Leu Val Ser Glu Lys Val Gly Gln Ala Cys
85 90 95

Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn
100 105 110

Leu Val Tyr His Ile Leu Arg Xaa His Ser Ala Lys Xaa Cys Gly Cys
115 120 125

Ile

<210> 39
<211> 46
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 39
tatacatatg cgtggacaac gtggtaaaca acgtggttgt gtgctg 46

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

<220>
<223> Synthetic Construct

<400> 40
ggtgctcgag ttattaaatg cagccgcaac gtttcgcgct 40

<210> 41
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 41
gtctggtgag cgagaaagtg ggtcag 26

<210> 42
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 42
ctgacccact ttctcgctca ccagac 26

<210> 43
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 43
cctatgataa aatcctggca aacctgagca agaacaaacg tctggtgagc gagaaag 57

<210> 44
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 44

ctttctcgct caccagacgt ttgttcttgc tcaggtttgc caggatttta tcatagg 57