

SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC

<120> PEPTIDE VACCINES FOR CANCERS EXPRESSING TUMOR-ASSOCIATED ANTIGENS

<130> ONC-A0704P

<150> US 60/902,949

<151> 2007-02-21

<160> 434

<170> PatentIn version 3.4

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Ile His Ser Gln Glu Pro Lys Asp Pro His Asp Leu Met Phe Thr Ile		260		265	270
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ttttaatagt taactgacta tagattgttt tctatgccat gtatgtgcca cttctgagag 4253
tagtaaatga ctctttgcta catttttaaaa gcaattgtat tagtaagaac tttgtaaata 4313
aatacctaaa acccaagtgt aaaaaaaaaa aaaaaa 4349

```

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<210> 6
<211> 882
<212> PRI
<213> Homo sapiens

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<400> 6

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Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu
1          5          10          15

```

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Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu
          20          25          30

```

```

Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Met Pro Gln Ile
          35          40          45

```

```

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

```

```

Ile Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu Ser
65          70          75          80

```

```

Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val Phe
          85          90          95

```

```

Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys Ala
          100          105          110

```

Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln Lys
115 120 125

Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser Met
130 135 140

Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu Leu
145 150 155 160

Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg Lys
165 170 175

Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln Gly
180 185 190

Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys Pro
195 200 205

Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe Tyr
210 215 220

Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe Gln
225 230 235 240

Asp Cys Ile Leu Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr Asn
245 250 255

Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu Gly
260 265 270

Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys Asp
275 280 285

Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu Trp
290 295 300

Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met Tyr
305 310 315 320

Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser Met
325 330 335

Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu Lys
340 345 350

Glu Thr Leu Ala Gln Leu Ser Arg Glu Thr Asp Val Ser Pro Phe Pro

355	360	365
Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser Leu		
370	375	380
Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp Thr		
385	390	395 400
Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro Ser		
405	410	415
Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr Glu		
420	425	430
Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln Val		
435	440	445
Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro Glu		
450	455	460
Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val His		
465	470	475 480
Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp Glu		
485	490	495
Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu Val		
500	505	510
Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu Thr		
515	520	525
Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys		
530	535	540
Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu		
545	550	555 560
Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn		
565	570	575
Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu		
580	585	590
Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu		
595	600	605

Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr
610 615 620

Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser Leu
625 630 635 640

Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp Arg
645 650 655

Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile Ala
660 665 670

Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln
675 680 685

Thr Arg Pro Pro Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser
690 695 700

Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn
705 710 715 720

Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu
725 730 735

Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu
740 745 750

Lys Met Leu Cys Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala
755 760 765

Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr
770 775 780

Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys
785 790 795 800

Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys
805 810 815

Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly
820 825 830

Arg Ser Pro Ser Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser
835 840 845

Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro
850 855 860

Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His
865 870 875 880

Leu Ile

<210> 7
<211> 1372
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (206)..(397)

<400> 7
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agtaaccgac ttctctccgg actcctgcac gacctgctcc tacagccggc gatccactcc 120
cggtctgttcc cccggagggt ccagaggcct ttcagaagga gaaggcagct ctgtttctct 180
gcagaggagt agggtccttt cagcc atg aag cat gtg ttg aac ctc tac ctg 232
Met Lys His Val Leu Asn Leu Tyr Leu
1 5
tta ggt gtg gta ctg acc cta ctc tcc atc ttc gtt aga gtg atg gag 280
Leu Gly Val Val Leu Thr Leu Leu Ser Ile Phe Val Arg Val Met Glu
10 15 20 25
tcc cta gaa ggc tta cta gag agc cca tcg cct ggg acc tcc tgg acc 328
Ser Leu Glu Gly Leu Leu Glu Ser Pro Ser Pro Gly Thr Ser Trp Thr
30 35 40
acc aga agc caa cta gcc aac aca gag ccc acc aag ggc ctt cca gac 376
Thr Arg Ser Gln Leu Ala Asn Thr Glu Pro Thr Lys Gly Leu Pro Asp
45 50 55
cat cca tcc aga agc atg tga taagacctcc ttccatactg gccatatttt 427
His Pro Ser Arg Ser Met
60
ggaacactga cctagacatg tccagatggg agtcccatc ctagcagaca agctgagcac 487
cgttgtaacc agagaactat tactaggcct tgaagaacct gtctaactgg atgctcattg 547
cctgggcaag gcctgttttag gccggttgcg gtggctcatg cctgtaatcc tagcactttg 607
ggaggctgag gtgggtggat cacctgaggt caggagtctg agaccagcct cgccaacatg 667
gcgaaacccc atctctacta aaaatacaaa agttagctgg gtgtggtggc agaggcctgt 727
aatcccagtt ccttgggagg ctgaggcggg agaattgctt gaaccggggg acggagggtt 787

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cagtgaaccg agatcgcaact gctgtaccca gcctgggcca cagtgaaga ctccatctca 847
aaaaaaaaa gaaaagaaaa agcctgttta atgcacaggt gtgagtggat tgcttatggc 907
tatgagatag gttgatctcg cccttaccoc ggggtctggg gtatgctgtg ctttctcag 967
cagtatggct ctgacatctc ttagatgtcc caacttcagc tgttgggaga tggatgatatt 1027
ttcaacccta cttctaaac atctgtctgg ggttccttta gtcttgaatg tcttatgctc 1087
aattatttgg tgttgagcct ctcttcaca agagctctc catgtttgga tagcagttga 1147
agaggttgtg tgggtgggct gttgggagt aggatggagt gttcagtgc catttctcat 1207
tttacatttt aaagtcgttc ctccaacata gtgtgtattg gtctgaagg ggtgggtggga 1267
tgccaaagcc tgcacaagt atggacattg tggccaccat gtggcttaaa tgattttttc 1327
taactaataa agtggaatat atatttcaaa aaaaaaaaaa aaaaa 1372

```

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<210> 8
<211> 63
<212> PRT
<213> Homo sapiens

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<400> 8
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Met Lys His Val Leu Asn Leu Tyr Leu Leu Gly Val Val Leu Thr Leu
1           5           10          15

```

```

Leu Ser Ile Phe Val Arg Val Met Glu Ser Leu Glu Gly Leu Leu Glu
          20          25          30

```

```

Ser Pro Ser Pro Gly Thr Ser Trp Thr Thr Arg Ser Gln Leu Ala Asn
          35          40          45

```

```

Thr Glu Pro Thr Lys Gly Leu Pro Asp His Pro Ser Arg Ser Met
          50          55          60

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```

<210> 9
<211> 3516
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (767)..(1990)

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<400> 9
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gggctcggcg ccgcctgtga gcgggcccgc gcggccggct ctccgggca ccaagcttgc 120
tccgcgccac tgcccgccgg ccgcggcgga ggaagacctg ccgtctccg ccgcggcggg 180

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cccttctctgg cgcgagggcag tgagggcgag ggcgtcaggt gcgagcgcg ggccccgcgcg	240
cagcgccccgc cgcagcgccg cgcgaagccg cgcggggctc cgctccgggg ggctccagcg	300
ccttcgcttc cgtctcagcc aagttgcgtg gaccgcgtct ttgcgcacct tccccagccg	360
cgggccgaac cgcgcgtccc actgacgctg ctttcgcttc acccgaaacg gggctgcggg	420
gccccgcacg cggaaaggat ggggagaagg ctgcagatgc cgaggcgccc cgagacgccc	480
gtgcggcagt gacccgcgac ctccgccccg ccggcgcggc ccctcggggc ccggggggccc	540
tcggcgcccc ttccttgccg cgcgggaacc ccgaggccc ggccggcccc ctccccctgc	600
gagccggcg cagccctccc ggcggggcgg cgggcgagg ccggggcggg cgcgggcgcg	660
ggcgggggcg gggcgggggc gcgcgcccgg agcccggagc ccggccctgc gctcggctcg	720
actcggctcg cctcgcggcg ggcgcctcgc tcgcagcgg cgcacc atg gac ggg	775
Met Asp Gly	
1	
ctg ccc ggt cgg gcg ctg ggg gcc gcc tgc ctt ctg ctg ctg gcg gcc	823
Leu Pro Gly Arg Ala Leu Gly Ala Ala Cys Leu Leu Leu Ala Ala	
5 10 15	
ggc tgg ctg ggg cct gag gcc tgg ggc tca ccc acg ccc ccg ccg acg	871
Gly Trp Leu Gly Pro Glu Ala Trp Gly Ser Pro Thr Pro Pro Pro Thr	
20 25 30 35	
cct gcc gcg ccg ccg cca ccc ccg cca ccc gga gcc ccg ggt ggc tgc	919
Pro Ala Ala Pro Pro Pro Pro Pro Pro Pro Gly Ala Pro Gly Gly Ser	
40 45 50	
cag gac acc tgt acg tgc tgc ggc ggc ttc cgg ccg cca gag gag ctc	967
Gln Asp Thr Cys Thr Ser Cys Gly Gly Phe Arg Arg Pro Glu Glu Leu	
55 60 65	
ggc cga gtg gac ggc gac ttc ctg gag gcg gtg aag ccg cac atc ttg	1015
Gly Arg Val Asp Gly Asp Phe Leu Glu Ala Val Lys Arg His Ile Leu	
70 75 80	
agc cgc ctg cag atg ccg ggc ccg ccc aac atc acg cac gcc gtg cct	1063
Ser Arg Leu Gln Met Arg Gly Arg Pro Asn Ile Thr His Ala Val Pro	
85 90 95	
aag gcc gcc atg gtc acg gcc ctg cgc aag ctg cac gcg ggc aag gtg	1111
Lys Ala Ala Met Val Thr Ala Leu Arg Lys Leu His Ala Gly Lys Val	
100 105 110 115	
cgc gag gac ggc cgc gtg gag atc ccg cac ctc gac ggc cac gcc agc	1159
Arg Glu Asp Gly Arg Val Glu Ile Pro His Leu Asp Gly His Ala Ser	
120 125 130	
ccg ggc gcc gac ggc cag gag ccg gtt tcc gaa atc atc agc ttc gcc	1207
Pro Gly Ala Asp Gly Gln Glu Arg Val Ser Glu Ile Ile Ser Phe Ala	
135 140 145	
gag aca gat ggc ctc gcc tcc tcc ccg gtc cgc cta tac ttc ttc atc	1255
Glu Thr Asp Gly Leu Ala Ser Ser Arg Val Arg Leu Tyr Phe Phe Ile	

150	155	160	
tcc aac gaa ggc aac cag aac ctg ttt gtg gtc cag gcc agc ctg tgg Ser Asn Glu Gly Asn Gln Asn Leu Phe Val Val Gln Ala Ser Leu Trp 165 170 175			1303
ctt tac ctg aaa ctc ctg ccc tac gtc ctg gag aag ggc agc cgg cgg Leu Tyr Leu Lys Leu Leu Pro Tyr Val Leu Glu Lys Gly Ser Arg Arg 180 185 190 195			1351
aag gtg cgg gtc aaa gtg tac ttc cag gag cag ggc cac ggt gac agg Lys Val Arg Val Lys Val Tyr Phe Gln Glu Gln Gly His Gly Asp Arg 200 205 210			1399
tgg aac atg gtg gag aag agg gtg gac ctc aag cgc agc ggc tgg cat Trp Asn Met Val Glu Lys Arg Val Asp Leu Lys Arg Ser Gly Trp His 215 220 225			1447
acc ttc cca ctc acg gag gcc atc cag gcc ttg ttt gag cgg ggc gag Thr Phe Pro Leu Thr Glu Ala Ile Gln Ala Leu Phe Glu Arg Gly Glu 230 235 240			1495
cgg cga ctc aac cta gac gtg cag tgt gac agc tgc cag gag ctg gcc Arg Arg Leu Asn Leu Asp Val Gln Cys Asp Ser Cys Gln Glu Leu Ala 245 250 255			1543
gtg gtg ccg gtg ttc gtg gac cca ggc gaa gag tcg cac cga ccc ttt Val Val Pro Val Phe Val Asp Pro Gly Glu Glu Ser His Arg Pro Phe 260 265 270 275			1591
gtg gtg gtg cag gct cgg ctg ggc gac agc agg cac cgc att cgc aag Val Val Val Gln Ala Arg Leu Gly Asp Ser Arg His Arg Ile Arg Lys 280 285 290			1639
cga ggc ctg gag tgc gat ggc cgg acc aac ctc tgt tgc agg caa cag Arg Gly Leu Glu Cys Asp Gly Arg Thr Asn Leu Cys Cys Arg Gln Gln 295 300 305			1687
ttc ttc att gac ttc cgc ctc atc ggc tgg aac gac tgg atc ata gca Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn Asp Trp Ile Ile Ala 310 315 320			1735
ccc acc ggc tac tac ggc aac tac tgt gag ggc agc tgc cca gcc tac Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly Ser Cys Pro Ala Tyr 325 330 335			1783
ctg gca ggg gtc ccc ggc tct gcc tcc tcc ttc cac acg gct gtg gtg Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe His Thr Ala Val Val 340 345 350 355			1831
aac cag tac cgc atg cgg ggt ctg aac ccc ggc acg gtg aac tcc tgc Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly Thr Val Asn Ser Cys 360 365 370			1879
tgc att ccc acc aag ctg agc acc atg tcc atg ctg tac ttc gat gat Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met Leu Tyr Phe Asp Asp 375 380 385			1927
gag tac aac atc gtc aag cgg gac gtg ccc aac atg att gtg gag gag Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn Met Ile Val Glu Glu 390 395 400			1975

tgc ggc tgc gcc tga cagtgcgaagg cagggggcacg gtggtggggc acggagggca 2030
 Cys Gly Cys Ala
 405

gtccccgggtg ggctttcttcc agccccccgc gggaacgggg tacacgggtg gctgagtaca 2090
 gtcatttctgt tgggctgtgg agatagtgcc aggggtgcggc ctgagatatt tttctacagc 2150
 ttcatagagc aaccagtcaa aaccagagcg agaaccctca actgacatga aatactttaa 2210
 aatgcacacg tagccacgca cagccagacg catcctgcca cccacacagc agcctccagg 2270
 ataccagcaa atggatgcgg tgacaaatgg cagcttagct acaaatgcct gtcagtcgga 2330
 gagaatgggg tgagcagcca ccattccacc agctggcccg gccacgtctc gaagttgcgc 2390
 cttcccgagc acacataaaa gcacaaagac agagacgcag agagagagag agagccacgg 2450
 agaggaaaag cagatgcagg ggtggggagc gcagctcggc ggaggctgcg tgtgccccgt 2510
 ggcttttacc aggcctgctc tgcttggtc gatgtctgt tttccacgc ctgggatacct 2570
 tcgtgcttca aggcctgggg agcctgtcct tccatgccct tgtcgaggga aagagaccca 2630
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 gcttgggcct ctgacatgac ttatgtgtgt gtgtgttttt ggggtgggga gggagggaga 2750
 gaagaggggg ctaaatttga tgctttaact gatctccaac agttgacagg tcatccttgc 2810
 cagttgtata actgaaaaag gacttttcta ccaggtatga ctttttaagt gaaaatctga 2870
 attgttctaa atggaaagaa aaaaagttgc aatctgtgcc cticattggg gacattcctc 2930
 taggactggt ttggggacgg gtgggaatga cccctaggca aggggatgag accgcaggag 2990
 gaaatggcgg ggagggtggca ttcttgaact gctgaggatg gggggtgtcc cctcagcgga 3050
 ggccaaggga ggggagcagc ctagttggtc ttggagagat ggggaaggct ttcagctgat 3110
 ttgcagaagt tgcccatgtg ggcccaacca tcagggtg cgtggacgt ggccccctgcc 3170
 cactcacctg ccgcctgcc cgcccgcccg catagcactt gcagacctgc ctgaacgcac 3230
 atgacatagc acttgccgat ctgcgtgtgc ccagaagtgg cccttggccg agcgccgaac 3290
 tcgctcgccc tctagatgtc caagtgccac gtgaactatg caatttaaag ggttgacca 3350
 cactagacga aactggactc gtacgactct tttatatatt tttatacttg aaatgaaatc 3410
 ctttgcttct tttttaagcg aatgattgct tttaatgttt gcactgattt agttgcatga 3470
 ttagtcagaa actgccattt gaaaaaaaaag ttatttttat agcagc 3516

<210> 10
 <211> 407
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Asp Gly Leu Pro Gly Arg Ala Leu Gly Ala Ala Cys Leu Leu Leu
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Leu Ala Ala Gly Trp Leu Gly Pro Glu Ala Trp Gly Ser Pro Thr Pro
20 25 30

Pro Pro Thr Pro Ala Ala Pro Pro Pro Pro Pro Pro Gly Ala Pro
35 40 45

Gly Gly Ser Gln Asp Thr Cys Thr Ser Cys Gly Gly Phe Arg Arg Pro
50 55 60

Glu Glu Leu Gly Arg Val Asp Gly Asp Phe Leu Glu Ala Val Lys Arg
65 70 75 80

His Ile Leu Ser Arg Leu Gln Met Arg Gly Arg Pro Asn Ile Thr His
85 90 95

Ala Val Pro Lys Ala Ala Met Val Thr Ala Leu Arg Lys Leu His Ala
100 105 110

Gly Lys Val Arg Glu Asp Gly Arg Val Glu Ile Pro His Leu Asp Gly
115 120 125

His Ala Ser Pro Gly Ala Asp Gly Gln Glu Arg Val Ser Glu Ile Ile
130 135 140

Ser Phe Ala Glu Thr Asp Gly Leu Ala Ser Ser Arg Val Arg Leu Tyr
145 150 155 160

Phe Phe Ile Ser Asn Glu Gly Asn Gln Asn Leu Phe Val Val Gln Ala
165 170 175

Ser Leu Trp Leu Tyr Leu Lys Leu Leu Pro Tyr Val Leu Glu Lys Gly
180 185 190

Ser Arg Arg Lys Val Arg Val Lys Val Tyr Phe Gln Glu Gln Gly His
195 200 205

Gly Asp Arg Trp Asn Met Val Glu Lys Arg Val Asp Leu Lys Arg Ser
210 215 220

Gly Trp His Thr Phe Pro Leu Thr Glu Ala Ile Gln Ala Leu Phe Glu
225 230 235 240

Arg Gly Glu Arg Arg Leu Asn Leu Asp Val Gln Cys Asp Ser Cys Gln
 245 250 255

Glu Leu Ala Val Val Pro Val Phe Val Asp Pro Gly Glu Glu Ser His
 260 265 270

Arg Pro Phe Val Val Val Gln Ala Arg Leu Gly Asp Ser Arg His Arg
 275 280 285

Ile Arg Lys Arg Gly Leu Glu Cys Asp Gly Arg Thr Asn Leu Cys Cys
 290 295 300

Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn Asp Trp
 305 310 315 320

Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly Ser Cys
 325 330 335

Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe His Thr
 340 345 350

Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly Thr Val
 355 360 365

Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met Leu Tyr
 370 375 380

Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn Met Ile
 385 390 395 400

Val Glu Glu Cys Gly Cys Ala
 405

<210> 11
 <211> 2972
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (28)..(2700)

<400> 11
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 Met Ser Gln Gly Ile Leu Ser Pro Pro
 1 5

gcg ggc ttg ctg tcc gat gac gat gtc gta gtt tct ccc atg ttt gag 102

Ala Gly Leu Leu Ser Asp Asp Asp Val Val Val Ser Pro Met Phe Glu	
10 15 20 25	
tcc aca gct gca gat ttg ggg tct gtg gta cgc aag aac ctg cta tca	150
Ser Thr Ala Ala Asp Leu Gly Ser Val Val Arg Lys Asn Leu Leu Ser	
30 35 40	
gac tgc tct gtc gtc tct acc tcc cta gag gac aag cag cag gtt cca	198
Asp Cys Ser Val Val Ser Thr Ser Leu Glu Asp Lys Gln Gln Val Pro	
45 50 55	
tct gag gac agt atg gag aag gtg aaa gta tac ttg agg gtt agg ccc	246
Ser Glu Asp Ser Met Glu Lys Val Lys Val Tyr Leu Arg Val Arg Pro	
60 65 70	
ttg tta cct tca gag ttg gaa cga cag gaa gat cag ggt tgt gtc cgt	294
Leu Leu Pro Ser Glu Leu Glu Arg Gln Glu Asp Gln Gly Cys Val Arg	
75 80 85	
att gag aat gtg gag acc ctt gtt cta caa gca ccc aag gac tcg ttt	342
Ile Glu Asn Val Glu Thr Leu Val Leu Gln Ala Pro Lys Asp Ser Phe	
90 95 100 105	
gcc ctg aag agc aat gaa cgg gga att ggc caa gcc aca cac agg ttc	390
Ala Leu Lys Ser Asn Glu Arg Gly Ile Gly Gln Ala Thr His Arg Phe	
110 115 120	
acc ttt tcc cag atc ttt ggg cca gaa gtg gga cag gca tcc ttc ttc	438
Thr Phe Ser Gln Ile Phe Gly Pro Glu Val Gly Gln Ala Ser Phe Phe	
125 130 135	
aac cta act gtg aag gag atg gta aag gat gta ctc aaa ggg cag aac	486
Asn Leu Thr Val Lys Glu Met Val Lys Asp Val Leu Lys Gly Gln Asn	
140 145 150	
tgg ctc atc tat aca tat gga gtc act aac tca ggg aaa acc cac acg	534
Trp Leu Ile Tyr Thr Tyr Gly Val Thr Asn Ser Gly Lys Thr His Thr	
155 160 165	
att caa ggt acc atc aag gat gga ggg att ctc ccc cgg tcc ctg gcg	582
Ile Gln Gly Thr Ile Lys Asp Gly Gly Ile Leu Pro Arg Ser Leu Ala	
170 175 180 185	
ctg atc ttc aat agc ctc caa ggc caa ctt cat cca aca cct gat ctg	630
Leu Ile Phe Asn Ser Leu Gln Gly Gln Leu His Pro Thr Pro Asp Leu	
190 195 200	
aag ccc ttg ctc tcc aat gag gta atc tgg cta gac agc aag cag atc	678
Lys Pro Leu Leu Ser Asn Glu Val Ile Trp Leu Asp Ser Lys Gln Ile	
205 210 215	
cga cag gag gaa atg aag aag ctg tcc ctg cta aat gga ggc ctc caa	726
Arg Gln Glu Glu Met Lys Lys Leu Ser Leu Leu Asn Gly Gly Leu Gln	
220 225 230	
gag gag gag ctg tcc act tcc ttg aag agg agt gtc tac atc gaa agt	774
Glu Glu Glu Leu Ser Thr Ser Leu Lys Arg Ser Val Tyr Ile Glu Ser	
235 240 245	
cgg ata ggt acc agc acc agc ttc gac agt ggc att gct ggg ctc tct	822
Arg Ile Gly Thr Ser Thr Ser Phe Asp Ser Gly Ile Ala Gly Leu Ser	

250	255	260	265	
tct atc agt cag tgt acc agc agt agc cag ctg gat gaa aca agt cat				870
Ser Ile Ser Gln Cys Thr Ser Ser Ser Gln Leu Asp Glu Thr Ser His				
	270	275	280	
cga tgg gca cag cca gac act gcc cca cta cct gtc ccg gca aac att				918
Arg Trp Ala Gln Pro Asp Thr Ala Pro Leu Pro Val Pro Ala Asn Ile				
	285	290	295	
cgc ttc tcc atc tgg atc tca ttc ttt gag atc tac aac gaa ctg ctt				966
Arg Phe Ser Ile Trp Ile Ser Phe Phe Glu Ile Tyr Asn Glu Leu Leu				
	300	305	310	
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Tyr Asp Leu Leu Glu Pro Pro Ser Gln Gln Arg Lys Arg Gln Thr Leu				
	315	320	325	
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Arg Leu Cys Glu Asp Gln Asn Gly Asn Pro Tyr Val Lys Asp Leu Asn				
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tgg att cat gtg caa gat gct gag gag gcc tgg aag ctc cta aaa gtg				1110
Trp Ile His Val Gln Asp Ala Glu Glu Ala Trp Lys Leu Leu Lys Val				
	350	355	360	
ggt cgt aag aac cag agc ttt gcc agc acc cac ctc aac cag aac tcc				1158
Gly Arg Lys Asn Gln Ser Phe Ala Ser Thr His Leu Asn Gln Asn Ser				
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agc cgc agt cac agc atc ttc tca atc agg atc cta cac ctt cag ggg				1206
Ser Arg Ser His Ser Ile Phe Ser Ile Arg Ile Leu His Leu Gln Gly				
	380	385	390	
gaa gga gat ata gtc ccc aag atc agc gag ctg tca ctc tgt gat ctg				1254
Glu Gly Asp Ile Val Pro Lys Ile Ser Glu Leu Ser Leu Cys Asp Leu				
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gct gcc tca gag cgc tgc aaa gat cag aag agt ggt gaa cgg ttg aag				1302
Ala Gly Ser Glu Arg Cys Lys Asp Gln Lys Ser Gly Glu Arg Leu Lys				
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gaa gca gga aac att aac acc tct cta cac acc ctg ggc cgc tgt att				1350
Glu Ala Gly Asn Ile Asn Thr Ser Leu His Thr Leu Gly Arg Cys Ile				
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Ala Ala Leu Arg Gln Asn Gln Gln Asn Arg Ser Lys Gln Asn Leu Val				
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Pro Phe Arg Asp Ser Lys Leu Thr Arg Val Phe Gln Gly Phe Phe Thr				
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Gly Arg Gly Arg Ser Cys Met Ile Val Asn Val Asn Pro Cys Ala Ser				
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acc tat gat gaa act ctt cat gtg gcc aag ttc tca gcc att gct agc				1542
Thr Tyr Asp Glu Thr Leu His Val Ala Lys Phe Ser Ala Ile Ala Ser				
	490	495	500	505

cag ctt gtg cat gcc cca cct atg caa ctg gga ttc cca tcc ctg cac Gln Leu Val His Ala Pro Pro Met Gln Leu Gly Phe Pro Ser Leu His 510 515 520	1590
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gcc aaa aag cgc ctt ggt acc aac cag gaa aat cag caa cca aac caa Ala Lys Lys Arg Leu Gly Thr Asn Gln Glu Asn Gln Gln Pro Asn Gln 830 835 840	2550
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Ala Pro Leu Pro Val Pro Ala Asn Ile Arg Phe Ser Ile Trp Ile Ser
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Phe Phe Glu Ile Tyr Asn Glu Leu Leu Tyr Asp Leu Leu Glu Pro Pro
305 310 315 320

Ser Gln Gln Arg Lys Arg Gln Thr Leu Arg Leu Cys Glu Asp Gln Asn
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Gly Asn Pro Tyr Val Lys Asp Leu Asn Trp Ile His Val Gln Asp Ala
340 345 350

Glu Glu Ala Trp Lys Leu Leu Lys Val Gly Arg Lys Asn Gln Ser Phe
355 360 365

Ala Ser Thr His Leu Asn Gln Asn Ser Ser Arg Ser His Ser Ile Phe
370 375 380

Ser Ile Arg Ile Leu His Leu Gln Gly Glu Gly Asp Ile Val Pro Lys
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Asp Gln Lys Ser Gly Glu Arg Leu Lys Glu Ala Gly Asn Ile Asn Thr
420 425 430

Ser Leu His Thr Leu Gly Arg Cys Ile Ala Ala Leu Arg Gln Asn Gln
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Gln Asn Arg Ser Lys Gln Asn Leu Val Pro Phe Arg Asp Ser Lys Leu
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Ile Val Asn Val Asn Pro Cys Ala Ser Thr Tyr Asp Glu Thr Leu His
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Met Gln Leu Gly Phe Pro Ser Leu His Ser Phe Ile Lys Glu His Ser
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580 585 590

Cys Asn Glu Met Val Glu Gln Met Gln Gln Arg Glu Gln Trp Cys Ser
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Glu His Leu Asp Thr Gln Lys Glu Leu Leu Glu Glu Met Tyr Glu Glu
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Lys Leu Asn Ile Leu Lys Glu Ser Leu Thr Ser Phe Tyr Gln Glu Glu
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Ile Gln Glu Arg Asp Glu Lys Ile Glu Glu Leu Glu Ala Leu Leu Gln
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 Met Lys Arg Ser
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 Ser Val Ser Ser Gly Gly Ala Gly Arg Leu Ser Met Gln Glu Leu Arg
 5 10 15 20
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 Ser Gln Asp Val Asn Lys Gln Gly Leu Tyr Thr Pro Gln Thr Lys Glu
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Lys Val Ser Leu Phe Gly Lys Arg Thr Ser Gly His Gly Ser Arg Asn	
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Ser Gln Leu Gly Ile Phe Ser Ser Ser Glu Lys Ile Lys Asp Pro Arg	
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Pro Leu Asn Asp Lys Ala Phe Ile Gln Gln Cys Ile Arg Gln Leu Cys	
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Glu Phe Leu Thr Glu Asn Gly Tyr Ala His Asn Val Ser Met Lys Ser	
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Tyr Gly Phe Leu Cys Pro Ser Tyr Glu Leu Pro Asp Thr Lys Phe Glu	
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Ser Lys Ser Ser Met Tyr Thr Val Gly Ala Pro His Thr Trp Pro His	
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Glu Glu Thr Glu Asp Gly Ile Met His Asn Lys Leu Phe Leu Asp Tyr	
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Thr Ile Lys Cys Tyr Glu Ser Phe Met Ser Gly Ala Asp Ser Phe Asp	
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Glu Met Asn Ala Glu Leu Gln Ser Lys Leu Lys Asp Leu Phe Asn Val	
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gat gct ttt aag ctg gaa tca tta gaa gca aaa aac aga gca ttg aat	932
Asp Ala Phe Lys Leu Glu Ser Leu Glu Ala Lys Asn Arg Ala Leu Asn	
265 270 275	
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Glu Gln Ile Ala Arg Leu Glu Gln Glu Arg Glu Lys Glu Pro Asn Arg	
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Leu Glu Ser Leu Arg Lys Leu Lys Ala Ser Leu Gln Gly Asp Val Gln	
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Lys Tyr Gln Ala Tyr Met Ser Asn Leu Glu Ser His Ser Ala Ile Leu	
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gac cag aaa tta aat ggt ctc aat gag gaa att gct aga gta gaa cta	1124
Asp Gln Lys Leu Asn Gly Leu Asn Glu Glu Ile Ala Arg Val Glu Leu	
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Arg Thr Leu Lys Glu Glu Val Gln Lys Leu Asp Asp Leu Tyr Gln Gln	
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Lys Ile Lys Glu Ala Glu Glu Glu Asp Glu Lys Cys Ala Ser Glu Leu	

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Glu Ser Leu Glu Lys His Lys His Leu Leu Glu Ser Thr Val Asn Gln			
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Gly Ser Arg Asn Ser Gln Leu Gly Ile Phe Ser Ser Ser Glu Lys Ile			
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Ser Met Lys Ser Leu Gln Ala Pro Ser Val Lys Asp Phe Leu Lys Ile
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Phe Thr Phe Leu Tyr Gly Phe Leu Cys Pro Ser Tyr Glu Leu Pro Asp
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Thr Trp Pro His Ile Val Ala Ala Leu Val Trp Leu Ile Asp Cys Ile
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Lys Ile His Thr Ala Met Lys Glu Ser Ser Pro Leu Phe Asp Asp Gly
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Gln Pro Trp Gly Glu Glu Thr Glu Asp Gly Ile Met His Asn Lys Leu
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Phe Leu Asp Tyr Thr Ile Lys Cys Tyr Glu Ser Phe Met Ser Gly Ala
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Ser Ala Ile Leu Asp Gln Lys Leu Asn Gly Leu Asn Glu Glu Ile Ala
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Arg Val Glu Leu Glu Cys Glu Thr Ile Lys Gln Glu Asn Thr Arg Leu
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Ile Asn His Glu Arg Asn Glu Leu Gln Gln Thr Ile Asn Lys Leu Thr
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Cys Leu Val Lys Tyr Arg Ala Gln Val Tyr Val Pro Leu Lys Glu Leu
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485 490 495

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500 505 510

Leu Tyr Gln Gln Lys Ile Lys Glu Ala Glu Glu Glu Asp Glu Lys Cys
515 520 525

Ala Ser Glu Leu Glu Ser Leu Glu Lys His Lys His Leu Leu Glu Ser
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Gln Arg Glu Tyr Gln Leu Val Val Gln Thr Thr Thr Glu Glu Arg Arg

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                    595                      600                      605

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30                      35                      40

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65                      70                      75

gtt ccg cta agt gat gct ctt tta aat aaa ttg att ggt cgt tac agt 350
Val Pro Leu Ser Asp Ala Leu Leu Asn Lys Leu Ile Gly Arg Tyr Ser
80                      85                      90

caa gca att gaa gcg ctt ccc cca gat aaa tat ggc caa aat gag agt 398

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Gln Ala Ile Glu Ala Leu Pro Pro Asp Lys Tyr Gly Gln Asn Glu Ser	
95 100 105	
ttt gct aga att caa gtg aga ttt gct gaa tta aaa gct att caa gag	446
Phe Ala Arg Ile Gln Val Arg Phe Ala Glu Leu Lys Ala Ile Gln Glu	
110 115 120	
cca gat gat gca cgt gac tac ttt caa atg gcc aga gca aac tgc aag	494
Pro Asp Asp Ala Arg Asp Tyr Phe Gln Met Ala Arg Ala Asn Cys Lys	
125 130 135 140	
aaa ttt gct ttt gtt cat ata tct ttt gca caa ttt gaa ctg tca caa	542
Lys Phe Ala Phe Val His Ile Ser Phe Ala Gln Phe Glu Leu Ser Gln	
145 150 155	
ggg aat gtc aaa aaa agt aaa caa ctt ctt caa aaa gct gta gaa cgt	590
Gly Asn Val Lys Lys Ser Lys Gln Leu Leu Gln Lys Ala Val Glu Arg	
160 165 170	
gga gca gta cca cta gaa atg ctg gaa att gcc ctg cgg aat tta aac	638
Gly Ala Val Pro Leu Glu Met Leu Glu Ile Ala Leu Arg Asn Leu Asn	
175 180 185	
ctc caa aaa aag cag ctg ctt tca gag gag gaa aag aag aat tta tca	686
Leu Gln Lys Lys Gln Leu Leu Ser Glu Glu Glu Lys Lys Asn Leu Ser	
190 195 200	
gca tct acg gta tta act gcc caa gaa tca ttt tcc ggt tca ctt ggg	734
Ala Ser Thr Val Leu Thr Ala Gln Glu Ser Phe Ser Gly Ser Leu Gly	
205 210 215 220	
cat tta cag aat agg aac aac agt tgt gat tcc aga gga cag act act	782
His Leu Gln Asn Arg Asn Asn Ser Cys Asp Ser Arg Gly Gln Thr Thr	
225 230 235	
aaa gcc agg ttt tta tat gga gag aac atg cca cca caa gat gca gaa	830
Lys Ala Arg Phe Leu Tyr Gly Glu Asn Met Pro Pro Gln Asp Ala Glu	
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ata ggt tac cgg aat tca ttg aga caa act aac aaa act aaa cag tca	878
Ile Gly Tyr Arg Asn Ser Leu Arg Gln Thr Asn Lys Thr Lys Gln Ser	
255 260 265	
tgc cca ttt gga aga gtc cca gtt aac ctt cta aat agc cca gat tgt	926
Cys Pro Phe Gly Arg Val Pro Val Asn Leu Leu Asn Ser Pro Asp Cys	
270 275 280	
gat gtg aag aca gat gat tca gtt gta cct tgt ttt atg aaa aga caa	974
Asp Val Lys Thr Asp Asp Ser Val Val Pro Cys Phe Met Lys Arg Gln	
285 290 295 300	
acc tct aga tca gaa tgc cga gat ttg gtt gtg cct gga tct aaa cca	1022
Thr Ser Arg Ser Glu Cys Arg Asp Leu Val Val Pro Gly Ser Lys Pro	
305 310 315	
agt gga aat gat tcc tgt gaa tta aga aat tta aag tct gtt caa aat	1070
Ser Gly Asn Asp Ser Cys Glu Leu Arg Asn Leu Lys Ser Val Gln Asn	
320 325 330	
agt cat ttc aag gaa cct ctg gtg tca gat gaa aag agt tct gaa ctt	1118
Ser His Phe Lys Glu Pro Leu Val Ser Asp Glu Lys Ser Ser Glu Leu	

335	340	345	
att att act gat tca ata acc ctg aag aat aaa acg gaa tca agt ctt Ile Ile Thr Asp Ser Ile Thr Leu Lys Asn Lys Thr Glu Ser Ser Leu 350 355 360			1166
cta gct aaa tta gaa gaa act aaa gag tat caa gaa cca gag gtt cca Leu Ala Lys Leu Glu Glu Thr Lys Glu Tyr Gln Glu Pro Glu Val Pro 365 370 375 380			1214
gag agt aac cag aaa cag tgg caa tct aag aga aag tca gag tgt att Glu Ser Asn Gln Lys Gln Trp Gln Ser Lys Arg Lys Ser Glu Cys Ile 385 390 395			1262
aac cag aat cct gct gca tct tca aat cac tgg cag att ccg gag tta Asn Gln Asn Pro Ala Ala Ser Ser Asn His Trp Gln Ile Pro Glu Leu 400 405 410			1310
gcc cga aaa gtt aat aca gag cag aaa cat acc act ttt gag caa cct Ala Arg Lys Val Asn Thr Glu Gln Lys His Thr Thr Phe Glu Gln Pro 415 420 425			1358
gtc ttt tca gtt tca aaa cag tca cca cca ata tca aca tct aaa tgg Val Phe Ser Val Ser Lys Gln Ser Pro Pro Ile Ser Thr Ser Lys Trp 430 435 440			1406
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gat tac atg agc tgt ttt aga act cca gtt gta aag aat gac ttt cca Asp Tyr Met Ser Cys Phe Arg Thr Pro Val Val Lys Asn Asp Phe Pro 465 470 475			1502
cct gct tgt cag ttg tca aca cct tat ggc caa cct gcc tgt ttc cag Pro Ala Cys Gln Leu Ser Thr Pro Tyr Gly Gln Pro Ala Cys Phe Gln 480 485 490			1550
cag caa cag cat caa ata ctt gcc act cca ctt caa aat tta cag gtt Gln Gln Gln His Gln Ile Leu Ala Thr Pro Leu Gln Asn Leu Gln Val 495 500 505			1598
tta gca tct tct tca gca aat gaa tgc att tcg gtt aaa gga aga att Leu Ala Ser Ser Ser Ala Asn Glu Cys Ile Ser Val Lys Gly Arg Ile 510 515 520			1646
tat tcc att tta aag cag ata gga agt gga ggt tca agc aag gta ttt Tyr Ser Ile Leu Lys Gln Ile Gly Ser Gly Gly Ser Ser Lys Val Phe 525 530 535 540			1694
cag gtg tta aat gaa aag aaa cag ata tat gct ata aaa tat gtg aac Gln Val Leu Asn Glu Lys Lys Gln Ile Tyr Ala Ile Lys Tyr Val Asn 545 550 555			1742
tta gaa gaa gca gat aac caa act ctt gat agt tac cgg aac gaa ata Leu Glu Glu Ala Asp Asn Gln Thr Leu Asp Ser Tyr Arg Asn Glu Ile 560 565 570			1790
gct tat ttg aat aaa cta caa caa cac agt gat aag atc atc cga ctt Ala Tyr Leu Asn Lys Leu Gln Gln His Ser Asp Lys Ile Ile Arg Leu 575 580 585			1838

tat gat tat gaa atc acg gac cag tac atc tac atg gta atg gag tgt Tyr Asp Tyr Glu Ile Thr Asp Gln Tyr Ile Tyr Met Val Met Glu Cys 590 595 600	1886
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cca tgg gaa cgc aag agt tac tgg aaa aat atg tta gag gca gtt cac Pro Trp Glu Arg Lys Ser Tyr Trp Lys Asn Met Leu Glu Ala Val His 625 630 635	1982
aca atc cat caa cat ggc att gtt cac agt gat ctt aaa cca gct aac Thr Ile His Gln His Gly Ile Val His Ser Asp Leu Lys Pro Ala Asn 640 645 650	2030
ttt ctg ata gtt gat gga atg cta aag cta att gat ttt ggg att gca Phe Leu Ile Val Asp Gly Met Leu Lys Leu Ile Asp Phe Gly Ile Ala 655 660 665	2078
aac caa atg caa cca gat aca aca agt gtt gtt aaa gat tct cag gtt Asn Gln Met Gln Pro Asp Thr Thr Ser Val Val Lys Asp Ser Gln Val 670 675 680	2126
ggc aca gtt aat tat atg cca cca gaa gca atc aaa gat atg tct tcc Gly Thr Val Asn Tyr Met Pro Pro Glu Ala Ile Lys Asp Met Ser Ser 685 690 695 700	2174
tcc aga gag aat ggg aaa tct aag tca aag ata agc ccc aaa agt gat Ser Arg Glu Asn Gly Lys Ser Lys Ser Lys Ile Ser Pro Lys Ser Asp 705 710 715	2222
gtt tgg tcc tta gga tgt att ttg tac tat atg act tac ggg aaa aca Val Trp Ser Leu Gly Cys Ile Leu Tyr Tyr Met Thr Tyr Gly Lys Thr 720 725 730	2270
cca ttt cag cag ata att aat cag att tct aaa tta cat gcc ata att Pro Phe Gln Gln Ile Ile Asn Gln Ile Ser Lys Leu His Ala Ile Ile 735 740 745	2318
gat cct aat cat gaa att gaa ttt ccc gat att cca gag aaa gat ctt Asp Pro Asn His Glu Ile Glu Phe Pro Asp Ile Pro Glu Lys Asp Leu 750 755 760	2366
caa gat gtg tta aag tgt tgt tta aaa agg gac cca aaa cag agg ata Gln Asp Val Leu Lys Cys Cys Leu Lys Arg Asp Pro Lys Gln Arg Ile 765 770 775 780	2414
tcc att cct gag ctg ctg gct cat ccc tat gtt caa att caa act cat Ser Ile Pro Glu Leu Leu Ala His Pro Tyr Val Gln Ile Gln Thr His 785 790 795	2462
cca gtt aac caa atg gcc aag gga acc act gaa gaa atg aaa tat gtt Pro Val Asn Gln Met Ala Lys Gly Thr Thr Glu Glu Met Lys Tyr Val 800 805 810	2510
ctg ggc caa ctt gtt ggt ctg aat tct cct aac tcc att ttg aaa gct Leu Gly Gln Leu Val Gly Leu Asn Ser Pro Asn Ser Ile Leu Lys Ala 815 820 825	2558

gct aaa act tta tat gaa cac tat agt ggt ggt gaa agt cat aat tct 2606
Ala Lys Thr Leu Tyr Glu His Tyr Ser Gly Gly Glu Ser His Asn Ser
830 835 840

tca tcc tcc aag act ttt gaa aaa aaa agg gga aaa aaa tga 2648
Ser Ser Ser Lys Thr Phe Glu Lys Lys Arg Gly Lys Lys
845 850 855

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20 25 30

Thr Asp Glu Leu Ser Leu Asn Lys Ile Ser Ala Asp Thr Thr Asp Asn
35 40 45

Ser Gly Thr Val Asn Gln Ile Met Met Met Ala Asn Asn Pro Glu Asp
50 55 60

Trp Leu Ser Leu Leu Lys Leu Glu Lys Asn Ser Val Pro Leu Ser
65 70 75 80

Asp Ala Leu Leu Asn Lys Leu Ile Gly Arg Tyr Ser Gln Ala Ile Glu
85 90 95

Ala Leu Pro Pro Asp Lys Tyr Gly Gln Asn Glu Ser Phe Ala Arg Ile
100 105 110

Gln Val Arg Phe Ala Glu Leu Lys Ala Ile Gln Glu Pro Asp Asp Ala
115 120 125

Arg Asp Tyr Phe Gln Met Ala Arg Ala Asn Cys Lys Lys Phe Ala Phe

130		135		140
Val His Ile Ser Phe Ala Gln Phe Glu Leu Ser Gln Gly Asn Val Lys				
145		150		155
				160
Lys Ser Lys Gln Leu Leu Gln Lys Ala Val Glu Arg Gly Ala Val Pro				
		165		170
				175
Leu Glu Met Leu Glu Ile Ala Leu Arg Asn Leu Asn Leu Gln Lys Lys				
		180		185
				190
Gln Leu Leu Ser Glu Glu Glu Lys Lys Asn Leu Ser Ala Ser Thr Val				
		195		200
				205
Leu Thr Ala Gln Glu Ser Phe Ser Gly Ser Leu Gly His Leu Gln Asn				
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				220
Arg Asn Asn Ser Cys Asp Ser Arg Gly Gln Thr Thr Lys Ala Arg Phe				
		225		230
				235
Leu Tyr Gly Glu Asn Met Pro Pro Gln Asp Ala Glu Ile Gly Tyr Arg				
		245		250
				255
Asn Ser Leu Arg Gln Thr Asn Lys Thr Lys Gln Ser Cys Pro Phe Gly				
		260		265
				270
Arg Val Pro Val Asn Leu Leu Asn Ser Pro Asp Cys Asp Val Lys Thr				
		275		280
				285
Asp Asp Ser Val Val Pro Cys Phe Met Lys Arg Gln Thr Ser Arg Ser				
		290		295
				300
Glu Cys Arg Asp Leu Val Val Pro Gly Ser Lys Pro Ser Gly Asn Asp				
		305		310
				315
				320
Ser Cys Glu Leu Arg Asn Leu Lys Ser Val Gln Asn Ser His Phe Lys				
		325		330
				335
Glu Pro Leu Val Ser Asp Glu Lys Ser Ser Glu Leu Ile Ile Thr Asp				
		340		345
				350
Ser Ile Thr Leu Lys Asn Lys Thr Glu Ser Ser Leu Leu Ala Lys Leu				
		355		360
				365
Glu Glu Thr Lys Glu Tyr Gln Glu Pro Glu Val Pro Glu Ser Asn Gln				
		370		375
				380

Lys Gln Trp Gln Ser Lys Arg Lys Ser Glu Cys Ile Asn Gln Asn Pro
 385 390 395 400

Ala Ala Ser Ser Asn His Trp Gln Ile Pro Glu Leu Ala Arg Lys Val
 405 410 415

Asn Thr Glu Gln Lys His Thr Thr Phe Glu Gln Pro Val Phe Ser Val
 420 425 430

Ser Lys Gln Ser Pro Pro Ile Ser Thr Ser Lys Trp Phe Asp Pro Lys
 435 440 445

Ser Ile Cys Lys Thr Pro Ser Ser Asn Thr Leu Asp Asp Tyr Met Ser
 450 455 460

Cys Phe Arg Thr Pro Val Val Lys Asn Asp Phe Pro Pro Ala Cys Gln
 465 470 475 480

Leu Ser Thr Pro Tyr Gly Gln Pro Ala Cys Phe Gln Gln Gln Gln His
 485 490 495

Gln Ile Leu Ala Thr Pro Leu Gln Asn Leu Gln Val Leu Ala Ser Ser
 500 505 510

Ser Ala Asn Glu Cys Ile Ser Val Lys Gly Arg Ile Tyr Ser Ile Leu
 515 520 525

Lys Gln Ile Gly Ser Gly Gly Ser Ser Lys Val Phe Gln Val Leu Asn
 530 535 540

Glu Lys Lys Gln Ile Tyr Ala Ile Lys Tyr Val Asn Leu Glu Glu Ala
 545 550 555 560

Asp Asn Gln Thr Leu Asp Ser Tyr Arg Asn Glu Ile Ala Tyr Leu Asn
 565 570 575

Lys Leu Gln Gln His Ser Asp Lys Ile Ile Arg Leu Tyr Asp Tyr Glu
 580 585 590

Ile Thr Asp Gln Tyr Ile Tyr Met Val Met Glu Cys Gly Asn Ile Asp
 595 600 605

Leu Asn Ser Trp Leu Lys Lys Lys Lys Ser Ile Asp Pro Trp Glu Arg
 610 615 620

Lys Ser Tyr Trp Lys Asn Met Leu Glu Ala Val His Thr Ile His Gln
625 630 635 640

His Gly Ile Val His Ser Asp Leu Lys Pro Ala Asn Phe Leu Ile Val
645 650 655

Asp Gly Met Leu Lys Leu Ile Asp Phe Gly Ile Ala Asn Gln Met Gln
660 665 670

Pro Asp Thr Thr Ser Val Val Lys Asp Ser Gln Val Gly Thr Val Asn
675 680 685

Tyr Met Pro Pro Glu Ala Ile Lys Asp Met Ser Ser Ser Arg Glu Asn
690 695 700

Gly Lys Ser Lys Ser Lys Ile Ser Pro Lys Ser Asp Val Trp Ser Leu
705 710 715 720

Gly Cys Ile Leu Tyr Tyr Met Thr Tyr Gly Lys Thr Pro Phe Gln Gln
725 730 735

Ile Ile Asn Gln Ile Ser Lys Leu His Ala Ile Ile Asp Pro Asn His
740 745 750

Glu Ile Glu Phe Pro Asp Ile Pro Glu Lys Asp Leu Gln Asp Val Leu
755 760 765

Lys Cys Cys Leu Lys Arg Asp Pro Lys Gln Arg Ile Ser Ile Pro Glu
770 775 780

Leu Leu Ala His Pro Tyr Val Gln Ile Gln Thr His Pro Val Asn Gln
785 790 795 800

Met Ala Lys Gly Thr Thr Glu Glu Met Lys Tyr Val Leu Gly Gln Leu
805 810 815

Val Gly Leu Asn Ser Pro Asn Ser Ile Leu Lys Ala Ala Lys Thr Leu
820 825 830

Tyr Glu His Tyr Ser Gly Gly Glu Ser His Asn Ser Ser Ser Ser Lys
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Thr Phe Glu Lys Lys Arg Gly Lys Lys
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gcagacacaag gcgggactca gaaccggcgt tcagggccgc cagcggccgc gaggcctga      240

g atg agg ctc caa aga ccc cga cag gcc ccg gcg ggt ggg agg cgc gcg      289
Met Arg Leu Gln Arg Pro Arg Gln Ala Pro Ala Gly Gly Arg Arg Ala
  1          5          10          15

ccc cgg ggc ggg cgg ggc tcc ccc tac cgg cca gac ccg ggg aga ggc      337
Pro Arg Gly Gly Arg Gly Ser Pro Tyr Arg Pro Asp Pro Gly Arg Gly
          20          25          30

gcg cgg agg ctg cga agg ttc cag aag gcc ggg gag ggg gcg ccg cgc      385
Ala Arg Arg Leu Arg Arg Phe Gln Lys Gly Gly Glu Gly Ala Pro Arg
          35          40          45

gct gac cct ccc tgg gca ccg ctg ggg acg atg gcg ctg ctc gcc ttg      433
Ala Asp Pro Pro Trp Ala Pro Leu Gly Thr Met Ala Leu Leu Ala Leu
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ctg ctg gtc gtg gcc cta ccg cgg gtg tgg aca gac gcc aac ctg act      481
Leu Leu Val Val Ala Leu Pro Arg Val Trp Thr Asp Ala Asn Leu Thr
          65          70          75          80

gcg aga caa cga gat cca gag gac tcc cag cga acg gac gag ggt gac      529
Ala Arg Gln Arg Asp Pro Glu Asp Ser Gln Arg Thr Asp Glu Gly Asp
          85          90          95

aat aga gtg tgg tgt cat gtt tgt gag aga gaa aac act ttc gag tgc      577
Asn Arg Val Trp Cys His Val Cys Glu Arg Glu Asn Thr Phe Glu Cys
          100          105          110

cag aac cca agg agg tgc aaa tgg aca gag cca tac tgc gtt ata gcg      625
Gln Asn Pro Arg Arg Cys Lys Trp Thr Glu Pro Tyr Cys Val Ile Ala
          115          120          125

gcc gtg aaa ata ttt cca cgt ttt ttc atg gtt gcg aag cag tgc tcc      673
Ala Val Lys Ile Phe Pro Arg Phe Phe Met Val Ala Lys Gln Cys Ser
          130          135          140

gct ggt tgt gca gcg atg gag aga ccc aag cca gag gag aag cgg ttt      721
Ala Gly Cys Ala Ala Met Glu Arg Pro Lys Pro Glu Glu Lys Arg Phe
          145          150          155          160

ctc ctg gaa gag ccc atg ccc ttc ttt tac ctc aag tgt tgt aaa att      769
Leu Leu Glu Glu Pro Met Pro Phe Phe Tyr Leu Lys Cys Cys Lys Ile
  
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cgc tac tgc aat tta gag ggg cca cct atc aac tca tca gtg ttc aaa			817
Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile Asn Ser Ser Val Phe Lys			
180	185	190	
gaa tat gct ggg agc atg ggt gag agc tgt ggt ggg ctg tgg ctg gcc			865
Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly Leu Trp Leu Ala			
195	200	205	
atc ctc ctg ctg ctg gcc tcc att gca gcc ggc ctc agc ctg tct tga			913
Ile Leu Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser			
210	215	220	
gccacgggac tgccacagac tgagccttcc ggagcatgga ctgctccag accgttgtca			973
cctgttgcat taaacttggt ttctgttgat tacctcttgg ttgacttcc cagggctcttg			1033
ggatgggaga gtggggatca ggtgcagttg gctcttaacc ctcaaggggt ctttaactca			1093
cattcagagg aagtccagat ctcttgagta gtgattttgg tgacaagttt ttctctttga			1153
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ggtgaagaca tccctggagt gaaggactcc tcagcatggg gggcagtggg gcacacgtta			1393
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		20						25					30		

Ala	Arg	Arg	Leu	Arg	Arg	Phe	Gln	Lys	Gly	Gly	Glu	Gly	Ala	Pro	Arg
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50 55 60

Leu Leu Val Val Ala Leu Pro Arg Val Trp Thr Asp Ala Asn Leu Thr
65 70 75 80

Ala Arg Gln Arg Asp Pro Glu Asp Ser Gln Arg Thr Asp Glu Gly Asp
85 90 95

Asn Arg Val Trp Cys His Val Cys Glu Arg Glu Asn Thr Phe Glu Cys
100 105 110

Gln Asn Pro Arg Arg Cys Lys Trp Thr Glu Pro Tyr Cys Val Ile Ala
115 120 125

Ala Val Lys Ile Phe Pro Arg Phe Phe Met Val Ala Lys Gln Cys Ser
130 135 140

Ala Gly Cys Ala Ala Met Glu Arg Pro Lys Pro Glu Glu Lys Arg Phe
145 150 155 160

Leu Leu Glu Glu Pro Met Pro Phe Phe Tyr Leu Lys Cys Cys Lys Ile
165 170 175

Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile Asn Ser Ser Val Phe Lys
180 185 190

Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly Leu Trp Leu Ala
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Ile Leu Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser
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<210> 23
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<210> 24
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<210> 25

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Thr Tyr Asn Gly Val Val Ala Tyr Ser Ile
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Leu Phe Leu Leu Leu Val Leu Leu Leu Leu
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