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ttgttttttg ttttttgag atggagtctc actctttcgc ccaggctgga gtgcagtggt 1920

atgatctcag ctcactgcaa gctccacctc ccgggttcac gccattctcc tgcctcagcc 1980

tcctgagtag ctgggactac aggcgcccgc caccacaccc ggctaatttt ttgtattttt 2040

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cacctgcctc ggcctcccaa agtgctggga ttacgggtgt gagccaccgt gcccagcctt 2160

ttttttttta atagaaaaaa taatccgact cccactacat caagactaat cttgttttgt 2220

gtgtttttca catgtattat agaatgcttt tgcatggact atcctcttgt ttttattaaa 2280

aacaaatgat ttttttaaaa gtcacaaaaa caattcacta aaaataaata tgtcattgtg 2340

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<222> (408)..(514)
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<222> (515)..(652)
<223> Exon 5

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<222> (653)..(769)
<223> Exon 6v1

<220>
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<223> Exon 7

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tggagtcgtt ggtgaagttt ttcattcctc agaggagaaa atctgtggct ggggagattg 180

ttctcattac tggagctggg catggaatag gcaggcagac tacttatgaa tttgcaaaac 240

gacagagcat attggttctg tgggatatta ataaggtgaa gaaagaagtg ggtgatgtaa 300

caatcgtggt gaataatgct gggacagtat atccagccga tcttctcagc accaaggatg 360

aagagattac caagacattt gaggtcaaca tcctaggaca tttttggatc acaaaagcac 420

ttcttccatc gatgatggag agaaatcatg gccacatcgt cacagtggct tcagtgtgcg 480

gccacgaagg gattccttac ctcatcccat attgttccag caaatttgcc gctgttggct 540

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ctgtattgga gacagatgaa gtcgtaagaa gtctgataga tggaatactt accaataaga 720

aaatgatttt tgttccatcg tatatcaata tctttctgag actacagaag tttcttcctg 780

aacgcgcctc agcgatttta aatcgtatgc agaatattca atttgaagca gtggttggcc 840

acaaaatcaa aatgaaatga ataaataagc tccagccaga gatgtatgca tgataatgat 900

atgaatagtt tcgaatcaat gctgcaaagc tttatttcac atttttcag tcctgataat 960

attaaaaaca ttggtttggc actagcagca gtcaaacgaa caagattaat tacctgtctt 1020

cctgtttctc aagaatattt acgtagtttt tcataggtct gtttttcctt tcatgcctct 1080

taaaaacttc tgtgcttaca taaacatact taaaaggttt tctttaagat attttatttt 1140

tccatttaaa ggtggacaaa agctacctcc ctaaaagtaa atacaaagag aacttattta 1200

cacagggaag gtttaagact gttcaagtag cattccaatc tgtagccatg ccacagaata 1260

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ctcaacctgg acatatttta agattcagca tttgaaagat ttccctagcc tcttcctttt 1380

tcattagccc aaaacggtgc aactctattc tggactttat tacttgattc tgtcttctgt 1440

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aagatacatt atgaaaggtg accgactcta ttttaaatct cagaatttta agttctagcc 1560

ccatgataac ctttttcttt gtaatttatg ctttcatata tccttggtcc cagagatgtt 1620

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gacctcgtga tccacctgcc tcggcctccc aaagtgctgg gattacgggt gtgagccacc 2040

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atcttgtttt gtgtgttttt cacatgtatt atagaatgct tttgcatgga ctatcctctt 2160

gtttttatta aaaacaaatg atttttttaa aagtcacaaa aacaattcac taaaaataaa 2220

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taaactctg 2289

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<211> 2280
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<213> Homo sapiens

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<223> Exon 2

<220>
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<223> Exon 3

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<222> (516)..(622)
<223> Exon 4

<220>
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<222> (623)..(760)
<223> Exon 5

<220>
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<223> Exon 7

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tggagtcgtt ggtgaagttt ttcattcctc agaggagaaa atctgtggct ggggagattg 180

ttctcattac tggagctggg catggaatag gcaggcagac tacttatgaa tttgcaaaac 240

gacagagcat attggttctg tgggatatta ataagcgcgg tgtggaggaa actgcagctg 300

agtgccgaaa actaggcgtc actgcgcatg cgtatgtggt agactgcagc aacagagaag 360

agatctatcg ctctctaaat caggtgaaga aagaagtggg tgatgtaaca atcgtggtga 420

ataatgctgg gacagtatat ccagccgatc ttctcagcac caaggatgaa gagattacca 480

agacatttga ggtcaacatc ctaggacatt tttggatcac aaaagcactt cttccatcga 540

tgatggagag aaatcatggc cacatcgtca cagtggcttc agtgtgcggc cacgaaggga 600

ttccttacct catcccatat tgttccagca aatttgccgc tgttggcttt cacagaggtc 660

tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa aacctcatgt ctctgcccag 720

tttttgtgaa tactgggttc accaaaaatc caagcacaag gtttcttcct gaacgcgcct 780

cagcgatttt aaatcgtatg cagaatattc aatttgaagc agtggttggc cacaaaatca 840

aaatgaaatg aataaataag ctccagccag agatgtatgc atgataatga tatgaatagt 900

ttcgaatcaa tgctgcaaag ctttatttca cattttttca gtcctgataa tattaaaaac 960

attggtttgg cactagcagc agtcaaacga acaagattaa ttacctgtct tcctgtttct 1020

caagaatatt tacgtagttt ttcataggtc tgtttttcct ttcatgcctc ttaaaaactt 1080

ctgtgcttac ataaacatac ttaaaaggtt ttctttaaga tattttattt ttccatttaa 1140

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ggtttaagac tgttcaagta gcattccaat ctgtagccat gccacagaat atcaacaaga 1260

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gacatatttt aagattcagc atttgaaaga tttccctagc ctcttccttt ttcattagcc 1380

caaaacggtg caactctatt ctggacttta ttacttgatt ctgtcttctg tataactctg 1440

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aaaaacaaat gatttttta aaagtcacaa aaacaattca ctaaaaataa atatgtcatt 2220

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<212> DNA
<213> Homo sapiens

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<222> (276)..(383)
<223> Exon 2

<220>
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<222> (384)..(515)
<223> Exon 3

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<222> (516)..(622)
<223> Exon 4

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<222> (623)..(760)
<223> Exon 5

<220>
<221> misc_feature
<222> (761)..(878)
<223> Exon 6v2 - includes additional residue 878 at 3' end

<220>
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<222> (879)..(2398)
<223> Exon 7

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tggagtcgtt ggtgaagttt ttcattcctc agaggagaaa atctgtggct ggggagattg 180

ttctcattac tggagctggg catggaatag gcaggcagac tacttatgaa tttgcaaaac 240

gacagagcat attggttctg tgggatatta ataagcgcgg tgtggaggaa actgcagctg 300

agtgccgaaa actaggcgtc actgcgcatg cgtatgtggt agactgcagc aacagagaag 360

agatctatcg ctctctaaat caggtgaaga aagaagtggg tgatgtaaca atcgtggtga 420

ataatgctgg gacagtatat ccagccgatc ttctcagcac caaggatgaa gagattacca 480

agacatttga ggtcaacatc ctaggacatt tttggatcac aaaagcactt cttccatcga 540

tgatggagag aaatcatggc cacatcgtca cagtggcttc agtgtgcggc cacgaaggga 600

ttccttacct catcccatat tgttccagca aatttgccgc tgttggcttt cacagaggtc 660

tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa aacctcatgt ctctgcccag 720

tttttgtgaa tactgggttc accaaaaatc caagcacaag attatggcct gtattggaga 780

cagatgaagt cgtaagaagt ctgatagatg gaatacttac caataagaaa atgatttttg 840

ttccatcgta tatcaatatc tttctgagac tacagaaggt ttcttcctga acgcgcctca 900

gcgattttaa atcgtatgca gaatattcaa tttgaagcag tggttggcca caaaatcaaa 960

atgaaatgaa taaataagct ccagccagag atgtatgcat gataatgata tgaatagttt 1020

cgaatcaatg ctgcaaagct ttatttcaca ttttttcagt cctgataata ttaaaaacat 1080

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gtgcttacat aaacatactt aaaaggtttt ctttaagata ttttattttt ccatttaaag 1260

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tgtgtttttc acatgtatta tagaatgctt ttgcatggac tatcctcttg tttttattaa 2280

aaacaaatga ttttttaaa agtcacaaaa acaattcact aaaaataaat atgtcattgt 2340

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<210> 8
<211> 2469
<212> DNA
<213> Homo sapiens

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<220>
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<223> Exon 7

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ataatgctgg gacagtatat ccagccgatc ttctcagcac caaggatgaa gagattacca 480

agacatttga ggtcaacatc ctaggacatt tttggaatgg aaaggacatc agaagtaatt 540

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aaatgatttt tgttccatcg tatatcaata tctttctgag actacagaag tttcttcctg 960

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taaactctg 2469

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<211> 1715
<212> DNA
<213> Homo sapiens

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<222> (623)..(760)
<223> Exon 5

<220>
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<222> (761)..(1715)
<223> Exon 6v3

<220>
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<223> Read-through from exon 6 into intron 6

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<222> (1716)..(1715)
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agtgccgaaa actaggcgtc actgcgcatg cgtatgtggt agactgcagc aacagagaag 360

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tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa aacctcatgt ctctgcccag 720

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tatttcctct gttattttcc tacccagtct ataaaaagag agtgattcat tttctctacc 1380

aaatctactg tctctgccca aactttgctg aagactattc taactaaagg aaacacagtt 1440

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tggaagtttg gttgggattg cactgaatct atagagcaat tggggagtat tgacatatca 1560

acaatattga gttttctaat ccaagaacat aatatctatt tttaaaatct tcttcaaaat 1620

ctttaaatct ttaaattgta ttttgtagtt tttggtgttt aagtcttgca catattttgt 1680

cagatttatt ccaaagtatt tcacgggttc ttttt 1715

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<223> Exon 6v2 - includes additional residue 770 at 3' end

<220>

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<223> Exon 7

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tggagtcgtt ggtgaagttt ttcattcctc agaggagaaa atctgtggct ggggagattg 180

ttctcattac tggagctggg catggaatag gcaggcagac tacttatgaa tttgcaaaac 240

gacagagcat attggttctg tgggatatta ataaggtgaa gaaagaagtg ggtgatgtaa 300

caatcgtggt gaataatgct gggacagtat atccagccga tcttctcagc accaaggatg 360

aagagattac caagacattt gaggtcaaca tcctaggaca tttttggatc acaaaagcac 420

ttcttccatc gatgatggag agaaatcatg gccacatcgt cacagtggct tcagtgtgcg 480

gccacgaagg gattccttac ctcatcccat attgttccag caaatttgcc gctgttggct 540

ttcacagagg tctgacatca gaacttcagg ccttgggaaa aactggtatc aaaacctcat 600

gtctctgccc agtttttgtg aatactgggt tcaccaaaaa tccaagcaca agattatggc 660

ctgtattgga gacagatgaa gtcgtaagaa gtctgataga tggaatactt accaataaga 720

aaatgatttt tgttccatcg tatatcaata tctttctgag actacagaag gtttcttcct 780

gaacgcgcct cagcgatttt aaatcgtatg cagaatattc aatttgaagc agtggttggc 840

cacaaaatca aaatgaaatg aataaataag ctccagccag agatgtatgc atgataatga 900

tatgaatagt ttcgaatcaa tgctgcaaag ctttatttca catttttca gtcctgataa 960

tattaaaaac attggtttgg cactagcagc agtcaaacga acaagattaa ttacctgtct 1020

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ttaaaaactt ctgtgcttac ataaacatac ttaaaaggtt ttctttaaga tattttattt 1140

ttccatttaa aggtggacaa aagctacctc cctaaaagta aatacaaaga gaacttattt 1200

acacagggaa ggtttaagac tgttcaagta gcattccaat ctgtagccat gccacagaat 1260

atcaacaaga acacagaatg agtgcacagc taagagatca agtttcagca ggcagcttta 1320

tctcaacctg gacatatttt aagattcagc atttgaaaga tttccctagc ctcttccttt 1380

ttcattagcc caaaacggtg caactctatt ctggacttta ttacttgatt ctgtcttctg 1440

tataactctg aagtccacca aaagtggacc ctctatattt cctccctttt tatagtctta 1500

taagatacat tatgaaaggt gaccgactct attttaaatc tcagaatttt aagttctagc 1560

cccatgataa ccttttttctt tgtaatttat gctttcatat atccttggtc ccagagatgt 1620

ttagacaatt ttaggctcaa aaattaaagc taacacagga aaaggaactg tactggctat 1680

tacataagaa acaatggacc caagagaaga aaaggaagaa agaaaggttt tttggttttt 1740

gttttgtttt gttttgtttt ttgtttttttt gagatggagt ctcactcttt cgcccaggct 1800

ggagtgcagt ggtatgatct cagctcactg caagctccac ctcccgggtt cacgccattc 1860

tcctgcctca gcctcctgag tagctgggac tacaggcgcc cgccaccaca cccggctaat 1920

tttttgtatt ttttgtagag acggggtttc accatgttag ccaagatggt ctcgatctcc 1980

tgacctcgtg atccacctgc ctcggcctcc caaagtgctg ggattacggg tgtgagccac 2040

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aatcttgttt tgtgtgtttt tcacatgtat tatagaatgc ttttgcatgg actatcctct 2160

tgtttttatt aaaaacaaat gatttttttta aaagtcacaa aaacaattca ctaaaaataa 2220

atatgtcatt gtgctttaaa aaaataacct cttgtagtta taaaataaaa cgtttgactt 2280

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<223> Exon 3

<220>
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<223> Exon 3'

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<222> (588)..(694)
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<223> Exon 5

<220>
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<222> (833)..(950)
<223> Exon 6v2 - includes additional residue 950 at 3' end

<220>
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<223> Exon 7

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tggagtcgtt ggtgaagttt ttcattcctc agaggagaaa atctgtggct ggggagattg 180

ttctcattac tggagctggg catggaatag gcaggcagac tacttatgaa tttgcaaaac 240

gacagagcat attggttctg tgggatatta ataagcgcgg tgtggaggaa actgcagctg 300

agtgccgaaa actaggcgtc actgcgcatg cgtatgtggt agactgcagc aacagagaag 360

agatctatcg ctctctaaat caggtgaaga aagaagtggg tgatgtaaca atcgtggtga 420

ataatgctgg gacagtatat ccagccgatc ttctcagcac caaggatgaa gagattacca 480

agacatttga ggtcaacatc ctaggacatt tttggaatgg aaaggacatc agaagtaatt 540

acttggatgt atataggatc gaggacactt ttggacgaga ctctgagatc acaaaagcac 600

ttcttccatc gatgatggag agaaatcatg gccacatcgt cacagtggct tcagtgtgcg 660

gccacgaagg gattccttac ctcatcccat attgttccag caaatttgcc gctgttggct 720

ttcacagagg tctgacatca gaacttcagg ccttgggaaa aactggtatc aaaacctcat 780

gtctctgccc agtttttgtg aatactgggt tcaccaaaaa tccaagcaca agattatggc 840

ctgtattgga gacagatgaa gtcgtaagaa gtctgataga tggaatactt accaataaga 900

aaatgatttt tgttccatcg tatatcaata tctttctgag actacagaag gtttcttcct 960

gaacgcgcct cagcgatttt aaatcgtatg cagaatattc aatttgaagc agtggttggc 1020

cacaaaatca aaatgaaatg aataaataag ctccagccag agatgtatgc atgataatga 1080

tatgaatagt ttcgaatcaa tgctgcaaag ctttatttca catttttca gtcctgataa 1140

tattaaaaac attggtttgg cactagcagc agtcaaacga acaagattaa ttacctgtct 1200

tcctgtttct caagaatatt tacgtagttt ttcataggtc tgtttttcct ttcatgcctc 1260

ttaaaaactt ctgtgcttac ataaacatac ttaaaaggtt ttctttaaga tattttattt 1320

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acacagggaa ggtttaagac tgttcaagta gcattccaat ctgtagccat gccacagaat 1440

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tataactctg aagtccacca aaagtggacc ctctatattt cctccctttt tatagtctta 1680

taagatacat tatgaaaggt gaccgactct attttaaatc tcagaatttt aagttctagc 1740

cccatgataa ccttttttctt tgtaatttat gctttcatat atccttggtc ccagagatgt 1800

ttagacaatt ttaggctcaa aaattaaagc taacacagga aaaggaactg tactggctat 1860

tacataagaa acaatggacc caagagaaga aaaggaagaa agaaaggttt tttggttttt 1920

gttttgtttt gttttgtttt ttgtttttttt gagatggagt ctcactcttt cgcccaggct 1980

ggagtgcagt ggtatgatct cagctcactg caagctccac ctcccgggtt cacgccattc 2040

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tgacctcgtg atccacctgc ctcggcctcc caaagtgctg ggattacggg tgtgagccac 2220

cgtgcccagc cttttttttt ttaatagaaa aaataatccg actcccacta catcaagact 2280

aatcttgttt tgtgtgtttt tcacatgtat tatagaatgc ttttgcatgg actatcctct 2340

tgtttttatt aaaaacaaat gatttttta aaagtcacaa aaacaattca ctaaaaataa 2400

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<223> Region Encoded by Exon 6v1

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<222> (272)..(300)
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<400> 12

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1               5                  10                  15


Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys
            20                  25                  30


Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
        35                  40                  45


Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
    50                  55                  60
```

```
Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu Thr Ala Ala Glu Cys
65                  70                  75                  80

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

Arg Glu Glu Ile Tyr Arg Ser Leu Asn Gln Val Lys Lys Glu Val Gly
            100                 105                 110

Asp Val Thr Ile Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp
        115                 120                 125

Leu Leu Ser Thr Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn
    130                 135                 140

Ile Leu Gly His Phe Trp Ile Thr Lys Ala Leu Leu Pro Ser Met Met
145                 150                 155                 160

Glu Arg Asn His Gly His Ile Val Thr Val Ala Ser Val Cys Gly His
                165                 170                 175

Glu Gly Ile Pro Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala
            180                 185                 190

Val Gly Phe His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys
        195                 200                 205

Thr Gly Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly
    210                 215                 220

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

Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys Met
                245                 250                 255

Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln Lys Phe
            260                 265                 270

Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln Asn Ile Gln
        275                 280                 285
```

```
Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys
    290                 295                 300


<210>  13
<211>  264
<212>  PRT
<213>  Homo sapiens


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<222>  (71)..(114)
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<223>  Region Encoded by Exon 4

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<223>  Region Encoded by Exon 5

<220>
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<223>  Region Encoded by Exon 6v1

<220>
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<223>  Region Encoded by Exon 7

<400>  13

Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile Tyr
1               5                   10                  15


Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys
            20                  25                  30


Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
        35                  40                  45
```

```
Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
    50                  55                  60

Leu Trp Asp Ile Asn Lys Val Lys Lys Glu Val Gly Asp Val Thr Ile
65                  70                  75                  80

Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr
                85                  90                  95

Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His
            100                 105                 110

Phe Trp Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His
        115                 120                 125

Gly His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro
    130                 135                 140

Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe His
145                 150                 155                 160

Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly Ile Lys
                165                 170                 175

Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe Thr Lys Asn
            180                 185                 190

Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp Glu Val Val Arg
        195                 200                 205

Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys Met Ile Phe Val Pro
    210                 215                 220

Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln Lys Phe Leu Pro Glu Arg
225                 230                 235                 240

Ala Ser Ala Ile Leu Asn Arg Met Gln Asn Ile Gln Phe Glu Ala Val
                245                 250                 255

Val Gly His Lys Ile Lys Met Lys
            260
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<210> 14
<211> 261
<212> PRT
<213> Homo sapiens

<220>
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<223> Region Encoded by Exon 2

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<223> Region Encoded by Exon 3

<220>
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<223> Region Encoded by Exon 4

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<220>
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<223> Region Encoded by Exon 7

<400> 14

Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile Tyr
1 5 10 15

Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys
20 25 30

Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
35 40 45

Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
50 55 60

```
Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu Thr Ala Ala Glu Cys
65                  70                  75                  80

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

Arg Glu Glu Ile Tyr Arg Ser Leu Asn Gln Val Lys Lys Glu Val Gly
            100                 105                 110

Asp Val Thr Ile Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp
        115                 120                 125

Leu Leu Ser Thr Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn
    130                 135                 140

Ile Leu Gly His Phe Trp Ile Thr Lys Ala Leu Leu Pro Ser Met Met
145                 150                 155                 160

Glu Arg Asn His Gly His Ile Val Thr Val Ala Ser Val Cys Gly His
                165                 170                 175

Glu Gly Ile Pro Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala
            180                 185                 190

Val Gly Phe His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys
        195                 200                 205

Thr Gly Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly
    210                 215                 220

Phe Thr Lys Asn Pro Ser Thr Arg Phe Leu Pro Glu Arg Ala Ser Ala
225                 230                 235                 240

Ile Leu Asn Arg Met Gln Asn Ile Gln Phe Glu Ala Val Val Gly His
                245                 250                 255

Lys Ile Lys Met Lys
            260
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<210> 15
<211> 274
<212> PRT

<213> Homo sapiens

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<220>
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<220>
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<220>
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<220>
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<223> Region Encoded by Exon 7

<400> 15

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Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile Tyr
1               5                  10                  15


Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys
            20                  25                  30


Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
        35                  40                  45


Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
    50                  55                  60
```

```
Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu Thr Ala Ala Glu Cys
65                  70                  75                  80

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

Arg Glu Glu Ile Tyr Arg Ser Leu Asn Gln Val Lys Lys Glu Val Gly
            100                 105                 110

Asp Val Thr Ile Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp
        115                 120                 125

Leu Leu Ser Thr Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn
    130                 135                 140

Ile Leu Gly His Phe Trp Ile Thr Lys Ala Leu Leu Pro Ser Met Met
145                 150                 155                 160

Glu Arg Asn His Gly His Ile Val Thr Val Ala Ser Val Cys Gly His
                165                 170                 175

Glu Gly Ile Pro Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala
            180                 185                 190

Val Gly Phe His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys
        195                 200                 205

Thr Gly Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly
    210                 215                 220

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

Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys Met
                245                 250                 255

Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln Lys Val
            260                 265                 270

Ser Ser
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<210> 16
<211> 324
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<222> (151)..(174)
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<222> (175)..(209)
<223> Region Encoded by Exon 4

<220>
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<222> (210)..(256)
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<220>
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<223> Region Encoded by Exon 6v1

<220>
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<222> (296)..(324)
<223> Region Encoded by Exon 7

<400> 16

Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile Tyr
1 5 10 15

Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys

```
            20                  25                  30

Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
        35                  40                  45

Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
    50                  55                  60

Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu Thr Ala Ala Glu Cys
65                  70                  75                  80

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

Arg Glu Glu Ile Tyr Arg Ser Leu Asn Gln Val Lys Lys Glu Val Gly
            100                 105                 110

Asp Val Thr Ile Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp
        115                 120                 125

Leu Leu Ser Thr Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn
    130                 135                 140

Ile Leu Gly His Phe Trp Asn Gly Lys Asp Ile Arg Ser Asn Tyr Leu
145                 150                 155                 160

Asp Val Tyr Arg Ile Glu Asp Thr Phe Gly Arg Asp Ser Glu Ile Thr
                165                 170                 175

Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly His Ile Val
            180                 185                 190

Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro Tyr Leu Ile Pro
        195                 200                 205

Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe His Arg Gly Leu Thr
    210                 215                 220

Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly Ile Lys Thr Ser Cys Leu
225                 230                 235                 240
```

```
Cys Pro Val Phe Val Asn Thr Gly Phe Thr Lys Asn Pro Ser Thr Arg
                245                 250                 255


Leu Trp Pro Val Leu Glu Thr Asp Glu Val Val Arg Ser Leu Ile Asp
            260                 265                 270


Gly Ile Leu Thr Asn Lys Lys Met Ile Phe Val Pro Ser Tyr Ile Asn
        275                 280                 285


Ile Phe Leu Arg Leu Gln Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile
    290                 295                 300


Leu Asn Arg Met Gln Asn Ile Gln Phe Glu Ala Val Val Gly His Lys
305                 310                 315                 320


Ile Lys Met Lys
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<210> 17
<211> 284
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(70)
<223> Region Encoded by Exon 1

<220>
<221> MISC_FEATURE
<222> (71)..(106)
<223> Region Encoded by Exon 2

<220>
<221> MISC_FEATURE
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<220>
<221> MISC_FEATURE
<222> (151)..(185)
<223> Region Encoded by Exon 4

<220>
<221> MISC_FEATURE
<222> (186)..(232)
<223> Region Encoded by Exon 5

<220>
<221> MISC_FEATURE
<222> (233)..(284)
<223> Region Encoded by Exon 6v3

<220>
<221> MISC_FEATURE
<222> (272)..(284)
<223> Region Encoded by Read-Through Into Intron 6

<400> 17

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Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile Tyr
1               5                  10                  15


Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys
            20                  25                  30


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Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
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Asp Val Thr Ile Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp
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Glu Arg Asn His Gly His Ile Val Thr Val Ala Ser Val Cys Gly His
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Phe Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp
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Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys Met
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Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln Lys Leu
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Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
        35                  40                  45


Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
    50                  55                  60


Leu Trp Asp Ile Asn Lys Val Lys Lys Glu Val Gly Asp Val Thr Ile
65                  70                  75                  80


Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr
                85                  90                  95


Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His
            100                 105                 110


Phe Trp Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His
        115                 120                 125


Gly His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro
    130                 135                 140


Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe His
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Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly Ile Lys
                165                 170                 175
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Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
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Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu Thr Ala Ala Glu Cys
65                  70                  75                  80


Arg Lys Leu Gly Val Thr Ala His Ala Tyr Val Val Asp Cys Ser Asn
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Arg Glu Glu Ile Tyr Arg Ser Leu Asn Gln Val Lys Lys Glu Val Gly
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Asp Val Thr Ile Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp
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Leu Leu Ser Thr Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn
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Ile Leu Gly His Phe Trp Asn Gly Lys Asp Ile Arg Ser Asn Tyr Leu
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Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly His Ile Val
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Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly Ile Lys Thr Ser Cys Leu
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Cys Pro Val Phe Val Asn Thr Gly Phe Thr Lys Asn Pro Ser Thr Arg
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20 25 30

Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
35 40 45

Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
50 55 60

Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu Thr Ala Ala Glu Cys

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65                  70                  75                  80

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

Arg Glu Glu Ile Tyr Arg Ser Leu Asn Gln Val Lys Lys Glu Val Gly
            100                 105                 110

Asp Val Thr Ile Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp
        115                 120                 125

Leu Leu Ser Thr Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn
    130                 135                 140

Ile Leu Gly His Phe Trp Ile Thr Lys Ala Leu Leu Pro Ser Met Met
145                 150                 155                 160

Glu Arg Asn His Gly His Ile Val Thr Val Ala Ser Val Cys Gly His
                165                 170                 175

Glu Gly Ile Pro Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala
            180                 185                 190

Val Gly Phe His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys
        195                 200                 205

Thr Gly Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly
    210                 215                 220

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

Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys Met
                245                 250                 255

Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln Lys Phe
            260                 265                 270

Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln Asn Ile Gln
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Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys
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<213>  Homo sapiens

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Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys
            20                  25                  30


Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
        35                  40                  45


Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
    50                  55                  60


Leu Trp Asp Ile Asn Lys Val Lys Lys Glu Val Gly Asp Val Thr Ile
65                  70                  75                  80


Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr
                85                  90                  95


Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His
            100                 105                 110


Phe Trp Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His
        115                 120                 125


Gly His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro
    130                 135                 140


Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe His
145                 150                 155                 160


Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly Ile Lys
                165                 170                 175
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Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe Thr Lys Asn
            180                 185                 190

Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp Glu Val Val Arg
        195                 200                 205

Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys Met Ile Phe Val Pro
    210                 215                 220

Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln Lys Phe Leu Pro Glu Arg
225                 230                 235                 240

Ala Ser Ala Ile Leu Asn Arg Met Gln Asn Ile Gln Phe Glu Ala Val
                245                 250                 255

Val Gly His Lys Ile Lys Met Lys
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Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys
            20                  25                  30

Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
        35                  40                  45

Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
    50                  55                  60

Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu Thr Ala Ala Glu Cys
65                  70                  75                  80

Arg Lys Leu Gly Val Thr Ala His Ala Tyr Val Val Asp Cys Ser Asn
                85                  90                  95
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Arg Glu Glu Ile Tyr Arg Ser Leu Asn Gln Val Lys Lys Glu Val Gly
            100                 105                 110

Asp Val Thr Ile Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp
        115                 120                 125

Leu Leu Ser Thr Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn
    130                 135                 140

Ile Leu Gly His Phe Trp Ile Thr Lys Ala Leu Leu Pro Ser Met Met
145                 150                 155                 160

Glu Arg Asn His Gly His Ile Val Thr Val Ala Ser Val Cys Gly His
                165                 170                 175

Glu Gly Ile Pro Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala
            180                 185                 190

Val Gly Phe His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys
        195                 200                 205

Thr Gly Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly
    210                 215                 220

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

Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys Met
                245                 250                 255

Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln Lys Phe
            260                 265                 270

Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln Asn Ile Gln
        275                 280                 285

Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys
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<213> Homo sapiens

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Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys
            20                  25                  30

Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
        35                  40                  45

Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
    50                  55                  60

Leu Trp Asp Ile Asn Lys Val Lys Lys Glu Val Gly Asp Val Thr Ile
65                  70                  75                  80

Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr
                85                  90                  95

Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His
            100                 105                 110

Phe Trp Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His
        115                 120                 125

Gly His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro
    130                 135                 140

Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe His
145                 150                 155                 160

Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly Ile Lys
                165                 170                 175

Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe Thr Lys Asn
            180                 185                 190

Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp Glu Val Val Arg
        195                 200                 205
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Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys Met Ile Phe Val Pro
210 215 220

Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln Lys Phe Leu Pro Glu Arg
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Ala Ser Ala Ile Leu Asn Arg Met Gln Asn Ile Gln Phe Glu Ala Val
245 250 255

Val Gly His Lys Ile Lys Met Lys
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ttctcattac tggagctggg catggaatag gcaggcagac tacttatgaa tttgcaaaac 240

gacagagcat attggttctg tgggatatta ataagcgcgg tgtggaggaa actgcagctg 300

agtgccgaaa actaggcgtc actgcgcatg cgtatgtggt agactgcagc aacagagaag 360

agatctatcg ctctctaaat caggtgaaga aagaagtggg tgatgtaaca atcgtggtga 420

ataatgctgg gacagtatat ccagccgatc ttctcagcac caaggatgaa gagattacca 480

agacatttga ggtcaacatc ctaggacatt tttggatcac aaaagcactt cttccatcga 540

tgatggagag aaatcatggc cacatcgtca cagtggcttc agtgtgcggc cacgaaggga 600

ttccttacct catcccatat tgttccagca aatttgccgc tgttggcttt cacagaggtc 660

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tttttgtgaa tactgggttc accaaaaatc caagcacaag attatggcct gtattggaga 780

cagatgaagt cgtaagaagt ctgatagatg gaatacttac caataagaaa atgatttttg 840

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tgaaatgaat aaataagctc cagccagaga tgtatgcatg ataatgatat gaatagtttc 1020

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ggtttggcac tagcagcagt caaacgaaca agattaatta cctgtcttcc tgtttctcaa 1140

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cagaatgagt gcacagctaa gagatcaagt ttcagcaggc agctttatct caacctggac 1440

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aacggtgcaa ctctattctg gactttatta cttgattctg tcttctgtat aactctgaag 1560

tccaccaaaa gtggaccctc tatatttcct ccctttttat agtcttataa gatacattat 1620

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atggacccaa gagaagaaaa ggaagaaaga aaggtttttt ggtttttgtt ttgttttgtt 1860

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<213> Homo sapiens

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gacagagcat attggttctg tgggatatta ataaggtgaa gaaagaagtg ggtgatgtaa 300

caatcgtggt gaataatgct gggacagtat atccagccga tcttctcagc accaaggatg 360

aagagattac caagacattt gaggtcaaca tcctaggaca tttttggatc acaaaagcac 420

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<221> MISC_FEATURE
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<400> 247

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1 5 10 15

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Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
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Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
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Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu Thr Ala Ala Glu Cys
65                  70                  75                  80

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

Arg Glu Glu Ile Tyr Arg Ser Leu Asn Gln Val Lys Lys Glu Val Gly
            100                 105                 110

Asp Val Thr Ile Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp
        115                 120                 125

Leu Leu Ser Thr Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn
    130                 135                 140

Ile Leu Gly His Phe Trp Ile Thr Lys Ala Leu Leu Pro Ser Met Met
145                 150                 155                 160

Glu Arg Asn His Gly His Ile Val Thr Val Ala Ser Val Cys Gly His
                165                 170                 175

Glu Gly Ile Pro Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala
            180                 185                 190

Val Gly Phe His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys
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Thr Gly Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly
    210                 215                 220

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

Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys Met
245 250 255

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<210> 250
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<222> (3)..(23)
<223> n = A, T, C, or G

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atcagaactt caggccttgg 20

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<210> 258
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cguuaucaac uugaaaaagu ggcaccgagu cggugc 96

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

<210> 1242
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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

<210> 1247

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

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