

1020001191 - P17-158 Sequence Listing
SEQUENCE LISTING

<110> TAIHO PHARMACEUTICAL CO., LTD.

<120> Fusion peptide of DCTN1 protein and RET protein

<130> P17-158W0

<150> JP 2017-158796

<151> 2017-08-21

<160> 77

<170> PatentIn version 3.5

<210> 1

<211> 4908

<212> DNA

<213> Artificial Sequence

<220>

<223> coding sequence of fusion peptide

<400> 1

atggcacaga gcaagaggca cgtgtacagc cggacgcca gcggcagcag gatgagtgcg	60
gaggcaagcg cccggcctct gcgggtgggc tcccgtag aggtgattgg aaaaggccac	120
cgaggcactg tggcctatgt tggagccaca ctgtttgcca ctggcaaagtg gtaggcctg	180
attctggatg aagcaaagg caaaaatgat ggaactgttc aaggcaggaa gtacttcact	240
tgtgatgaag ggcattggcat ctttgtgctc cagtcccaga tccaggtatt tgaagatgga	300
gcagatacta cttccccaga gacacctgat tcttctgctt caaaagtcct caaaagagag	360
ggaactgata caactgcaaa gactagcaaa ctgcggggac tgaagcctaa gaaggcaccg	420
acagcccgaa agaccacaac tcggcgacct aagcccacgc gccagccag tactgggggtg	480
gctggggcca gtagctccct gggcccctct ggctcagcgt cagcaggtga gctgagcagc	540
agtgagccca gcaccccggtc tcagactccg ctggcagcac ccatcatccc cacgccggtc	600
ctcacctctc ctggagcagt cccccgctt cttccccat ccaaggagga ggagggacta	660
agggctcagg tgcgggacct ggaggagaaa ctagagacct tgagactgaa acgggcagaa	720
gacaaagcaa agctaaaaga gctggagaaa caaaaatcc agctggagca ggtgcaggaa	780
tggaagagca aaatgcagga gcagcaggcc gacctgcagc ggcgctcaa ggaggcgaga	840

1020001191 - P17-158 Sequence Listing

aaggaagcca aggaggcgct ggaggcaaag gaacgctata tggaggagat ggctgatact	900
gctgatgcca ttgagatggc cactttggac aaggagatgg ctgaagagcg ggctgagtcc	960
ctgcagcagg aggtggaggc actgaaggag cgggtggacg agctcactac tgacttagag	1020
atcctcaagg ctgagattga agagaagggc tcagatggcg ctgcatccag ttatcagctc	1080
aagcagcttg aggagcagaa tgcccgctg aaggatgccc tggtaggat gcgggatctt	1140
tcttcctcag agaagcagga gcatgtgaag ctccagaagc tcatggaaaa gaagaaccaa	1200
gagctggaag ttgtgaggca acagcgggag cgtctgcagg aggagctaag ccaggcagag	1260
agcaccattg atgagctcaa ggagcaggtg gatgctgctc tgggtgctga ggagatggtg	1320
gagatgctga cagatcggaa cctgaatctg gaagagaaag tgcgcgagtt gagggagact	1380
gtgggagact tggaagcgat gaatgagatg aacgatgagc tgcaggagaa tgcacgtgag	1440
acagaactgg agctgcggga gcagctggac atggcaggcg cgcgggttcg tgaggcccag	1500
aagcgtgtgg aggagccca ggagacggtt gcagactacc agcagaccat caagaagtac	1560
cgccagctga ccgcccattc acaggatgtg aatcgggaaac tgacaaaacca gcaggaagca	1620
tctgtggaga ggcaacagca gccacctcca gagacctttg acttcaaaat caagtttgct	1680
gagactaagg cccatgccaa ggcaattgag atggaattga ggcagatgga ggtggcccag	1740
gccaatcgac acatgtccct gctgacagcc ttcatgcctg acagcttcct tcggccaggt	1800
ggggaccatg actgcgttct ggtgctgttg ctcatgcctc gtctcatttg caaggcagag	1860
ctgatccgga agcaggccca ggagaagttt gaactaagtg agaactgttc agagcggcct	1920
gggctgcgag gagctgctgg ggagcaactc agctttgctg ctggactggt gtactcgctg	1980
agcctgctgc aggccacgct acaccgctat gagcatgccc tctctcagtg cagtgtggat	2040
gtgtataaga aagtgggcag cctgtaccct gagatgagtg cccatgagcg ctccttggat	2100
ttcctcattg aactgctgca caaggatcag ctggatgaga ctgtcaatgt ggagcctctc	2160
accaaggcca tcaagtacta tcagcatctg tacagcatcc accttgccga acagcctgag	2220
gactgtacta tgcagctggc tgaccacatt aagttcacgc agagtgtctt ggactgcatg	2280
agtgtggagg taggacggct gcgtgccttc ttgcagggtg ggcaggaggc tacagatatt	2340
gccctcctgc tccgggatct ggaaacttca tgcagtgaca tccgccagtt ctgcaagaag	2400

1020001191 - P17-158 Sequence Listing

atccgaaggc gaatgccagg gacagatgct cctgggatcc cagctgcact ggcctttgga	2460
ccacaggtat ctgacacgct cctagactgc aggaaacact tgacgtgggt cgtggctgtg	2520
ctgcaggagg tggcagctgc tgctgcccag ctcatgtccc cactggcaga gaatgagggg	2580
ctacttgtgg ctgctctgga ggaactggct ttcaaagcaa gcgagcagat ctatgggacc	2640
ccctccagca gcccctatga gtgtctgctgc cagtcattgca acatcctcat cagtaccatg	2700
aacaagctgg ccacagccat gcaggagggg gagtatgatg cagagcggcc cccagcaag	2760
cctccaccgg ttgaactgct ggctgctgcc cttcgtgcag agatcacaga tgctgaaggc	2820
ctgggtttga agctcgaaga tcgagagaca gttattaagg agttgaagaa gtcactcaag	2880
attaagggag aggagctaag tgaggccaat gtgcggctga gcctcctgga gaagaagttg	2940
gacagtgttg ccaaggatgc agatgagcgc atcgagaaag tccagactcg gctggaggag	3000
accagggcac tgctgcgaaa gaaggagaaa gagtttgagg agacaatgga tgcactccag	3060
gctgacatcg accagctgga ggcagagaag gcagaactaa agcagcgtct gaacagccag	3120
tccaaacgca cgattgaggg actccggggc cctcctcctt caggcattgc tactctggtc	3180
tctggcattg ctggtgaaga acagcagcga ggagccatcc ctgggcaggc tccagggtct	3240
gtgccaggcc cagggtggt gaaggactca ccactgctgc ttcagcagat ctctgccatg	3300
aggctgcaca tctcccagct ccagcatgag aacagcatcc tcaaggagag ccagatgaag	3360
gcatccttgg catccctgcc ccctctgcat gttgcaaagc tatcccatga gggccctggc	3420
agtgagttac cagctggagc gctgtatcgt aagaccagcc agctgctgga gacattgaat	3480
caattgagca cacacacgca cgtagtagac atcactcgca ccagccctgc tgccaagagc	3540
ccgtcggccc aacttatgga gcaagtggct cagcttaagt ccctgagtga caccgtcgag	3600
aagctcaagg atgaggtcct caaggagaca gtatctcagc gccctggagc cacagtaccc	3660
actgactttg ccaccttccc ttcactcagc ttcctcaggg aggatccaaa gtgggaattc	3720
cctcggaaga acttggttct tggaaaaact ctaggagaag gcgaatttgg aaaagtggctc	3780
aaggcaacgg ctttccatct gaaaggcaga gcagggtaca ccacggtggc cgtgaagatg	3840
ctgaaagaga acgcctcccc gagtgagctt cgagacctgc tgtcagagtt caacgtcctg	3900
aagcaggtca accaccaca tgtcatcaaa ttgtatgggg cctgcagcca ggatggcccg	3960

1020001191 - P17-158 Sequence Listing

ctcctcctca tcgtggagta cgccaaatac ggctccctgc ggggcttcct ccgcgagagc	4020
cgcaaagtgg ggcctggcta cctgggcagt ggaggcagcc gcaactccag ctccctggac	4080
cacccggatg agcgggccct caccatgggc gacctcatct catttgctg gcagatctca	4140
caggggatgc agtatctggc cgagatgaag ctcgttcacg gggacttggc agccagaaac	4200
atcctggtag ctgaggggcg gaagatgaag atttcggatt tcggcttgct ccgagatggt	4260
tatgaagagg attcctacgt gaagaggagc cagggtcggg ttccagttaa atggatggca	4320
attgaatccc tttttgatca tatctacacc acgcaaagtg atgtatggct ttttggtgct	4380
ctgctgtggg agatcgtgac cctaggggga aaccctatc ctgggattcc tcctgagcgg	4440
ctcttcaacc ttctgaagac cggccaccgg atggagaggc cagacaactg cagcgaggag	4500
atgtaccgcc tgatgctgca atgctggaag caggagccgg aaaaaaggcc ggtgtttgct	4560
gacatcagca aagacctgga gaagatgatg gttaagagga gagactactt ggaccttgct	4620
gcgctccactc catctgactc cctgatttat gacgacggcc tctcagagga ggagacaccg	4680
ctggtggact gtaataatgc cccctccct cgagccctcc cttccacatg gattgaaaac	4740
aaactctatg gcatgtcaga cccgaactgg cctggagaga gtcctgtacc actcacgaga	4800
gctgatggca ctaacactgg gtttccaaga tatccaaatg atagtgtata tgctaactgg	4860
atgctttcac cctcagcggc aaaattaatg gacacgtttg atagttaa	4908

<210> 2
 <211> 1635
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion peptide

<400> 2

Met	Ala	Gln	Ser	Lys	Arg	His	Val	Tyr	Ser	Arg	Thr	Pro	Ser	Gly	Ser
1				5				10						15	

Arg	Met	Ser	Ala	Glu	Ala	Ser	Ala	Arg	Pro	Leu	Arg	Val	Gly	Ser	Arg
			20					25					30		

Val	Glu	Val	Ile	Gly	Lys	Gly	His	Arg	Gly	Thr	Val	Ala	Tyr	Val	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1020001191 - P17-158 Sequence Listing

35

40

45

Ala Thr Leu Phe Ala Thr Gly Lys Trp Val Gly Val Ile Leu Asp Glu
 50 55 60

Ala Lys Gly Lys Asn Asp Gly Thr Val Gln Gly Arg Lys Tyr Phe Thr
 65 70 75 80

Cys Asp Glu Gly His Gly Ile Phe Val Arg Gln Ser Gln Ile Gln Val
 85 90 95

Phe Glu Asp Gly Ala Asp Thr Thr Ser Pro Glu Thr Pro Asp Ser Ser
 100 105 110

Ala Ser Lys Val Leu Lys Arg Glu Gly Thr Asp Thr Thr Ala Lys Thr
 115 120 125

Ser Lys Leu Arg Gly Leu Lys Pro Lys Lys Ala Pro Thr Ala Arg Lys
 130 135 140

Thr Thr Thr Arg Arg Pro Lys Pro Thr Arg Pro Ala Ser Thr Gly Val
 145 150 155 160

Ala Gly Ala Ser Ser Ser Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly
 165 170 175

Glu Leu Ser Ser Ser Glu Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala
 180 185 190

Ala Pro Ile Ile Pro Thr Pro Val Leu Thr Ser Pro Gly Ala Val Pro
 195 200 205

Pro Leu Pro Ser Pro Ser Lys Glu Glu Glu Gly Leu Arg Ala Gln Val
 210 215 220

Arg Asp Leu Glu Glu Lys Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu
 225 230 235 240

Asp Lys Ala Lys Leu Lys Glu Leu Glu Lys His Lys Ile Gln Leu Glu

1020001191 - P17-158 Sequence Listing

245

250

255

Gln Val Gln Glu Trp Lys Ser Lys Met Gln Glu Gln Gln Ala Asp Leu
 260 265 270

Gln Arg Arg Leu Lys Glu Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu
 275 280 285

Ala Lys Glu Arg Tyr Met Glu Glu Met Ala Asp Thr Ala Asp Ala Ile
 290 295 300

Glu Met Ala Thr Leu Asp Lys Glu Met Ala Glu Glu Arg Ala Glu Ser
 305 310 315 320

Leu Gln Gln Glu Val Glu Ala Leu Lys Glu Arg Val Asp Glu Leu Thr
 325 330 335

Thr Asp Leu Glu Ile Leu Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp
 340 345 350

Gly Ala Ala Ser Ser Tyr Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala
 355 360 365

Arg Leu Lys Asp Ala Leu Val Arg Met Arg Asp Leu Ser Ser Ser Glu
 370 375 380

Lys Gln Glu His Val Lys Leu Gln Lys Leu Met Glu Lys Lys Asn Gln
 385 390 395 400

Glu Leu Glu Val Val Arg Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu
 405 410 415

Ser Gln Ala Glu Ser Thr Ile Asp Glu Leu Lys Glu Gln Val Asp Ala
 420 425 430

Ala Leu Gly Ala Glu Glu Met Val Glu Met Leu Thr Asp Arg Asn Leu
 435 440 445

Asn Leu Glu Glu Lys Val Arg Glu Leu Arg Glu Thr Val Gly Asp Leu

1020001191 - P17-158 Sequence Listing

450

455

460

Glu Ala Met Asn Glu Met Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu
465 470 475 480

Thr Glu Leu Glu Leu Arg Glu Gln Leu Asp Met Ala Gly Ala Arg Val
485 490 495

Arg Glu Ala Gln Lys Arg Val Glu Ala Ala Gln Glu Thr Val Ala Asp
500 505 510

Tyr Gln Gln Thr Ile Lys Lys Tyr Arg Gln Leu Thr Ala His Leu Gln
515 520 525

Asp Val Asn Arg Glu Leu Thr Asn Gln Gln Glu Ala Ser Val Glu Arg
530 535 540

Gln Gln Gln Pro Pro Pro Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala
545 550 555 560

Glu Thr Lys Ala His Ala Lys Ala Ile Glu Met Glu Leu Arg Gln Met
565 570 575

Glu Val Ala Gln Ala Asn Arg His Met Ser Leu Leu Thr Ala Phe Met
580 585 590

Pro Asp Ser Phe Leu Arg Pro Gly Gly Asp His Asp Cys Val Leu Val
595 600 605

Leu Leu Leu Met Pro Arg Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys
610 615 620

Gln Ala Gln Glu Lys Phe Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro
625 630 635 640

Gly Leu Arg Gly Ala Ala Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu
645 650 655

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

1020001191 - P17-158 Sequence Listing

660

665

670

Ala Leu Ser Gln Cys Ser Val Asp Val Tyr Lys Lys Val Gly Ser Leu
675 680 685

Tyr Pro Glu Met Ser Ala His Glu Arg Ser Leu Asp Phe Leu Ile Glu
690 695 700

Leu Leu His Lys Asp Gln Leu Asp Glu Thr Val Asn Val Glu Pro Leu
705 710 715 720

Thr Lys Ala Ile Lys Tyr Tyr Gln His Leu Tyr Ser Ile His Leu Ala
725 730 735

Glu Gln Pro Glu Asp Cys Thr Met Gln Leu Ala Asp His Ile Lys Phe
740 745 750

Thr Gln Ser Ala Leu Asp Cys Met Ser Val Glu Val Gly Arg Leu Arg
755 760 765

Ala Phe Leu Gln Gly Gly Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu
770 775 780

Arg Asp Leu Glu Thr Ser Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys
785 790 795 800

Ile Arg Arg Arg Met Pro Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala
805 810 815

Leu Ala Phe Gly Pro Gln Val Ser Asp Thr Leu Leu Asp Cys Arg Lys
820 825 830

His Leu Thr Trp Val Val Ala Val Leu Gln Glu Val Ala Ala Ala Ala
835 840 845

Ala Gln Leu Ile Ala Pro Leu Ala Glu Asn Glu Gly Leu Leu Val Ala
850 855 860

Ala Leu Glu Glu Leu Ala Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr

1020001191 - P17-158 Sequence Listing

865		870		875		880
Pro	Ser	Ser	Ser	Pro	Tyr	Leu
				885		890
						895
Ile	Ser	Thr	Met	Asn	Lys	Leu
			900			905
						910
Asp	Ala	Glu	Arg	Pro	Pro	Ser
		915				920
						925
Ala	Ala	Leu	Arg	Ala	Glu	Ile
		930				935
						940
Leu	Glu	Asp	Arg	Glu	Thr	Val
945						950
						955
						960
Ile	Lys	Gly	Glu	Glu	Leu	Ser
				965		970
						975
Glu	Lys	Lys	Leu	Asp	Ser	Ala
			980			985
						990
Lys	Val	Gln	Thr	Arg	Leu	Glu
		995				1000
						1005
Glu	Lys	Glu	Phe	Glu	Glu	Thr
	1010					1015
						1020
Asp	Gln	Leu	Glu	Ala	Glu	Lys
	1025					1030
						1035
Ser	Gln	Ser	Lys	Arg	Thr	Ile
	1040					1045
						1050
Ser	Gly	Ile	Ala	Thr	Leu	Val
	1055					1060
						1065
Gln	Arg	Gly	Ala	Ile	Pro	Gly

1020001191 - P17-158 Sequence Listing

1070													
Pro	Gly	Leu	Val	Lys	Asp	Ser	Pro	Leu	Leu	Leu	Gln	Gln	Ile Ser
1085						1090					1095		
Ala	Met	Arg	Leu	His	Ile	Ser	Gln	Leu	Gln	His	Glu	Asn	Ser Ile
1100						1105					1110		
Leu	Lys	Gly	Ala	Gln	Met	Lys	Ala	Ser	Leu	Ala	Ser	Leu	Pro Pro
1115						1120					1125		
Leu	His	Val	Ala	Lys	Leu	Ser	His	Glu	Gly	Pro	Gly	Ser	Glu Leu
1130						1135					1140		
Pro	Ala	Gly	Ala	Leu	Tyr	Arg	Lys	Thr	Ser	Gln	Leu	Leu	Glu Thr
1145						1150					1155		
Leu	Asn	Gln	Leu	Ser	Thr	His	Thr	His	Val	Val	Asp	Ile	Thr Arg
1160						1165					1170		
Thr	Ser	Pro	Ala	Ala	Lys	Ser	Pro	Ser	Ala	Gln	Leu	Met	Glu Gln
1175						1180					1185		
Val	Ala	Gln	Leu	Lys	Ser	Leu	Ser	Asp	Thr	Val	Glu	Lys	Leu Lys
1190						1195					1200		
Asp	Glu	Val	Leu	Lys	Glu	Thr	Val	Ser	Gln	Arg	Pro	Gly	Ala Thr
1205						1210					1215		
Val	Pro	Thr	Asp	Phe	Ala	Thr	Phe	Pro	Ser	Ser	Ala	Phe	Leu Arg
1220						1225					1230		
Glu	Asp	Pro	Lys	Trp	Glu	Phe	Pro	Arg	Lys	Asn	Leu	Val	Leu Gly
1235						1240					1245		
Lys	Thr	Leu	Gly	Glu	Gly	Glu	Phe	Gly	Lys	Val	Val	Lys	Ala Thr
1250						1255					1260		
Ala	Phe	His	Leu	Lys	Gly	Arg	Ala	Gly	Tyr	Thr	Thr	Val	Ala Val

1020001191 - P17-158 Sequence Listing

1265														
Lys	Met	Leu	Lys	Glu	Asn	Ala	Ser	Pro	Ser	Glu	Leu	Arg	Asp	Leu
1280						1285					1290			
Leu	Ser	Glu	Phe	Asn	Val	Leu	Lys	Gln	Val	Asn	His	Pro	His	Val
1295						1300					1305			
Ile	Lys	Leu	Tyr	Gly	Ala	Cys	Ser	Gln	Asp	Gly	Pro	Leu	Leu	Leu
1310						1315					1320			
Ile	Val	Glu	Tyr	Ala	Lys	Tyr	Gly	Ser	Leu	Arg	Gly	Phe	Leu	Arg
1325						1330					1335			
Glu	Ser	Arg	Lys	Val	Gly	Pro	Gly	Tyr	Leu	Gly	Ser	Gly	Gly	Ser
1340						1345					1350			
Arg	Asn	Ser	Ser	Ser	Leu	Asp	His	Pro	Asp	Glu	Arg	Ala	Leu	Thr
1355						1360					1365			
Met	Gly	Asp	Leu	Ile	Ser	Phe	Ala	Trp	Gln	Ile	Ser	Gln	Gly	Met
1370						1375					1380			
Gln	Tyr	Leu	Ala	Glu	Met	Lys	Leu	Val	His	Arg	Asp	Leu	Ala	Ala
1385						1390					1395			
Arg	Asn	Ile	Leu	Val	Ala	Glu	Gly	Arg	Lys	Met	Lys	Ile	Ser	Asp
1400						1405					1410			
Phe	Gly	Leu	Ser	Arg	Asp	Val	Tyr	Glu	Glu	Asp	Ser	Tyr	Val	Lys
1415						1420					1425			
Arg	Ser	Gln	Gly	Arg	Ile	Pro	Val	Lys	Trp	Met	Ala	Ile	Glu	Ser
1430						1435					1440			
Leu	Phe	Asp	His	Ile	Tyr	Thr	Thr	Gln	Ser	Asp	Val	Trp	Ser	Phe
1445						1450					1455			
Gly	Val	Leu	Leu	Trp	Glu	Ile	Val	Thr	Leu	Gly	Gly	Asn	Pro	Tyr

1020001191 - P17-158 Sequence Listing

1460

1465

1470

Pro Gly Ile Pro Pro Glu Arg Leu Phe Asn Leu Leu Lys Thr Gly
1475 1480 1485

His Arg Met Glu Arg Pro Asp Asn Cys Ser Glu Glu Met Tyr Arg
1490 1495 1500

Leu Met Leu Gln Cys Trp Lys Gln Glu Pro Asp Lys Arg Pro Val
1505 1510 1515

Phe Ala Asp Ile Ser Lys Asp Leu Glu Lys Met Met Val Lys Arg
1520 1525 1530

Arg Asp Tyr Leu Asp Leu Ala Ala Ser Thr Pro Ser Asp Ser Leu
1535 1540 1545

Ile Tyr Asp Asp Gly Leu Ser Glu Glu Glu Thr Pro Leu Val Asp
1550 1555 1560

Cys Asn Asn Ala Pro Leu Pro Arg Ala Leu Pro Ser Thr Trp Ile
1565 1570 1575

Glu Asn Lys Leu Tyr Gly Met Ser Asp Pro Asn Trp Pro Gly Glu
1580 1585 1590

Ser Pro Val Pro Leu Thr Arg Ala Asp Gly Thr Asn Thr Gly Phe
1595 1600 1605

Pro Arg Tyr Pro Asn Asp Ser Val Tyr Ala Asn Trp Met Leu Ser
1610 1615 1620

Pro Ser Ala Ala Lys Leu Met Asp Thr Phe Asp Ser
1625 1630 1635

<210> 3

<211> 4782

<212> DNA

<213> Artificial Sequence

1020001191 - P17-158 Sequence Listing

<220>

<223> coding sequence of fusion peptide

<400> 3

atggcacaga gcaagaggca cgtgtacagc cggacgcca gcggcagcag gatgagtgcg	60
gaggcaagcg cccggcctct gcgggtgggc tcccgtgtag aggtgattgg aaaaggccac	120
cgaggcactg tggcctatgt tggagccaca ctgtttgcc a ctggcaa atg ggtaggcgtg	180
attctggatg aagcaaaggg caaaaatgat ggaactgttc aaggcaggaa gtacttcact	240
tgtgatgaag ggcatggcat ctttgtgcgc cagtcccaga tccaggtatt tgaagatgga	300
gcagatacta cttccccaga gacacctgat tcttctgctt caaaagtcct caaaagagag	360
ggaactgata caactgcaaa gactagcaaa ctgcggggac tgaagcctaa gaaggcacccg	420
acagcccgaa agaccacaac tcggcgaccc aagccacgc gccagccag tactgggggtg	480
gctggggcca gtagctccct gggcccctct ggctcagcgt cagcaggtga gctgagcagc	540
agtgagccca gcaccccggc tcagactccg ctggcagcac ccatcatccc cagccggtc	600
ctcacctctc ctggagcagt cccccgctt ctttccccat ccaaggagga ggagggacta	660
agggctcagg tgcgggacct ggaggagaaa ctagagaccc tgagactgaa acgggcagaa	720
gacaaagcaa agctaaaaga gctggagaaa cacaaaatcc agctggagca ggtgcaggaa	780
tggaagagca aaatgcagga gcagcaggcc gacctgcagc ggcgctcaa ggaggcgaga	840
aaggaagcca aggaggcgct ggaggcaaag gaacgctata tggaggagat ggctgatact	900
gctgatgcca ttgagatggc cactttggac aaggagatgg ctgaagagcg ggctgagtcc	960
ctgcagcagg aggtggaggc actgaaggag cgggtggacg agctcactac tgacttagag	1020
atcctcaagg ctgagattga agagaagggc tcagatggcg ctgcatccag ttatcagctc	1080
aagcagcttg aggagcagaa tgcccgctg aaggatgccc tgggtaggat gcgggatctt	1140
tcttcctcag agaagcagga gcatgtgaag ctccagaagc tcatggaaaa gaagaaccaa	1200
gagctggaag ttgtgaggca acagcgggag cgtctgcagg aggagctaag ccaggcagag	1260
agcaccattg atgagctcaa ggagcaggtg gatgctgctc tgggtgctga ggagatgggtg	1320
gagatgctga cagatcggaa cctgaatctg gaagagaaag tgcgcgagtt gagggagact	1380
gtgggagact tggaagcgat gaatgagatg aacgatgagc tgcaggagaa tgcacgtgag	1440

1020001191 - P17-158 Sequence Listing

acagaactgg agctgcggga gcagctggac atggcaggcg cgcgggttcg tgaggcccag	1500
aagcgtgtgg aggagccca ggagacggtt gcagactacc agcagaccat caagaagtac	1560
cgccagctga ccgcccattc acaggatgtg aatcggaac tgacaaacca gcaggaagca	1620
tctgtggaga ggcaacagca gccacctcca gagacctttg acttcaaaat caagtttgct	1680
gagactaagg cccatgccaa ggcaattgag atggaattga ggcagatgga ggtggcccag	1740
gccaatcgac acatgtccct gctgacagcc ttcatgcctg acagcttcct tcggccaggt	1800
ggggaccatg actgcgttct ggtgctgttg ctcatgcctc gtctcatttg caaggcagag	1860
ctgatccgga agcaggccca ggagaagttt gaactaagtg agaactgttc agagcggcct	1920
gggctgcgag gagctgctgg ggagcaactc agctttgctg ctggactggg gtactcgctg	1980
agcctgctgc aggccacgct acaccgctat gagcatgccc tctctcagtg cagtgtggat	2040
gtgtataaga aagtgggcag cctgtaccct gagatgagtg cccatgagcg ctccttggat	2100
ttcctcattg aactgctgca caaggatcag ctggatgaga ctgtcaatgt ggagcctctc	2160
accaaggcca tcaagtacta tcagcatctg tacagcatcc accttgccga acagcctgag	2220
gactgtacta tgcagctggc tgaccacatt aagttcacgc agagtgtctt ggactgcatg	2280
agtgtggagg taggacggct gcgtgccttc ttgcagggtg ggcaggaggc tacagatatt	2340
gccctcctgc tccgggatct ggaaacttca tgcagtgaca tccgccagtt ctgcaagaag	2400
atccgaaggc gaatgccagg gacagatgct cctgggatcc cagctgcact ggcctttgga	2460
ccacaggtat ctgacacgct cctagactgc aggaaacact tgacgtgggt cgtggctgtg	2520
ctgcaggagg tggcagctgc tgctgcccag ctcatgccc cactggcaga gaatgagggg	2580
ctacttgtgg ctgctctgga ggaactggct ttcaaagcaa gcgagcagat ctatgggacc	2640
ccctccagca gcccctatga gtgtctgctc cagtcatgca acatcctcat cagtaccatg	2700
aacaagctgg ccacagccat gcaggagggg gagtatgatg cagagcggcc cccagcaag	2760
cctccaccgg ttgaactgct ggctgctgcc cttcgtgcag agatcacaga tgctgaaggc	2820
ctggggttga agctcgaaga tcgagagaca gttattaagg agttgaagaa gtcactcaag	2880
attaagggag aggagctaag tgaggccaat gtgcggctga gcctcctgga gaagaagttg	2940
gacagtgtg ccaaggatgc agatgagcgc atcgagaaag tccagactcg gctggaggag	3000

1020001191 - P17-158 Sequence Listing

acccaggcac tgctgcgaaa gaaggagaaa gagtttgagg agacaatgga tgcactccag	3060
gctgacatcg accagctgga ggcagagaag gcagaactaa agcagcgtct gaacagccag	3120
tccaaacgca cgattgaggg actccggggc cctcctcctt caggcattgc tactctggtc	3180
tctggcattg ctggtgaaga acagcagcga ggagccatcc ctgggcaggc tccagggtct	3240
gtgccaggcc cagggctggt gaaggactca cactgctgc ttccagcagat ctctgccatg	3300
aggctgcaca tctcccagct ccagcatgag aacagcatcc tcaaggagc ccagatgaag	3360
gcatccttgg catccctgcc ccctctgcat gttgcaaagc tatcccatga gggccctggc	3420
agtgagttac cagctggagc gctgtatcgt aagaccagcc agctgctgga gacattgaat	3480
caattgagca cacacacgca cgtagtagac atcactcgca ccagccctgc tgccaagagc	3540
ccgtcggccc aacttatgga gcaagtggct cagcttaagt ccctgagtga caccgtcgag	3600
aagctcaagg atgaggtcct caaggagaca gtatctcagc gccctggagc cacagtaccc	3660
actgactttg ccaccttccc ttcatcagcc ttctcaggg aggatccaaa gtgggaattc	3720
cctcgggaaga acttggttct tggaaaaact ctaggagaag gcgaatttgg aaaagtggtc	3780
aaggcaacgg ctttccatct gaaaggcaga gcagggtaca ccacggtggc cgtgaagatg	3840
ctgaaagaga acgcctcccc gagtgagctt cgagacctgc tgtcagagtt caacgtcctg	3900
aagcaggtca accaccaca tgtcatcaaa ttgtatgggg cctgcagcca ggatggcccc	3960
ctcctcctca tcgtggagta cgccaaatac ggctccctgc ggggcttcct ccgcgagagc	4020
cgcaaagtgg ggcctggcta cctgggcagt ggaggcagcc gcaactccag ctccctggac	4080
cacccggatg agcgggccct caccatgggc gacctcatct catttgcctg gcagatctca	4140
caggggatgc agtatctggc cgagatgaag ctcgttcacg gggacttggc agccagaaac	4200
atcctggtag ctgaggggcg gaagatgaag atttcggatt tcggcttgtc ccgagatgtt	4260
tatgaagagg attcctacgt gaagaggagc cagggtcgga ttccagttaa atggatggca	4320
attgaatccc tttttgatca tatctacacc acgcaaagtg atgtatggtc ttttgggtgc	4380
ctgctgtggg agatcgtgac cctaggggga aaccctatc ctgggattcc tcctgagcgg	4440
ctcttcaacc ttctgaagac cggccaccgg atggagaggc cagacaactg cagcgaggag	4500
atgtaccgcc tgatgctgca atgctggaag caggagccgg aaaaaggcc ggtgtttgcg	4560

1020001191 - P17-158 Sequence Listing

gacatcagca aagacctgga gaagatgatg gttaagagga gagactactt ggaccttgcg 4620
 gcgtccactc catctgactc cctgatttat gacgacggcc tctcagagga ggagacaccg 4680
 ctggtggact gtaataatgc cccctccct cgagccctcc cttccacatg gattgaaaac 4740
 aaactctatg gtagaatttc ccatgcattt actagattct ag 4782

<210> 4
 <211> 1593
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion peptide

<400> 4

Met Ala Gln Ser Lys Arg His Val Tyr Ser Arg Thr Pro Ser Gly Ser
 1 5 10 15

Arg Met Ser Ala Glu Ala Ser Ala Arg Pro Leu Arg Val Gly Ser Arg
 20 25 30

Val Glu Val Ile Gly Lys Gly His Arg Gly Thr Val Ala Tyr Val Gly
 35 40 45

Ala Thr Leu Phe Ala Thr Gly Lys Trp Val Gly Val Ile Leu Asp Glu
 50 55 60

Ala Lys Gly Lys Asn Asp Gly Thr Val Gln Gly Arg Lys Tyr Phe Thr
 65 70 75 80

Cys Asp Glu Gly His Gly Ile Phe Val Arg Gln Ser Gln Ile Gln Val
 85 90 95

Phe Glu Asp Gly Ala Asp Thr Thr Ser Pro Glu Thr Pro Asp Ser Ser
 100 105 110

Ala Ser Lys Val Leu Lys Arg Glu Gly Thr Asp Thr Thr Ala Lys Thr
 115 120 125

Ser Lys Leu Arg Gly Leu Lys Pro Lys Lys Ala Pro Thr Ala Arg Lys

1020001191 - P17-158 Sequence Listing

130

135

140

Thr Thr Thr Arg Arg Pro Lys Pro Thr Arg Pro Ala Ser Thr Gly Val
145 150 155 160

Ala Gly Ala Ser Ser Ser Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly
165 170 175

Glu Leu Ser Ser Ser Glu Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala
180 185 190

Ala Pro Ile Ile Pro Thr Pro Val Leu Thr Ser Pro Gly Ala Val Pro
195 200 205

Pro Leu Pro Ser Pro Ser Lys Glu Glu Glu Gly Leu Arg Ala Gln Val
210 215 220

Arg Asp Leu Glu Glu Lys Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu
225 230 235 240

Asp Lys Ala Lys Leu Lys Glu Leu Glu Lys His Lys Ile Gln Leu Glu
245 250 255

Gln Val Gln Glu Trp Lys Ser Lys Met Gln Glu Gln Gln Ala Asp Leu
260 265 270

Gln Arg Arg Leu Lys Glu Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu
275 280 285

Ala Lys Glu Arg Tyr Met Glu Glu Met Ala Asp Thr Ala Asp Ala Ile
290 295 300

Glu Met Ala Thr Leu Asp Lys Glu Met Ala Glu Glu Arg Ala Glu Ser
305 310 315 320

Leu Gln Gln Glu Val Glu Ala Leu Lys Glu Arg Val Asp Glu Leu Thr
325 330 335

Thr Asp Leu Glu Ile Leu Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp

1020001191 - P17-158 Sequence Listing

340

345

350

Gly Ala Ala Ser Ser Tyr Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala
355 360 365

Arg Leu Lys Asp Ala Leu Val Arg Met Arg Asp Leu Ser Ser Ser Glu
370 375 380

Lys Gln Glu His Val Lys Leu Gln Lys Leu Met Glu Lys Lys Asn Gln
385 390 395 400

Glu Leu Glu Val Val Arg Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu
405 410 415

Ser Gln Ala Glu Ser Thr Ile Asp Glu Leu Lys Glu Gln Val Asp Ala
420 425 430

Ala Leu Gly Ala Glu Glu Met Val Glu Met Leu Thr Asp Arg Asn Leu
435 440 445

Asn Leu Glu Glu Lys Val Arg Glu Leu Arg Glu Thr Val Gly Asp Leu
450 455 460

Glu Ala Met Asn Glu Met Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu
465 470 475 480

Thr Glu Leu Glu Leu Arg Glu Gln Leu Asp Met Ala Gly Ala Arg Val
485 490 495

Arg Glu Ala Gln Lys Arg Val Glu Ala Ala Gln Glu Thr Val Ala Asp
500 505 510

Tyr Gln Gln Thr Ile Lys Lys Tyr Arg Gln Leu Thr Ala His Leu Gln
515 520 525

Asp Val Asn Arg Glu Leu Thr Asn Gln Gln Glu Ala Ser Val Glu Arg
530 535 540

Gln Gln Gln Pro Pro Pro Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala

545 550 555 560

Thr Gln Ser Ala Leu Asp Cys Met Ser Val Glu Val Gly Arg Leu Arg

1020001191 - P17-158 Sequence Listing

755

760

765

Ala Phe Leu Gln Gly Gly Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu
 770 775 780

Arg Asp Leu Glu Thr Ser Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys
 785 790 795 800

Ile Arg Arg Arg Met Pro Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala
 805 810 815

Leu Ala Phe Gly Pro Gln Val Ser Asp Thr Leu Leu Asp Cys Arg Lys
 820 825 830

His Leu Thr Trp Val Val Ala Val Leu Gln Glu Val Ala Ala Ala Ala
 835 840 845

Ala Gln Leu Ile Ala Pro Leu Ala Glu Asn Glu Gly Leu Leu Val Ala
 850 855 860

Ala Leu Glu Glu Leu Ala Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr
 865 870 875 880

Pro Ser Ser Ser Pro Tyr Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu
 885 890 895

Ile Ser Thr Met Asn Lys Leu Ala Thr Ala Met Gln Glu Gly Glu Tyr
 900 905 910

Asp Ala Glu Arg Pro Pro Ser Lys Pro Pro Pro Val Glu Leu Arg Ala
 915 920 925

Ala Ala Leu Arg Ala Glu Ile Thr Asp Ala Glu Gly Leu Gly Leu Lys
 930 935 940

Leu Glu Asp Arg Glu Thr Val Ile Lys Glu Leu Lys Lys Ser Leu Lys
 945 950 955 960

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

1020001191 - P17-158 Sequence Listing

965 970 975

Glu Lys Lys Leu Asp Ser Ala Ala Lys Asp Ala Asp Glu Arg Ile Glu
980 985 990

Lys Val Gln Thr Arg Leu Glu Glu Thr Gln Ala Leu Leu Arg Lys Lys
995 1000 1005

Glu Lys Glu Phe Glu Glu Thr Met Asp Ala Leu Gln Ala Asp Ile
1010 1015 1020

Asp Gln Leu Glu Ala Glu Lys Ala Glu Leu Lys Gln Arg Leu Asn
1025 1030 1035

Ser Gln Ser Lys Arg Thr Ile Glu Gly Leu Arg Gly Pro Pro Pro
1040 1045 1050

Ser Gly Ile Ala Thr Leu Val Ser Gly Ile Ala Gly Glu Glu Gln
1055 1060 1065

Gln Arg Gly Ala Ile Pro Gly Gln Ala Pro Gly Ser Val Pro Gly
1070 1075 1080

Pro Gly Leu Val Lys Asp Ser Pro Leu Leu Leu Gln Gln Ile Ser
1085 1090 1095

Ala Met Arg Leu His Ile Ser Gln Leu Gln His Glu Asn Ser Ile
1100 1105 1110

Leu Lys Gly Ala Gln Met Lys Ala Ser Leu Ala Ser Leu Pro Pro
1115 1120 1125

Leu His Val Ala Lys Leu Ser His Glu Gly Pro Gly Ser Glu Leu
1130 1135 1140

Pro Ala Gly Ala Leu Tyr Arg Lys Thr Ser Gln Leu Leu Glu Thr
1145 1150 1155

Leu Asn Gln Leu Ser Thr His Thr His Val Val Asp Ile Thr Arg

1020001191 - P17-158 Sequence Listing

1160														
Thr	Ser	Pro	Ala	Ala	Lys	Ser	Pro	Ser	Ala	Gln	Leu	Met	Glu	Gln
1175						1180					1185			
Val	Ala	Gln	Leu	Lys	Ser	Leu	Ser	Asp	Thr	Val	Glu	Lys	Leu	Lys
1190						1195					1200			
Asp	Glu	Val	Leu	Lys	Glu	Thr	Val	Ser	Gln	Arg	Pro	Gly	Ala	Thr
1205						1210					1215			
Val	Pro	Thr	Asp	Phe	Ala	Thr	Phe	Pro	Ser	Ser	Ala	Phe	Leu	Arg
1220						1225					1230			
Glu	Asp	Pro	Lys	Trp	Glu	Phe	Pro	Arg	Lys	Asn	Leu	Val	Leu	Gly
1235						1240					1245			
Lys	Thr	Leu	Gly	Glu	Gly	Glu	Phe	Gly	Lys	Val	Val	Lys	Ala	Thr
1250						1255					1260			
Ala	Phe	His	Leu	Lys	Gly	Arg	Ala	Gly	Tyr	Thr	Thr	Val	Ala	Val
1265						1270					1275			
Lys	Met	Leu	Lys	Glu	Asn	Ala	Ser	Pro	Ser	Glu	Leu	Arg	Asp	Leu
1280						1285					1290			
Leu	Ser	Glu	Phe	Asn	Val	Leu	Lys	Gln	Val	Asn	His	Pro	His	Val
1295						1300					1305			
Ile	Lys	Leu	Tyr	Gly	Ala	Cys	Ser	Gln	Asp	Gly	Pro	Leu	Leu	Leu
1310						1315					1320			
Ile	Val	Glu	Tyr	Ala	Lys	Tyr	Gly	Ser	Leu	Arg	Gly	Phe	Leu	Arg
1325						1330					1335			
Glu	Ser	Arg	Lys	Val	Gly	Pro	Gly	Tyr	Leu	Gly	Ser	Gly	Gly	Ser
1340						1345					1350			
Arg	Asn	Ser	Ser	Ser	Leu	Asp	His	Pro	Asp	Glu	Arg	Ala	Leu	Thr

1020001191 - P17-158 Sequence Listing

1355

1360

1365

Met Gly Asp Leu Ile Ser Phe Ala Trp Gln Ile Ser Gln Gly Met
1370 1375 1380

Gln Tyr Leu Ala Glu Met Lys Leu Val His Arg Asp Leu Ala Ala
1385 1390 1395

Arg Asn Ile Leu Val Ala Glu Gly Arg Lys Met Lys Ile Ser Asp
1400 1405 1410

Phe Gly Leu Ser Arg Asp Val Tyr Glu Glu Asp Ser Tyr Val Lys
1415 1420 1425

Arg Ser Gln Gly Arg Ile Pro Val Lys Trp Met Ala Ile Glu Ser
1430 1435 1440

Leu Phe Asp His Ile Tyr Thr Thr Gln Ser Asp Val Trp Ser Phe
1445 1450 1455

Gly Val Leu Leu Trp Glu Ile Val Thr Leu Gly Gly Asn Pro Tyr
1460 1465 1470

Pro Gly Ile Pro Pro Glu Arg Leu Phe Asn Leu Leu Lys Thr Gly
1475 1480 1485

His Arg Met Glu Arg Pro Asp Asn Cys Ser Glu Glu Met Tyr Arg
1490 1495 1500

Leu Met Leu Gln Cys Trp Lys Gln Glu Pro Asp Lys Arg Pro Val
1505 1510 1515

Phe Ala Asp Ile Ser Lys Asp Leu Glu Lys Met Met Val Lys Arg
1520 1525 1530

Arg Asp Tyr Leu Asp Leu Ala Ala Ser Thr Pro Ser Asp Ser Leu
1535 1540 1545

Ile Tyr Asp Asp Gly Leu Ser Glu Glu Glu Thr Pro Leu Val Asp

1020001191 - P17-158 Sequence Listing

1550

1555

1560

Cys Asn Asn Ala Pro Leu Pro Arg Ala Leu Pro Ser Thr Trp Ile
1565 1570 1575

Glu Asn Lys Leu Tyr Gly Arg Ile Ser His Ala Phe Thr Arg Phe
1580 1585 1590

<210> 5

<211> 4506

<212> DNA

<213> Artificial Sequence

<220>

<223> coding sequence of fusion peptide

<400> 5

atgatgagac aggcaccgac agcccgaaag accacaactc ggcgacccaa gcccacgcgc	60
ccagccagta ctgggggtggc tggggccagt agctccctgg gccctctctgg ctcagcgtca	120
gcaggtgagc tgagcagcag tgagcccagc accccggctc agactccgct ggcagcaccc	180
atcatcccca cgccggtcct cacctctcct ggagcagtcc ccccgcttcc ttcccatcc	240
aaggaggagg agggactaag ggctcaggtg cgggacctgg aggagaaact agagaccctg	300
agactgaaac gggcagaaga caaagcaaag ctaaaagagc tggagaaaca caaaatccag	360
ctggagcagg tgcaggaatg gaagagcaaa atgcaggagc agcaggccga cctgcagcgg	420
cgcctcaagg aggcgagaaa ggaagccaag gaggcgctgg aggcaaagga acgctatatg	480
gaggagatgg ctgatactgc tgatgccatt gagatggcca ctttggacaa ggagatggct	540
gaagagcggg ctgagtccct gcagcaggag gtggaggcac tgaaggagcg ggtggacgag	600
ctcactactg acttagagat cctcaaggct gagattgaag agaagggtc agatggcgct	660
gcatccagtt atcagctcaa gcagcttgag gagcagaatg cccgcctgaa ggatgccctg	720
gtgaggatgc gggatctttc ttcctcagag aagcaggagc atgtgaagct ccagaagctc	780
atggaaaaga agaaccaaga gctggaagtt gtgaggcaac agcgggagcg tctgcaggag	840
gagctaagcc aggcagagag caccattgat gagctcaagg agcaggtgga tgctgctctg	900
ggtgctgagg agatggtgga gatgctgaca gatcggaacc tgaatctgga agagaaagtg	960

1020001191 - P17-158 Sequence Listing

cgcgagttga gggagactgt gggagacttg gaagcgatga atgagatgaa cgatgagctg	1020
caggagaatg cacgtgagac agaactggag ctgctgggagc agctggacat ggcaggcgcg	1080
cgggttcgtg aggcccagaa gcgtgtggag gcagcccagg agacggttgc agactaccag	1140
cagaccatca agaagtaccg ccagctgacc gcccattctac aggatgtgaa tcgggaactg	1200
acaaaccagc aggaagcatc tgtggagagg caacagcagc cacctccaga gacctttgac	1260
ttcaaaatca agtttgctga gactaaggcc catgccaaagg caattgagat ggaattgagg	1320
cagatggagg tggcccaggc caatcgacac atgtccctgc tgacagcctt catgcctgac	1380
agcttccttc ggccagggtg ggaccatgac tgcgttcttg tgctgttgct catgcctcgt	1440
ctcatttgca aggagagct gatccggaag caggcccagg agaagtttga actaagttag	1500
aactgttcag agcggcctgg gctgctgagga gctgctgggg agcaactcag ctttgctgct	1560
ggactggtgt actcgctgag cctgctgcag gccacgtac accgctatga gcatgccctc	1620
tctcagtga gtgtggatgt gtataagaaa gtgggcagcc tgtaccctga gatgagtgcc	1680
catgagcgct ctttggttt cctcattgaa ctgctgcaca aggatcagct ggatgagact	1740
gtcaatgtgg agcctctcac caaggccatc aagtactatc agcatctgta cagcatccac	1800
cttgccgaac agcctgagga ctgtactatg cagctggctg accacattaa gttcacgcag	1860
agtgtcttgg actgcatgag tgtggaggta ggacggctgc gtgccttctt gcagggtggg	1920
caggaggcta cagatattgc cctcctgctc cgggatctgg aaacttcatg cagtgcacac	1980
cgccagttct gcaagaagat ccgaaggcga atgccaggga cagatgctcc tgggatccca	2040
gctgcactgg cctttggacc acaggtatct gacacgtcc tagactgcag gaaacacttg	2100
acgtgggtcg tggctgtgct gcaggagggt gcagctgctg ctgcccagct cattgccccca	2160
ctggcagaga atgaggggct acttgtggct gctctggagg aactggcttt caaagcaagc	2220
gagcagatct atgggacccc ctccagcagc ccctatgagt gtctgcgcca gtcattgcaac	2280
atcctcatca gtaccatgaa caagctggcc acagccatgc aggaggggga gtatgatgca	2340
gagcggcccc ccagcaagcc tccaccggtt gaactgcggg ctgctgccct tcgtgcagag	2400
atcacagatg ctgaaggcct gggtttgaag ctcgaagatc gagagacagt tattaaggag	2460
ttgaagaagt cactcaagat taaggagag gagctaagtg aggccaatgt gcggctgagc	2520

1020001191 - P17-158 Sequence Listing

ctcctggaga agaagttgga cagtgtgcc aaggatgcag atgagcgcag cgagaaagtc	2580
cagactcggc tggaggagac ccaggcactg ctgcgaaaga aggagaaaga gtttgaggag	2640
acaatggatg cactccaggc tgacatcgac cagctggagg cagagaaggc agaactaaag	2700
cagcgtctga acagccagtc caaacgcacg attgagggac tccggggccc tcctccttca	2760
ggcattgcta ctctggtctc tggcattgct ggtgaagaac agcagcgagg agccatccct	2820
gggcaggctc cagggtctgt gccaggccca gggctggtga aggactcacc actgctgctt	2880
cagcagatct ctgccatgag gctgcacatc tcccagctcc agcatgagaa cagcatcctc	2940
aaggagagccc agatgaaggc atccttggca tccctgcccc ctctgcatgt tgcaaagcta	3000
tcccatgagg gccctggcag tgagttacca gctggagcgc tgtatcgtaa gaccagccag	3060
ctgctggaga cattgaatca attgagcaca cacacgcacg tagtagacat cactcgcacc	3120
agccctgctg ccaagagccc gtcggcccaa cttatggagc aagtggctca gcttaagtcc	3180
ctgagtgaca ccgtcgagaa gctcaaggat gaggtcctca aggagacagt atctcagcgc	3240
cctggagcca cagtaccac tgactttgcc accttcctt catcagcctt cctcaggag	3300
gatccaaagt gggaattccc tcggaagaac ttggttcttg gaaaaactct aggagaaggc	3360
gaatttgga aagtgggtcaa ggcaacggcc ttccatctga aaggcagagc aggggtacacc	3420
acgggtggccg tgaagatgct gaaagagaac gcctccccga gtgagcttcg agacctgctg	3480
tcagagttca acgtcctgaa gcagggtcaac caccacatg tcatcaaatt gtatggggcc	3540
tgcagccagg atggcccgtc cctcctcatc gtggagtacg ccaaatacgg ctccctgcgg	3600
ggcttcctcc gcgagagccg caaagtgggg cctggctacc tgggcagtgg aggcagccgc	3660
aactccagct ccctggacca cccggatgag cgggccctca ccatgggcga cctcatctca	3720
tttgctggc agatctcaca ggggatgcag tatctggccg agatgaagct cgttcatcgg	3780
gacttggcag ccagaaacat cctggtagct gaggggcgga agatgaagat ttcggatttc	3840
ggcttgctccc gagatgttta tgaagaggat tcctacgtga agaggagcca gggtcggatt	3900
ccagttaa at ggatggcaat tgaatccctt tttgatcata tctacaccac gcaaagtgat	3960
gtatggtctt ttggtgtcct gctgtgggag atcgtgaccc tagggggaaa cccctatcct	4020
gggattcctc ctgagcggct cttcaacctt ctgaagaccg gccaccggat ggagaggcca	4080

1020001191 - P17-158 Sequence Listing

gacaactgca gcgaggagat gtaccgcctg atgctgcaat gctggaagca ggagccggac	4140
aaaaggccgg tgtttgcgga catcagcaaa gacctggaga agatgatggg taagaggaga	4200
gactacttgg accttgcggc gtccactcca tctgactccc tgatttatga cgacggcctc	4260
tcagaggagg agacaccgct ggtggactgt aataatgccc ccctccctcg agccctccct	4320
tccacatgga ttgaaaacaa actctatggc atgtcagacc cgaactggcc tggagagagt	4380
cctgtaccac tcacgagagc tgatggcact aacactgggt ttccaagata tccaaatgat	4440
agtgtatatg ctaactggat gctttcacc ctcagcggcaa aattaatgga cacgtttgat	4500
agttaa	4506

<210>	6
<211>	1501
<212>	PRT
<213>	Artificial Sequence

<220>
<223> fusion peptide

<400> 6

Met Met Arg Gln Ala Pro Thr Ala Arg Lys Thr Thr Thr Arg Arg Pro
1 5 10 15

Lys Pro Thr Arg Pro Ala Ser Thr Gly Val Ala Gly Ala Ser Ser Ser
20 25 30

Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser Ser Glu
35 40 45

Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile Pro Thr
50 55 60

Pro Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser Pro Ser
65 70 75 80

Lys Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu Glu Lys
85 90 95

Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys Leu Lys

1020001191 - P17-158 Sequence Listing

100

105

110

Glu Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu Trp Lys
115 120 125

Ser Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu Lys Glu
130 135 140

Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg Tyr Met
145 150 155 160

Glu Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr Leu Asp
165 170 175

Lys Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu Val Glu
180 185 190

Ala Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu Ile Leu
195 200 205

Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser Ser Tyr
210 215 220

Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp Ala Leu
225 230 235 240

Val Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His Val Lys
245 250 255

Leu Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val Val Arg
260 265 270

Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu Ser Thr
275 280 285

Ile Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala Glu Glu
290 295 300

Met Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu Lys Val

1020001191 - P17-158 Sequence Listing

305 310 315 320

Arg Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn Glu Met
325 330 335

Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu Leu Arg
340 345 350

Glu Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln Lys Arg
355 360 365

Val Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr Ile Lys
370 375 380

Lys Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg Glu Leu
385 390 395 400

Thr Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro Pro Pro
405 410 415

Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala His Ala
420 425 430

Lys Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln Ala Asn
435 440 445

Arg His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe Leu Arg
450 455 460

Pro Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met Pro Arg
465 470 475 480

Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu Lys Phe
485 490 495

Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro Gly Leu Arg Gly Ala Ala
500 505 510

Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu Ser Leu

1020001191 - P17-158 Sequence Listing

515

520

525

Leu Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln Cys Ser
 530 535 540

Val Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met Ser Ala
 545 550 555 560

His Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys Asp Gln
 565 570 575

Leu Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile Lys Tyr
 580 585 590

Tyr Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu Asp Cys
 595 600 605

Thr Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala Leu Asp
 610 615 620

Cys Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln Gly Gly
 625 630 635 640

Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu Thr Ser
 645 650 655

Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg Met Pro
 660 665 670

Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly Pro Gln
 675 680 685

Val Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp Val Val
 690 695 700

Ala Val Leu Gln Glu Val Ala Ala Ala Ala Ala Gln Leu Ile Ala Pro
 705 710 715 720

Leu Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu Leu Ala

1020001191 - P17-158 Sequence Listing

725 730 735

Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser Pro Tyr
740 745 750

Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met Asn Lys
755 760 765

Leu Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg Pro Pro
770 775 780

Ser Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg Ala Glu
785 790 795 800

Ile Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg Glu Thr
805 810 815

Val Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu Glu Leu
820 825 830

Ser Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu Asp Ser
835 840 845

Ala Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr Arg Leu
850 855 860

Glu Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe Glu Glu
865 870 875 880

Thr Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala Glu Lys
885 890 895

Ala Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg Thr Ile Glu
900 905 910

Gly Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr Leu Val Ser Gly
915 920 925

Ile Ala Gly Glu Glu Gln Gln Arg Gly Ala Ile Pro Gly Gln Ala Pro

1020001191 - P17-158 Sequence Listing

930

935

940

Gly Ser Val Pro Gly Pro Gly Leu Val Lys Asp Ser Pro Leu Leu Leu
945 950 955 960

Gln Gln Ile Ser Ala Met Arg Leu His Ile Ser Gln Leu Gln His Glu
965 970 975

Asn Ser Ile Leu Lys Gly Ala Gln Met Lys Ala Ser Leu Ala Ser Leu
980 985 990

Pro Pro Leu His Val Ala Lys Leu Ser His Glu Gly Pro Gly Ser Glu
995 1000 1005

Leu Pro Ala Gly Ala Leu Tyr Arg Lys Thr Ser Gln Leu Leu Glu
1010 1015 1020

Thr Leu Asn Gln Leu Ser Thr His Thr His Val Val Asp Ile Thr
1025 1030 1035

Arg Thr Ser Pro Ala Ala Lys Ser Pro Ser Ala Gln Leu Met Glu
1040 1045 1050

Gln Val Ala Gln Leu Lys Ser Leu Ser Asp Thr Val Glu Lys Leu
1055 1060 1065

Lys Asp Glu Val Leu Lys Glu Thr Val Ser Gln Arg Pro Gly Ala
1070 1075 1080

Thr Val Pro Thr Asp Phe Ala Thr Phe Pro Ser Ser Ala Phe Leu
1085 1090 1095

Arg Glu Asp Pro Lys Trp Glu Phe Pro Arg Lys Asn Leu Val Leu
1100 1105 1110

Gly Lys Thr Leu Gly Glu Gly Glu Phe Gly Lys Val Val Lys Ala
1115 1120 1125

Thr Ala Phe His Leu Lys Gly Arg Ala Gly Tyr Thr Thr Val Ala

1020001191 - P17-158 Sequence Listing

1130

1135

1140

Val Lys Met Leu Lys Glu Asn Ala Ser Pro Ser Glu Leu Arg Asp
1145 1150 1155

Leu Leu Ser Glu Phe Asn Val Leu Lys Gln Val Asn His Pro His
1160 1165 1170

Val Ile Lys Leu Tyr Gly Ala Cys Ser Gln Asp Gly Pro Leu Leu
1175 1180 1185

Leu Ile Val Glu Tyr Ala Lys Tyr Gly Ser Leu Arg Gly Phe Leu
1190 1195 1200

Arg Glu Ser Arg Lys Val Gly Pro Gly Tyr Leu Gly Ser Gly Gly
1205 1210 1215

Ser Arg Asn Ser Ser Ser Leu Asp His Pro Asp Glu Arg Ala Leu
1220 1225 1230

Thr Met Gly Asp Leu Ile Ser Phe Ala Trp Gln Ile Ser Gln Gly
1235 1240 1245

Met Gln Tyr Leu Ala Glu Met Lys Leu Val His Arg Asp Leu Ala
1250 1255 1260

Ala Arg Asn Ile Leu Val Ala Glu Gly Arg Lys Met Lys Ile Ser
1265 1270 1275

Asp Phe Gly Leu Ser Arg Asp Val Tyr Glu Glu Asp Ser Tyr Val
1280 1285 1290

Lys Arg Ser Gln Gly Arg Ile Pro Val Lys Trp Met Ala Ile Glu
1295 1300 1305

Ser Leu Phe Asp His Ile Tyr Thr Thr Gln Ser Asp Val Trp Ser
1310 1315 1320

Phe Gly Val Leu Leu Trp Glu Ile Val Thr Leu Gly Gly Asn Pro

1020001191 - P17-158 Sequence Listing

1325

1330

1335

Tyr Pro Gly Ile Pro Pro Glu Arg Leu Phe Asn Leu Leu Lys Thr
1340 1345 1350

Gly His Arg Met Glu Arg Pro Asp Asn Cys Ser Glu Glu Met Tyr
1355 1360 1365

Arg Leu Met Leu Gln Cys Trp Lys Gln Glu Pro Asp Lys Arg Pro
1370 1375 1380

Val Phe Ala Asp Ile Ser Lys Asp Leu Glu Lys Met Met Val Lys
1385 1390 1395

Arg Arg Asp Tyr Leu Asp Leu Ala Ala Ser Thr Pro Ser Asp Ser
1400 1405 1410

Leu Ile Tyr Asp Asp Gly Leu Ser Glu Glu Glu Thr Pro Leu Val
1415 1420 1425

Asp Cys Asn Asn Ala Pro Leu Pro Arg Ala Leu Pro Ser Thr Trp
1430 1435 1440

Ile Glu Asn Lys Leu Tyr Gly Met Ser Asp Pro Asn Trp Pro Gly
1445 1450 1455

Glu Ser Pro Val Pro Leu Thr Arg Ala Asp Gly Thr Asn Thr Gly
1460 1465 1470

Phe Pro Arg Tyr Pro Asn Asp Ser Val Tyr Ala Asn Trp Met Leu
1475 1480 1485

Ser Pro Ser Ala Ala Lys Leu Met Asp Thr Phe Asp Ser
1490 1495 1500

<210> 7

<211> 4380

<212> DNA

<213> Artificial Sequence

1020001191 - P17-158 Sequence Listing

<220>

<223> coding sequence of fusion peptide

<400> 7

atgatgagac aggcaccgac agcccgaaag accacaactc ggcgacccaa gcccacgcgc	60
ccagccagta ctgggggtggc tggggccagt agctccctgg gccctcttgg ctcagcgtca	120
gcaggtgagc tgagcagcag tgagcccagc accccggctc agactccgct ggcagcaccc	180
atcatcccca cgccggctct cacctctcct ggagcagtcc ccccgttcc ttccccatcc	240
aaggaggagg agggactaag ggctcaggtg cgggacctgg aggagaaact agagaccctg	300
agactgaaac gggcagaaga caaagcaaag ctaaaagagc tggagaaaca caaaatccag	360
ctggagcagg tgcaggaatg gaagagcaaa atgcaggagc agcaggccga cctgcagcgg	420
cgcctcaagg aggcgagaaa ggaagccaag gaggcgctgg aggcaaagga acgctatatg	480
gaggagatgg ctgatactgc tgatgccatt gagatggcca ctttggacaa ggagatggct	540
gaagagcggg ctgagtccct gcagcaggag gtggaggcac tgaaggagcg ggtggacgag	600
ctcactactg acttagagat cctcaaggct gagattgaag agaagggtc agatggcgct	660
gcatccagtt atcagctcaa gcagcttgag gagcagaatg cccgcctgaa ggatgccctg	720
gtgaggatgc gggatctttc ttcctcagag aagcaggagc atgtgaagct ccagaagctc	780
atggaaaaga agaaccaaga gctggaagtt gtgaggcaac agcgggagcg tctgcaggag	840
gagctaagcc aggcagagag caccattgat gagctcaagg agcaggtgga tgctgctctg	900
ggtgctgagg agatggtgga gatgctgaca gatcggaacc tgaatctgga agagaaagtg	960
cgcgagttga gggagactgt gggagacttg gaagcgatga atgagatgaa cgatgagctg	1020
caggagaatg cacgtgagac agaactggag ctgcgggagc agctggacat ggcaggcgcg	1080
cgggttcgtg aggccagaa gcgtgtggag gcagcccagg agacggttgc agactaccag	1140
cagaccatca agaagtaccg ccagctgacc gccatctac aggatgtgaa tcgggaactg	1200
acaaaccagc aggaagcatc tgtggagagg caacagcagc cacctccaga gacctttgac	1260
ttcaaaatca agtttgctga gactaaggcc catgccaagg caattgagat ggaattgagg	1320
cagatggagg tggcccaggc caatcgacac atgtccctgc tgacagcctt catgcctgac	1380
agcttccttc ggccaggtgg ggaccatgac tgcgttctgg tgctgttgct catgcctcgt	1440

1020001191 - P17-158 Sequence Listing

ctcatttgca aggcagagct gatccggaag caggcccagg agaagtttga actaagtgag	1500
aactgttcag agcggcctgg gctgcgagga gctgctgggg agcaactcag ctttgctgct	1560
ggactgggtgt actcgctgag cctgctgcag gccacgctac accgctatga gcatgccctc	1620
tctcagtgca gtgtggatgt gtataagaaa gtgggcagcc tgtaccctga gatgagtgcc	1680
catgagcgct ctttgattt cctcattgaa ctgctgcaca aggatcagct ggatgagact	1740
gtcaatgtgg agcctctcac caaggccatc aagtactatc agcatctgta cagcatccac	1800
cttgccgaac agcctgagga ctgtactatg cagctggctg accacattaa gttcacgcag	1860
agtgctctgg actgcatgag tgtggaggta ggacggctgc gtgccttctt gcagggtggg	1920
caggaggcta cagatattgc cctcctgctc cgggatctgg aaacttcatg cagtgcacac	1980
cgccagttct gcaagaagat ccgaaggcga atgccaggga cagatgctcc tgggatccca	2040
gctgcactgg cttttggacc acaggtatct gacacgctcc tagactgcag gaaacacttg	2100
acgtgggtcg tggctgtgct gcaggaggtg gcagctgctg ctgccagct cattgcccc	2160
ctggcagaga atgaggggct acttgtggct gctctggagg aactggcttt caaagcaagc	2220
gagcagatct atgggacccc ctccagcagc ccctatgagt gtctgcgcca gtcatgcaac	2280
atcctcatca gtaccatgaa caagctggcc acagccatgc aggaggggga gtatgatgca	2340
gagcggcccc ccagcaagcc tccaccggtt gaactgcggg ctgctgccct tcgtgcagag	2400
atcacagatg ctgaaggcct gggtttgaag ctgaagatc gagagacagt tattaaggag	2460
ttgaagaagt cactcaagat taaggagag gagctaagtg aggccaatgt gcggctgagc	2520
ctcctggaga agaagttgga cagtgtgcc aaggatgcag atgagcgcac cgagaaagtc	2580
cagactcggc tggaggagac ccaggcactg ctgcgaaaga aggagaaaga gtttgaggag	2640
acaatggatg cactccaggc tgacatcgac cagctggagg cagagaaggc agaactaaag	2700
cagcgtctga acagccagtc caaacgcacg attgagggac tccggggccc tcctccttca	2760
ggcattgcta ctctggtctc tggcattgct ggtgaagaac agcagcgagg agccatccct	2820
gggcaggctc cagggtctgt gccaggccca gggctggtga aggactcacc actgctgctt	2880
cagcagatct ctgccatgag gctgcacatc tcccagctcc agcatgagaa cagcatcctc	2940
aaggagagccc agatgaaggc atccttggca tccctgcccc ctctgcatgt tgcaaagcta	3000

1020001191 - P17-158 Sequence Listing

tcccatgagg gccctggcag tgagttacca gctggagcgc tgtatcgtaa gaccagccag	3060
ctgctggaga cattgaatca attgagcaca cacacgcacg tagtagacat cactcgcacc	3120
agccctgctg ccaagagccc gtcggcccaa cttatggagc aagtggctca gcttaagtcc	3180
ctgagtgaca ccgtcgagaa gctcaaggat gaggtcctca aggagacagt atctcagcgc	3240
cctggagcca cagtaccac tgactttgcc accttcctt catcagcctt cctcagggag	3300
gatccaaagt gggaattccc tcggaagaac ttggttcttg gaaaaactct aggagaaggc	3360
gaatttggaa aagtgggtcaa ggcaacggcc ttccatctga aaggcagagc agggtagacc	3420
acgggtggccg tgaagatgct gaaagagaac gcctccccga gtgagcttcg agacctgctg	3480
tcagagttca acgtcctgaa gcaggtcaac caccacatg tcatcaaatt gtatggggcc	3540
tgcagccagg atggcccgt cctcctcatc gtggagtacg ccaaatacgg ctccctgcgg	3600
ggcttcctcc gcgagagccg caaagtgggg cctggctacc tgggcagtgg aggcagccgc	3660
aactccagct ccctggacca cccggatgag cgggccctca ccatgggcga cctcatctca	3720
tttgctggc agatctcaca ggggatgcag tatctggccg agatgaagct cgttcacg	3780
gacttggcag ccagaaacat cctggtagct gaggggcgga agatgaagat ttcggatttc	3840
ggcttgctcc gagatgttta tgaagaggat tcctacgtga agaggagcca gggtcggatt	3900
ccagttaaatt ggatggcaat tgaatccctt tttgatcata tctacaccac gcaaagtgat	3960
gtatggtctt ttggtgtcct gctgtgggag atcgtgacct tagggggaaa cccctatcct	4020
gggattcctc ctgagcggct cttcaacctt ctgaagaccg gccaccgat ggagaggcca	4080
gacaactgca gcgaggagat gtaccgcctg atgctgcaat gctggaagca ggagccggac	4140
aaaaggccgg tgtttgcgga catcagcaaa gacctggaga agatgatggt taagaggaga	4200
gactacttgg accttgcggc gtccactcca tctgactccc tgatttatga cgacggcctc	4260
tcagaggagg agacaccgct ggtggactgt aataatgccc ccctccctcg agccctcct	4320
tccacatgga ttgaaaacaa actctatggt agaatttccc atgcatttac tagattctag	4380

<210> 8

<211> 1459

<212> PRT

<213> Artificial Sequence

1020001191 - P17-158 Sequence Listing

<220>

<223> fusion peptide

<400> 8

Met Met Arg Gln Ala Pro Thr Ala Arg Lys Thr Thr Thr Arg Arg Pro
1 5 10 15

Lys Pro Thr Arg Pro Ala Ser Thr Gly Val Ala Gly Ala Ser Ser Ser
20 25 30

Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser Ser Glu
35 40 45

Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile Pro Thr
50 55 60

Pro Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser Pro Ser
65 70 75 80

Lys Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu Glu Lys
85 90 95

Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys Leu Lys
100 105 110

Glu Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu Trp Lys
115 120 125

Ser Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu Lys Glu
130 135 140

Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg Tyr Met
145 150 155 160

Glu Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr Leu Asp
165 170 175

Lys Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu Val Glu
180 185 190

1020001191 - P17-158 Sequence Listing

Ala Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu Ile Leu
195 200 205

Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser Ser Tyr
210 215 220

Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp Ala Leu
225 230 235 240

Val Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His Val Lys
245 250 255

Leu Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val Val Arg
260 265 270

Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu Ser Thr
275 280 285

Ile Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala Glu Glu
290 295 300

Met Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu Lys Val
305 310 315 320

Arg Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn Glu Met
325 330 335

Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu Leu Arg
340 345 350

Glu Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln Lys Arg
355 360 365

Val Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr Ile Lys
370 375 380

Lys Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg Glu Leu
385 390 395 400

1020001191 - P17-158 Sequence Listing

Thr Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro Pro Pro
405 410 415

Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala His Ala
420 425 430

Lys Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln Ala Asn
435 440 445

Arg His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe Leu Arg
450 455 460

Pro Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met Pro Arg
465 470 475 480

Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu Lys Phe
485 490 495

Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro Gly Leu Arg Gly Ala Ala
500 505 510

Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu Ser Leu
515 520 525

Leu Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln Cys Ser
530 535 540

Val Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met Ser Ala
545 550 555 560

His Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys Asp Gln
565 570 575

Leu Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile Lys Tyr
580 585 590

Tyr Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu Asp Cys
595 600 605

1020001191 - P17-158 Sequence Listing

Thr Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala Leu Asp
610 615 620

Cys Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln Gly Gly
625 630 635 640

Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu Thr Ser
645 650 655

Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg Met Pro
660 665 670

Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly Pro Gln
675 680 685

Val Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp Val Val
690 695 700

Ala Val Leu Gln Glu Val Ala Ala Ala Ala Ala Gln Leu Ile Ala Pro
705 710 715 720

Leu Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu Leu Ala
725 730 735

Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser Pro Tyr
740 745 750

Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met Asn Lys
755 760 765

Leu Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg Pro Pro
770 775 780

Ser Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg Ala Glu
785 790 795 800

Ile Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg Glu Thr
805 810 815

1020001191 - P17-158 Sequence Listing

Val Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu Glu Leu
820 825 830

Ser Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu Asp Ser
835 840 845

Ala Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr Arg Leu
850 855 860

Glu Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe Glu Glu
865 870 875 880

Thr Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala Glu Lys
885 890 895

Ala Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg Thr Ile Glu
900 905 910

Gly Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr Leu Val Ser Gly
915 920 925

Ile Ala Gly Glu Glu Gln Gln Arg Gly Ala Ile Pro Gly Gln Ala Pro
930 935 940

Gly Ser Val Pro Gly Pro Gly Leu Val Lys Asp Ser Pro Leu Leu Leu
945 950 955 960

Gln Gln Ile Ser Ala Met Arg Leu His Ile Ser Gln Leu Gln His Glu
965 970 975

Asn Ser Ile Leu Lys Gly Ala Gln Met Lys Ala Ser Leu Ala Ser Leu
980 985 990

Pro Pro Leu His Val Ala Lys Leu Ser His Glu Gly Pro Gly Ser Glu
995 1000 1005

Leu Pro Ala Gly Ala Leu Tyr Arg Lys Thr Ser Gln Leu Leu Glu
1010 1015 1020

1020001191 - P17-158 Sequence Listing

Thr	Leu	Asn	Gln	Leu	Ser	Thr	His	Thr	His	Val	Val	Asp	Ile	Thr
1025						1030					1035			
Arg	Thr	Ser	Pro	Ala	Ala	Lys	Ser	Pro	Ser	Ala	Gln	Leu	Met	Glu
1040						1045					1050			
Gln	Val	Ala	Gln	Leu	Lys	Ser	Leu	Ser	Asp	Thr	Val	Glu	Lys	Leu
1055						1060					1065			
Lys	Asp	Glu	Val	Leu	Lys	Glu	Thr	Val	Ser	Gln	Arg	Pro	Gly	Ala
1070						1075					1080			
Thr	Val	Pro	Thr	Asp	Phe	Ala	Thr	Phe	Pro	Ser	Ser	Ala	Phe	Leu
1085						1090					1095			
Arg	Glu	Asp	Pro	Lys	Trp	Glu	Phe	Pro	Arg	Lys	Asn	Leu	Val	Leu
1100						1105					1110			
Gly	Lys	Thr	Leu	Gly	Glu	Gly	Glu	Phe	Gly	Lys	Val	Val	Lys	Ala
1115						1120					1125			
Thr	Ala	Phe	His	Leu	Lys	Gly	Arg	Ala	Gly	Tyr	Thr	Thr	Val	Ala
1130						1135					1140			
Val	Lys	Met	Leu	Lys	Glu	Asn	Ala	Ser	Pro	Ser	Glu	Leu	Arg	Asp
1145						1150					1155			
Leu	Leu	Ser	Glu	Phe	Asn	Val	Leu	Lys	Gln	Val	Asn	His	Pro	His
1160						1165					1170			
Val	Ile	Lys	Leu	Tyr	Gly	Ala	Cys	Ser	Gln	Asp	Gly	Pro	Leu	Leu
1175						1180					1185			
Leu	Ile	Val	Glu	Tyr	Ala	Lys	Tyr	Gly	Ser	Leu	Arg	Gly	Phe	Leu
1190						1195					1200			
Arg	Glu	Ser	Arg	Lys	Val	Gly	Pro	Gly	Tyr	Leu	Gly	Ser	Gly	Gly
1205						1210					1215			

1020001191 - P17-158 Sequence Listing

Ser	Arg	Asn	Ser	Ser	Ser	Leu	Asp	His	Pro	Asp	Glu	Arg	Ala	Leu
1220						1225					1230			
Thr	Met	Gly	Asp	Leu	Ile	Ser	Phe	Ala	Trp	Gln	Ile	Ser	Gln	Gly
1235						1240					1245			
Met	Gln	Tyr	Leu	Ala	Glu	Met	Lys	Leu	Val	His	Arg	Asp	Leu	Ala
1250						1255					1260			
Ala	Arg	Asn	Ile	Leu	Val	Ala	Glu	Gly	Arg	Lys	Met	Lys	Ile	Ser
1265						1270					1275			
Asp	Phe	Gly	Leu	Ser	Arg	Asp	Val	Tyr	Glu	Glu	Asp	Ser	Tyr	Val
1280						1285					1290			
Lys	Arg	Ser	Gln	Gly	Arg	Ile	Pro	Val	Lys	Trp	Met	Ala	Ile	Glu
1295						1300					1305			
Ser	Leu	Phe	Asp	His	Ile	Tyr	Thr	Thr	Gln	Ser	Asp	Val	Trp	Ser
1310						1315					1320			
Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile	Val	Thr	Leu	Gly	Gly	Asn	Pro
1325						1330					1335			
Tyr	Pro	Gly	Ile	Pro	Pro	Glu	Arg	Leu	Phe	Asn	Leu	Leu	Lys	Thr
1340						1345					1350			
Gly	His	Arg	Met	Glu	Arg	Pro	Asp	Asn	Cys	Ser	Glu	Glu	Met	Tyr
1355						1360					1365			
Arg	Leu	Met	Leu	Gln	Cys	Trp	Lys	Gln	Glu	Pro	Asp	Lys	Arg	Pro
1370						1375					1380			
Val	Phe	Ala	Asp	Ile	Ser	Lys	Asp	Leu	Glu	Lys	Met	Met	Val	Lys
1385						1390					1395			
Arg	Arg	Asp	Tyr	Leu	Asp	Leu	Ala	Ala	Ser	Thr	Pro	Ser	Asp	Ser
1400						1405					1410			

1020001191 - P17-158 Sequence Listing

Leu Ile Tyr Asp Asp Gly Leu Ser Glu Glu Glu Thr Pro Leu Val
1415 1420 1425

Asp Cys Asn Asn Ala Pro Leu Pro Arg Ala Leu Pro Ser Thr Trp
1430 1435 1440

Ile Glu Asn Lys Leu Tyr Gly Arg Ile Ser His Ala Phe Thr Arg
1445 1450 1455

Phe

<210> 9

<211> 4833

<212> DNA

<213> Artificial Sequence

<220>

<223> coding sequence of fusion peptide

<400> 9

atggcacaga gcaagaggca cgtgtacagc cggacgcca gcggcagcag gatgagtgcg	60
gaggcaagcg cccggcctct gcgggtgggc tcccgtgtag aggtgattgg aaaaggccac	120
cgaggcactg tggcctatgt tggagccaca ctgtttgccca ctggcaaattg ggtaggcgtg	180
attctggatg aagcaaaggg caaaaatgat ggaactgttc aaggcaggaa gtacttcact	240
tgtgatgaag ggcatggcat ctttgtgctc cagtcccaga tccaggtatt tgaagatgga	300
gcagatacta cttccccaga gacacctgat tcttctgctt caaaagtcct caaaagagag	360
ggaactgata caactgcaaa gactagcaaa ctgcccacgc gccagccag tactgggggtg	420
gctggggcca gtagctccct gggcccctct ggctcagcgt cagcaggtga gctgagcagc	480
agtgagccca gcaccccggc tcagactccg ctggcagcac ccatcatccc cacgccggtc	540
ctcacctctc ctggagcagt cccccgctt ctttccccat ccaaggagga ggagggacta	600
agggctcagg tgcgggacct ggaggagaaa ctagagaccc tgagactgaa acgggcagaa	660
gacaaagcaa agctaaaaga gctggagaaa cacaaaatcc agctggagca ggtgcaggaa	720
tggaagagca aaatgcagga gcagcaggcc gacctgcagc ggcgcctcaa ggaggcgaga	780

1020001191 - P17-158 Sequence Listing

aaggaagcca aggaggcgct ggaggcaaag gaacgctata tggaggagat ggctgatact	840
gctgatgcca ttgagatggc cactttggac aaggagatgg ctgaagagcg ggctgagtcc	900
ctgcagcagg aggtggaggc actgaaggag cgggtggacg agctcactac tgacttagag	960
atcctcaagg ctgagattga agagaagggc tcagatggcg ctgcatccag ttatcagctc	1020
aagcagcttg aggagcagaa tgcccgctg aaggatgccc tggtaggat gcgggatctt	1080
tcttcctcag agaagcagga gcatgtgaag ctccagaagc tcatggaaaa gaagaaccaa	1140
gagctggaag ttgtgaggca acagcgggag cgtctgcagg aggagctaag ccaggcagag	1200
agcaccattg atgagctcaa ggagcaggtg gatgctgctc tgggtgctga ggagatggtg	1260
gagatgctga cagatcggaa cctgaatctg gaagagaaag tgcgcgagtt gagggagact	1320
gtgggagact tggaagcgat gaatgagatg aacgatgagc tgcaggagaa tgcacgtgag	1380
acagaactgg agctgcggga gcagctggac atggcaggcg cgcgggttcg tgaggcccag	1440
aagcgtgtgg aggagccca ggagacggtt gcagactacc agcagaccat caagaagtac	1500
cgccagctga ccgcccattc acaggatgtg aatcgggaaac tgacaaaacca gcaggaagca	1560
tctgtggaga ggcaacagca gccacctcca gagacctttg acttcaaaat caagtttgct	1620
gagactaagg cccatgccaa ggcaattgag atggaattga ggcagatgga ggtggcccag	1680
gccaatcgac acatgtccct gctgacagcc ttcatgcctg acagcttcct tcggccaggt	1740
ggggaccatg actgcgttct ggtgctgttg ctcatgcctc gtctcatttg caaggcagag	1800
ctgatccgga agcaggccca ggagaagttt gaactaagtg agaactgttc agagcggcct	1860
gggctgcgag gagctgctgg ggagcaactc agctttgctg ctggactggt gtactcgctg	1920
agcctgctgc aggccacgct acaccgctat gagcatgccc tctctcagtg cagtgtggat	1980
gtgtataaga aagtgggcag cctgtaccct gagatgagtg cccatgagcg ctccttggat	2040
ttcctcattg aactgctgca caaggatcag ctggatgaga ctgtcaatgt ggagcctctc	2100
accaaggcca tcaagtacta tcagcatctg tacagcatcc accttgccga acagcctgag	2160
gactgtacta tgcagctggc tgaccacatt aagttcacgc agagtgtctt ggactgcatg	2220
agtgtggagg taggacggct gcgtgccttc ttgcagggtg ggcaggaggc tacagatatt	2280
gccctcctgc tccgggatct ggaaacttca tgcagtgaca tccgccagtt ctgcaagaag	2340

1020001191 - P17-158 Sequence Listing

atccgaaggc gaatgccagg gacagatgct cctgggatcc cagctgcact ggccttttga	2400
ccacaggtat ctgacacgct cctagactgc aggaaacact tgacgtgggt cgtggctgtg	2460
ctgcaggagg tggcagctgc tgctgcccag ctcatgtccc cactggcaga gaatgagggg	2520
ctacttgtgg ctgctctgga ggaactggct ttcaaagcaa gcgagcagat ctatgggacc	2580
ccctccagca gcccctatga gtgtctgctg cagtcattgca acatcctcat cagtaccatg	2640
aacaagctgg ccacagccat gcaggagggg gagtatgatg cagagcggcc cccagcaag	2700
cctccaccgg ttgaactgct ggctgctgcc cttcgtgcag agatcacaga tgctgaaggc	2760
ctgggtttga agctcgaaga tcgagagaca gttattaagg agttgaagaa gtcactcaag	2820
attaagggag aggagctaag tgaggccaat gtgcggctga gcctcctgga gaagaagttg	2880
gacagtgtg ccaaggatgc agatgagcgc atcgagaaag tccagactcg gctggaggag	2940
accagggcac tgctgcgaaa gaaggagaaa gagtttgagg agacaatgga tgcactccag	3000
gctgacatcg accagctgga ggcagagaag gcagaactaa agcagcgtct gaacagccag	3060
tccaaacgca cgattgaggg actccggggc cctcctcctt caggcattgc tactctggtc	3120
tctggcattg ctgggtggagc catccctggg caggctccag ggtctgtgcc aggcccaggg	3180
ctggtgaagg actcaccact gctgcttcag cagatctctg ccatgaggct gcacatctcc	3240
cagctccagc atgagaacag catcctcaag ggagcccaga tgaaggcatc cttggcatcc	3300
ctgccccctc tgcatgttgc aaagctatcc catgagggcc ctggcagtga gttaccagct	3360
ggagcgtgt atcgtaagac cagccagctg ctggagacat tgaatcaatt gagcacacac	3420
acgcacgtag tagacatcac tcgcaccagc cctgctgcca agagcccgtc ggcccaactt	3480
atggagcaag tggctcagct taagtccctg agtgacaccg tcgagaagct caaggatgag	3540
gtcctcaagg agacagtatc tcagcgccct ggagccacag taccactga ctttgccacc	3600
ttcccttcat cagccttcct caggaggat ccaaagtggg aattccctcg gaagaacttg	3660
gttcttgga aaactctagg agaaggcgaa tttggaaaag tggtaaggc aacggccttc	3720
catctgaaag gcagagcagg gtacaccacg gtggccgtga agatgctgaa agagaacgcc	3780
tccccgagtg agcttcgaga cctgctgtca gagttcaacg tcctgaagca ggtcaaccac	3840
ccacatgtca tcaaattgta tggggcctgc agccaggatg gcccgtcct cctcatcgtg	3900

1020001191 - P17-158 Sequence Listing

gagtacgcca aatacggctc cctgcggggc ttcctccgcg agagccgcaa agtggggcct	3960
ggctacctgg gcagtggagg cagccgcaac tccagctccc tggaccaccc ggatgagcgg	4020
gccctcacca tgggcgacct catctcattt gcctggcaga tctcacaggg gatgcagtat	4080
ctggccgaga tgaagctcgt tcatcgggac ttggcagcca gaaacatcct ggtagctgag	4140
gggcggaaga tgaagatttc ggatttcggc ttgtcccgag atgtttatga agaggattcc	4200
tacgtgaaga ggagccaggg tcggattcca gttaaattga tggcaattga atcccttttt	4260
gatcatatct acaccacgca aagtgatgta tggctctttg gtgtcctgct gtgggagatc	4320
gtgaccctag ggggaaaccc ctatcctggg attcctcctg agcggctctt caaccttctg	4380
aagaccggcc accggatgga gaggccagac aactgcagcg aggagatgta ccgcctgatg	4440
ctgcaatgct ggaagcagga gccggacaaa aggccggtgt ttgcggacat cagcaaagac	4500
ctggagaaga tgatggttaa gaggagagac tacttggacc ttgcggcgtc cactccatct	4560
gactccctga tttatgacga cggcctctca gaggaggaga caccgctggt ggactgtaat	4620
aatgcccccc tccctcgagc cctcccttcc acatggattg aaaacaaact ctatggcatg	4680
tcagaccgga actggcctgg agagagtcct gtaccactca cgagagctga tggcactaac	4740
actgggtttc caagatatcc aaatgatagt gtatatgcta actggatgct ttcaccctca	4800
gcggcaaaat taatggacac gtttgatagt taa	4833

<210> 10
 <211> 1610
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion peptide

<400> 10

Met	Ala	Gln	Ser	Lys	Arg	His	Val	Tyr	Ser	Arg	Thr	Pro	Ser	Gly	Ser
1				5					10					15	

Arg	Met	Ser	Ala	Glu	Ala	Ser	Ala	Arg	Pro	Leu	Arg	Val	Gly	Ser	Arg
			20					25					30		

Val	Glu	Val	Ile	Gly	Lys	Gly	His	Arg	Gly	Thr	Val	Ala	Tyr	Val	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1020001191 - P17-158 Sequence Listing

35

40

45

Ala Thr Leu Phe Ala Thr Gly Lys Trp Val Gly Val Ile Leu Asp Glu
 50 55 60

Ala Lys Gly Lys Asn Asp Gly Thr Val Gln Gly Arg Lys Tyr Phe Thr
 65 70 75 80

Cys Asp Glu Gly His Gly Ile Phe Val Arg Gln Ser Gln Ile Gln Val
 85 90 95

Phe Glu Asp Gly Ala Asp Thr Thr Ser Pro Glu Thr Pro Asp Ser Ser
 100 105 110

Ala Ser Lys Val Leu Lys Arg Glu Gly Thr Asp Thr Thr Ala Lys Thr
 115 120 125

Ser Lys Leu Pro Thr Arg Pro Ala Ser Thr Gly Val Ala Gly Ala Ser
 130 135 140

Ser Ser Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser
 145 150 155 160

Ser Glu Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile
 165 170 175

Pro Thr Pro Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser
 180 185 190

Pro Ser Lys Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu
 195 200 205

Glu Lys Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys
 210 215 220

Leu Lys Glu Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu
 225 230 235 240

Trp Lys Ser Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu

1020001191 - P17-158 Sequence Listing

245

250

255

Lys Glu Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg
 260 265 270

Tyr Met Glu Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr
 275 280 285

Leu Asp Lys Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu
 290 295 300

Val Glu Ala Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu
 305 310 315 320

Ile Leu Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser
 325 330 335

Ser Tyr Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp
 340 345 350

Ala Leu Val Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His
 355 360 365

Val Lys Leu Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val
 370 375 380

Val Arg Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu
 385 390 395 400

Ser Thr Ile Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala
 405 410 415

Glu Glu Met Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu
 420 425 430

Lys Val Arg Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn
 435 440 445

Glu Met Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu

1020001191 - P17-158 Sequence Listing

450

455

460

Leu Arg Glu Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln
 465 470 475 480

Lys Arg Val Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr
 485 490 495

Ile Lys Lys Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg
 500 505 510

Glu Leu Thr Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro
 515 520 525

Pro Pro Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala
 530 535 540

His Ala Lys Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln
 545 550 555 560

Ala Asn Arg His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe
 565 570 575

Leu Arg Pro Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met
 580 585 590

Pro Arg Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu
 595 600 605

Lys Phe Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro Gly Leu Arg Gly
 610 615 620

Ala Ala Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu
 625 630 635 640

Ser Leu Leu Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln
 645 650 655

Cys Ser Val Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met

1020001191 - P17-158 Sequence Listing

660

665

670

Ser Ala His Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys
675 680 685

Asp Gln Leu Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile
690 695 700

Lys Tyr Tyr Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu
705 710 715 720

Asp Cys Thr Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala
725 730 735

Leu Asp Cys Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln
740 745 750

Gly Gly Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu
755 760 765

Thr Ser Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg
770 775 780

Met Pro Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly
785 790 795 800

Pro Gln Val Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp
805 810 815

Val Val Ala Val Leu Gln Glu Val Ala Ala Ala Ala Ala Gln Leu Ile
820 825 830

Ala Pro Leu Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu
835 840 845

Leu Ala Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser
850 855 860

Pro Tyr Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met

865 870 875 880

Leu Gln Gln Ile Ser Ala Met Arg Leu His Ile Ser Gln Leu Gln

1020001191 - P17-158 Sequence Listing

1070

1075

1080

His Glu Asn Ser Ile Leu Lys Gly Ala Gln Met Lys Ala Ser Leu
1085 1090 1095

Ala Ser Leu Pro Pro Leu His Val Ala Lys Leu Ser His Glu Gly
1100 1105 1110

Pro Gly Ser Glu Leu Pro Ala Gly Ala Leu Tyr Arg Lys Thr Ser
1115 1120 1125

Gln Leu Leu Glu Thr Leu Asn Gln Leu Ser Thr His Thr His Val
1130 1135 1140

Val Asp Ile Thr Arg Thr Ser Pro Ala Ala Lys Ser Pro Ser Ala
1145 1150 1155

Gln Leu Met Glu Gln Val Ala Gln Leu Lys Ser Leu Ser Asp Thr
1160 1165 1170

Val Glu Lys Leu Lys Asp Glu Val Leu Lys Glu Thr Val Ser Gln
1175 1180 1185

Arg Pro Gly Ala Thr Val Pro Thr Asp Phe Ala Thr Phe Pro Ser
1190 1195 1200

Ser Ala Phe Leu Arg Glu Asp Pro Lys Trp Glu Phe Pro Arg Lys
1205 1210 1215

Asn Leu Val Leu Gly Lys Thr Leu Gly Glu Gly Glu Phe Gly Lys
1220 1225 1230

Val Val Lys Ala Thr Ala Phe His Leu Lys Gly Arg Ala Gly Tyr
1235 1240 1245

Thr Thr Val Ala Val Lys Met Leu Lys Glu Asn Ala Ser Pro Ser
1250 1255 1260

Glu Leu Arg Asp Leu Leu Ser Glu Phe Asn Val Leu Lys Gln Val

1020001191 - P17-158 Sequence Listing

1265

1270

1275

Asn His Pro His Val Ile Lys Leu Tyr Gly Ala Cys Ser Gln Asp
1280 1285 1290

Gly Pro Leu Leu Leu Ile Val Glu Tyr Ala Lys Tyr Gly Ser Leu
1295 1300 1305

Arg Gly Phe Leu Arg Glu Ser Arg Lys Val Gly Pro Gly Tyr Leu
1310 1315 1320

Gly Ser Gly Gly Ser Arg Asn Ser Ser Ser Leu Asp His Pro Asp
1325 1330 1335

Glu Arg Ala Leu Thr Met Gly Asp Leu Ile Ser Phe Ala Trp Gln
1340 1345 1350

Ile Ser Gln Gly Met Gln Tyr Leu Ala Glu Met Lys Leu Val His
1355 1360 1365

Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Ala Glu Gly Arg Lys
1370 1375 1380

Met Lys Ile Ser Asp Phe Gly Leu Ser Arg Asp Val Tyr Glu Glu
1385 1390 1395

Asp Ser Tyr Val Lys Arg Ser Gln Gly Arg Ile Pro Val Lys Trp
1400 1405 1410

Met Ala Ile Glu Ser Leu Phe Asp His Ile Tyr Thr Thr Gln Ser
1415 1420 1425

Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Val Thr Leu
1430 1435 1440

Gly Gly Asn Pro Tyr Pro Gly Ile Pro Pro Glu Arg Leu Phe Asn
1445 1450 1455

Leu Leu Lys Thr Gly His Arg Met Glu Arg Pro Asp Asn Cys Ser

1020001191 - P17-158 Sequence Listing

1460

1465

1470

Glu Glu Met Tyr Arg Leu Met Leu Gln Cys Trp Lys Gln Glu Pro
1475 1480 1485

Asp Lys Arg Pro Val Phe Ala Asp Ile Ser Lys Asp Leu Glu Lys
1490 1495 1500

Met Met Val Lys Arg Arg Asp Tyr Leu Asp Leu Ala Ala Ser Thr
1505 1510 1515

Pro Ser Asp Ser Leu Ile Tyr Asp Asp Gly Leu Ser Glu Glu Glu
1520 1525 1530

Thr Pro Leu Val Asp Cys Asn Asn Ala Pro Leu Pro Arg Ala Leu
1535 1540 1545

Pro Ser Thr Trp Ile Glu Asn Lys Leu Tyr Gly Met Ser Asp Pro
1550 1555 1560

Asn Trp Pro Gly Glu Ser Pro Val Pro Leu Thr Arg Ala Asp Gly
1565 1570 1575

Thr Asn Thr Gly Phe Pro Arg Tyr Pro Asn Asp Ser Val Tyr Ala
1580 1585 1590

Asn Trp Met Leu Ser Pro Ser Ala Ala Lys Leu Met Asp Thr Phe
1595 1600 1605

Asp Ser
1610

<210> 11

<211> 4707

<212> DNA

<213> Artificial Sequence

<220>

<223> coding sequence of fusion peptide

<400> 11

1020001191 - P17-158 Sequence Listing

atggcacaga gcaagaggca cgtgtacagc cggacgccc	gcggcagcag gatgagtgcg	60
gaggcaagcg cccggcctct gcgggtgggc tcccgtgtag	aggtgattgg aaaaggccac	120
cgaggcactg tggcctatgt tggagccaca ctgtttgcc	ctggcaaata ggtaggcgtg	180
attctggatg aagcaaagg caaaaatgat ggaactgttc	aaggcaggaa gtacttcact	240
tgtgatgaag ggcatggcat ctttgtgctg cagtcccaga	tccaggtatt tgaagatgga	300
gcagatacta cttccccaga gacacctgat tcttctgctt	caaaagtcct caaaagagag	360
ggaactgata caactgcaaa gactagcaaa ctgccacgc	gccagccag tactggggtg	420
gctggggcca gtagctccct gggcccctct ggctcagcgt	cagcaggtga gctgagcagc	480
agtgagccca gcacccggc tcagactccg ctggcagcac	ccatcatccc cagccggctc	540
ctcacctctc ctggagcagt ccccccgtt cttccccat	ccaaggagga ggagggacta	600
agggctcagg tgcgggacct ggaggagaaa ctagagaccc	tgagactgaa acgggcagaa	660
gacaaagcaa agctaaaaga gctggagaaa cacaaaatcc	agctggagca ggtgcaggaa	720
tggaagagca aaatgcagga gcagcaggcc gacctgcagc	ggcgctcaa ggaggcgaga	780
aaggaagcca aggaggcgct ggaggcaaag gaacgctata	tggaggagat ggctgatact	840
gctgatgcca ttgagatggc cactttggac aaggagatgg	ctgaagagcg ggctgagtcc	900
ctgcagcagg aggtggaggc actgaaggag cgggtggacg	agctcactac tgacttagag	960
atcctcaagg ctgagattga agagaagggc tcagatggcg	ctgcatccag ttatcagctc	1020
aagcagcttg aggagcagaa tgcccgctg aaggatgccc	tggtgaggat gcgggatctt	1080
tcttcctcag agaagcagga gcatgtgaag ctccagaagc	tcatggaaaa gaagaaccaa	1140
gagctggaag ttgtgaggca acagcgggag cgtctgcagg	aggagctaag ccaggcagag	1200
agcaccattg atgagctcaa ggagcagggtg gatgctgctc	tgggtgctga ggagatgggtg	1260
gagatgctga cagatcggaa cctgaatctg gaagagaaag	tgcgcgagtt gagggagact	1320
gtgggagact tggaagcgat gaatgagatg aacgatgagc	tgaggagaa tgcacgtgag	1380
acagaactgg agctgcggga gcagctggac atggcaggcg	cgcgggttcg tgaggcccag	1440
aagcgtgtgg aggagccca ggagacggtt gcagactacc	agcagaccat caagaagtac	1500
cgccagctga ccgcccattc acaggatgtg aatcggaac	tgacaaacca gcaggaagca	1560

1020001191 - P17-158 Sequence Listing

tctgtggaga ggcaacagca gccacctcca gagacctttg acttcaaaat caagtttgct	1620
gagactaagg cccatgccaa ggcaattgag atggaattga ggcagatgga ggtggcccag	1680
gccaatcgac acatgtccct gctgacagcc ttcatgcctg acagcttcct tcggccaggt	1740
ggggaccatg actgcgttct ggtgctgttg ctcatgcctc gtctcatttg caaggcagag	1800
ctgatccgga agcaggccca ggagaagttt gaactaagtg agaactgttc agagcggcct	1860
gggctgagag gagctgctgg ggagcaactc agctttgctg ctggactggt gtactcgctg	1920
agcctgctgc aggccacgct acaccgctat gagcatgccc tctctcagtg cagtgtggat	1980
gtgtataaga aagtgggcag cctgtaccct gagatgagtg cccatgagcg ctccttggat	2040
ttcctcattg aactgctgca caaggatcag ctggatgaga ctgtcaatgt ggagcctctc	2100
accaaggcca tcaagtacta tcagcatctg tacagcatcc accttgccga acagcctgag	2160
gactgtacta tgcagctggc tgaccacatt aagttcacgc agagtgtctt ggactgcatg	2220
agtgtggagg taggacggct gcgtgccttc ttgcagggtg ggcaggaggc tacagatatt	2280
gccctcctgc tccgggatct ggaaacttca tgcagtgaca tccgccagtt ctgcaagaag	2340
atccgaaggc gaatgccagg gacagatgct cctgggatcc cagctgcact ggcctttgga	2400
ccacaggtat ctgacacgct cctagactgc aggaaacact tgacgtgggt cgtggctgtg	2460
ctgcaggagg tggcagctgc tgctgcccag ctcatgccc cactggcaga gaatgagggg	2520
ctacttgtgg ctgctctgga ggaactggct ttcaaagcaa gcgagcagat ctatgggacc	2580
ccctccagca gccctatga gtgtctgctc cagtcatgca acatcctcat cagtaccatg	2640
aacaagctgg ccacagccat gcaggagggg gagtatgatg cagagcggcc cccagcaag	2700
cctccaccgg ttgaactgct ggctgctgcc cttcgtgcag agatcacaga tgctgaaggc	2760
ctgggtttga agctcgaaga tcgagagaca gttattaagg agttgaagaa gtcactcaag	2820
attaaggagag aggagctaag tgaggccaat gtgcggctga gcctcctgga gaagaagttg	2880
gacagtgtg ccaaggatgc agatgagcgc atcgagaaag tccagactcg gctggaggag	2940
acccaggcac tgctgcgaaa gaaggagaaa gagtttgagg agacaatgga tgcactccag	3000
gctgacatcg accagctgga ggcagagaag gcagaactaa agcagcgtct gaacagccag	3060
tccaaacgca cgattgaggg actccggggc cctcctcctt caggcattgc tactctggtc	3120

1020001191 - P17-158 Sequence Listing

tctggcattg ctggtggagc catccctggg caggctccag ggtctgtgcc aggcccaggg	3180
ctggtgaagg actcaccact gctgcttcag cagatctctg ccatgaggct gcacatctcc	3240
cagctccagc atgagaacag catcctcaag ggagcccaga tgaaggcatc cttggcatcc	3300
ctgccccctc tgcatgttgc aaagctatcc catgagggcc ctggcagtga gttaccagct	3360
ggagcgctgt atcgtaagac cagccagctg ctggagacat tgaatcaatt gagcacacac	3420
acgcacgtag tagacatcac tcgcaccagc cctgctgcca agagcccgtc ggcccaactt	3480
atggagcaag tggctcagct taagtccctg agtgacaccg tcgagaagct caaggatgag	3540
gtcctcaagg agacagtatc tcagcgcctt ggagccacag taccactga ctttgccacc	3600
ttcccttcat cagccttcct cagggaggat ccaaagtggg aattccctcg gaagaacttg	3660
gttcttggaa aaactctagg agaaggcgaa tttggaaaag tgggtcaaggc aacggccttc	3720
catctgaaag gcagagcagg gtacaccacg gtggccgtga agatgctgaa agagaacgcc	3780
tccccgagtg agcttcgaga cctgctgtca gagttcaacg tcctgaagca ggtcaaccac	3840
ccacatgtca tcaaattgta tggggcctgc agccaggatg gcccgtcct cctcatcgtg	3900
gagtacgcca aatacggctc cctgcggggc ttctccgcg agagccgcaa agtggggcct	3960
ggctacctgg gcagtggagg cagccgcaac tccagctccc tggaccaccg ggatgagcgg	4020
gccctcacca tgggcgacct catctcattt gcctggcaga tctcacaggg gatgcagtat	4080
ctggccgaga tgaagctcgt tcatcgggac ttggcagcca gaaacatcct ggtagctgag	4140
gggcggaaga tgaagatttc ggatttcggc ttgtcccag atgtttatga agaggattcc	4200
tacgtgaaga ggagccaggg tcggattcca gttaaattga tggcaattga atcccttttt	4260
gatcatatct acaccacgca aagtgatgta tggctctttt gtgtcctgct gtgggagatc	4320
gtgaccctag ggggaaaccc ctatcctggg attcctcctg agcggctctt caaccttctg	4380
aagaccggcc accggatgga gaggccagac aactgcagcg aggagatgta ccgcctgatg	4440
ctgcaatgct ggaagcagga gccggacaaa aggccggtgt ttgcggacat cagcaaagac	4500
ctggagaaga tgatggttaa gaggagagac tacttggacc ttgcggcgtc cactccatct	4560
gactccctga tttatgacga cggcctctca gaggaggaga caccgctggg ggactgtaat	4620
aatgcccccc tccctcgagc cctcccttcc acatggattg aaaacaaact ctatggtaga	4680

1020001191 - P17-158 Sequence Listing

atttcccatg catttactag attctag

4707

<210> 12
 <211> 1568
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion peptide

<400> 12

Met Ala Gln Ser Lys Arg His Val Tyr Ser Arg Thr Pro Ser Gly Ser
 1 5 10 15

Arg Met Ser Ala Glu Ala Ser Ala Arg Pro Leu Arg Val Gly Ser Arg
 20 25 30

Val Glu Val Ile Gly Lys Gly His Arg Gly Thr Val Ala Tyr Val Gly
 35 40 45

Ala Thr Leu Phe Ala Thr Gly Lys Trp Val Gly Val Ile Leu Asp Glu
 50 55 60

Ala Lys Gly Lys Asn Asp Gly Thr Val Gln Gly Arg Lys Tyr Phe Thr
 65 70 75 80

Cys Asp Glu Gly His Gly Ile Phe Val Arg Gln Ser Gln Ile Gln Val
 85 90 95

Phe Glu Asp Gly Ala Asp Thr Thr Ser Pro Glu Thr Pro Asp Ser Ser
 100 105 110

Ala Ser Lys Val Leu Lys Arg Glu Gly Thr Asp Thr Thr Ala Lys Thr
 115 120 125

Ser Lys Leu Pro Thr Arg Pro Ala Ser Thr Gly Val Ala Gly Ala Ser
 130 135 140

Ser Ser Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser
 145 150 155 160

1020001191 - P17-158 Sequence Listing

Ser Glu Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile
165 170 175

Pro Thr Pro Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser
180 185 190

Pro Ser Lys Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu
195 200 205

Glu Lys Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys
210 215 220

Leu Lys Glu Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu
225 230 235 240

Trp Lys Ser Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu
245 250 255

Lys Glu Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg
260 265 270

Tyr Met Glu Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr
275 280 285

Leu Asp Lys Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu
290 295 300

Val Glu Ala Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu
305 310 315 320

Ile Leu Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser
325 330 335

Ser Tyr Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp
340 345 350

Ala Leu Val Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His
355 360 365

1020001191 - P17-158 Sequence Listing

Val Lys Leu Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val
370 375 380

Val Arg Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu
385 390 395 400

Ser Thr Ile Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala
405 410 415

Glu Glu Met Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu
420 425 430

Lys Val Arg Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn
435 440 445

Glu Met Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu
450 455 460

Leu Arg Glu Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln
465 470 475 480

Lys Arg Val Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr
485 490 495

Ile Lys Lys Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg
500 505 510

Glu Leu Thr Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro
515 520 525

Pro Pro Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala
530 535 540

His Ala Lys Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln
545 550 555 560

Ala Asn Arg His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe
565 570 575

1020001191 - P17-158 Sequence Listing

Leu Arg Pro Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met
580 585 590

Pro Arg Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu
595 600 605

Lys Phe Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro Gly Leu Arg Gly
610 615 620

Ala Ala Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu
625 630 635 640

Ser Leu Leu Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln
645 650 655

Cys Ser Val Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met
660 665 670

Ser Ala His Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys
675 680 685

Asp Gln Leu Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile
690 695 700

Lys Tyr Tyr Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu
705 710 715 720

Asp Cys Thr Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala
725 730 735

Leu Asp Cys Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln
740 745 750

Gly Gly Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu
755 760 765

Thr Ser Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg
770 775 780

1020001191 - P17-158 Sequence Listing

Met Pro Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly
785 790 795 800

Pro Gln Val Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp
805 810 815

Val Val Ala Val Leu Gln Glu Val Ala Ala Ala Ala Ala Gln Leu Ile
820 825 830

Ala Pro Leu Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu
835 840 845

Leu Ala Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser
850 855 860

Pro Tyr Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met
865 870 875 880

Asn Lys Leu Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg
885 890 895

Pro Pro Ser Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg
900 905 910

Ala Glu Ile Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg
915 920 925

Glu Thr Val Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu
930 935 940

Glu Leu Ser Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu
945 950 955 960

Asp Ser Ala Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr
965 970 975

Arg Leu Glu Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe
980 985 990

1020001191 - P17-158 Sequence Listing

Glu Glu Thr Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala
 995 1000 1005

Glu Lys Ala Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg
 1010 1015 1020

Thr Ile Glu Gly Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr
 1025 1030 1035

Leu Val Ser Gly Ile Ala Gly Gly Ala Ile Pro Gly Gln Ala Pro
 1040 1045 1050

Gly Ser Val Pro Gly Pro Gly Leu Val Lys Asp Ser Pro Leu Leu
 1055 1060 1065

Leu Gln Gln Ile Ser Ala Met Arg Leu His Ile Ser Gln Leu Gln
 1070 1075 1080

His Glu Asn Ser Ile Leu Lys Gly Ala Gln Met Lys Ala Ser Leu
 1085 1090 1095

Ala Ser Leu Pro Pro Leu His Val Ala Lys Leu Ser His Glu Gly
 1100 1105 1110

Pro Gly Ser Glu Leu Pro Ala Gly Ala Leu Tyr Arg Lys Thr Ser
 1115 1120 1125

Gln Leu Leu Glu Thr Leu Asn Gln Leu Ser Thr His Thr His Val
 1130 1135 1140

Val Asp Ile Thr Arg Thr Ser Pro Ala Ala Lys Ser Pro Ser Ala
 1145 1150 1155

Gln Leu Met Glu Gln Val Ala Gln Leu Lys Ser Leu Ser Asp Thr
 1160 1165 1170

Val Glu Lys Leu Lys Asp Glu Val Leu Lys Glu Thr Val Ser Gln
 1175 1180 1185

1020001191 - P17-158 Sequence Listing

Arg	Pro	Gly	Ala	Thr	Val	Pro	Thr	Asp	Phe	Ala	Thr	Phe	Pro	Ser
1190						1195					1200			
Ser	Ala	Phe	Leu	Arg	Glu	Asp	Pro	Lys	Trp	Glu	Phe	Pro	Arg	Lys
1205						1210					1215			
Asn	Leu	Val	Leu	Gly	Lys	Thr	Leu	Gly	Glu	Gly	Glu	Phe	Gly	Lys
1220						1225					1230			
Val	Val	Lys	Ala	Thr	Ala	Phe	His	Leu	Lys	Gly	Arg	Ala	Gly	Tyr
1235						1240					1245			
Thr	Thr	Val	Ala	Val	Lys	Met	Leu	Lys	Glu	Asn	Ala	Ser	Pro	Ser
1250						1255					1260			
Glu	Leu	Arg	Asp	Leu	Leu	Ser	Glu	Phe	Asn	Val	Leu	Lys	Gln	Val
1265						1270					1275			
Asn	His	Pro	His	Val	Ile	Lys	Leu	Tyr	Gly	Ala	Cys	Ser	Gln	Asp
1280						1285					1290			
Gly	Pro	Leu	Leu	Leu	Ile	Val	Glu	Tyr	Ala	Lys	Tyr	Gly	Ser	Leu
1295						1300					1305			
Arg	Gly	Phe	Leu	Arg	Glu	Ser	Arg	Lys	Val	Gly	Pro	Gly	Tyr	Leu
1310						1315					1320			
Gly	Ser	Gly	Gly	Ser	Arg	Asn	Ser	Ser	Ser	Leu	Asp	His	Pro	Asp
1325						1330					1335			
Glu	Arg	Ala	Leu	Thr	Met	Gly	Asp	Leu	Ile	Ser	Phe	Ala	Trp	Gln
1340						1345					1350			
Ile	Ser	Gln	Gly	Met	Gln	Tyr	Leu	Ala	Glu	Met	Lys	Leu	Val	His
1355						1360					1365			
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Ala	Glu	Gly	Arg	Lys
1370						1375					1380			

1020001191 - P17-158 Sequence Listing

Met	Lys	Ile	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Asp	Val	Tyr	Glu	Glu
1385						1390					1395			
Asp	Ser	Tyr	Val	Lys	Arg	Ser	Gln	Gly	Arg	Ile	Pro	Val	Lys	Trp
1400						1405					1410			
Met	Ala	Ile	Glu	Ser	Leu	Phe	Asp	His	Ile	Tyr	Thr	Thr	Gln	Ser
1415						1420					1425			
Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile	Val	Thr	Leu
1430						1435					1440			
Gly	Gly	Asn	Pro	Tyr	Pro	Gly	Ile	Pro	Pro	Glu	Arg	Leu	Phe	Asn
1445						1450					1455			
Leu	Leu	Lys	Thr	Gly	His	Arg	Met	Glu	Arg	Pro	Asp	Asn	Cys	Ser
1460						1465					1470			
Glu	Glu	Met	Tyr	Arg	Leu	Met	Leu	Gln	Cys	Trp	Lys	Gln	Glu	Pro
1475						1480					1485			
Asp	Lys	Arg	Pro	Val	Phe	Ala	Asp	Ile	Ser	Lys	Asp	Leu	Glu	Lys
1490						1495					1500			
Met	Met	Val	Lys	Arg	Arg	Asp	Tyr	Leu	Asp	Leu	Ala	Ala	Ser	Thr
1505						1510					1515			
Pro	Ser	Asp	Ser	Leu	Ile	Tyr	Asp	Asp	Gly	Leu	Ser	Glu	Glu	Glu
1520						1525					1530			
Thr	Pro	Leu	Val	Asp	Cys	Asn	Asn	Ala	Pro	Leu	Pro	Arg	Ala	Leu
1535						1540					1545			
Pro	Ser	Thr	Trp	Ile	Glu	Asn	Lys	Leu	Tyr	Gly	Arg	Ile	Ser	His
1550						1555					1560			
Ala	Phe	Thr	Arg	Phe										
1565														

1020001191 - P17-158 Sequence Listing

<210> 13
 <211> 4491
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coding sequence of fusion peptide

<400> 13
 atgatgagac aggcaccgac agcccgaaag accacaactc ggcgacccaa gcccacgcgc 60
 ccagccagta ctgggggtggc tggggccagt agctccctgg gcccctctgg ctcagcgtca 120
 gcaggtgagc tgagcagcag tgagcccagc accccggctc agactccgct ggcagcaccc 180
 atcatcccca cgccggctct cacctctcct ggagcagtcc ccccgcttcc ttccccatcc 240
 aaggaggagg agggactaag ggctcaggtg cgggacctgg aggagaaact agagaccctg 300
 agactgaaac gggcagaaga caaagcaaag ctaaaagagc tggagaaaca caaaatccag 360
 ctggagcagg tgcaggaatg gaagagcaaa atgcaggagc agcaggccga cctgcagcgg 420
 cgcctcaagg aggcgagaaa ggaagccaag gaggcgctgg aggcaaagga acgctatatg 480
 gaggagatgg ctgatactgc tgatgccatt gagatggcca ctttggacaa ggagatggct 540
 gaagagcggg ctgagtcctt gcagcaggag gtggaggcac tgaaggagcg ggtggacgag 600
 ctactactg acttagagat cctcaaggct gagattgaag agaagggctc agatggcgct 660
 gcatccagtt atcagctcaa gcagcttgag gaggagaatg cccgcctgaa ggatgccctg 720
 gtgaggatgc gggatctttc ttcctcagag aagcaggagc atgtgaagct ccagaagctc 780
 atggaaaaga agaaccaaga gctggaagtt gtgaggcaac agcgggagcg tctgcaggag 840
 gagctaagcc aggcagagag caccattgat gagctcaagg agcagggtgga tgctgctctg 900
 ggtgctgagg agatgggtgga gatgctgaca gatcggaacc tgaatctgga agagaaagtg 960
 cgcgagttga gggagactgt gggagacttg gaagcgatga atgagatgaa cgatgagctg 1020
 caggagaatg cacgtgagac agaactggag ctgcgggagc agctggacat ggcaggcgcg 1080
 cgggttcgtg agggccagaa gcgtgtggag gcagcccagg agacggttgc agactaccag 1140
 cagaccatca agaagtaccg ccagctgacc gcccatctac aggatgtgaa tcgggaactg 1200
 acaaaccagc aggaagcatc tgtggagagg caacagcagc cacctccaga gacctttgac 1260

1020001191 - P17-158 Sequence Listing

ttcaaaatca agtttgctga gactaaggcc catgccaagg caattgagat ggaattgagg	1320
cagatggagg tggcccaggc caatcgacac atgtccctgc tgacagcctt catgcctgac	1380
agcttccttc ggccagggtgg ggaccatgac tgcgttctgg tgctgttgct catgcctcgt	1440
ctcatttgca aggcaagct gatccggaag caggcccagg agaagtttga actaagtgag	1500
aactgttcag agcggcctgg gctgctgagga gctgctgggg agcaactcag ctttgctgct	1560
ggactgggtg actcgctgag cctgctgcag gccacgctac accgctatga gcatgccctc	1620
tctcagtga gtgtggatgt gtataagaaa gtgggcagcc tgtaccctga gatgagtgcc	1680
catgagcgt ccttggtatt cctcattgaa ctgctgcaca aggatcagct ggatgagact	1740
gtcaatgtgg agcctctcac caaggccatc aagtactatc agcatctgta cagcatccac	1800
cttgccgaac agcctgagga ctgtactatg cagctggctg accacattaa gttcacgcag	1860
agtgtcttgg actgcatgag tgtggaggta ggacggctgc gtgccttctt gcagggtggg	1920
caggaggcta cagatattgc cctcctgctc cgggatctgg aaacttcatg cagtgcacac	1980
cgccagttct gcaagaagat ccgaaggcga atgccaggga cagatgctcc tgggatccca	2040
gctgcactgg ctttggacc acaggtatct gacacgctcc tagactgcag gaaacacttg	2100
acgtgggtcg tggctgtgct gcaggaggtg gcagctgctg ctgccagct cattgcccc	2160
ctggcagaga atgaggggct acttgtggct gctctggagg aactggcttt caaagcaagc	2220
gagcagatct atgggacccc ctccagcagc ccctatgagt gtctgcgcca gtcatgcaac	2280
atcctcatca gtaccatgaa caagctggcc acagccatgc aggaggggga gtatgatgca	2340
gagcggcccc ccagcaagcc tccaccggtt gaactgcggg ctgctgccct tcgtgcagag	2400
atcacagatg ctgaaggcct gggtttgaag ctcgaagatc gagagacagt tattaaggag	2460
ttgaagaagt cactcaagat taaggagag gagctaagtg aggccaatgt gcggctgagc	2520
ctcctggaga agaagttgga cagtgtgcc aaggatgcag atgagcgcac cgagaaagtc	2580
cagactcggc tggaggagac ccaggcactg ctgcgaaaga aggagaaaga gtttgaggag	2640
acaatggatg cactccaggc tgacatcgac cagctggagg cagagaaggc agaactaaag	2700
cagcgtctga acagccagtc caaacgcacg attgagggac tccggggccc tcctccttca	2760
ggcattgcta ctctggtctc tggcattgct ggtggagcca tccctgggca ggctccaggg	2820

1020001191 - P17-158 Sequence Listing

tctgtgccag gccagggct ggtgaaggac tcaccactgc tgcttcagca gatctctgcc	2880
atgaggctgc acatctccca gctccagcat gagaacagca tcctcaaggg agcccagatg	2940
aaggcatcct tggcatccct gccccctctg catgttgcaa agctatccca tgagggccct	3000
ggcagtgagt taccagctgg agcgtgtat cgtaagacca gccagctgct ggagacattg	3060
aatcaattga gcacacacac gcacgtagta gacatcactc gcaccagccc tgctgccaag	3120
agcccgctcg cccaacttat ggagcaagtg gctcagctta agtccctgag tgacaccgtc	3180
gagaagctca aggatgaggt cctcaaggag acagtatctc agcgccctgg agccacagta	3240
cccactgact ttgccacctt cccttcatca gccttcctca gggaggatcc aaagtgggaa	3300
ttccctcgga agaacttgggt tcttggaata actctaggag aaggcgaatt tggaaaagt	3360
gtcaaggcaa cggccttcca tctgaaaggc agagcagggt acaccacggt ggccgtgaag	3420
atgctgaaag agaacgcctc cccgagttag cttcgagacc tgctgtcaga gttcaacgtc	3480
ctgaagcagg tcaaccaccc acatgtcatc aaattgtatg gggcctgcag ccaggatggc	3540
ccgctcctcc tcatcgtgga gtacgcaaaa tacggctccc tgcggggctt cctccgcgag	3600
agccgcaaag tggggcctgg ctacctgggc agtggaggca gccgcaactc cagctccctg	3660
gaccacccgg atgagcgggc cctcaccatg ggcgacctca tctcatttgc ctggcagatc	3720
tcacagggga tgcagtatct ggccgagatg aagctcgttc atcgggactt ggcagccaga	3780
aacatcctgg tagctgaggg gcggaagatg aagatttcgg atttcggctt gtcccagat	3840
gtttatgaag aggattccta cgtgaagagg agccagggtc ggattccagt taaatggatg	3900
gcaattgaat ccccttttga tcatatctac accacgcaaa gtgatgtatg gtcttttgg	3960
gtcctgctgt gggagatcgt gaccctaggg ggaaaccct atcctgggat tcctcctgag	4020
cggctcttca accttctgaa gaccggccac cggatggaga ggccagacaa ctgcagcgag	4080
gagatgtacc gcctgatgct gcaatgctgg aagcaggagc cggacaaaag gccggtgttt	4140
gcggacatca gcaaagacct ggagaagatg atggttaaga ggagagacta cttggacctt	4200
gcggcgtcca ctccatctga ctccctgatt tatgacgacg gcctctcaga ggaggagaca	4260
ccgctgggtgg actgtaataa tgccccctc cctcgagccc tcccttcac atggattgaa	4320
aacaaactct atggcatgtc agaccgaac tggcctggag agagtcctgt accactcacg	4380

1020001191 - P17-158 Sequence Listing

agagctgatg gcactaacac tgggtttcca agatatccaa atgatatgtg atatgctaac 4440

tggatgcttt caccctcagc ggcaaaatta atggacacgt ttgatagtta a 4491

<210> 14

<211> 1496

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion peptide

<400> 14

Met Met Arg Gln Ala Pro Thr Ala Arg Lys Thr Thr Thr Arg Arg Pro
1 5 10 15

Lys Pro Thr Arg Pro Ala Ser Thr Gly Val Ala Gly Ala Ser Ser Ser
20 25 30

Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser Ser Glu
35 40 45

Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile Pro Thr
50 55 60

Pro Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser Pro Ser
65 70 75 80

Lys Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu Glu Lys
85 90 95

Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys Leu Lys
100 105 110

Glu Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu Trp Lys
115 120 125

Ser Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu Lys Glu
130 135 140

Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg Tyr Met

1020001191 - P17-158 Sequence Listing

145 150 155 160

Glu Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr Leu Asp
165 170 175

Lys Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu Val Glu
180 185 190

Ala Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu Ile Leu
195 200 205

Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser Ser Tyr
210 215 220

Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp Ala Leu
225 230 235 240

Val Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His Val Lys
245 250 255

Leu Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val Val Arg
260 265 270

Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu Ser Thr
275 280 285

Ile Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala Glu Glu
290 295 300

Met Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu Lys Val
305 310 315 320

Arg Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn Glu Met
325 330 335

Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu Leu Arg
340 345 350

Glu Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln Lys Arg

1020001191 - P17-158 Sequence Listing

355

360

365

Val Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr Ile Lys
 370 375 380

Lys Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg Glu Leu
 385 390 395 400

Thr Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro Pro Pro
 405 410 415

Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala His Ala
 420 425 430

Lys Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln Ala Asn
 435 440 445

Arg His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe Leu Arg
 450 455 460

Pro Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met Pro Arg
 465 470 475 480

Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu Lys Phe
 485 490 495

Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro Gly Leu Arg Gly Ala Ala
 500 505 510

Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu Ser Leu
 515 520 525

Leu Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln Cys Ser
 530 535 540

Val Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met Ser Ala
 545 550 555 560

His Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys Asp Gln

1020001191 - P17-158 Sequence Listing

565 570 575

Leu Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile Lys Tyr
580 585 590

Tyr Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu Asp Cys
595 600 605

Thr Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala Leu Asp
610 615 620

Cys Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln Gly Gly
625 630 635 640

Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu Thr Ser
645 650 655

Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg Met Pro
660 665 670

Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly Pro Gln
675 680 685

Val Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp Val Val
690 695 700

Ala Val Leu Gln Glu Val Ala Ala Ala Ala Gln Leu Ile Ala Pro
705 710 715 720

Leu Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu Leu Ala
725 730 735

Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser Pro Tyr
740 745 750

Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met Asn Lys
755 760 765

Leu Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg Pro Pro

1020001191 - P17-158 Sequence Listing

770

775

780

Ser Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg Ala Glu
785 790 795 800

Ile Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg Glu Thr
805 810 815

Val Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu Glu Leu
820 825 830

Ser Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu Asp Ser
835 840 845

Ala Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr Arg Leu
850 855 860

Glu Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe Glu Glu
865 870 875 880

Thr Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala Glu Lys
885 890 895

Ala Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg Thr Ile Glu
900 905 910

Gly Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr Leu Val Ser Gly
915 920 925

Ile Ala Gly Gly Ala Ile Pro Gly Gln Ala Pro Gly Ser Val Pro Gly
930 935 940

Pro Gly Leu Val Lys Asp Ser Pro Leu Leu Leu Gln Gln Ile Ser Ala
945 950 955 960

Met Arg Leu His Ile Ser Gln Leu Gln His Glu Asn Ser Ile Leu Lys
965 970 975

Gly Ala Gln Met Lys Ala Ser Leu Ala Ser Leu Pro Pro Leu His Val

1020001191 - P17-158 Sequence Listing

980

985

990

Ala Lys Leu Ser His Glu Gly Pro Gly Ser Glu Leu Pro Ala Gly Ala
 995 1000 1005

Leu Tyr Arg Lys Thr Ser Gln Leu Leu Glu Thr Leu Asn Gln Leu
 1010 1015 1020

Ser Thr His Thr His Val Val Asp Ile Thr Arg Thr Ser Pro Ala
 1025 1030 1035

Ala Lys Ser Pro Ser Ala Gln Leu Met Glu Gln Val Ala Gln Leu
 1040 1045 1050

Lys Ser Leu Ser Asp Thr Val Glu Lys Leu Lys Asp Glu Val Leu
 1055 1060 1065

Lys Glu Thr Val Ser Gln Arg Pro Gly Ala Thr Val Pro Thr Asp
 1070 1075 1080

Phe Ala Thr Phe Pro Ser Ser Ala Phe Leu Arg Glu Asp Pro Lys
 1085 1090 1095

Trp Glu Phe Pro Arg Lys Asn Leu Val Leu Gly Lys Thr Leu Gly
 1100 1105 1110

Glu Gly Glu Phe Gly Lys Val Val Lys Ala Thr Ala Phe His Leu
 1115 1120 1125

Lys Gly Arg Ala Gly Tyr Thr Thr Val Ala Val Lys Met Leu Lys
 1130 1135 1140

Glu Asn Ala Ser Pro Ser Glu Leu Arg Asp Leu Leu Ser Glu Phe
 1145 1150 1155

Asn Val Leu Lys Gln Val Asn His Pro His Val Ile Lys Leu Tyr
 1160 1165 1170

Gly Ala Cys Ser Gln Asp Gly Pro Leu Leu Leu Ile Val Glu Tyr

1020001191 - P17-158 Sequence Listing

1175														
Ala	Lys	Tyr	Gly	Ser	Leu	Arg	Gly	Phe	Leu	Arg	Glu	Ser	Arg	Lys
1190						1195					1200			
Val	Gly	Pro	Gly	Tyr	Leu	Gly	Ser	Gly	Gly	Ser	Arg	Asn	Ser	Ser
1205						1210					1215			
Ser	Leu	Asp	His	Pro	Asp	Glu	Arg	Ala	Leu	Thr	Met	Gly	Asp	Leu
1220						1225					1230			
Ile	Ser	Phe	Ala	Trp	Gln	Ile	Ser	Gln	Gly	Met	Gln	Tyr	Leu	Ala
1235						1240					1245			
Glu	Met	Lys	Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu
1250						1255					1260			
Val	Ala	Glu	Gly	Arg	Lys	Met	Lys	Ile	Ser	Asp	Phe	Gly	Leu	Ser
1265						1270					1275			
Arg	Asp	Val	Tyr	Glu	Glu	Asp	Ser	Tyr	Val	Lys	Arg	Ser	Gln	Gly
1280						1285					1290			
Arg	Ile	Pro	Val	Lys	Trp	Met	Ala	Ile	Glu	Ser	Leu	Phe	Asp	His
1295						1300					1305			
Ile	Tyr	Thr	Thr	Gln	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu
1310						1315					1320			
Trp	Glu	Ile	Val	Thr	Leu	Gly	Gly	Asn	Pro	Tyr	Pro	Gly	Ile	Pro
1325						1330					1335			
Pro	Glu	Arg	Leu	Phe	Asn	Leu	Leu	Lys	Thr	Gly	His	Arg	Met	Glu
1340						1345					1350			
Arg	Pro	Asp	Asn	Cys	Ser	Glu	Glu	Met	Tyr	Arg	Leu	Met	Leu	Gln
1355						1360					1365			
Cys	Trp	Lys	Gln	Glu	Pro	Asp	Lys	Arg	Pro	Val	Phe	Ala	Asp	Ile

1020001191 - P17-158 Sequence Listing

1370

1375

1380

Ser Lys Asp Leu Glu Lys Met Met Val Lys Arg Arg Asp Tyr Leu
1385 1390 1395

Asp Leu Ala Ala Ser Thr Pro Ser Asp Ser Leu Ile Tyr Asp Asp
1400 1405 1410

Gly Leu Ser Glu Glu Glu Thr Pro Leu Val Asp Cys Asn Asn Ala
1415 1420 1425

Pro Leu Pro Arg Ala Leu Pro Ser Thr Trp Ile Glu Asn Lys Leu
1430 1435 1440

Tyr Gly Met Ser Asp Pro Asn Trp Pro Gly Glu Ser Pro Val Pro
1445 1450 1455

Leu Thr Arg Ala Asp Gly Thr Asn Thr Gly Phe Pro Arg Tyr Pro
1460 1465 1470

Asn Asp Ser Val Tyr Ala Asn Trp Met Leu Ser Pro Ser Ala Ala
1475 1480 1485

Lys Leu Met Asp Thr Phe Asp Ser
1490 1495

<210> 15

<211> 4365

<212> DNA

<213> Artificial Sequence

<220>

<223> coding sequence of fusion peptide

<400> 15

atgatgagac aggcaccgac agcccgaaag accacaactc ggcgacccaa gccacgcgc 60

ccagccagta ctgggggtggc tggggccagt agctccctgg gccctctgg ctcagcgta 120

gcaggtgagc tgagcagcag tgagcccagc accccggctc agactccgct ggcagcacc 180

atcatcccca cgccggtcct cacctctcct ggagcagtcc ccccgcttcc ttcccatcc 240

1020001191 - P17-158 Sequence Listing

aaggaggagg agggactaag ggctcaggtg cgggacctgg aggagaaact agagaccctg	300
agactgaaac gggcagaaga caaagcaaag ctaaaagagc tggagaaaca caaaatccag	360
ctggagcagg tgcaggaatg gaagagcaaa atgcaggagc agcaggccga cctgcagcgg	420
cgcctcaagg aggcgagaaa ggaagccaag gaggcgctgg aggcaaagga acgctatatg	480
gaggagatgg ctgatactgc tgatgccatt gagatggcca ctttggacaa ggagatggct	540
gaagagcggg ctgagtccct gcagcaggag gtggaggcac tgaaggagcg ggtggacgag	600
ctcactactg acttagagat cctcaaggct gagattgaag agaagggtc agatggcgct	660
gcatccagtt atcagctcaa gcagcttgag gagcagaatg cccgcctgaa ggatgccctg	720
gtgaggatgc gggatctttc ttcctcagag aagcaggagc atgtgaagct ccagaagctc	780
atggaaaaga agaaccaaga gctggaagt tggaggcaac agcgggagcg tctgcaggag	840
gagctaagcc aggcagagag caccattgat gagctcaagg agcaggtgga tgctgctctg	900
ggtgctgagg agatggtgga gatgctgaca gatcggaacc tgaatctgga agagaaagtg	960
cgcgagttga gggagactgt gggagacttg gaagcgatga atgagatgaa cgatgagctg	1020
caggagaatg cacgtgagac agaactggag ctgcgggagc agctggacat ggcaggcgcg	1080
cgggttcgtg agggccagaa gcgtgtggag gcagcccagg agacggttgc agactaccag	1140
cagaccatca agaagtaccg ccagctgacc gccatctac aggatgtgaa tcgggaactg	1200
acaaaccagc aggaagcatc tgtgggagagg caacagcagc cacctccaga gacctttgac	1260
ttcaaaatca agtttgctga gactaaggcc catgccaaagg caattgagat ggaattgagg	1320
cagatggagg tggcccaggc caatcgacac atgtccctgc tgacagcctt catgcctgac	1380
agcttccttc ggccagggtg ggacatgac tgcgttctgg tgctgttgct catgcctcgt	1440
ctcatttgca aggcagagct gatccggaag caggcccagg agaagtttga actaagtgag	1500
aactgttcag agcggcctgg gctgcgagga gctgctgggg agcaactcag ctttgctgct	1560
ggactgggtg actcgctgag cctgctgcag gccacgtac accgctatga gcatgccctc	1620
tctcagtgca gtgtggatgt gtataagaaa gtgggcagcc tgtaccctga gatgagtgcc	1680
catgagcgct ccttggaatt cctcattgaa ctgctgcaca aggatcagct ggatgagact	1740
gtcaatgtgg agcctctcac caaggccatc aagtactatc agcatctgta cagcatccac	1800

1020001191 - P17-158 Sequence Listing

cttgccgaac agcctgagga ctgtactatg cagctggctg accacattaa gttcacgcag	1860
agtgtctctgg actgcatgag tgtggaggta ggacggctgc gtgccttctt gcagggtggg	1920
caggaggcta cagatattgc cctcctgctc cgggatctgg aaacttcatg cagtgcacatc	1980
cgccagttct gcaagaagat ccgaaggcga atgccaggga cagatgctcc tgggatccca	2040
gctgcactgg cttttggacc acaggtatct gacacgctcc tagactgcag gaaacacttg	2100
acgtgggtcg tggctgtgct gcaggaggtg gcagctgctg ctgccagct cattgccccca	2160
ctggcagaga atgaggggct acttgtggct gctctggagg aactggcttt caaagcaagc	2220
gagcagatct atgggacccc ctccagcagc ccctatgagt gtctgcgcca gtcatgcaac	2280
atcctcatca gtacatgaa caagctggcc acagccatgc aggaggggga gtatgatgca	2340
gagcggcccc ccagcaagcc tccaccggtt gaactgcggg ctgctgccct tcgtgcagag	2400
atcacagatg ctgaaggcct gggtttgaag ctcgaagatc gagagacagt tattaaggag	2460
ttgaagaagt cactcaagat taaggagag gagctaagtg aggccaatgt gcggctgagc	2520
ctcctggaga agaagttgga cagtgtgcc aaggatgcag atgagcgcac cgagaaagtc	2580
cagactcggc tggaggagac ccaggcactg ctgcgaaaga aggagaaaga gtttgaggag	2640
acaatggatg cactccaggc tgacatcgac cagctggagg cagagaaggc agaactaaag	2700
cagcgtctga acagccagtc caaacgcacg attgaggggac tccggggccc tcctccttca	2760
ggcattgcta ctctggtctc tggcattgct ggtggagcca tccctgggca ggctccaggg	2820
tctgtgccag gccagggct ggtgaaggac tcaccactgc tgcttcagca gatctctgcc	2880
atgaggctgc acatctccca gctccagcat gagaacagca tcctcaaggg agcccagatg	2940
aaggcatcct tggcatccct gccccctctg catgttgcaa agctatccca tgagggcct	3000
ggcagtgagt taccagctgg agcgctgtat cgtaagacca gccagctgct ggagacattg	3060
aatcaattga gcacacacac gcacgtagta gacatcactc gcaccagccc tgctgccaaag	3120
agcccgtcgg cccaacttat ggagcaagtg gctcagctta agtccctgag tgacaccgtc	3180
gagaagctca aggatgaggt cctcaaggag acagtatctc agcgccctgg agccacagta	3240
cccactgact ttgccacctt cccttcatca gccttcctca gggaggatcc aaagtgggaa	3300
ttccctcgga agaacttgggt tcttgaaaaa actctaggag aaggcgaatt tggaaaagtg	3360

1020001191 - P17-158 Sequence Listing

gtcaaggcaa cggccttcca tctgaaaggc agagcagggt acaccacggt ggccgtgaag	3420
atgctgaaag agaacgcctc cccgagttag cttcgagacc tgctgtcaga gttcaacgtc	3480
ctgaagcagg tcaaccaccc acatgtcatc aaattgtatg gggcctgcag ccaggatggc	3540
ccgctcctcc tcatcgtgga gtacgcaaaa tacggctccc tgcggggctt cctccgcgag	3600
agccgcaaag tggggcctgg ctacctgggc agtggaggca gccgcaactc cagctccctg	3660
gaccacccgg atgagcgggc cctcaccatg ggcgacctca tctcatttgc ctggcagatc	3720
tcacagggga tgagtagtct ggccgagatg aagctcgttc atcgggactt ggcagccaga	3780
aacatcctgg tagctgaggg gcggaagatg aagatttcgg atttcggctt gtcccagat	3840
gtttatgaag aggattccta cgtgaagagg agccagggtc ggattccagt taaatggatg	3900
gcaattgaat ccctttttga tcatatctac accacgcaaa gtgatgtatg gtcttttgg	3960
gtcctgctgt gggagatcgt gaccctaggg ggaaaccct atcctgggat tcctcctgag	4020
cggctcttca accttctgaa gaccggccac cggatggaga ggccagacaa ctgcagcgag	4080
gagatgtacc gcctgatgct gcaatgctgg aagcaggagc cggacaaaag gccggtgttt	4140
gcggacatca gcaaagacct ggagaagatg atggttaaga ggagagacta cttggacctt	4200
gcggcgtcca ctccatctga ctccctgatt tatgacgacg gcctctcaga ggaggagaca	4260
ccgctggtgg actgtaataa tgccccctc cctcgagccc tcccttcac atggattgaa	4320
aacaaactct atggtagaat ttcccatgca ttactagat tctag	4365

<210> 16
 <211> 1454
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion peptide

<400> 16

Met	Met	Arg	Gln	Ala	Pro	Thr	Ala	Arg	Lys	Thr	Thr	Thr	Arg	Arg	Pro
1				5					10					15	

Lys	Pro	Thr	Arg	Pro	Ala	Ser	Thr	Gly	Val	Ala	Gly	Ala	Ser	Ser	Ser
			20					25					30		

1020001191 - P17-158 Sequence Listing

Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser Ser Glu
35 40 45

Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile Pro Thr
50 55 60

Pro Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser Pro Ser
65 70 75 80

Lys Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu Glu Lys
85 90 95

Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys Leu Lys
100 105 110

Glu Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu Trp Lys
115 120 125

Ser Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu Lys Glu
130 135 140

Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg Tyr Met
145 150 155 160

Glu Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr Leu Asp
165 170 175

Lys Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu Val Glu
180 185 190

Ala Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu Ile Leu
195 200 205

Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser Ser Tyr
210 215 220

Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp Ala Leu
225 230 235 240

1020001191 - P17-158 Sequence Listing

Val Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His Val Lys
245 250 255

Leu Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val Val Arg
260 265 270

Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu Ser Thr
275 280 285

Ile Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala Glu Glu
290 295 300

Met Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu Lys Val
305 310 315 320

Arg Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn Glu Met
325 330 335

Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu Leu Arg
340 345 350

Glu Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln Lys Arg
355 360 365

Val Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr Ile Lys
370 375 380

Lys Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg Glu Leu
385 390 395 400

Thr Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro Pro Pro
405 410 415

Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala His Ala
420 425 430

Lys Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln Ala Asn
435 440 445

1020001191 - P17-158 Sequence Listing

Arg His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe Leu Arg
450 455 460

Pro Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met Pro Arg
465 470 475 480

Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu Lys Phe
485 490 495

Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro Gly Leu Arg Gly Ala Ala
500 505 510

Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu Ser Leu
515 520 525

Leu Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln Cys Ser
530 535 540

Val Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met Ser Ala
545 550 555 560

His Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys Asp Gln
565 570 575

Leu Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile Lys Tyr
580 585 590

Tyr Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu Asp Cys
595 600 605

Thr Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala Leu Asp
610 615 620

Cys Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln Gly Gly
625 630 635 640

Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu Thr Ser
645 650 655

1020001191 - P17-158 Sequence Listing

Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg Met Pro
660 665 670

Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly Pro Gln
675 680 685

Val Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp Val Val
690 695 700

Ala Val Leu Gln Glu Val Ala Ala Ala Ala Ala Gln Leu Ile Ala Pro
705 710 715 720

Leu Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu Leu Ala
725 730 735

Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser Pro Tyr
740 745 750

Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met Asn Lys
755 760 765

Leu Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg Pro Pro
770 775 780

Ser Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg Ala Glu
785 790 795 800

Ile Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg Glu Thr
805 810 815

Val Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu Glu Leu
820 825 830

Ser Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu Asp Ser
835 840 845

Ala Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr Arg Leu
850 855 860

1020001191 - P17-158 Sequence Listing

Glu Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe Glu Glu
865 870 875 880

Thr Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala Glu Lys
885 890 895

Ala Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg Thr Ile Glu
900 905 910

Gly Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr Leu Val Ser Gly
915 920 925

Ile Ala Gly Gly Ala Ile Pro Gly Gln Ala Pro Gly Ser Val Pro Gly
930 935 940

Pro Gly Leu Val Lys Asp Ser Pro Leu Leu Leu Gln Gln Ile Ser Ala
945 950 955 960

Met Arg Leu His Ile Ser Gln Leu Gln His Glu Asn Ser Ile Leu Lys
965 970 975

Gly Ala Gln Met Lys Ala Ser Leu Ala Ser Leu Pro Pro Leu His Val
980 985 990

Ala Lys Leu Ser His Glu Gly Pro Gly Ser Glu Leu Pro Ala Gly Ala
995 1000 1005

Leu Tyr Arg Lys Thr Ser Gln Leu Leu Glu Thr Leu Asn Gln Leu
1010 1015 1020

Ser Thr His Thr His Val Val Asp Ile Thr Arg Thr Ser Pro Ala
1025 1030 1035

Ala Lys Ser Pro Ser Ala Gln Leu Met Glu Gln Val Ala Gln Leu
1040 1045 1050

Lys Ser Leu Ser Asp Thr Val Glu Lys Leu Lys Asp Glu Val Leu
1055 1060 1065

1020001191 - P17-158 Sequence Listing

Lys	Glu	Thr	Val	Ser	Gln	Arg	Pro	Gly	Ala	Thr	Val	Pro	Thr	Asp
1070						1075					1080			
Phe	Ala	Thr	Phe	Pro	Ser	Ser	Ala	Phe	Leu	Arg	Glu	Asp	Pro	Lys
1085						1090					1095			
Trp	Glu	Phe	Pro	Arg	Lys	Asn	Leu	Val	Leu	Gly	Lys	Thr	Leu	Gly
1100						1105					1110			
Glu	Gly	Glu	Phe	Gly	Lys	Val	Val	Lys	Ala	Thr	Ala	Phe	His	Leu
1115						1120					1125			
Lys	Gly	Arg	Ala	Gly	Tyr	Thr	Thr	Val	Ala	Val	Lys	Met	Leu	Lys
1130						1135					1140			
Glu	Asn	Ala	Ser	Pro	Ser	Glu	Leu	Arg	Asp	Leu	Leu	Ser	Glu	Phe
1145						1150					1155			
Asn	Val	Leu	Lys	Gln	Val	Asn	His	Pro	His	Val	Ile	Lys	Leu	Tyr
1160						1165					1170			
Gly	Ala	Cys	Ser	Gln	Asp	Gly	Pro	Leu	Leu	Leu	Ile	Val	Glu	Tyr
1175						1180					1185			
Ala	Lys	Tyr	Gly	Ser	Leu	Arg	Gly	Phe	Leu	Arg	Glu	Ser	Arg	Lys
1190						1195					1200			
Val	Gly	Pro	Gly	Tyr	Leu	Gly	Ser	Gly	Gly	Ser	Arg	Asn	Ser	Ser
1205						1210					1215			
Ser	Leu	Asp	His	Pro	Asp	Glu	Arg	Ala	Leu	Thr	Met	Gly	Asp	Leu
1220						1225					1230			
Ile	Ser	Phe	Ala	Trp	Gln	Ile	Ser	Gln	Gly	Met	Gln	Tyr	Leu	Ala
1235						1240					1245			
Glu	Met	Lys	Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu
1250						1255					1260			

1020001191 - P17-158 Sequence Listing

Val	Ala	Glu	Gly	Arg	Lys	Met	Lys	Ile	Ser	Asp	Phe	Gly	Leu	Ser
1265						1270					1275			
Arg	Asp	Val	Tyr	Glu	Glu	Asp	Ser	Tyr	Val	Lys	Arg	Ser	Gln	Gly
1280						1285					1290			
Arg	Ile	Pro	Val	Lys	Trp	Met	Ala	Ile	Glu	Ser	Leu	Phe	Asp	His
1295						1300					1305			
Ile	Tyr	Thr	Thr	Gln	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu
1310						1315					1320			
Trp	Glu	Ile	Val	Thr	Leu	Gly	Gly	Asn	Pro	Tyr	Pro	Gly	Ile	Pro
1325						1330					1335			
Pro	Glu	Arg	Leu	Phe	Asn	Leu	Leu	Lys	Thr	Gly	His	Arg	Met	Glu
1340						1345					1350			
Arg	Pro	Asp	Asn	Cys	Ser	Glu	Glu	Met	Tyr	Arg	Leu	Met	Leu	Gln
1355						1360					1365			
Cys	Trp	Lys	Gln	Glu	Pro	Asp	Lys	Arg	Pro	Val	Phe	Ala	Asp	Ile
1370						1375					1380			
Ser	Lys	Asp	Leu	Glu	Lys	Met	Met	Val	Lys	Arg	Arg	Asp	Tyr	Leu
1385						1390					1395			
Asp	Leu	Ala	Ala	Ser	Thr	Pro	Ser	Asp	Ser	Leu	Ile	Tyr	Asp	Asp
1400						1405					1410			
Gly	Leu	Ser	Glu	Glu	Glu	Thr	Pro	Leu	Val	Asp	Cys	Asn	Asn	Ala
1415						1420					1425			
Pro	Leu	Pro	Arg	Ala	Leu	Pro	Ser	Thr	Trp	Ile	Glu	Asn	Lys	Leu
1430						1435					1440			
Tyr	Gly	Arg	Ile	Ser	His	Ala	Phe	Thr	Arg	Phe				
1445						1450								

1020001191 - P17-158 Sequence Listing

<210> 17
 <211> 4782
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coding sequence of fusion peptide

<400> 17
 atgagtgcgg aggcaagcgc ccggcctctg cgggtgggct cccgtgtaga ggtgattgga 60
 aaaggccacc gaggcactgt ggcctatgtt ggagccacac tgtttgccac tggcaaatgg 120
 gtaggcgtga ttctggatga agcaaagggc aaaaatgatg gaactgttca aggcaggaag 180
 tacttcactt gtgatgaagg gcatggcatc tttgtgcgcc agtcccagat ccaggtatatt 240
 gaagatggag cagatactac ttccccagag acacctgatt cttctgcttc aaaagtcctc 300
 aaaagagagg gaactgatac aactgcaaag actagcaaac tgcccacgcg cccagccagt 360
 actgggggtgg ctggggccag tagctccctg ggcccctctg gctcagcgtc agcaggtgag 420
 ctgagcagca gtgagcccag caccgccgct cagactccgc tggcagcacc catcatcccc 480
 acgccggtcc tcacctctcc tggagcagtc cccccgcttc cttccccatc caaggaggag 540
 gagggactaa gggctcaggt gcgggacctg gaggagaaac tagagaccct gagactgaaa 600
 cgggcagaag acaaagcaaa gctaaaagag ctggagaaac aaaaaatcca gctggagcag 660
 gtgcaggaat ggaagagcaa aatgcaggag cagcaggccg acctgcagcg gcgcctcaag 720
 gaggcgagaa aggaagccaa ggaggcgctg gaggcaaagg aacgctatat ggaggagatg 780
 gctgatactg ctgatgccat tgagatggcc acttttgaca aggagatggc tgaagagcgg 840
 gctgagtccc tgcagcagga ggtggaggca ctgaaggagc ggggtggacga gctcactact 900
 gacttagaga tcctcaaggc tgagattgaa gagaagggtc cagatggcgc tgcattcagt 960
 tatcagctca agcagcttga ggagcagaat gcccgcctga aggatgccct ggtgaggatg 1020
 cgggatcttt cttcctcaga gaagcaggag catgtgaagc tccagaagct catggaaaag 1080
 aagaaccaag agctggaagt tgtgaggcaa cagcgggagc gtctgcagga ggagctaagc 1140
 caggcagaga gcaccattga tgagctcaag gagcaggtgg atgctgctct ggggtgctgag 1200
 gagatgggtg agatgctgac agatcggaac ctgaatctgg aagagaaagt gcgcgagttg 1260

1020001191 - P17-158 Sequence Listing

agggagactg tgggagactt ggaagcgatg aatgagatga acgatgagct gcaggagaat	1320
gcacgtgaga cagaactgga gctgcgggag cagctggaca tggcaggcgc gcgggttcgt	1380
gaggcccaga agcgtgtgga ggagagcccag gagacggttg cagactacca gcagaccatc	1440
aagaagtacc gccagctgac cgcccatcta caggatgtga atcggaact gacaaaccag	1500
caggaagcat ctgtggagag gcaacagcag ccacctccag agacctttga cttcaaaatc	1560
aagtttgctg agactaaggc ccatgccaaag gcaattgaga tggaattgag gcagatggag	1620
gtggcccagg ccaatcgaca catgtccctg ctgacagcct tcatgcctga cagcttcctt	1680
cggccagggtg gggacatga ctgcgttctg gtgctgttgc tcatgcctcg tctcatttgc	1740
aaggcagagc tgatccggaa gcaggcccag gagaagtttg aactaagtga gaactgttca	1800
gagcggcctg ggctgcgagg agctgctggg gagcaactca gctttgctgc tggactgggtg	1860
tactcgctga gcctgctgca ggccacgcta caccgctatg agcatgccct ctctcagtgc	1920
agtgtggatg tgtataagaa agtgggcagc ctgtaccctg agatgagtgc ccatgagcgc	1980
tccttggatt tcctcattga actgctgcac aaggatcagc tggatgagac tgtcaatgtg	2040
gagcctctca ccaaggccat caagtactat cagcatctgt acagcatcca ccttgccgaa	2100
cagcctgagg actgtactat gcagctggct gaccacatta agttcacgca gagtgcctctg	2160
gactgcatga gtgtggaggt aggacggctg cgtgccttct tgcagggtgg gcaggaggct	2220
acagatattg ccctcctgct ccgggatctg gaaacttcat gcagtgacat ccgccagttc	2280
tgcaagaaga tccgaaggcg aatgccaggg acagatgctc ctgggatccc agctgcactg	2340
gcctttggac cacaggtatc tgacacgctc ctagactgca ggaaacactt gacgtgggtc	2400
gtggctgtgc tgcaggaggt ggagctgct gctgcccagc tcattgcccc actggcagag	2460
aatgaggggc tacttgtggc tgctctggag gaactggctt tcaaagcaag cgagcagatc	2520
tatgggaccc cctccagcag cccctatgag tgtctgcgcc agtcatgcaa catcctcatc	2580
agtaccatga acaagctggc cacagccatg caggaggggg agtatgatgc agagcggccc	2640
cccagcaagc ctccaccggt tgaactgcgg gctgctgccc ttcgtgcaga gatcacagat	2700
gctgaaggcc tgggtttgaa gctcgaagat cgagagacag ttattaagga gttgaagaag	2760
tcactcaaga ttaagggaga ggagctaagt gaggccaatg tgcggctgag cctcctggag	2820

1020001191 - P17-158 Sequence Listing

aagaagttgg acagtgctgc caaggatgca gatgagcgca tcgagaaagt ccagactcgg	2880
ctggaggaga cccaggcact gctgcgaaag aaggagaaag agtttgagga gacaatggat	2940
gcactccagg ctgacatcga ccagctggag gcagagaagg cagaactaaa gcagcgtctg	3000
aacagccagt ccaaacgcac gattgaggga ctccggggcc ctcttccttc aggcattgct	3060
actctggtct ctggcattgc tgggtggagcc atccctgggc aggctccagg gtctgtgcca	3120
ggcccagggc tggatgaagga ctcaccactg ctgcttcagc agatctctgc catgaggctg	3180
cacatctccc agctccagca tgagaacagc atcctcaagg gagcccagat gaaggcatcc	3240
ttggcatccc tgccccctct gcatgttgca aagctatccc atgagggccc tggcagttag	3300
ttaccagctg gagcgctgta tcgtaagacc agccagctgc tggagacatt gaatcaattg	3360
agcacacaca cgcacgtagt agacatcact cgcaccagcc ctgctgcca gagcccgtcg	3420
gcccactta tggagcaagt ggctcagctt aagtccctga gtgacaccgt cgagaagctc	3480
aaggatgagg tcctcaagga gacagtatct cagcgccctg gagccacagt acccactgac	3540
tttgccacct tcccttcac agccttcctc agggaggatc caaagtggga attcctcgg	3600
aagaacttgg ttcttgga aaactctagga gaaggcgaat ttggaaaagt ggtcaaggca	3660
acggccttcc atctgaaagg cagagcaggg tacaccacgg tggccgtgaa gatgctgaaa	3720
gagaacgcct ccccgagtga gcttcgagac ctgctgtcag agttcaacgt cctgaagcag	3780
gtcaaccacc cacatgtcat caaattgtat ggggcctgca gccaggatgg cccgctcctc	3840
ctcatcgtgg agtacgcaa atacggctcc ctgcggggct tcctccgca gagccgcaaa	3900
gtggggcctg gctacctggg cagtggaggc agccgcaact ccagctccct ggaccacccg	3960
gatgagcggg ccctcacat gggcgacctc atctcatttg cctggcagat ctcacagggg	4020
atgcagtatc tggccgagat gaagctcggt catcgggact tggcagccag aaacatcctg	4080
gtagctgagg ggcggaagat gaagatttcg gatttcggct tgtcccaga tgtttatgaa	4140
gaggattcct acgtgaagag gagccagggt cggattccag ttaaattgat ggcaattgaa	4200
tccctttttg atcatatcta caccacgcaa agtgatgtat ggtcttttgg tgtcctgctg	4260
tgggagatcg tgaccctagg gggaaacccc tatcctggga ttctcctga gcggctcttc	4320
aaccttctga agaccggcca ccgatggag aggccagaca actgcagcga ggagatgtac	4380

1020001191 - P17-158 Sequence Listing

cgctgatgc tgcaatgctg gaagcaggag ccggacaaaa ggccggtgtt tgcggacatc	4440
agcaaagacc tggagaagat gatggttaag aggagagact acttggacct tgcggcgctcc	4500
actccatctg actccctgat ttatgacgac ggcctctcag aggaggagac accgctggtg	4560
gactgtaata atgccccct ccctcgagcc ctcccttcca catggattga aaacaaactc	4620
tatggcatgt cagacccgaa ctggcctgga gagagtcctg taccactcac gagagctgat	4680
ggcactaaca ctgggtttcc aagatatcca aatgatagtg tatatgctaa ctggatgctt	4740
tcaccctcag cggcaaaatt aatggacacg tttgatagtt aa	4782

<210> 18
 <211> 1593
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion peptide

<400> 18

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

Glu	Val	Ile	Gly	Lys	Gly	His	Arg	Gly	Thr	Val	Ala	Tyr	Val	Gly	Ala
			20					25					30		

Thr	Leu	Phe	Ala	Thr	Gly	Lys	Trp	Val	Gly	Val	Ile	Leu	Asp	Glu	Ala
		35					40					45			

Lys	Gly	Lys	Asn	Asp	Gly	Thr	Val	Gln	Gly	Arg	Lys	Tyr	Phe	Thr	Cys
	50					55					60				

Asp	Glu	Gly	His	Gly	Ile	Phe	Val	Arg	Gln	Ser	Gln	Ile	Gln	Val	Phe
65					70					75					80

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

Ser	Lys	Val	Leu	Lys	Arg	Glu	Gly	Thr	Asp	Thr	Thr	Ala	Lys	Thr	Ser
			100					105					110		

1020001191 - P17-158 Sequence Listing

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

Ser Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser Ser
130 135 140

Glu Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile Pro
145 150 155 160

Thr Pro Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser Pro
165 170 175

Ser Lys Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu Glu
180 185 190

Lys Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys Leu
195 200 205

Lys Glu Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu Trp
210 215 220

Lys Ser Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu Lys
225 230 235 240

Glu Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg Tyr
245 250 255

Met Glu Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr Leu
260 265 270

Asp Lys Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu Val
275 280 285

Glu Ala Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu Ile
290 295 300

Leu Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser Ser
305 310 315 320

1020001191 - P17-158 Sequence Listing

Tyr Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp Ala
325 330 335

Leu Val Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His Val
340 345 350

Lys Leu Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val Val
355 360 365

Arg Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu Ser
370 375 380

Thr Ile Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala Glu
385 390 395 400

Glu Met Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu Lys
405 410 415

Val Arg Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn Glu
420 425 430

Met Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu Leu
435 440 445

Arg Glu Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln Lys
450 455 460

Arg Val Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr Ile
465 470 475 480

Lys Lys Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg Glu
485 490 495

Leu Thr Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro Pro
500 505 510

Pro Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala His
515 520 525

1020001191 - P17-158 Sequence Listing

Ala Lys Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln Ala
530 535 540

Asn Arg His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe Leu
545 550 555 560

Arg Pro Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met Pro
565 570 575

Arg Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu Lys
580 585 590

Phe Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro Gly Leu Arg Gly Ala
595 600 605

Ala Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu Ser
610 615 620

Leu Leu Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln Cys
625 630 635 640

Ser Val Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met Ser
645 650 655

Ala His Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys Asp
660 665 670

Gln Leu Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile Lys
675 680 685

Tyr Tyr Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu Asp
690 695 700

Cys Thr Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala Leu
705 710 715 720

Asp Cys Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln Gly
725 730 735

1020001191 - P17-158 Sequence Listing

Gly Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu Thr
740 745 750

Ser Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg Met
755 760 765

Pro Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly Pro
770 775 780

Gln Val Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp Val
785 790 795 800

Val Ala Val Leu Gln Glu Val Ala Ala Ala Ala Gln Leu Ile Ala
805 810 815

Pro Leu Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu Leu
820 825 830

Ala Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser Pro
835 840 845

Tyr Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met Asn
850 855 860

Lys Leu Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg Pro
865 870 875 880

Pro Ser Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg Ala
885 890 895

Glu Ile Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg Glu
900 905 910

Thr Val Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu Glu
915 920 925

Leu Ser Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu Asp
930 935 940

1020001191 - P17-158 Sequence Listing

Ser Ala Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr Arg
945 950 955 960

Leu Glu Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe Glu
965 970 975

Glu Thr Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala Glu
980 985 990

Lys Ala Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg Thr Ile
995 1000 1005

Glu Gly Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr Leu Val
1010 1015 1020

Ser Gly Ile Ala Gly Gly Ala Ile Pro Gly Gln Ala Pro Gly Ser
1025 1030 1035

Val Pro Gly Pro Gly Leu Val Lys Asp Ser Pro Leu Leu Leu Gln
1040 1045 1050

Gln Ile Ser Ala Met Arg Leu His Ile Ser Gln Leu Gln His Glu
1055 1060 1065

Asn Ser Ile Leu Lys Gly Ala Gln Met Lys Ala Ser Leu Ala Ser
1070 1075 1080

Leu Pro Pro Leu His Val Ala Lys Leu Ser His Glu Gly Pro Gly
1085 1090 1095

Ser Glu Leu Pro Ala Gly Ala Leu Tyr Arg Lys Thr Ser Gln Leu
1100 1105 1110

Leu Glu Thr Leu Asn Gln Leu Ser Thr His Thr His Val Val Asp
1115 1120 1125

Ile Thr Arg Thr Ser Pro Ala Ala Lys Ser Pro Ser Ala Gln Leu
1130 1135 1140

1020001191 - P17-158 Sequence Listing

Met	Glu	Gln	Val	Ala	Gln	Leu	Lys	Ser	Leu	Ser	Asp	Thr	Val	Glu	1145	1150	1155
Lys	Leu	Lys	Asp	Glu	Val	Leu	Lys	Glu	Thr	Val	Ser	Gln	Arg	Pro	1160	1165	1170
Gly	Ala	Thr	Val	Pro	Thr	Asp	Phe	Ala	Thr	Phe	Pro	Ser	Ser	Ala	1175	1180	1185
Phe	Leu	Arg	Glu	Asp	Pro	Lys	Trp	Glu	Phe	Pro	Arg	Lys	Asn	Leu	1190	1195	1200
Val	Leu	Gly	Lys	Thr	Leu	Gly	Glu	Gly	Glu	Phe	Gly	Lys	Val	Val	1205	1210	1215
Lys	Ala	Thr	Ala	Phe	His	Leu	Lys	Gly	Arg	Ala	Gly	Tyr	Thr	Thr	1220	1225	1230
Val	Ala	Val	Lys	Met	Leu	Lys	Glu	Asn	Ala	Ser	Pro	Ser	Glu	Leu	1235	1240	1245
Arg	Asp	Leu	Leu	Ser	Glu	Phe	Asn	Val	Leu	Lys	Gln	Val	Asn	His	1250	1255	1260
Pro	His	Val	Ile	Lys	Leu	Tyr	Gly	Ala	Cys	Ser	Gln	Asp	Gly	Pro	1265	1270	1275
Leu	Leu	Leu	Ile	Val	Glu	Tyr	Ala	Lys	Tyr	Gly	Ser	Leu	Arg	Gly	1280	1285	1290
Phe	Leu	Arg	Glu	Ser	Arg	Lys	Val	Gly	Pro	Gly	Tyr	Leu	Gly	Ser	1295	1300	1305
Gly	Gly	Ser	Arg	Asn	Ser	Ser	Ser	Leu	Asp	His	Pro	Asp	Glu	Arg	1310	1315	1320
Ala	Leu	Thr	Met	Gly	Asp	Leu	Ile	Ser	Phe	Ala	Trp	Gln	Ile	Ser	1325	1330	1335

1020001191 - P17-158 Sequence Listing

Gln Gly	Met Gln Tyr	Leu Ala	Glu Met Lys	Leu Val	His Arg Asp
1340		1345		1350	
Leu Ala	Ala Arg Asn Ile	Leu Val	Ala Glu Gly	Arg Lys Met Lys	
1355		1360		1365	
Ile Ser	Asp Phe Gly Leu	Ser Arg Asp Val Tyr	Glu Glu Asp Ser		
1370		1375	1380		
Tyr Val	Lys Arg Ser Gln	Gly Arg Ile Pro Val	Lys Trp Met Ala		
1385		1390	1395		
Ile Glu	Ser Leu Phe Asp	His Ile Tyr Thr Thr	Gln Ser Asp Val		
1400		1405	1410		
Trp Ser	Phe Gly Val Leu	Leu Trp Glu Ile Val	Thr Leu Gly Gly		
1415		1420	1425		
Asn Pro	Tyr Pro Gly Ile	Pro Pro Glu Arg Leu	Phe Asn Leu Leu		
1430		1435	1440		
Lys Thr	Gly His Arg Met	Glu Arg Pro Asp Asn	Cys Ser Glu Glu		
1445		1450	1455		
Met Tyr	Arg Leu Met Leu	Gln Cys Trp Lys Gln	Glu Pro Asp Lys		
1460		1465	1470		
Arg Pro	Val Phe Ala Asp	Ile Ser Lys Asp Leu	Glu Lys Met Met		
1475		1480	1485		
Val Lys	Arg Arg Asp Tyr	Leu Asp Leu Ala Ala	Ser Thr Pro Ser		
1490		1495	1500		
Asp Ser	Leu Ile Tyr Asp	Asp Gly Leu Ser Glu	Glu Glu Thr Pro		
1505		1510	1515		
Leu Val	Asp Cys Asn Asn	Ala Pro Leu Pro Arg	Ala Leu Pro Ser		
1520		1525	1530		

1020001191 - P17-158 Sequence Listing

Thr Trp Ile Glu Asn Lys Leu Tyr Gly Met Ser Asp Pro Asn Trp
1535 1540 1545

Pro Gly Glu Ser Pro Val Pro Leu Thr Arg Ala Asp Gly Thr Asn
1550 1555 1560

Thr Gly Phe Pro Arg Tyr Pro Asn Asp Ser Val Tyr Ala Asn Trp
1565 1570 1575

Met Leu Ser Pro Ser Ala Ala Lys Leu Met Asp Thr Phe Asp Ser
1580 1585 1590

<210> 19
<211> 4656
<212> DNA
<213> Artificial Sequence

<220>
<223> coding sequence of fusion peptide

<400> 19
atgagtgcgg aggcaagcgc ccggcctctg cgggtgggct cccgtgtaga ggtgattgga 60
aaaggccacc gaggcactgt ggcctatgtt ggagccacac tgtttgccac tggcaaatgg 120
gtaggcgtga ttctggatga agcaaagggc aaaaatgatg gaactgttca aggcaggaag 180
tacttcactt gtgatgaagg gcatggcatc tttgtgcgcc agtcccagat ccaggtatatt 240
gaagatggag cagatactac ttccccagag acacctgatt cttctgcttc aaaagtcctc 300
aaaagagagg gaactgatac aactgcaaag actagcaaac tgcccacgcg cccagccagt 360
actgggggtgg ctggggccag tagctccctg ggcccctctg gctcagcgtc agcaggtgag 420
ctgagcagca gtgagcccag caccgccggt cagactccgc tggcagcacc catcatcccc 480
acgccggtcc tcacctctcc tggagcagtc cccccgttc cttccccatc caaggaggag 540
gagggactaa gggctcaggt gcgggacctg gaggagaaac tagagaccct gagactgaaa 600
cgggcagaag acaaagcaaa gctaaaagag ctggagaaac aaaaatcca gctggagcag 660
gtgcaggaat ggaagagcaa aatgcaggag cagcaggccg acctgcagcg gcgcctcaag 720
gaggcgagaa aggaagccaa ggaggcgctg gaggcaaagg aacgctatat ggaggagatg 780

1020001191 - P17-158 Sequence Listing

gctgatactg ctgatgccat tgagatggcc acttttgaca aggagatggc tgaagagcgg	840
gctgagtccc tgcagcagga ggtggaggca ctgaaggagc ggggtggacga gctcactact	900
gacttagaga tcctcaaggc tgagattgaa gagaagggtc cagatggcgc tgcattcagt	960
tatcagctca agcagcttga ggagcagaat gcccgcctga aggatgccct ggtgaggatg	1020
cgggatcttt cttcctcaga gaagcaggag catgtgaagc tccagaagct catggaaaag	1080
aagaaccaag agctggaagt tgtgaggcaa cagcgggagc gtctgcagga ggagctaagc	1140
caggcagaga gcaccattga tgagctcaag gagcagggtg atgctgctct gggtgctgag	1200
gagatgggtg agatgctgac agatcggaac ctgaatctgg aagagaaagt gcgcgagttg	1260
agggagactg tgggagactt ggaagcgatg aatgagatga acgatgagct gcaggagaat	1320
gcacgtgaga cagaactgga gctgcgggag cagctggaca tggcaggcgc gcgggttcgt	1380
gaggcccaga agcgtgtgga ggcagcccag gagacggttg cagactacca gcagaccatc	1440
aagaagtacc gccagctgac cgcccatcta caggatgtga atcggaact gacaaaccag	1500
caggaagcat ctgtggagag gcaacagcag ccacctccag agacctttga cttcaaaatc	1560
aagtttgctg agactaaggc ccatgccaaag gcaattgaga tggaattgag gcagatggag	1620
gtggcccagg ccaatcgaca catgtccctg ctgacagcct tcatgcctga cagcttcctt	1680
cggccagggtg gggaccatga ctgcgttctg gtgctgttgc tcatgcctcg tctcatttgc	1740
aaggcagagc tgatccggaa gcaggcccag gagaagtttg aactaagtga gaactgttca	1800
gagcggcctg ggctgcgagg agctgctggg gagcaactca gctttgctgc tggactggtg	1860
tactcgctga gcctgctgca ggccacgcta caccgctatg agcatgccct ctctcagtgc	1920
agtgtggatg tgtataagaa agtgggcagc ctgtaccctg agatgagtgc ccatgagcgc	1980
tccttggatt tcctcattga actgctgcac aaggatcagc tggatgagac tgtcaatgtg	2040
gagccttca ccaaggccat caagtactat cagcatctgt acagcatcca cttgcccga	2100
cagcctgagg actgtactat gcagctggct gaccacatta agttcacgca gagtgctctg	2160
gactgcatga gtgtggagggt aggacggctg cgtgccttct tgcagggttg gcaggaggct	2220
acagatattg ccctcctgct ccgggatctg gaaacttcat gcagtgacat ccgccagttc	2280
tgcaagaaga tccgaaggcg aatgccaggg acagatgctc ctgggatccc agctgcactg	2340

1020001191 - P17-158 Sequence Listing

gcctttggac cacaggtatc tgacacgctc ctagactgca ggaaacactt gacgtgggtc	2400
gtggctgtgc tgcaggaggt ggacagctgct gctgcccagc tcattgcccc actggcagag	2460
aatgaggggc tacttgtggc tgctctggag gaactggctt tcaaagcaag cgagcagatc	2520
tatgggaccc cctccagcag cccctatgag tgtctgcgcc agtcatgcaa catcctcatc	2580
agtaccatga acaagctggc cacagccatg caggaggggg agtatgatgc agagcggccc	2640
cccagcaagc ctccaccggt tgaactgcgg gctgctgccc ttcgtgcaga gatcacagat	2700
gctgaaggcc tgggtttgaa gctcgaagat cgagagacag ttattaagga gttgaagaag	2760
tcactcaaga ttaagggaga ggagctaagt gaggccaatg tgcggctgag cctcctggag	2820
aagaagttgg acagtgtgc caaggatgca gatgagcgca tcgagaaagt ccagactcgg	2880
ctggaggaga cccaggcact gctgcgaaag aaggagaaag agtttgagga gacaatggat	2940
gcactccagg ctgacatcga ccagctggag gcagagaagg cagaactaaa gcagcgtctg	3000
aacagccagt ccaaacgcac gattgagggc ctccggggcc ctctccttc aggcattgct	3060
actctggtct ctggcattgc tgggtggagcc atccctgggc aggctccagg gtctgtgcca	3120
ggcccagggc tgggtgaagga ctcaccactg ctgcttcagc agatctctgc catgaggctg	3180
cacatctccc agctccagca tgagaacagc atcctcaagg gagcccagat gaaggcatcc	3240
ttggcatccc tgccccctct gcatgttgca aagctatccc atgaggggccc tggcagttag	3300
ttaccagctg gagcgctgta tcgtaagacc agccagctgc tggagacatt gaatcaattg	3360
agcacacaca cgcacgtagt agacatcact cgcaccagcc ctgctgccaa gagcccgtcg	3420
gcccactta tggagcaagt ggctcagctt aagtccctga gtgacaccgt cgagaagctc	3480
aaggatgagg tcctcaagga gacagtatct cagcgccctg gagccacagt acccactgac	3540
tttgccacct tcccttcac agccttcctc agggaggatc caaagtggga attcctcgg	3600
aagaacttgg ttcttgaaa aactctagga gaaggcgaat ttggaaaagt ggtcaaggca	3660
acggccttcc atctgaaagg cagagcaggg tacaccacgg tggccgtgaa gatgctgaaa	3720
gagaacgcct ccccgagtga gcttcgagac ctgctgtcag agttcaacgt cctgaagcag	3780
gtcaaccacc cacatgtcat caaattgtat ggggcctgca gccaggatgg cccgctcctc	3840
ctcatcgtgg agtacgcaa atacggctcc ctgcggggct tcctccgca gagccgcaaa	3900

1020001191 - P17-158 Sequence Listing

gtggggcctg gctacctggg cagtggaggc agccgcaact ccagctccct ggaccacccg 3960
 gatgagcggg ccctcaccat gggcgacctc atctcatttg cctggcagat ctcacagggg 4020
 atgcagtatc tggccgagat gaagctcgtt catcgggact tggcagccag aaacatcctg 4080
 gtagctgagg ggcggaagat gaagatttcg gatttcggct tgtcccgaga tgtttatgaa 4140
 gaggattcct acgtgaagag gagccagggt cggattccag ttaaattgat ggcaattgaa 4200
 tccctttttg atcatatcta caccacgcaa agtgatgtat ggtcttttgg tgtcctgctg 4260
 tgggagatcg tgaccctagg gggaaacccc tctcctggga ttcctcctga gcggctcttc 4320
 aaccttctga agaccggcca ccggatggag aggccagaca actgcagcga ggagatgtac 4380
 cgctgatgc tgcaatgctg gaagcaggag ccggacaaaa ggccggtgtt tgcggacatc 4440
 agcaaagacc tggagaagat gatggttaag aggagagact acttgacact tgcggcgtcc 4500
 actccatctg actccctgat ttatgacgac ggcctctcag aggaggagac accgctggtg 4560
 gactgtaata atgccccct ccctcgagcc ctcccttcca catggattga aaacaaactc 4620
 tatggtagaa tttcccatgc atttactaga ttctag 4656

<210> 20
 <211> 1551
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion peptide

<400> 20

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

Glu Val Ile Gly Lys Gly His Arg Gly Thr Val Ala Tyr Val Gly Ala
 20 25 30

Thr Leu Phe Ala Thr Gly Lys Trp Val Gly Val Ile Leu Asp Glu Ala
 35 40 45

Lys Gly Lys Asn Asp Gly Thr Val Gln Gly Arg Lys Tyr Phe Thr Cys
 50 55 60

1020001191 - P17-158 Sequence Listing

Asp Glu Gly His Gly Ile Phe Val Arg Gln Ser Gln Ile Gln Val Phe
65 70 75 80

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

Ser Lys Val Leu Lys Arg Glu Gly Thr Asp Thr Thr Ala Lys Thr Ser
100 105 110

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

Ser Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser Ser
130 135 140

Glu Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile Pro
145 150 155 160

Thr Pro Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser Pro
165 170 175

Ser Lys Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu Glu
180 185 190

Lys Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys Leu
195 200 205

Lys Glu Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu Trp
210 215 220

Lys Ser Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu Lys
225 230 235 240

Glu Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg Tyr
245 250 255

Met Glu Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr Leu
260 265 270

1020001191 - P17-158 Sequence Listing

Asp Lys Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu Val
275 280 285

Glu Ala Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu Ile
290 295 300

Leu Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser Ser
305 310 315 320

Tyr Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp Ala
325 330 335

Leu Val Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His Val
340 345 350

Lys Leu Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val Val
355 360 365

Arg Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu Ser
370 375 380

Thr Ile Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala Glu
385 390 395 400

Glu Met Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu Lys
405 410 415

Val Arg Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn Glu
420 425 430

Met Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu Leu
435 440 445

Arg Glu Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln Lys
450 455 460

Arg Val Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr Ile
465 470 475 480

1020001191 - P17-158 Sequence Listing

Lys Lys Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg Glu
485 490 495

Leu Thr Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro Pro
500 505 510

Pro Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala His
515 520 525

Ala Lys Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln Ala
530 535 540

Asn Arg His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe Leu
545 550 555 560

Arg Pro Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met Pro
565 570 575

Arg Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu Lys
580 585 590

Phe Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro Gly Leu Arg Gly Ala
595 600 605

Ala Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu Ser
610 615 620

Leu Leu Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln Cys
625 630 635 640

Ser Val Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met Ser
645 650 655

Ala His Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys Asp
660 665 670

Gln Leu Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile Lys
675 680 685

1020001191 - P17-158 Sequence Listing

Tyr Tyr Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu Asp
690 695 700

Cys Thr Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala Leu
705 710 715 720

Asp Cys Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln Gly
725 730 735

Gly Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu Thr
740 745 750

Ser Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg Met
755 760 765

Pro Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly Pro
770 775 780

Gln Val Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp Val
785 790 795 800

Val Ala Val Leu Gln Glu Val Ala Ala Ala Ala Ala Gln Leu Ile Ala
805 810 815

Pro Leu Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu Leu
820 825 830

Ala Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser Pro
835 840 845

Tyr Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met Asn
850 855 860

Lys Leu Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg Pro
865 870 875 880

Pro Ser Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg Ala
885 890 895

1020001191 - P17-158 Sequence Listing

Glu Ile Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg Glu
900 905 910

Thr Val Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu Glu
915 920 925

Leu Ser Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu Asp
930 935 940

Ser Ala Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr Arg
945 950 955 960

Leu Glu Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe Glu
965 970 975

Glu Thr Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala Glu
980 985 990

Lys Ala Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg Thr Ile
995 1000 1005

Glu Gly Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr Leu Val
1010 1015 1020

Ser Gly Ile Ala Gly Gly Ala Ile Pro Gly Gln Ala Pro Gly Ser
1025 1030 1035

Val Pro Gly Pro Gly Leu Val Lys Asp Ser Pro Leu Leu Leu Gln
1040 1045 1050

Gln Ile Ser Ala Met Arg Leu His Ile Ser Gln Leu Gln His Glu
1055 1060 1065

Asn Ser Ile Leu Lys Gly Ala Gln Met Lys Ala Ser Leu Ala Ser
1070 1075 1080

Leu Pro Pro Leu His Val Ala Lys Leu Ser His Glu Gly Pro Gly
1085 1090 1095

1020001191 - P17-158 Sequence Listing

Ser	Glu	Leu	Pro	Ala	Gly	Ala	Leu	Tyr	Arg	Lys	Thr	Ser	Gln	Leu
1100						1105					1110			
Leu	Glu	Thr	Leu	Asn	Gln	Leu	Ser	Thr	His	Thr	His	Val	Val	Asp
1115						1120					1125			
Ile	Thr	Arg	Thr	Ser	Pro	Ala	Ala	Lys	Ser	Pro	Ser	Ala	Gln	Leu
1130						1135					1140			
Met	Glu	Gln	Val	Ala	Gln	Leu	Lys	Ser	Leu	Ser	Asp	Thr	Val	Glu
1145						1150					1155			
Lys	Leu	Lys	Asp	Glu	Val	Leu	Lys	Glu	Thr	Val	Ser	Gln	Arg	Pro
1160						1165					1170			
Gly	Ala	Thr	Val	Pro	Thr	Asp	Phe	Ala	Thr	Phe	Pro	Ser	Ser	Ala
1175						1180					1185			
Phe	Leu	Arg	Glu	Asp	Pro	Lys	Trp	Glu	Phe	Pro	Arg	Lys	Asn	Leu
1190						1195					1200			
Val	Leu	Gly	Lys	Thr	Leu	Gly	Glu	Gly	Glu	Phe	Gly	Lys	Val	Val
1205						1210					1215			
Lys	Ala	Thr	Ala	Phe	His	Leu	Lys	Gly	Arg	Ala	Gly	Tyr	Thr	Thr
1220						1225					1230			
Val	Ala	Val	Lys	Met	Leu	Lys	Glu	Asn	Ala	Ser	Pro	Ser	Glu	Leu
1235						1240					1245			
Arg	Asp	Leu	Leu	Ser	Glu	Phe	Asn	Val	Leu	Lys	Gln	Val	Asn	His
1250						1255					1260			
Pro	His	Val	Ile	Lys	Leu	Tyr	Gly	Ala	Cys	Ser	Gln	Asp	Gly	Pro
1265						1270					1275			
Leu	Leu	Leu	Ile	Val	Glu	Tyr	Ala	Lys	Tyr	Gly	Ser	Leu	Arg	Gly
1280						1285					1290			

1020001191 - P17-158 Sequence Listing

Phe	Leu	Arg	Glu	Ser	Arg	Lys	Val	Gly	Pro	Gly	Tyr	Leu	Gly	Ser
1295						1300					1305			
Gly	Gly	Ser	Arg	Asn	Ser	Ser	Ser	Leu	Asp	His	Pro	Asp	Glu	Arg
1310						1315					1320			
Ala	Leu	Thr	Met	Gly	Asp	Leu	Ile	Ser	Phe	Ala	Trp	Gln	Ile	Ser
1325						1330					1335			
Gln	Gly	Met	Gln	Tyr	Leu	Ala	Glu	Met	Lys	Leu	Val	His	Arg	Asp
1340						1345					1350			
Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Ala	Glu	Gly	Arg	Lys	Met	Lys
1355						1360					1365			
Ile	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Asp	Val	Tyr	Glu	Glu	Asp	Ser
1370						1375					1380			
Tyr	Val	Lys	Arg	Ser	Gln	Gly	Arg	Ile	Pro	Val	Lys	Trp	Met	Ala
1385						1390					1395			
Ile	Glu	Ser	Leu	Phe	Asp	His	Ile	Tyr	Thr	Thr	Gln	Ser	Asp	Val
1400						1405					1410			
Trp	Ser	Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile	Val	Thr	Leu	Gly	Gly
1415						1420					1425			
Asn	Pro	Tyr	Pro	Gly	Ile	Pro	Pro	Glu	Arg	Leu	Phe	Asn	Leu	Leu
1430						1435					1440			
Lys	Thr	Gly	His	Arg	Met	Glu	Arg	Pro	Asp	Asn	Cys	Ser	Glu	Glu
1445						1450					1455			
Met	Tyr	Arg	Leu	Met	Leu	Gln	Cys	Trp	Lys	Gln	Glu	Pro	Asp	Lys
1460						1465					1470			
Arg	Pro	Val	Phe	Ala	Asp	Ile	Ser	Lys	Asp	Leu	Glu	Lys	Met	Met
1475						1480					1485			

1020001191 - P17-158 Sequence Listing

Val Lys Arg Arg Asp Tyr Leu Asp Leu Ala Ala Ser Thr Pro Ser
1490 1495 1500

Asp Ser Leu Ile Tyr Asp Asp Gly Leu Ser Glu Glu Glu Thr Pro
1505 1510 1515

Leu Val Asp Cys Asn Asn Ala Pro Leu Pro Arg Ala Leu Pro Ser
1520 1525 1530

Thr Trp Ile Glu Asn Lys Leu Tyr Gly Arg Ile Ser His Ala Phe
1535 1540 1545

Thr Arg Phe
1550

<210> 21
<211> 4887
<212> DNA
<213> Artificial Sequence

<220>
<223> coding sequence of fusion peptide

<400> 21
atggcacaga gcaagaggca cgtgtacagc cggacgccca gcggcagcag gatgagtgcg 60
gaggcaagcg cccggcctct gcgggtgggc tcccgtgtag aggtgattgg aaaaggccac 120
cgaggcactg tggcctatgt tggagccaca ctgtttgcc a ctggcaa atg ggtaggcgtg 180
attctggatg aagcaaagg caaaaatgat ggaactgttc aaggcaggaa gtacttcact 240
tgtgatgaag ggcatggcat ctttgtg cgc cagtcccaga tccaggtatt tgaagatgga 300
gcagatacta cttccccaga gacacctgat tcttctgctt caaaagtcct caaaagagag 360
ggaactgata caactgcaaa gactagcaaa ctggcaccga cagcccga aa gaccacaact 420
cggcgaccca agcccacgcg ccagccagt actgggggtgg ctggggccag tagctccctg 480
ggcccctctg gctcagcgtc agcaggtgag ctgagcagca gtgagcccag caccgccgct 540
cagactccgc tggcagcacc catcatcccc acgccggtcc tcacctctcc tggagcagtc 600
ccccgccttc cttccccatc caaggaggag gagggactaa gggctcaggt gcgggacctg 660

1020001191 - P17-158 Sequence Listing

gaggagaaac tagagaccct gagactgaaa cgggcagaag acaaagcaaa gctaaaagag	720
ctggagaaac acaaaatcca gctggagcag gtgcaggaat ggaagagcaa aatgcaggag	780
cagcaggccg acctgcagcg gcgcctcaag gaggcagaaa aggaagccaa ggaggcgctg	840
gaggcaaagg aacgctatat ggaggagatg gctgatactg ctgatgccat tgagatggcc	900
actttggaca aggagatggc tgaagagcgg gctgagtccc tgcagcagga ggtggaggca	960
ctgaaggagc ggggtggacga gctcactact gacttagaga tcctcaaggc tgagattgaa	1020
gagaagggtc cagatggcgc tgcattccagt tatcagctca agcagcttga ggagcagaat	1080
gccccctga aggatgccct ggtgaggatg cgggatcttt cttcctcaga gaagcaggag	1140
catgtgaagc tccagaagct catggaaaag aagaaccaag agctggaagt tgtgaggcaa	1200
cagcgggagc gtctgcagga ggagctaagc caggcagaga gcaccattga tgagctcaag	1260
gagcagggtg atgctgctct ggggtgctgag gagatgggtg agatgctgac agatcggaac	1320
ctgaatctgg aagagaaaagt gcgcgagttg agggagactg tgggagactt ggaagcagtg	1380
aatgagatga acgatgagct gcaggagaat gcacgtgaga cagaactgga gctgcgggag	1440
cagctggaca tggcaggcgc gcgggttcgt gagggccaga agcgtgtgga ggcagcccag	1500
gagacggttg cagactacca gcagaccatc aagaagtacc gccagctgac cgcccatcta	1560
caggatgtga atcgggaact gacaaaccag caggaagcat ctgtggagag gcaacagcag	1620
ccacctccag agacctttga cttcaaaatc aagtttgctg agactaaggc ccatgccaa	1680
gcaattgaga tggaattgag gcagatggag gtggcccagg ccaatcgaca catgtccctg	1740
ctgacagcct tcatgcctga cagcttcctt cggccaggtg gggaccatga ctgcgttctg	1800
gtgctgttgc tcatgcctcg tctcatttgc aaggcagagc tgatccggaa gcaggcccag	1860
gagaagtttg aactaagtga gaactgttca gagcggcctg ggctgcgagg agctgctggg	1920
gagcaactca gctttgctgc tggactggtg tactcgctga gcctgctgca ggccacgcta	1980
caccgctatg agcatgccct ctctcagtgc agtgtggatg tgtataagaa agtgggcagc	2040
ctgtaccctg agatgagtgc ccatgagcgc tccttggttgc tcctcattga actgctgcac	2100
aaggatcagc tggatgagac tgtcaatgtg gagcctctca ccaaggccat caagtactat	2160
cagcatctgt acagcatcca ccttgccgaa cagcctgagg actgtactat gcagctggct	2220

1020001191 - P17-158 Sequence Listing

gaccacatta agttcacgca gagtgtctctg gactgcatga gtgtggaggt aggacggctg	2280
cgtgccttct tgcagggtgg gcaggaggct acagatatctg ccctcctgct ccgggatctg	2340
gaaacttcat gcagtgacat ccgccagttc tgcaagaaga tccgaaggcg aatgccaggg	2400
acagatgctc ctgggatccc agctgcactg gcctttggac cacaggtatc tgacacgctc	2460
ctagactgca ggaaacactt gacgtgggtc gtggctgtgc tgcaggaggt ggcagctgct	2520
gctgcccagc tcattgcccc actggcagag aatgaggggc tacttgtggc tgctctggag	2580
gaactggctt tcaaagcaag cgagcagatc tatgggaccc cctccagcag cccctatgag	2640
tgtctgcgcc agtcatgcaa catcctcatc agtaccatga acaagctggc cacagccatg	2700
caggaggggg agtatgatgc agagcggccc cccagcaagc ctccaccggt tgaactgcgg	2760
gctgctgccc ttcgtgcaga gatcacagat gctgaaggcc tgggtttgaa gctcgaagat	2820
cgagagacag ttattaagga gttgaagaag tcaactaaga ttaagggaga ggagctaagt	2880
gaggccaatg tgcggctgag cctcctggag aagaagttgg acagtgtctc caaggatgca	2940
gatgagcgca tcgagaaagt ccagactcgg ctggaggaga cccaggcact gctgcgaaag	3000
aaggagaaag agtttgagga gacaatggat gcactccagg ctgacatcga ccagctggag	3060
gcagagaagg cagaactaaa gcagcgtctg aacagccagt ccaaacgcac gattgagggga	3120
ctccggggcc ctctccttc aggcattgct actctggtct ctggcattgc tgggtgaagaa	3180
cagcagcgag gagccatccc tgggcaggct ccagggtctg tgccaggccc agggctggtg	3240
aaggactcac cactgctgct tcagcagatc tctgcatga ggctgcacat ctcccagctc	3300
cagcatgaga acagcatcct caaggagacc cagatgaagg catccttggc atccctgccc	3360
cctctgcatg ttgcaaagct atcccatgag ggccctggca gtgagttacc agctggagcg	3420
ctgtatcgta agaccagcca gctgctggag acattgaatc aattgagcac acacacgcac	3480
gtagtagaca tcaactgcac cagccctgct gccaaagacc cgtcggccca acttatggag	3540
caagtggctc agcttaagtc cctgagtgc accgtcgaga agctcaagga tgaggtcctc	3600
aaggagacag tatctcagcg ccctggagcc acagtaccca ctgactttgc caccttcctt	3660
tcatcagcct tcctcagggg ggatccaaag tgggaattcc ctcggaagaa cttggttctt	3720
ggaaaaactc taggagaagg cgaatttgga aaagtgttca aggcaacggc cttccatctg	3780

1020001191 - P17-158 Sequence Listing

aaaggcagag cagggtacac cacggtggcc gtgaagatgc tgaaagagaa cgcctccccg	3840
agtgagcttc gagacctgct gtcagagttc aacgtcctga agcaggtcaa ccacccacat	3900
gtcatcaaat tgtatggggc ctgcagccag gatggcccgc tcctcctcat cgtggagtac	3960
gccaaatacg gctccctgcg gggcttcctc cgcgagagcc gcaaagtggg gcctggctac	4020
ctgggcagtg gaggcagccg caactccagc tccctggacc acccggatga gcgggcccctc	4080
accatgggcg acctcatctc atttgcctgg cagatctcac aggggatgca gtatctggcc	4140
gagatgaagc tcgttcatcg ggacttggca gccagaaaca tcctggtagc tgaggggcgg	4200
aagatgaaga tttcggattt cggcttgtcc cgagatgttt atgaagagga ttcctacgtg	4260
aagaggagcc agggtcggat tccagttaaa tggatggcaa ttgaatccct ttttgatcat	4320
atctacacca cgcaaagtga tgtatggtct tttggtgtcc tgctgtggga gatcgtgacc	4380
ctagggggaa acccctatcc tgggattcct cctgagcggc tcttcaacct tctgaagacc	4440
ggccaccgga tggagaggcc agacaactgc agcaggagga tgtaccgcct gatgctgcaa	4500
tgctggaagc aggagccgga caaaaggccg gtgtttgcgg acatcagcaa agacctggag	4560
aagatgatgg ttaagaggag agactacttg gaccttgcgg cgtccactcc atctgactcc	4620
ctgatttatg acgacggcct ctcagaggag gagacaccgc tgggtggactg taataatgcc	4680
ccccccctc gagccctccc ttccacatgg attgaaaaca aactctatgg catgtcagac	4740
ccgaactggc ctggagagag tcctgtacca ctcacgagag ctgatggcac taacactggg	4800
tttccaagat atccaaatga tagtgtatat gctaactgga tgctttcacc ctcagcggca	4860
aaattaatgg acacgtttga tagttaa	4887

<210> 22
 <211> 1628
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion peptide

<400> 22

Met	Ala	Gln	Ser	Lys	Arg	His	Val	Tyr	Ser	Arg	Thr	Pro	Ser	Gly	Ser
1				5				10						15	

1020001191 - P17-158 Sequence Listing

Arg Met Ser Ala Glu Ala Ser Ala Arg Pro Leu Arg Val Gly Ser Arg
20 25 30

Val Glu Val Ile Gly Lys Gly His Arg Gly Thr Val Ala Tyr Val Gly
35 40 45

Ala Thr Leu Phe Ala Thr Gly Lys Trp Val Gly Val Ile Leu Asp Glu
50 55 60

Ala Lys Gly Lys Asn Asp Gly Thr Val Gln Gly Arg Lys Tyr Phe Thr
65 70 75 80

Cys Asp Glu Gly His Gly Ile Phe Val Arg Gln Ser Gln Ile Gln Val
85 90 95

Phe Glu Asp Gly Ala Asp Thr Thr Ser Pro Glu Thr Pro Asp Ser Ser
100 105 110

Ala Ser Lys Val Leu Lys Arg Glu Gly Thr Asp Thr Thr Ala Lys Thr
115 120 125

Ser Lys Leu Ala Pro Thr Ala Arg Lys Thr Thr Thr Arg Arg Pro Lys
130 135 140

Pro Thr Arg Pro Ala Ser Thr Gly Val Ala Gly Ala Ser Ser Ser Leu
145 150 155 160

Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser Ser Glu Pro
165 170 175

Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile Pro Thr Pro
180 185 190

Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser Pro Ser Lys
195 200 205

Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu Glu Lys Leu
210 215 220

1020001191 - P17-158 Sequence Listing

Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys Leu Lys Glu
225 230 235 240

Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu Trp Lys Ser
245 250 255

Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu Lys Glu Ala
260 265 270

Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg Tyr Met Glu
275 280 285

Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr Leu Asp Lys
290 295 300

Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu Val Glu Ala
305 310 315 320

Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu Ile Leu Lys
325 330 335

Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser Ser Tyr Gln
340 345 350

Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp Ala Leu Val
355 360 365

Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His Val Lys Leu
370 375 380

Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val Val Arg Gln
385 390 395 400

Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu Ser Thr Ile
405 410 415

Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala Glu Glu Met
420 425 430

1020001191 - P17-158 Sequence Listing

Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu Lys Val Arg
 435 440 445

Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn Glu Met Asn
 450 455 460

Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu Leu Arg Glu
 465 470 475 480

Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln Lys Arg Val
 485 490 495

Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr Ile Lys Lys
 500 505 510

Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg Glu Leu Thr
 515 520 525

Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro Pro Pro Glu
 530 535 540

Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala His Ala Lys
 545 550 555 560

Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln Ala Asn Arg
 565 570 575

His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe Leu Arg Pro
 580 585 590

Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met Pro Arg Leu
 595 600 605

Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu Lys Phe Glu
 610 615 620

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

1020001191 - P17-158 Sequence Listing

Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu Ser Leu Leu
645 650 655

Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln Cys Ser Val
660 665 670

Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met Ser Ala His
675 680 685

Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys Asp Gln Leu
690 695 700

Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile Lys Tyr Tyr
705 710 715 720

Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu Asp Cys Thr
725 730 735

Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala Leu Asp Cys
740 745 750

Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln Gly Gly Gln
755 760 765

Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu Thr Ser Cys
770 775 780

Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg Met Pro Gly
785 790 795 800

Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly Pro Gln Val
805 810 815

Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp Val Val Ala
820 825 830

Val Leu Gln Glu Val Ala Ala Ala Ala Ala Gln Leu Ile Ala Pro Leu
835 840 845

1020001191 - P17-158 Sequence Listing

Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu Leu Ala Phe
850 855 860

Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser Pro Tyr Glu
865 870 875 880

Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met Asn Lys Leu
885 890 895

Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg Pro Pro Ser
900 905 910

Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg Ala Glu Ile
915 920 925

Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg Glu Thr Val
930 935 940

Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu Glu Leu Ser
945 950 955 960

Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu Asp Ser Ala
965 970 975

Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr Arg Leu Glu
980 985 990

Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe Glu Glu Thr
995 1000 1005

Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala Glu Lys
1010 1015 1020

Ala Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg Thr Ile
1025 1030 1035

Glu Gly Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr Leu Val
1040 1045 1050

1020001191 - P17-158 Sequence Listing

Ser	Gly	Ile	Ala	Gly	Glu	Glu	Gln	Gln	Arg	Gly	Ala	Ile	Pro	Gly	
1055						1060					1065				
Gln	Ala	Pro	Gly	Ser	Val	Pro	Gly	Pro	Gly	Leu	Val	Lys	Asp	Ser	
1070						1075					1080				
Pro	Leu	Leu	Leu	Gln	Gln	Ile	Ser	Ala	Met	Arg	Leu	His	Ile	Ser	
1085						1090					1095				
Gln	Leu	Gln	His	Glu	Asn	Ser	Ile	Leu	Lys	Gly	Ala	Gln	Met	Lys	
1100						1105					1110				
Ala	Ser	Leu	Ala	Ser	Leu	Pro	Pro	Leu	His	Val	Ala	Lys	Leu	Ser	
1115						1120					1125				
His	Glu	Gly	Pro	Gly	Ser	Glu	Leu	Pro	Ala	Gly	Ala	Leu	Tyr	Arg	
1130						1135					1140				
Lys	Thr	Ser	Gln	Leu	Leu	Glu	Thr	Leu	Asn	Gln	Leu	Ser	Thr	His	
1145						1150					1155				
Thr	His	Val	Val	Asp	Ile	Thr	Arg	Thr	Ser	Pro	Ala	Ala	Lys	Ser	
1160						1165					1170				
Pro	Ser	Ala	Gln	Leu	Met	Glu	Gln	Val	Ala	Gln	Leu	Lys	Ser	Leu	
1175						1180					1185				
Ser	Asp	Thr	Val	Glu	Lys	Leu	Lys	Asp	Glu	Val	Leu	Lys	Glu	Thr	
1190						1195					1200				
Val	Ser	Gln	Arg	Pro	Gly	Ala	Thr	Val	Pro	Thr	Asp	Phe	Ala	Thr	
1205						1210					1215				
Phe	Pro	Ser	Ser	Ala	Phe	Leu	Arg	Glu	Asp	Pro	Lys	Trp	Glu	Phe	
1220						1225					1230				
Pro	Arg	Lys	Asn	Leu	Val	Leu	Gly	Lys	Thr	Leu	Gly	Glu	Gly	Glu	
1235						1240					1245				

1020001191 - P17-158 Sequence Listing

Phe	Gly	Lys	Val	Val	Lys	Ala	Thr	Ala	Phe	His	Leu	Lys	Gly	Arg
1250						1255					1260			
Ala	Gly	Tyr	Thr	Thr	Val	Ala	Val	Lys	Met	Leu	Lys	Glu	Asn	Ala
1265						1270					1275			
Ser	Pro	Ser	Glu	Leu	Arg	Asp	Leu	Leu	Ser	Glu	Phe	Asn	Val	Leu
1280						1285					1290			
Lys	Gln	Val	Asn	His	Pro	His	Val	Ile	Lys	Leu	Tyr	Gly	Ala	Cys
1295						1300					1305			
Ser	Gln	Asp	Gly	Pro	Leu	Leu	Leu	Ile	Val	Glu	Tyr	Ala	Lys	Tyr
1310						1315					1320			
Gly	Ser	Leu	Arg	Gly	Phe	Leu	Arg	Glu	Ser	Arg	Lys	Val	Gly	Pro
1325						1330					1335			
Gly	Tyr	Leu	Gly	Ser	Gly	Gly	Ser	Arg	Asn	Ser	Ser	Ser	Leu	Asp
1340						1345					1350			
His	Pro	Asp	Glu	Arg	Ala	Leu	Thr	Met	Gly	Asp	Leu	Ile	Ser	Phe
1355						1360					1365			
Ala	Trp	Gln	Ile	Ser	Gln	Gly	Met	Gln	Tyr	Leu	Ala	Glu	Met	Lys
1370						1375					1380			
Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Ala	Glu
1385						1390					1395			
Gly	Arg	Lys	Met	Lys	Ile	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Asp	Val
1400						1405					1410			
Tyr	Glu	Glu	Asp	Ser	Tyr	Val	Lys	Arg	Ser	Gln	Gly	Arg	Ile	Pro
1415						1420					1425			
Val	Lys	Trp	Met	Ala	Ile	Glu	Ser	Leu	Phe	Asp	His	Ile	Tyr	Thr
1430						1435					1440			

1020001191 - P17-158 Sequence Listing

Thr	Gln	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile
1445						1450					1455			
Val	Thr	Leu	Gly	Gly	Asn	Pro	Tyr	Pro	Gly	Ile	Pro	Pro	Glu	Arg
1460						1465					1470			
Leu	Phe	Asn	Leu	Leu	Lys	Thr	Gly	His	Arg	Met	Glu	Arg	Pro	Asp
1475						1480					1485			
Asn	Cys	Ser	Glu	Glu	Met	Tyr	Arg	Leu	Met	Leu	Gln	Cys	Trp	Lys
1490						1495					1500			
Gln	Glu	Pro	Asp	Lys	Arg	Pro	Val	Phe	Ala	Asp	Ile	Ser	Lys	Asp
1505						1510					1515			
Leu	Glu	Lys	Met	Met	Val	Lys	Arg	Arg	Asp	Tyr	Leu	Asp	Leu	Ala
1520						1525					1530			
Ala	Ser	Thr	Pro	Ser	Asp	Ser	Leu	Ile	Tyr	Asp	Asp	Gly	Leu	Ser
1535						1540					1545			
Glu	Glu	Glu	Thr	Pro	Leu	Val	Asp	Cys	Asn	Asn	Ala	Pro	Leu	Pro
1550						1555					1560			
Arg	Ala	Leu	Pro	Ser	Thr	Trp	Ile	Glu	Asn	Lys	Leu	Tyr	Gly	Met
1565						1570					1575			
Ser	Asp	Pro	Asn	Trp	Pro	Gly	Glu	Ser	Pro	Val	Pro	Leu	Thr	Arg
1580						1585					1590			
Ala	Asp	Gly	Thr	Asn	Thr	Gly	Phe	Pro	Arg	Tyr	Pro	Asn	Asp	Ser
1595						1600					1605			
Val	Tyr	Ala	Asn	Trp	Met	Leu	Ser	Pro	Ser	Ala	Ala	Lys	Leu	Met
1610						1615					1620			
Asp	Thr	Phe	Asp	Ser										
1625														

1020001191 - P17-158 Sequence Listing

<210> 23
 <211> 4761
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coding sequence of fusion peptide

<400> 23
 atggcacaga gcaagaggca cgtgtacagc cggacgcccc gcggcagcag gatgagtgcg 60
 gaggcaagcg cccggcctct gcgggtgggc tcccgtgtag aggtgattgg aaaaggccac 120
 cgaggcactg tggcctatgt tggagccaca ctgtttgcc a ctggcaa atg ggtaggcgtg 180
 attctggatg aagcaaaggg caaaaatgat ggaactgttc aaggcaggaa gtacttcact 240
 tgtgatgaag ggcatggcat ctttgtg cgc cagtcccaga tccaggtatt tgaagatgga 300
 gcagatacta cttccccaga gacacctgat tcttctgctt caaaagtcct caaaagagag 360
 ggaactgata caactgcaaa gactagcaaa ctggcaccga cagcccga aa gaccacaact 420
 cggcgaccca agcccacgcg ccagccagt actgggggtgg ctggggccag tagctccctg 480
 ggccccctctg gctcagcgtc agcaggtgag ctgagcagca gtgagcccag cccccggct 540
 cagactccgc tggcagcacc catcatcccc acgccggtcc tcacctctcc tggagcagtc 600
 cccccgcttc cttccccatc caaggaggag gagggactaa gggctcaggt gcgggacctg 660
 gaggagaaac tagagaccct gagactgaaa cgggcagaag acaaagcaaa gctaaaagag 720
 ctggagaaac acaaaatcca gctggagcag gtgcaggaat ggaagagcaa aatgcaggag 780
 cagcaggccg acctgcagcg gcgcctcaag gaggcgagaa aggaagccaa ggaggcgctg 840
 gaggcaaagg aacgctatat ggaggagatg gctgatactg ctgatgccat tgagatggcc 900
 actttggaca aggagatggc tgaagagcgg gctgagtccc tgcagcagga ggtggaggca 960
 ctgaaggagc ggggtggacga gctcactact gacttagaga tcctcaaggc tgagattgaa 1020
 gagaagggct cagatggcgc tgcattccagt tatcagctca agcagcttga ggagcagaat 1080
 gcccgctga aggatgccct ggtgaggatg cgggatcttt cttcctcaga gaagcaggag 1140
 catgtgaagc tccagaagct catggaaaag aagaaccaag agctggaagt tgtgaggcaa 1200
 cagcgggagc gtctgcagga ggagctaagc caggcagaga gcaccattga tgagctcaag 1260

1020001191 - P17-158 Sequence Listing

gagcaggtgg atgctgctct ggggtgctgag gagatgggtgg agatgctgac agatcggaac	1320
ctgaatctgg aagagaaaagt gcgcgagttg agggagactg tgggagactt ggaagcgatg	1380
aatgagatga acgatgagct gcaggagaaat gcacgtgaga cagaactgga gctgcgggag	1440
cagctggaca tggcaggcgc gcgggttcgt gaggcccaga agcgtgtgga ggcagcccag	1500
gagacggttg cagactacca gcagaccatc aagaagtacc gccagctgac cgcccatcta	1560
caggatgtga atcgggaaact gacaaaccag caggaagcat ctgtggagag gcaacagcag	1620
ccacctccag agacctttga cttcaaaatc aagtttgctg agactaaggc ccatgccaaag	1680
gcaattgaga tggaattgag gcagatggag gtggcccagg ccaatcgaca catgtccctg	1740
ctgacagcct tcatgcctga cagcttcctt cggccagggtg gggaccatga ctgcgttctg	1800
gtgctgttgc tcatgcctcg tctcatttgc aaggcagagc tgatccggaa gcaggcccag	1860
gagaagtttg aactaagtga gaactgttca gagcggcctg ggctgcgagg agctgctggg	1920
gagcaactca gctttgctgc tggactggtg tactcgctga gcctgctgca ggccacgcta	1980
caccgctatg agcatgccct ctctcagtgc agtgtggatg tgtataagaa agtgggcagc	2040
ctgtaccctg agatgagtgc ccatgagcgc tccttggttgc tcctcattga actgctgcac	2100
aaggatcagc tggatgagac tgtcaatgtg gagcctctca ccaaggccat caagtactat	2160
cagcatctgt acagcatcca ccttgccgaa cagcctgagg actgtactat gcagctggct	2220
gaccacatta agttcacgca gagtgtcttg gactgcatga gtgtggaggt aggacggctg	2280
cgtgccttct tgcagggtgg gcaggaggct acagatatg ccctcctgct ccgggatctg	2340
gaaacttcat gcagtacat ccgccagttc tgcaagaaga tccgaaggcg aatgccaggg	2400
acagatgctc ctgggatccc agctgcactg gcctttggac cacaggtatc tgacacgctc	2460
ctagactgca ggaaacactt gacgtgggtc gtggctgtgc tgcaggaggt ggcagctgct	2520
gctgcccagc tcattgcccc actggcagag aatgaggggc tacttgtggc tgctctggag	2580
gaactggctt tcaaagcaag cgagcagatc tatgggaccc cctccagcag cccctatgag	2640
tgtctgcgcc agtcatgcaa catcctcatc agtaccatga acaagctggc cacagccatg	2700
caggaggggg agtatgatgc agagcggccc cccagcaagc ctccaccggt tgaactgcgg	2760
gctgctgccc ttcgtgcaga gatcacagat gctgaaggcc tgggtttgaa gctcgaagat	2820

1020001191 - P17-158 Sequence Listing

cgagagacag ttattaagga gttgaagaag tcactcaaga ttaagggaga ggagctaagt	2880
gaggccaatg tgcggctgag cctcctggag aagaagttgg acagtgctgc caaggatgca	2940
gatgagcgca tcgagaaagt ccagactcgg ctggaggaga cccaggcact gctgcgaaag	3000
aaggagaaaag agtttgagga gacaatggat gcactccagg ctgacatcga ccagctggag	3060
gcagagaagg cagaactaaa gcagcgtctg aacagccagt ccaaacgcac gattgaggga	3120
ctccggggcc ctctccttc aggcattgct actctggtct ctggcattgc tggatgaaga	3180
cagcagcgag gagccatccc tgggcaggct ccagggtctg tgccaggccc agggctggtg	3240
aaggactcac cactgctgct tcagcagatc tctgccatga ggctgcacat ctcccagctc	3300
cagcatgaga acagcatcct caaggagacc cagatgaagg catccttggc atccctgccc	3360
cctctgcatg ttgcaaagct atcccatgag ggccctggca gtgagttacc agctggagcg	3420
ctgtatcgta agaccagcca gctgctggag acattgaatc aattgagcac acacacgcac	3480
gtagtagaca tcactcgac cagccctgct gccaaagacc cgtcggccca acttatggag	3540
caagtggctc agcttaagtc cctgagtga accgtcgaga agctcaagga tgaggtcctc	3600
aaggagacag tatctcagcg ccctggagcc acagtaccca ctgactttgc caccttcctt	3660
tcatcagcct tcctcagga ggatccaaag tgggaattcc ctcggaagaa cttggttctt	3720
ggaaaaactc taggagaagg cgaatttga aaagtggta aggcaacggc cttccatctg	3780
aaaggcagag cagggtacac cacggtggcc gtgaagatgc tgaaagagaa cgcctccccg	3840
agtgaacttc gagacctgct gtcagagttc aacgtcctga agcaggtcaa ccaccacat	3900
gtcatcaaat tgtatggggc ctgcagccag gatggccgc tcctcctcat cgtggagtac	3960
gccaaatacg gtcctctgc gggcttcctc cgcgagagcc gcaaagtggg gcctggctac	4020
ctgggcagtg gaggcagccg caactccagc tccctggacc acccgatga gcgggcccctc	4080
accatgggag acctcatctc atttgcctgg cagatctcac aggggatgca gtatctggcc	4140
gagatgaagc tcgttcatcg ggacttggca gccagaaaca tcctggtagc tgaggggagg	4200
aagatgaaga tttcggattt cggcttgtcc cgagatgttt atgaagagga ttcctacgtg	4260
aagaggagcc agggtcggat tccagttaaa tggatggcaa ttgaatccct ttttgatcat	4320
atctacacca cgcaaagtga tgtatggtct tttggtgtcc tgctgtggga gatcgtgacc	4380

1020001191 - P17-158 Sequence Listing

ctagggggaa acccctatcc tgggattcct cctgagcggc tcttcaacct tctgaagacc	4440
ggccaccgga tggagaggcc agacaactgc agcgaggaga tgtaccgcct gatgctgcaa	4500
tgctggaagc aggagccgga caaaaggccg gtgtttgcgg acatcagcaa agacctggag	4560
aagatgatgg ttaagaggag agactacttg gaccttgcgg cgtccactcc atctgactcc	4620
ctgatttatg acgacggcct ctgagaggag gagacaccgc tgggtggactg taataatgcc	4680
cccctccctc gagccctccc ttccacatgg attgaaaaca aactctatgg tagaatttcc	4740
catgcattta ctagattcta g	4761

<210> 24
 <211> 1586
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion peptide

<400> 24

Met	Ala	Gln	Ser	Lys	Arg	His	Val	Tyr	Ser	Arg	Thr	Pro	Ser	Gly	Ser
1				5					10					15	

Arg	Met	Ser	Ala	Glu	Ala	Ser	Ala	Arg	Pro	Leu	Arg	Val	Gly	Ser	Arg
			20					25					30		

Val	Glu	Val	Ile	Gly	Lys	Gly	His	Arg	Gly	Thr	Val	Ala	Tyr	Val	Gly
		35					40					45			

Ala	Thr	Leu	Phe	Ala	Thr	Gly	Lys	Trp	Val	Gly	Val	Ile	Leu	Asp	Glu
	50					55					60				

Ala	Lys	Gly	Lys	Asn	Asp	Gly	Thr	Val	Gln	Gly	Arg	Lys	Tyr	Phe	Thr
65				70					75					80	

Cys	Asp	Glu	Gly	His	Gly	Ile	Phe	Val	Arg	Gln	Ser	Gln	Ile	Gln	Val
				85					90					95	

Phe	Glu	Asp	Gly	Ala	Asp	Thr	Thr	Ser	Pro	Glu	Thr	Pro	Asp	Ser	Ser
			100					105					110		

1020001191 - P17-158 Sequence Listing

Ala Ser Lys Val Leu Lys Arg Glu Gly Thr Asp Thr Thr Ala Lys Thr
115 120 125

Ser Lys Leu Ala Pro Thr Ala Arg Lys Thr Thr Thr Arg Arg Pro Lys
130 135 140

Pro Thr Arg Pro Ala Ser Thr Gly Val Ala Gly Ala Ser Ser Ser Leu
145 150 155 160

Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser Ser Glu Pro
165 170 175

Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile Pro Thr Pro
180 185 190

Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser Pro Ser Lys
195 200 205

Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu Glu Lys Leu
210 215 220

Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys Leu Lys Glu
225 230 235 240

Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu Trp Lys Ser
245 250 255

Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu Lys Glu Ala
260 265 270

Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg Tyr Met Glu
275 280 285

Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr Leu Asp Lys
290 295 300

Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu Val Glu Ala
305 310 315 320

1020001191 - P17-158 Sequence Listing

Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu Ile Leu Lys
325 330 335

Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser Ser Tyr Gln
340 345 350

Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp Ala Leu Val
355 360 365

Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His Val Lys Leu
370 375 380

Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val Val Arg Gln
385 390 395 400

Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu Ser Thr Ile
405 410 415

Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala Glu Glu Met
420 425 430

Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu Lys Val Arg
435 440 445

Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn Glu Met Asn
450 455 460

Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu Leu Arg Glu
465 470 475 480

Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln Lys Arg Val
485 490 495

Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr Ile Lys Lys
500 505 510

Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg Glu Leu Thr
515 520 525

1020001191 - P17-158 Sequence Listing

Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro Pro Pro Glu
530 535 540

Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala His Ala Lys
545 550 555 560

Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln Ala Asn Arg
565 570 575

His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe Leu Arg Pro
580 585 590

Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met Pro Arg Leu
595 600 605

Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu Lys Phe Glu
610 615 620

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

Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu Ser Leu Leu
645 650 655

Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln Cys Ser Val
660 665 670

Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met Ser Ala His
675 680 685

Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys Asp Gln Leu
690 695 700

Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile Lys Tyr Tyr
705 710 715 720

Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu Asp Cys Thr
725 730 735

1020001191 - P17-158 Sequence Listing

Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala Leu Asp Cys
740 745 750

Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln Gly Gly Gln
755 760 765

Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu Thr Ser Cys
770 775 780

Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg Met Pro Gly
785 790 795 800

Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly Pro Gln Val
805 810 815

Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp Val Val Ala
820 825 830

Val Leu Gln Glu Val Ala Ala Ala Ala Gln Leu Ile Ala Pro Leu
835 840 845

Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu Leu Ala Phe
850 855 860

Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser Pro Tyr Glu
865 870 875 880

Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met Asn Lys Leu
885 890 895

Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg Pro Pro Ser
900 905 910

Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg Ala Glu Ile
915 920 925

Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg Glu Thr Val
930 935 940

1020001191 - P17-158 Sequence Listing

Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu Glu Leu Ser
945 950 955 960

Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu Asp Ser Ala
965 970 975

Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr Arg Leu Glu
980 985 990

Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe Glu Glu Thr
995 1000 1005

Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala Glu Lys
1010 1015 1020

Ala Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg Thr Ile
1025 1030 1035

Glu Gly Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr Leu Val
1040 1045 1050

Ser Gly Ile Ala Gly Glu Glu Gln Gln Arg Gly Ala Ile Pro Gly
1055 1060 1065

Gln Ala Pro Gly Ser Val Pro Gly Pro Gly Leu Val Lys Asp Ser
1070 1075 1080

Pro Leu Leu Leu Gln Gln Ile Ser Ala Met Arg Leu His Ile Ser
1085 1090 1095

Gln Leu Gln His Glu Asn Ser Ile Leu Lys Gly Ala Gln Met Lys
1100 1105 1110

Ala Ser Leu Ala Ser Leu Pro Pro Leu His Val Ala Lys Leu Ser
1115 1120 1125

His Glu Gly Pro Gly Ser Glu Leu Pro Ala Gly Ala Leu Tyr Arg
1130 1135 1140

1020001191 - P17-158 Sequence Listing

Lys	Thr	Ser	Gln	Leu	Leu	Glu	Thr	Leu	Asn	Gln	Leu	Ser	Thr	His
1145						1150					1155			
Thr	His	Val	Val	Asp	Ile	Thr	Arg	Thr	Ser	Pro	Ala	Ala	Lys	Ser
1160						1165					1170			
Pro	Ser	Ala	Gln	Leu	Met	Glu	Gln	Val	Ala	Gln	Leu	Lys	Ser	Leu
1175						1180					1185			
Ser	Asp	Thr	Val	Glu	Lys	Leu	Lys	Asp	Glu	Val	Leu	Lys	Glu	Thr
1190						1195					1200			
Val	Ser	Gln	Arg	Pro	Gly	Ala	Thr	Val	Pro	Thr	Asp	Phe	Ala	Thr
1205						1210					1215			
Phe	Pro	Ser	Ser	Ala	Phe	Leu	Arg	Glu	Asp	Pro	Lys	Trp	Glu	Phe
1220						1225					1230			
Pro	Arg	Lys	Asn	Leu	Val	Leu	Gly	Lys	Thr	Leu	Gly	Glu	Gly	Glu
1235						1240					1245			
Phe	Gly	Lys	Val	Val	Lys	Ala	Thr	Ala	Phe	His	Leu	Lys	Gly	Arg
1250						1255					1260			
Ala	Gly	Tyr	Thr	Thr	Val	Ala	Val	Lys	Met	Leu	Lys	Glu	Asn	Ala
1265						1270					1275			
Ser	Pro	Ser	Glu	Leu	Arg	Asp	Leu	Leu	Ser	Glu	Phe	Asn	Val	Leu
1280						1285					1290			
Lys	Gln	Val	Asn	His	Pro	His	Val	Ile	Lys	Leu	Tyr	Gly	Ala	Cys
1295						1300					1305			
Ser	Gln	Asp	Gly	Pro	Leu	Leu	Leu	Ile	Val	Glu	Tyr	Ala	Lys	Tyr
1310						1315					1320			
Gly	Ser	Leu	Arg	Gly	Phe	Leu	Arg	Glu	Ser	Arg	Lys	Val	Gly	Pro
1325						1330					1335			

1020001191 - P17-158 Sequence Listing

Gly	Tyr	Leu	Gly	Ser	Gly	Gly	Ser	Arg	Asn	Ser	Ser	Ser	Leu	Asp
1340						1345					1350			
His	Pro	Asp	Glu	Arg	Ala	Leu	Thr	Met	Gly	Asp	Leu	Ile	Ser	Phe
1355						1360					1365			
Ala	Trp	Gln	Ile	Ser	Gln	Gly	Met	Gln	Tyr	Leu	Ala	Glu	Met	Lys
1370						1375					1380			
Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Ala	Glu
1385						1390					1395			
Gly	Arg	Lys	Met	Lys	Ile	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Asp	Val
1400						1405					1410			
Tyr	Glu	Glu	Asp	Ser	Tyr	Val	Lys	Arg	Ser	Gln	Gly	Arg	Ile	Pro
1415						1420					1425			
Val	Lys	Trp	Met	Ala	Ile	Glu	Ser	Leu	Phe	Asp	His	Ile	Tyr	Thr
1430						1435					1440			
Thr	Gln	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile
1445						1450					1455			
Val	Thr	Leu	Gly	Gly	Asn	Pro	Tyr	Pro	Gly	Ile	Pro	Pro	Glu	Arg
1460						1465					1470			
Leu	Phe	Asn	Leu	Leu	Lys	Thr	Gly	His	Arg	Met	Glu	Arg	Pro	Asp
1475						1480					1485			
Asn	Cys	Ser	Glu	Glu	Met	Tyr	Arg	Leu	Met	Leu	Gln	Cys	Trp	Lys
1490						1495					1500			
Gln	Glu	Pro	Asp	Lys	Arg	Pro	Val	Phe	Ala	Asp	Ile	Ser	Lys	Asp
1505						1510					1515			
Leu	Glu	Lys	Met	Met	Val	Lys	Arg	Arg	Asp	Tyr	Leu	Asp	Leu	Ala
1520						1525					1530			

1020001191 - P17-158 Sequence Listing

Ala Ser Thr Pro Ser Asp Ser Leu Ile Tyr Asp Asp Gly Leu Ser
1535 1540 1545

Glu Glu Glu Thr Pro Leu Val Asp Cys Asn Asn Ala Pro Leu Pro
1550 1555 1560

Arg Ala Leu Pro Ser Thr Trp Ile Glu Asn Lys Leu Tyr Gly Arg
1565 1570 1575

Ile Ser His Ala Phe Thr Arg Phe
1580 1585

<210> 25
<211> 1278
<212> PRT
<213> Homo sapiens

<400> 25

Met Ala Gln Ser Lys Arg His Val Tyr Ser Arg Thr Pro Ser Gly Ser
1 5 10 15

Arg Met Ser Ala Glu Ala Ser Ala Arg Pro Leu Arg Val Gly Ser Arg
20 25 30

Val Glu Val Ile Gly Lys Gly His Arg Gly Thr Val Ala Tyr Val Gly
35 40 45

Ala Thr Leu Phe Ala Thr Gly Lys Trp Val Gly Val Ile Leu Asp Glu
50 55 60

Ala Lys Gly Lys Asn Asp Gly Thr Val Gln Gly Arg Lys Tyr Phe Thr
65 70 75 80

Cys Asp Glu Gly His Gly Ile Phe Val Arg Gln Ser Gln Ile Gln Val
85 90 95

Phe Glu Asp Gly Ala Asp Thr Thr Ser Pro Glu Thr Pro Asp Ser Ser
100 105 110

1020001191 - P17-158 Sequence Listing

Ala Ser Lys Val Leu Lys Arg Glu Gly Thr Asp Thr Thr Ala Lys Thr
115 120 125

Ser Lys Leu Arg Gly Leu Lys Pro Lys Lys Ala Pro Thr Ala Arg Lys
130 135 140

Thr Thr Thr Arg Arg Pro Lys Pro Thr Arg Pro Ala Ser Thr Gly Val
145 150 155 160

Ala Gly Ala Ser Ser Ser Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly
165 170 175

Glu Leu Ser Ser Ser Glu Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala
180 185 190

Ala Pro Ile Ile Pro Thr Pro Val Leu Thr Ser Pro Gly Ala Val Pro
195 200 205

Pro Leu Pro Ser Pro Ser Lys Glu Glu Glu Gly Leu Arg Ala Gln Val
210 215 220

Arg Asp Leu Glu Glu Lys Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu
225 230 235 240

Asp Lys Ala Lys Leu Lys Glu Leu Glu Lys His Lys Ile Gln Leu Glu
245 250 255

Gln Val Gln Glu Trp Lys Ser Lys Met Gln Glu Gln Gln Ala Asp Leu
260 265 270

Gln Arg Arg Leu Lys Glu Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu
275 280 285

Ala Lys Glu Arg Tyr Met Glu Glu Met Ala Asp Thr Ala Asp Ala Ile
290 295 300

Glu Met Ala Thr Leu Asp Lys Glu Met Ala Glu Glu Arg Ala Glu Ser
305 310 315 320

1020001191 - P17-158 Sequence Listing

Leu Gln Gln Glu Val Glu Ala Leu Lys Glu Arg Val Asp Glu Leu Thr
325 330 335

Thr Asp Leu Glu Ile Leu Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp
340 345 350

Gly Ala Ala Ser Ser Tyr Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala
355 360 365

Arg Leu Lys Asp Ala Leu Val Arg Met Arg Asp Leu Ser Ser Ser Glu
370 375 380

Lys Gln Glu His Val Lys Leu Gln Lys Leu Met Glu Lys Lys Asn Gln
385 390 395 400

Glu Leu Glu Val Val Arg Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu
405 410 415

Ser Gln Ala Glu Ser Thr Ile Asp Glu Leu Lys Glu Gln Val Asp Ala
420 425 430

Ala Leu Gly Ala Glu Glu Met Val Glu Met Leu Thr Asp Arg Asn Leu
435 440 445

Asn Leu Glu Glu Lys Val Arg Glu Leu Arg Glu Thr Val Gly Asp Leu
450 455 460

Glu Ala Met Asn Glu Met Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu
465 470 475 480

Thr Glu Leu Glu Leu Arg Glu Gln Leu Asp Met Ala Gly Ala Arg Val
485 490 495

Arg Glu Ala Gln Lys Arg Val Glu Ala Ala Gln Glu Thr Val Ala Asp
500 505 510

Tyr Gln Gln Thr Ile Lys Lys Tyr Arg Gln Leu Thr Ala His Leu Gln
515 520 525

1020001191 - P17-158 Sequence Listing

Asp Val Asn Arg Glu Leu Thr Asn Gln Gln Glu Ala Ser Val Glu Arg
530 535 540

Gln Gln Gln Pro Pro Pro Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala
545 550 555 560

Glu Thr Lys Ala His Ala Lys Ala Ile Glu Met Glu Leu Arg Gln Met
565 570 575

Glu Val Ala Gln Ala Asn Arg His Met Ser Leu Leu Thr Ala Phe Met
580 585 590

Pro Asp Ser Phe Leu Arg Pro Gly Gly Asp His Asp Cys Val Leu Val
595 600 605

Leu Leu Leu Met Pro Arg Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys
610 615 620

Gln Ala Gln Glu Lys Phe Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro
625 630 635 640

Gly Leu Arg Gly Ala Ala Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu
645 650 655

Val Tyr Ser Leu Ser Leu Leu Gln Ala Thr Leu His Arg Tyr Glu His
660 665 670

Ala Leu Ser Gln Cys Ser Val Asp Val Tyr Lys Lys Val Gly Ser Leu
675 680 685

Tyr Pro Glu Met Ser Ala His Glu Arg Ser Leu Asp Phe Leu Ile Glu
690 695 700

Leu Leu His Lys Asp Gln Leu Asp Glu Thr Val Asn Val Glu Pro Leu
705 710 715 720

Thr Lys Ala Ile Lys Tyr Tyr Gln His Leu Tyr Ser Ile His Leu Ala
725 730 735

1020001191 - P17-158 Sequence Listing

Glu Gln Pro Glu Asp Cys Thr Met Gln Leu Ala Asp His Ile Lys Phe
740 745 750

Thr Gln Ser Ala Leu Asp Cys Met Ser Val Glu Val Gly Arg Leu Arg
755 760 765

Ala Phe Leu Gln Gly Gly Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu
770 775 780

Arg Asp Leu Glu Thr Ser Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys
785 790 795 800

Ile Arg Arg Arg Met Pro Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala
805 810 815

Leu Ala Phe Gly Pro Gln Val Ser Asp Thr Leu Leu Asp Cys Arg Lys
820 825 830

His Leu Thr Trp Val Val Ala Val Leu Gln Glu Val Ala Ala Ala Ala
835 840 845

Ala Gln Leu Ile Ala Pro Leu Ala Glu Asn Glu Gly Leu Leu Val Ala
850 855 860

Ala Leu Glu Glu Leu Ala Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr
865 870 875 880

Pro Ser Ser Ser Pro Tyr Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu
885 890 895

Ile Ser Thr Met Asn Lys Leu Ala Thr Ala Met Gln Glu Gly Glu Tyr
900 905 910

Asp Ala Glu Arg Pro Pro Ser Lys Pro Pro Pro Val Glu Leu Arg Ala
915 920 925

Ala Ala Leu Arg Ala Glu Ile Thr Asp Ala Glu Gly Leu Gly Leu Lys
930 935 940

1020001191 - P17-158 Sequence Listing

Leu Glu Asp Arg Glu Thr Val Ile Lys Glu Leu Lys Lys Ser Leu Lys
945 950 955 960

Ile Lys Gly Glu Glu Leu Ser Glu Ala Asn Val Arg Leu Ser Leu Leu
965 970 975

Glu Lys Lys Leu Asp Ser Ala Ala Lys Asp Ala Asp Glu Arg Ile Glu
980 985 990

Lys Val Gln Thr Arg Leu Glu Glu Thr Gln Ala Leu Leu Arg Lys Lys
995 1000 1005

Glu Lys Glu Phe Glu Glu Thr Met Asp Ala Leu Gln Ala Asp Ile
1010 1015 1020

Asp Gln Leu Glu Ala Glu Lys Ala Glu Leu Lys Gln Arg Leu Asn
1025 1030 1035

Ser Gln Ser Lys Arg Thr Ile Glu Gly Leu Arg Gly Pro Pro Pro
1040 1045 1050

Ser Gly Ile Ala Thr Leu Val Ser Gly Ile Ala Gly Glu Glu Gln
1055 1060 1065

Gln Arg Gly Ala Ile Pro Gly Gln Ala Pro Gly Ser Val Pro Gly
1070 1075 1080

Pro Gly Leu Val Lys Asp Ser Pro Leu Leu Leu Gln Gln Ile Ser
1085 1090 1095

Ala Met Arg Leu His Ile Ser Gln Leu Gln His Glu Asn Ser Ile
1100 1105 1110

Leu Lys Gly Ala Gln Met Lys Ala Ser Leu Ala Ser Leu Pro Pro
1115 1120 1125

Leu His Val Ala Lys Leu Ser His Glu Gly Pro Gly Ser Glu Leu
1130 1135 1140

1020001191 - P17-158 Sequence Listing

Pro Ala Gly Ala Leu Tyr Arg Lys Thr Ser Gln Leu Leu Glu Thr
1145 1150 1155

Leu Asn Gln Leu Ser Thr His Thr His Val Val Asp Ile Thr Arg
1160 1165 1170

Thr Ser Pro Ala Ala Lys Ser Pro Ser Ala Gln Leu Met Glu Gln
1175 1180 1185

Val Ala Gln Leu Lys Ser Leu Ser Asp Thr Val Glu Lys Leu Lys
1190 1195 1200

Asp Glu Val Leu Lys Glu Thr Val Ser Gln Arg Pro Gly Ala Thr
1205 1210 1215

Val Pro Thr Asp Phe Ala Thr Phe Pro Ser Ser Ala Phe Leu Arg
1220 1225 1230

Ala Lys Glu Glu Gln Gln Asp Asp Thr Val Tyr Met Gly Lys Val
1235 1240 1245

Thr Phe Ser Cys Ala Ala Gly Phe Gly Gln Arg His Arg Leu Val
1250 1255 1260

Leu Thr Gln Glu Gln Leu His Gln Leu His Ser Arg Leu Ile Ser
1265 1270 1275

<210> 26
<211> 1144
<212> PRT
<213> Homo sapiens

<400> 26

Met Met Arg Gln Ala Pro Thr Ala Arg Lys Thr Thr Thr Arg Arg Pro
1 5 10 15

Lys Pro Thr Arg Pro Ala Ser Thr Gly Val Ala Gly Ala Ser Ser Ser
20 25 30

Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser Ser Glu

1020001191 - P17-158 Sequence Listing

35

40

45

Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile Pro Thr
 50 55 60

Pro Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser Pro Ser
 65 70 75 80

Lys Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu Glu Lys
 85 90 95

Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys Leu Lys
 100 105 110

Glu Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu Trp Lys
 115 120 125

Ser Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu Lys Glu
 130 135 140

Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg Tyr Met
 145 150 155 160

Glu Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr Leu Asp
 165 170 175

Lys Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu Val Glu
 180 185 190

Ala Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu Ile Leu
 195 200 205

Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser Ser Tyr
 210 215 220

Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp Ala Leu
 225 230 235 240

Val Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His Val Lys

245 250 255

Arg His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe Leu Arg

1020001191 - P17-158 Sequence Listing

450

455

460

Pro Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met Pro Arg
465 470 475 480

Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu Lys Phe
485 490 495

Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro Gly Leu Arg Gly Ala Ala
500 505 510

Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu Ser Leu
515 520 525

Leu Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln Cys Ser
530 535 540

Val Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met Ser Ala
545 550 555 560

His Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys Asp Gln
565 570 575

Leu Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile Lys Tyr
580 585 590

Tyr Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu Asp Cys
595 600 605

Thr Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala Leu Asp
610 615 620

Cys Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln Gly Gly
625 630 635 640

Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu Thr Ser
645 650 655

Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg Met Pro

1020001191 - P17-158 Sequence Listing

660

665

670

Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly Pro Gln
675 680 685

Val Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp Val Val
690 695 700

Ala Val Leu Gln Glu Val Ala Ala Ala Ala Ala Gln Leu Ile Ala Pro
705 710 715 720

Leu Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu Leu Ala
725 730 735

Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser Pro Tyr
740 745 750

Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met Asn Lys
755 760 765

Leu Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg Pro Pro
770 775 780

Ser Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg Ala Glu
785 790 795 800

Ile Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg Glu Thr
805 810 815

Val Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu Glu Leu
820 825 830

Ser Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu Asp Ser
835 840 845

Ala Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr Arg Leu
850 855 860

Glu Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe Glu Glu

1020001191 - P17-158 Sequence Listing

865		870		875		880
Thr Met Asp Ala	Leu Gln Ala Asp Ile	Asp Gln Leu Glu Ala	Glu Lys			
	885		890		895	
Ala Glu Leu Lys	Gln Arg Leu Asn Ser	Gln Ser Lys Arg	Thr Ile Glu			
	900		905		910	
Gly Leu Arg Gly	Pro Pro Pro Ser	Gly Ile Ala Thr	Leu Val Ser Gly			
	915		920		925	
Ile Ala Gly Glu	Glu Gln Gln Arg Gly	Ala Ile Pro Gly	Gln Ala Pro			
	930		935		940	
Gly Ser Val Pro	Gly Pro Gly Leu Val	Lys Asp Ser Pro	Leu Leu Leu			
945		950		955		960
Gln Gln Ile Ser	Ala Met Arg Leu His	Ile Ser Gln Leu	Gln His Glu			
	965		970		975	
Asn Ser Ile Leu	Lys Gly Ala Gln Met	Lys Ala Ser Leu	Ala Ser Leu			
	980		985		990	
Pro Pro Leu His	Val Ala Lys Leu	Ser His Glu Gly	Pro Gly Ser Glu			
	995		1000		1005	
Leu Pro Ala Gly	Ala Leu Tyr Arg	Lys Thr Ser Gln	Leu Leu Glu			
	1010		1015		1020	
Thr Leu Asn Gln	Leu Ser Thr His	Thr His Val Val	Asp Ile Thr			
	1025		1030		1035	
Arg Thr Ser Pro	Ala Ala Lys Ser	Pro Ser Ala Gln	Leu Met Glu			
	1040		1045		1050	
Gln Val Ala Gln	Leu Lys Ser Leu	Ser Asp Thr Val	Glu Lys Leu			
	1055		1060		1065	
Lys Asp Glu Val	Leu Lys Glu Thr	Val Ser Gln Arg	Pro Gly Ala			

1020001191 - P17-158 Sequence Listing

1070

1075

1080

Thr Val Pro Thr Asp Phe Ala Thr Phe Pro Ser Ser Ala Phe Leu
1085 1090 1095

Arg Ala Lys Glu Glu Gln Gln Asp Asp Thr Val Tyr Met Gly Lys
1100 1105 1110

Val Thr Phe Ser Cys Ala Ala Gly Phe Gly Gln Arg His Arg Leu
1115 1120 1125

Val Leu Thr Gln Glu Gln Leu His Gln Leu His Ser Arg Leu Ile
1130 1135 1140

Ser

<210> 27

<211> 1253

<212> PRT

<213> Homo sapiens

<400> 27

Met Ala Gln Ser Lys Arg His Val Tyr Ser Arg Thr Pro Ser Gly Ser
1 5 10 15

Arg Met Ser Ala Glu Ala Ser Ala Arg Pro Leu Arg Val Gly Ser Arg
20 25 30

Val Glu Val Ile Gly Lys Gly His Arg Gly Thr Val Ala Tyr Val Gly
35 40 45

Ala Thr Leu Phe Ala Thr Gly Lys Trp Val Gly Val Ile Leu Asp Glu
50 55 60

Ala Lys Gly Lys Asn Asp Gly Thr Val Gln Gly Arg Lys Tyr Phe Thr
65 70 75 80

Cys Asp Glu Gly His Gly Ile Phe Val Arg Gln Ser Gln Ile Gln Val
85 90 95

1020001191 - P17-158 Sequence Listing

Phe Glu Asp Gly Ala Asp Thr Thr Ser Pro Glu Thr Pro Asp Ser Ser
100 105 110

Ala Ser Lys Val Leu Lys Arg Glu Gly Thr Asp Thr Thr Ala Lys Thr
115 120 125

Ser Lys Leu Pro Thr Arg Pro Ala Ser Thr Gly Val Ala Gly Ala Ser
130 135 140

Ser Ser Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser
145 150 155 160

Ser Glu Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile
165 170 175

Pro Thr Pro Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser
180 185 190

Pro Ser Lys Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu
195 200 205

Glu Lys Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys
210 215 220

Leu Lys Glu Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu
225 230 235 240

Trp Lys Ser Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu
245 250 255

Lys Glu Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg
260 265 270

Tyr Met Glu Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr
275 280 285

Leu Asp Lys Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu
290 295 300

1020001191 - P17-158 Sequence Listing

Val Glu Ala Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu
305 310 315 320

Ile Leu Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser
325 330 335

Ser Tyr Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp
340 345 350

Ala Leu Val Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His
355 360 365

Val Lys Leu Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val
370 375 380

Val Arg Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu
385 390 395 400

Ser Thr Ile Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala
405 410 415

Glu Glu Met Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu
420 425 430

Lys Val Arg Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn
435 440 445

Glu Met Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu
450 455 460

Leu Arg Glu Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln
465 470 475 480

Lys Arg Val Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr
485 490 495

Ile Lys Lys Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg
500 505 510

1020001191 - P17-158 Sequence Listing

Glu Leu Thr Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro
515 520 525

Pro Pro Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala
530 535 540

His Ala Lys Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln
545 550 555 560

Ala Asn Arg His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe
565 570 575

Leu Arg Pro Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met
580 585 590

Pro Arg Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu
595 600 605

Lys Phe Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro Gly Leu Arg Gly
610 615 620

Ala Ala Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu
625 630 635 640

Ser Leu Leu Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln
645 650 655

Cys Ser Val Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met
660 665 670

Ser Ala His Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys
675 680 685

Asp Gln Leu Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile
690 695 700

Lys Tyr Tyr Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu
705 710 715 720

1020001191 - P17-158 Sequence Listing

Asp Cys Thr Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala
725 730 735

Leu Asp Cys Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln
740 745 750

Gly Gly Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu
755 760 765

Thr Ser Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg
770 775 780

Met Pro Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly
785 790 795 800

Pro Gln Val Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp
805 810 815

Val Val Ala Val Leu Gln Glu Val Ala Ala Ala Ala Ala Gln Leu Ile
820 825 830

Ala Pro Leu Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu
835 840 845

Leu Ala Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser
850 855 860

Pro Tyr Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met
865 870 875 880

Asn Lys Leu Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg
885 890 895

Pro Pro Ser Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg
900 905 910

Ala Glu Ile Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg
915 920 925

1020001191 - P17-158 Sequence Listing

Glu Thr Val Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu
930 935 940

Glu Leu Ser Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu
945 950 955 960

Asp Ser Ala Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr
965 970 975

Arg Leu Glu Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe
980 985 990

Glu Glu Thr Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala
995 1000 1005

Glu Lys Ala Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg
1010 1015 1020

Thr Ile Glu Gly Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr
1025 1030 1035

Leu Val Ser Gly Ile Ala Gly Gly Ala Ile Pro Gly Gln Ala Pro
1040 1045 1050

Gly Ser Val Pro Gly Pro Gly Leu Val Lys Asp Ser Pro Leu Leu
1055 1060 1065

Leu Gln Gln Ile Ser Ala Met Arg Leu His Ile Ser Gln Leu Gln
1070 1075 1080

His Glu Asn Ser Ile Leu Lys Gly Ala Gln Met Lys Ala Ser Leu
1085 1090 1095

Ala Ser Leu Pro Pro Leu His Val Ala Lys Leu Ser His Glu Gly
1100 1105 1110

Pro Gly Ser Glu Leu Pro Ala Gly Ala Leu Tyr Arg Lys Thr Ser
1115 1120 1125

1020001191 - P17-158 Sequence Listing

Gln Leu Leu Glu Thr Leu Asn Gln Leu Ser Thr His Thr His Val
1130 1135 1140

Val Asp Ile Thr Arg Thr Ser Pro Ala Ala Lys Ser Pro Ser Ala
1145 1150 1155

Gln Leu Met Glu Gln Val Ala Gln Leu Lys Ser Leu Ser Asp Thr
1160 1165 1170

Val Glu Lys Leu Lys Asp Glu Val Leu Lys Glu Thr Val Ser Gln
1175 1180 1185

Arg Pro Gly Ala Thr Val Pro Thr Asp Phe Ala Thr Phe Pro Ser
1190 1195 1200

Ser Ala Phe Leu Arg Ala Lys Glu Glu Gln Gln Asp Asp Thr Val
1205 1210 1215

Tyr Met Gly Lys Val Thr Phe Ser Cys Ala Ala Gly Phe Gly Gln
1220 1225 1230

Arg His Arg Leu Val Leu Thr Gln Glu Gln Leu His Gln Leu His
1235 1240 1245

Ser Arg Leu Ile Ser
1250

<210> 28
<211> 1139
<212> PRT
<213> Homo sapiens

<400> 28

Met Met Arg Gln Ala Pro Thr Ala Arg Lys Thr Thr Thr Arg Arg Pro
1 5 10 15

Lys Pro Thr Arg Pro Ala Ser Thr Gly Val Ala Gly Ala Ser Ser Ser
20 25 30

1020001191 - P17-158 Sequence Listing

Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser Ser Glu
35 40 45

Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile Pro Thr
50 55 60

Pro Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser Pro Ser
65 70 75 80

Lys Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu Glu Lys
85 90 95

Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys Leu Lys
100 105 110

Glu Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu Trp Lys
115 120 125

Ser Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu Lys Glu
130 135 140

Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg Tyr Met
145 150 155 160

Glu Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr Leu Asp
165 170 175

Lys Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu Val Glu
180 185 190

Ala Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu Ile Leu
195 200 205

Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser Ser Tyr
210 215 220

Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp Ala Leu
225 230 235 240

1020001191 - P17-158 Sequence Listing

Val Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His Val Lys
245 250 255

Leu Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val Val Arg
260 265 270

Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu Ser Thr
275 280 285

Ile Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala Glu Glu
290 295 300

Met Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu Lys Val
305 310 315 320

Arg Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn Glu Met
325 330 335

Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu Leu Arg
340 345 350

Glu Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln Lys Arg
355 360 365

Val Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr Ile Lys
370 375 380

Lys Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg Glu Leu
385 390 395 400

Thr Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro Pro Pro
405 410 415

Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala His Ala
420 425 430

Lys Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln Ala Asn
435 440 445

1020001191 - P17-158 Sequence Listing

Arg His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe Leu Arg
450 455 460

Pro Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met Pro Arg
465 470 475 480

Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu Lys Phe
485 490 495

Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro Gly Leu Arg Gly Ala Ala
500 505 510

Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu Ser Leu
515 520 525

Leu Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln Cys Ser
530 535 540

Val Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met Ser Ala
545 550 555 560

His Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys Asp Gln
565 570 575

Leu Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile Lys Tyr
580 585 590

Tyr Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu Asp Cys
595 600 605

Thr Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala Leu Asp
610 615 620

Cys Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln Gly Gly
625 630 635 640

Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu Thr Ser
645 650 655

1020001191 - P17-158 Sequence Listing

Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg Met Pro
660 665 670

Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly Pro Gln
675 680 685

Val Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp Val Val
690 695 700

Ala Val Leu Gln Glu Val Ala Ala Ala Ala Ala Gln Leu Ile Ala Pro
705 710 715 720

Leu Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu Leu Ala
725 730 735

Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser Pro Tyr
740 745 750

Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met Asn Lys
755 760 765

Leu Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg Pro Pro
770 775 780

Ser Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg Ala Glu
785 790 795 800

Ile Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg Glu Thr
805 810 815

Val Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu Glu Leu
820 825 830

Ser Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu Asp Ser
835 840 845

Ala Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr Arg Leu
850 855 860

1020001191 - P17-158 Sequence Listing

Glu Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe Glu Glu
865 870 875 880

Thr Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala Glu Lys
885 890 895

Ala Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg Thr Ile Glu
900 905 910

Gly Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr Leu Val Ser Gly
915 920 925

Ile Ala Gly Gly Ala Ile Pro Gly Gln Ala Pro Gly Ser Val Pro Gly
930 935 940

Pro Gly Leu Val Lys Asp Ser Pro Leu Leu Leu Gln Gln Ile Ser Ala
945 950 955 960

Met Arg Leu His Ile Ser Gln Leu Gln His Glu Asn Ser Ile Leu Lys
965 970 975

Gly Ala Gln Met Lys Ala Ser Leu Ala Ser Leu Pro Pro Leu His Val
980 985 990

Ala Lys Leu Ser His Glu Gly Pro Gly Ser Glu Leu Pro Ala Gly Ala
995 1000 1005

Leu Tyr Arg Lys Thr Ser Gln Leu Leu Glu Thr Leu Asn Gln Leu
1010 1015 1020

Ser Thr His Thr His Val Val Asp Ile Thr Arg Thr Ser Pro Ala
1025 1030 1035

Ala Lys Ser Pro Ser Ala Gln Leu Met Glu Gln Val Ala Gln Leu
1040 1045 1050

Lys Ser Leu Ser Asp Thr Val Glu Lys Leu Lys Asp Glu Val Leu
1055 1060 1065

1020001191 - P17-158 Sequence Listing

Lys Glu Thr Val Ser Gln Arg Pro Gly Ala Thr Val Pro Thr Asp
1070 1075 1080

Phe Ala Thr Phe Pro Ser Ser Ala Phe Leu Arg Ala Lys Glu Glu
1085 1090 1095

Gln Gln Asp Asp Thr Val Tyr Met Gly Lys Val Thr Phe Ser Cys
1100 1105 1110

Ala Ala Gly Phe Gly Gln Arg His Arg Leu Val Leu Thr Gln Glu
1115 1120 1125

Gln Leu His Gln Leu His Ser Arg Leu Ile Ser
1130 1135

<210> 29
<211> 1236
<212> PRT
<213> Homo sapiens

<400> 29

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

Glu Val Ile Gly Lys Gly His Arg Gly Thr Val Ala Tyr Val Gly Ala
20 25 30

Thr Leu Phe Ala Thr Gly Lys Trp Val Gly Val Ile Leu Asp Glu Ala
35 40 45

Lys Gly Lys Asn Asp Gly Thr Val Gln Gly Arg Lys Tyr Phe Thr Cys
50 55 60

Asp Glu Gly His Gly Ile Phe Val Arg Gln Ser Gln Ile Gln Val Phe
65 70 75 80

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

1020001191 - P17-158 Sequence Listing

Ser Lys Val Leu Lys Arg Glu Gly Thr Asp Thr Thr Ala Lys Thr Ser
100 105 110

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

Ser Leu Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser Ser
130 135 140

Glu Pro Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile Pro
145 150 155 160

Thr Pro Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser Pro
165 170 175

Ser Lys Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu Glu
180 185 190

Lys Leu Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys Leu
195 200 205

Lys Glu Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu Trp
210 215 220

Lys Ser Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu Lys
225 230 235 240

Glu Ala Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg Tyr
245 250 255

Met Glu Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr Leu
260 265 270

Asp Lys Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu Val
275 280 285

Glu Ala Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu Ile
290 295 300

1020001191 - P17-158 Sequence Listing

Leu Lys Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser Ser
305 310 315 320

Tyr Gln Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp Ala
325 330 335

Leu Val Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His Val
340 345 350

Lys Leu Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val Val
355 360 365

Arg Gln Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu Ser
370 375 380

Thr Ile Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala Glu
385 390 395 400

Glu Met Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu Lys
405 410 415

Val Arg Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn Glu
420 425 430

Met Asn Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu Leu
435 440 445

Arg Glu Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln Lys
450 455 460

Arg Val Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr Ile
465 470 475 480

Lys Lys Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg Glu
485 490 495

Leu Thr Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro Pro
500 505 510

1020001191 - P17-158 Sequence Listing

Pro Glu Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala His
515 520 525

Ala Lys Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln Ala
530 535 540

Asn Arg His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe Leu
545 550 555 560

Arg Pro Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met Pro
565 570 575

Arg Leu Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu Lys
580 585 590

Phe Glu Leu Ser Glu Asn Cys Ser Glu Arg Pro Gly Leu Arg Gly Ala
595 600 605

Ala Gly Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu Ser
610 615 620

Leu Leu Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln Cys
625 630 635 640

Ser Val Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met Ser
645 650 655

Ala His Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys Asp
660 665 670

Gln Leu Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile Lys
675 680 685

Tyr Tyr Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu Asp
690 695 700

Cys Thr Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala Leu
705 710 715 720

1020001191 - P17-158 Sequence Listing

Asp Cys Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln Gly
725 730 735

Gly Gln Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu Thr
740 745 750

Ser Cys Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg Met
755 760 765

Pro Gly Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly Pro
770 775 780

Gln Val Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp Val
785 790 795 800

Val Ala Val Leu Gln Glu Val Ala Ala Ala Ala Gln Leu Ile Ala
805 810 815

Pro Leu Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu Leu
820 825 830

Ala Phe Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser Pro
835 840 845

Tyr Glu Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met Asn
850 855 860

Lys Leu Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg Pro
865 870 875 880

Pro Ser Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg Ala
885 890 895

Glu Ile Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg Glu
900 905 910

Thr Val Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu Glu
915 920 925

1020001191 - P17-158 Sequence Listing

Leu Ser Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu Asp
 930 935 940

Ser Ala Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr Arg
 945 950 955 960

Leu Glu Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe Glu
 965 970 975

Glu Thr Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala Glu
 980 985 990

Lys Ala Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg Thr Ile
 995 1000 1005

Glu Gly Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr Leu Val
 1010 1015 1020

Ser Gly Ile Ala Gly Gly Ala Ile Pro Gly Gln Ala Pro Gly Ser
 1025 1030 1035

Val Pro Gly Pro Gly Leu Val Lys Asp Ser Pro Leu Leu Leu Gln
 1040 1045 1050

Gln Ile Ser Ala Met Arg Leu His Ile Ser Gln Leu Gln His Glu
 1055 1060 1065

Asn Ser Ile Leu Lys Gly Ala Gln Met Lys Ala Ser Leu Ala Ser
 1070 1075 1080

Leu Pro Pro Leu His Val Ala Lys Leu Ser His Glu Gly Pro Gly
 1085 1090 1095

Ser Glu Leu Pro Ala Gly Ala Leu Tyr Arg Lys Thr Ser Gln Leu
 1100 1105 1110

Leu Glu Thr Leu Asn Gln Leu Ser Thr His Thr His Val Val Asp
 1115 1120 1125

1020001191 - P17-158 Sequence Listing

Ile Thr Arg Thr Ser Pro Ala Ala Lys Ser Pro Ser Ala Gln Leu
1130 1135 1140

Met Glu Gln Val Ala Gln Leu Lys Ser Leu Ser Asp Thr Val Glu
1145 1150 1155

Lys Leu Lys Asp Glu Val Leu Lys Glu Thr Val Ser Gln Arg Pro
1160 1165 1170

Gly Ala Thr Val Pro Thr Asp Phe Ala Thr Phe Pro Ser Ser Ala
1175 1180 1185

Phe Leu Arg Ala Lys Glu Glu Gln Gln Asp Asp Thr Val Tyr Met
1190 1195 1200

Gly Lys Val Thr Phe Ser Cys Ala Ala Gly Phe Gly Gln Arg His
1205 1210 1215

Arg Leu Val Leu Thr Gln Glu Gln Leu His Gln Leu His Ser Arg
1220 1225 1230

Leu Ile Ser
1235

<210> 30
<211> 1271
<212> PRT
<213> Homo sapiens

<400> 30

Met Ala Gln Ser Lys Arg His Val Tyr Ser Arg Thr Pro Ser Gly Ser
1 5 10 15

Arg Met Ser Ala Glu Ala Ser Ala Arg Pro Leu Arg Val Gly Ser Arg
20 25 30

Val Glu Val Ile Gly Lys Gly His Arg Gly Thr Val Ala Tyr Val Gly
35 40 45

Ala Thr Leu Phe Ala Thr Gly Lys Trp Val Gly Val Ile Leu Asp Glu

1020001191 - P17-158 Sequence Listing

50

55

60

Ala Lys Gly Lys Asn Asp Gly Thr Val Gln Gly Arg Lys Tyr Phe Thr
65 70 75 80

Cys Asp Glu Gly His Gly Ile Phe Val Arg Gln Ser Gln Ile Gln Val
85 90 95

Phe Glu Asp Gly Ala Asp Thr Thr Ser Pro Glu Thr Pro Asp Ser Ser
100 105 110

Ala Ser Lys Val Leu Lys Arg Glu Gly Thr Asp Thr Thr Ala Lys Thr
115 120 125

Ser Lys Leu Ala Pro Thr Ala Arg Lys Thr Thr Thr Arg Arg Pro Lys
130 135 140

Pro Thr Arg Pro Ala Ser Thr Gly Val Ala Gly Ala Ser Ser Ser Leu
145 150 155 160

Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser Ser Glu Pro
165 170 175

Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile Pro Thr Pro
180 185 190

Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser Pro Ser Lys
195 200 205

Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu Glu Lys Leu
210 215 220

Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys Leu Lys Glu
225 230 235 240

Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu Trp Lys Ser
245 250 255

Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu Lys Glu Ala

1020001191 - P17-158 Sequence Listing

260

265

270

Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg Tyr Met Glu
 275 280 285

Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr Leu Asp Lys
 290 295 300

Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu Val Glu Ala
 305 310 315 320

Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu Ile Leu Lys
 325 330 335

Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser Ser Tyr Gln
 340 345 350

Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp Ala Leu Val
 355 360 365

Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His Val Lys Leu
 370 375 380

Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val Val Arg Gln
 385 390 395 400

Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu Ser Thr Ile
 405 410 415

Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala Glu Glu Met
 420 425 430

Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu Lys Val Arg
 435 440 445

Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn Glu Met Asn
 450 455 460

Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu Leu Arg Glu

1020001191 - P17-158 Sequence Listing

465 470 475 480

Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln Lys Arg Val
485 490 495

Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr Ile Lys Lys
500 505 510

Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg Glu Leu Thr
515 520 525

Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro Pro Pro Glu
530 535 540

Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala His Ala Lys
545 550 555 560

Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln Ala Asn Arg
565 570 575

His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe Leu Arg Pro
580 585 590

Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met Pro Arg Leu
595 600 605

Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu Lys Phe Glu
610 615 620

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

Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu Ser Leu Leu
645 650 655

Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln Cys Ser Val
660 665 670

Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met Ser Ala His

1020001191 - P17-158 Sequence Listing

675

680

685

Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys Asp Gln Leu
 690 695 700

Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile Lys Tyr Tyr
 705 710 715 720

Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu Asp Cys Thr
 725 730 735

Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala Leu Asp Cys
 740 745 750

Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln Gly Gly Gln
 755 760 765

Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu Thr Ser Cys
 770 775 780

Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg Met Pro Gly
 785 790 795 800

Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly Pro Gln Val
 805 810 815

Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp Val Val Ala
 820 825 830

Val Leu Gln Glu Val Ala Ala Ala Ala Glu Leu Ile Ala Pro Leu
 835 840 845

Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu Leu Ala Phe
 850 855 860

Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser Pro Tyr Glu
 865 870 875 880

Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met Asn Lys Leu

1020001191 - P17-158 Sequence Listing

885

890

895

Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg Pro Pro Ser
900 905 910

Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg Ala Glu Ile
915 920 925

Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg Glu Thr Val
930 935 940

Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu Glu Leu Ser
945 950 955 960

Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu Asp Ser Ala
965 970 975

Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr Arg Leu Glu
980 985 990

Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe Glu Glu Thr
995 1000 1005

Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala Glu Lys
1010 1015 1020

Ala Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg Thr Ile
1025 1030 1035

Glu Gly Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr Leu Val
1040 1045 1050

Ser Gly Ile Ala Gly Glu Glu Gln Gln Arg Gly Ala Ile Pro Gly
1055 1060 1065

Gln Ala Pro Gly Ser Val Pro Gly Pro Gly Leu Val Lys Asp Ser
1070 1075 1080

Pro Leu Leu Leu Gln Gln Ile Ser Ala Met Arg Leu His Ile Ser

1020001191 - P17-158 Sequence Listing

1085

1090

1095

Gln Leu Gln His Glu Asn Ser Ile Leu Lys Gly Ala Gln Met Lys
 1100 1105 1110

Ala Ser Leu Ala Ser Leu Pro Pro Leu His Val Ala Lys Leu Ser
 1115 1120 1125

His Glu Gly Pro Gly Ser Glu Leu Pro Ala Gly Ala Leu Tyr Arg
 1130 1135 1140

Lys Thr Ser Gln Leu Leu Glu Thr Leu Asn Gln Leu Ser Thr His
 1145 1150 1155

Thr His Val Val Asp Ile Thr Arg Thr Ser Pro Ala Ala Lys Ser
 1160 1165 1170

Pro Ser Ala Gln Leu Met Glu Gln Val Ala Gln Leu Lys Ser Leu
 1175 1180 1185

Ser Asp Thr Val Glu Lys Leu Lys Asp Glu Val Leu Lys Glu Thr
 1190 1195 1200

Val Ser Gln Arg Pro Gly Ala Thr Val Pro Thr Asp Phe Ala Thr
 1205 1210 1215

Phe Pro Ser Ser Ala Phe Leu Arg Ala Lys Glu Glu Gln Gln Asp
 1220 1225 1230

Asp Thr Val Tyr Met Gly Lys Val Thr Phe Ser Cys Ala Ala Gly
 1235 1240 1245

Phe Gly Gln Arg His Arg Leu Val Leu Thr Gln Glu Gln Leu His
 1250 1255 1260

Gln Leu His Ser Arg Leu Ile Ser
 1265 1270

<210> 31

1020001191 - P17-158 Sequence Listing

<211> 1114

<212> PRT

<213> Homo sapiens

<400> 31

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

Leu Leu Leu Pro Leu Leu Gly Lys Val Ala Leu Gly Leu Tyr Phe Ser
20 25 30

Arg Asp Ala Tyr Trp Glu Lys Leu Tyr Val Asp Gln Ala Ala Gly Thr
35 40 45

Pro Leu Leu Tyr Val His Ala Leu Arg Asp Ala Pro Glu Glu Val Pro
50 55 60

Ser Phe Arg Leu Gly Gln His Leu Tyr Gly Thr Tyr Arg Thr Arg Leu
65 70 75 80

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

Leu Asn Arg Ser Leu Asp His Ser Ser Trp Glu Lys Leu Ser Val Arg
100 105 110

Asn Arg Gly Phe Pro Leu Leu Thr Val Tyr Leu Lys Val Phe Leu Ser
115 120 125

Pro Thr Ser Leu Arg Glu Gly Glu Cys Gln Trp Pro Gly Cys Ala Arg
130 135 140

Val Tyr Phe Ser Phe Phe Asn Thr Ser Phe Pro Ala Cys Ser Ser Leu
145 150 155 160

Lys Pro Arg Glu Leu Cys Phe Pro Glu Thr Arg Pro Ser Phe Arg Ile
165 170 175

Arg Glu Asn Arg Pro Pro Gly Thr Phe His Gln Phe Arg Leu Leu Pro
180 185 190

1020001191 - P17-158 Sequence Listing

Val Gln Phe Leu Cys Pro Asn Ile Ser Val Ala Tyr Arg Leu Leu Glu
195 200 205

Gly Glu Gly Leu Pro Phe Arg Cys Ala Pro Asp Ser Leu Glu Val Ser
210 215 220

Thr Arg Trp Ala Leu Asp Arg Glu Gln Arg Glu Lys Tyr Glu Leu Val
225 230 235 240

Ala Val Cys Thr Val His Ala Gly Ala Arg Glu Glu Val Val Met Val
245 250 255

Pro Phe Pro Val Thr Val Tyr Asp Glu Asp Asp Ser Ala Pro Thr Phe
260 265 270

Pro Ala Gly Val Asp Thr Ala Ser Ala Val Val Glu Phe Lys Arg Lys
275 280 285

Glu Asp Thr Val Val Ala Thr Leu Arg Val Phe Asp Ala Asp Val Val
290 295 300

Pro Ala Ser Gly Glu Leu Val Arg Arg Tyr Thr Ser Thr Leu Leu Pro
305 310 315 320

Gly Asp Thr Trp Ala Gln Gln Thr Phe Arg Val Glu His Trp Pro Asn
325 330 335

Glu Thr Ser Val Gln Ala Asn Gly Ser Phe Val Arg Ala Thr Val His
340 345 350

Asp Tyr Arg Leu Val Leu Asn Arg Asn Leu Ser Ile Ser Glu Asn Arg
355 360 365

Thr Met Gln Leu Ala Val Leu Val Asn Asp Ser Asp Phe Gln Gly Pro
370 375 380

Gly Ala Gly Val Leu Leu Leu His Phe Asn Val Ser Val Leu Pro Val
385 390 395 400

1020001191 - P17-158 Sequence Listing

Ser Leu His Leu Pro Ser Thr Tyr Ser Leu Ser Val Ser Arg Arg Ala
405 410 415

Arg Arg Phe Ala Gln Ile Gly Lys Val Cys Val Glu Asn Cys Gln Ala
420 425 430

Phe Ser Gly Ile Asn Val Gln Tyr Lys Leu His Ser Ser Gly Ala Asn
435 440 445

Cys Ser Thr Leu Gly Val Val Thr Ser Ala Glu Asp Thr Ser Gly Ile
450 455 460

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

Leu His Tyr Met Val Val Ala Thr Asp Gln Gln Thr Ser Arg Gln Ala
485 490 495

Gln Ala Gln Leu Leu Val Thr Val Glu Gly Ser Tyr Val Ala Glu Glu
500 505 510

Ala Gly Cys Pro Leu Ser Cys Ala Val Ser Lys Arg Arg Leu Glu Cys
515 520 525

Glu Glu Cys Gly Gly Leu Gly Ser Pro Thr Gly Arg Cys Glu Trp Arg
530 535 540

Gln Gly Asp Gly Lys Gly Ile Thr Arg Asn Phe Ser Thr Cys Ser Pro
545 550 555 560

Ser Thr Lys Thr Cys Pro Asp Gly His Cys Asp Val Val Glu Thr Gln
565 570 575

Asp Ile Asn Ile Cys Pro Gln Asp Cys Leu Arg Gly Ser Ile Val Gly
580 585 590

Gly His Glu Pro Gly Glu Pro Arg Gly Ile Lys Ala Gly Tyr Gly Thr
595 600 605

1020001191 - P17-158 Sequence Listing

Cys Asn Cys Phe Pro Glu Glu Glu Lys Cys Phe Cys Glu Pro Glu Asp
610 615 620

Ile Gln Asp Pro Leu Cys Asp Glu Leu Cys Arg Thr Val Ile Ala Ala
625 630 635 640

Ala Val Leu Phe Ser Phe Ile Val Ser Val Leu Leu Ser Ala Phe Cys
645 650 655

Ile His Cys Tyr His Lys Phe Ala His Lys Pro Pro Ile Ser Ser Ala
660 665 670

Glu Met Thr Phe Arg Arg Pro Ala Gln Ala Phe Pro Val Ser Tyr Ser
675 680 685

Ser Ser Gly Ala Arg Arg Pro Ser Leu Asp Ser Met Glu Asn Gln Val
690 695 700

Ser Val Asp Ala Phe Lys Ile Leu Glu Asp Pro Lys Trp Glu Phe Pro
705 710 715 720

Arg Lys Asn Leu Val Leu Gly Lys Thr Leu Gly Glu Gly Glu Phe Gly
725 730 735

Lys Val Val Lys Ala Thr Ala Phe His Leu Lys Gly Arg Ala Gly Tyr
740 745 750

Thr Thr Val Ala Val Lys Met Leu Lys Glu Asn Ala Ser Pro Ser Glu
755 760 765

Leu Arg Asp Leu Leu Ser Glu Phe Asn Val Leu Lys Gln Val Asn His
770 775 780

Pro His Val Ile Lys Leu Tyr Gly Ala Cys Ser Gln Asp Gly Pro Leu
785 790 795 800

Leu Leu Ile Val Glu Tyr Ala Lys Tyr Gly Ser Leu Arg Gly Phe Leu
805 810 815

1020001191 - P17-158 Sequence Listing

Arg Glu Ser Arg Lys Val Gly Pro Gly Tyr Leu Gly Ser Gly Gly Ser
820 825 830

Arg Asn Ser Ser Ser Leu Asp His Pro Asp Glu Arg Ala Leu Thr Met
835 840 845

Gly Asp Leu Ile Ser Phe Ala Trp Gln Ile Ser Gln Gly Met Gln Tyr
850 855 860

Leu Ala Glu Met Lys Leu Val His Arg Asp Leu Ala Ala Arg Asn Ile
865 870 875 880

Leu Val Ala Glu Gly Arg Lys Met Lys Ile Ser Asp Phe Gly Leu Ser
885 890 895

Arg Asp Val Tyr Glu Glu Asp Ser Tyr Val Lys Arg Ser Gln Gly Arg
900 905 910

Ile Pro Val Lys Trp Met Ala Ile Glu Ser Leu Phe Asp His Ile Tyr
915 920 925

Thr Thr Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile
930 935 940

Val Thr Leu Gly Gly Asn Pro Tyr Pro Gly Ile Pro Pro Glu Arg Leu
945 950 955 960

Phe Asn Leu Leu Lys Thr Gly His Arg Met Glu Arg Pro Asp Asn Cys
965 970 975

Ser Glu Glu Met Tyr Arg Leu Met Leu Gln Cys Trp Lys Gln Glu Pro
980 985 990

Asp Lys Arg Pro Val Phe Ala Asp Ile Ser Lys Asp Leu Glu Lys Met
995 1000 1005

Met Val Lys Arg Arg Asp Tyr Leu Asp Leu Ala Ala Ser Thr Pro
1010 1015 1020

1020001191 - P17-158 Sequence Listing

Ser Asp Ser Leu Ile Tyr Asp Asp Gly Leu Ser Glu Glu Glu Thr
1025 1030 1035

Pro Leu Val Asp Cys Asn Asn Ala Pro Leu Pro Arg Ala Leu Pro
1040 1045 1050

Ser Thr Trp Ile Glu Asn Lys Leu Tyr Gly Met Ser Asp Pro Asn
1055 1060 1065

Trp Pro Gly Glu Ser Pro Val Pro Leu Thr Arg Ala Asp Gly Thr
1070 1075 1080

Asn Thr Gly Phe Pro Arg Tyr Pro Asn Asp Ser Val Tyr Ala Asn
1085 1090 1095

Trp Met Leu Ser Pro Ser Ala Ala Lys Leu Met Asp Thr Phe Asp
1100 1105 1110

Ser

<210> 32
<211> 1072
<212> PRT
<213> Homo sapiens

<400> 32

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

Leu Leu Leu Pro Leu Leu Gly Lys Val Ala Leu Gly Leu Tyr Phe Ser
20 25 30

Arg Asp Ala Tyr Trp Glu Lys Leu Tyr Val Asp Gln Ala Ala Gly Thr
35 40 45

Pro Leu Leu Tyr Val His Ala Leu Arg Asp Ala Pro Glu Glu Val Pro
50 55 60

1020001191 - P17-158 Sequence Listing

Ser Phe Arg Leu Gly Gln His Leu Tyr Gly Thr Tyr Arg Thr Arg Leu
65 70 75 80

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

Leu Asn Arg Ser Leu Asp His Ser Ser Trp Glu Lys Leu Ser Val Arg
100 105 110

Asn Arg Gly Phe Pro Leu Leu Thr Val Tyr Leu Lys Val Phe Leu Ser
115 120 125

Pro Thr Ser Leu Arg Glu Gly Glu Cys Gln Trp Pro Gly Cys Ala Arg
130 135 140

Val Tyr Phe Ser Phe Phe Asn Thr Ser Phe Pro Ala Cys Ser Ser Leu
145 150 155 160

Lys Pro Arg Glu Leu Cys Phe Pro Glu Thr Arg Pro Ser Phe Arg Ile
165 170 175

Arg Glu Asn Arg Pro Pro Gly Thr Phe His Gln Phe Arg Leu Leu Pro
180 185 190

Val Gln Phe Leu Cys Pro Asn Ile Ser Val Ala Tyr Arg Leu Leu Glu
195 200 205

Gly Glu Gly Leu Pro Phe Arg Cys Ala Pro Asp Ser Leu Glu Val Ser
210 215 220

Thr Arg Trp Ala Leu Asp Arg Glu Gln Arg Glu Lys Tyr Glu Leu Val
225 230 235 240

Ala Val Cys Thr Val His Ala Gly Ala Arg Glu Glu Val Val Met Val
245 250 255

Pro Phe Pro Val Thr Val Tyr Asp Glu Asp Asp Ser Ala Pro Thr Phe
260 265 270

1020001191 - P17-158 Sequence Listing

Pro Ala Gly Val Asp Thr Ala Ser Ala Val Val Glu Phe Lys Arg Lys
275 280 285

Glu Asp Thr Val Val Ala Thr Leu Arg Val Phe Asp Ala Asp Val Val
290 295 300

Pro Ala Ser Gly Glu Leu Val Arg Arg Tyr Thr Ser Thr Leu Leu Pro
305 310 315 320

Gly Asp Thr Trp Ala Gln Gln Thr Phe Arg Val Glu His Trp Pro Asn
325 330 335

Glu Thr Ser Val Gln Ala Asn Gly Ser Phe Val Arg Ala Thr Val His
340 345 350

Asp Tyr Arg Leu Val Leu Asn Arg Asn Leu Ser Ile Ser Glu Asn Arg
355 360 365

Thr Met Gln Leu Ala Val Leu Val Asn Asp Ser Asp Phe Gln Gly Pro
370 375 380

Gly Ala Gly Val Leu Leu Leu His Phe Asn Val Ser Val Leu Pro Val
385 390 395 400

Ser Leu His Leu Pro Ser Thr Tyr Ser Leu Ser Val Ser Arg Arg Ala
405 410 415

Arg Arg Phe Ala Gln Ile Gly Lys Val Cys Val Glu Asn Cys Gln Ala
420 425 430

Phe Ser Gly Ile Asn Val Gln Tyr Lys Leu His Ser Ser Gly Ala Asn
435 440 445

Cys Ser Thr Leu Gly Val Val Thr Ser Ala Glu Asp Thr Ser Gly Ile
450 455 460

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

1020001191 - P17-158 Sequence Listing

Leu His Tyr Met Val Val Ala Thr Asp Gln Gln Thr Ser Arg Gln Ala
485 490 495

Gln Ala Gln Leu Leu Val Thr Val Glu Gly Ser Tyr Val Ala Glu Glu
500 505 510

Ala Gly Cys Pro Leu Ser Cys Ala Val Ser Lys Arg Arg Leu Glu Cys
515 520 525

Glu Glu Cys Gly Gly Leu Gly Ser Pro Thr Gly Arg Cys Glu Trp Arg
530 535 540

Gln Gly Asp Gly Lys Gly Ile Thr Arg Asn Phe Ser Thr Cys Ser Pro
545 550 555 560

Ser Thr Lys Thr Cys Pro Asp Gly His Cys Asp Val Val Glu Thr Gln
565 570 575

Asp Ile Asn Ile Cys Pro Gln Asp Cys Leu Arg Gly Ser Ile Val Gly
580 585 590

Gly His Glu Pro Gly Glu Pro Arg Gly Ile Lys Ala Gly Tyr Gly Thr
595 600 605

Cys Asn Cys Phe Pro Glu Glu Glu Lys Cys Phe Cys Glu Pro Glu Asp
610 615 620

Ile Gln Asp Pro Leu Cys Asp Glu Leu Cys Arg Thr Val Ile Ala Ala
625 630 635 640

Ala Val Leu Phe Ser Phe Ile Val Ser Val Leu Leu Ser Ala Phe Cys
645 650 655

Ile His Cys Tyr His Lys Phe Ala His Lys Pro Pro Ile Ser Ser Ala
660 665 670

Glu Met Thr Phe Arg Arg Pro Ala Gln Ala Phe Pro Val Ser Tyr Ser
675 680 685

1020001191 - P17-158 Sequence Listing

Ser Ser Gly Ala Arg Arg Pro Ser Leu Asp Ser Met Glu Asn Gln Val
690 695 700

Ser Val Asp Ala Phe Lys Ile Leu Glu Asp Pro Lys Trp Glu Phe Pro
705 710 715 720

Arg Lys Asn Leu Val Leu Gly Lys Thr Leu Gly Glu Gly Glu Phe Gly
725 730 735

Lys Val Val Lys Ala Thr Ala Phe His Leu Lys Gly Arg Ala Gly Tyr
740 745 750

Thr Thr Val Ala Val Lys Met Leu Lys Glu Asn Ala Ser Pro Ser Glu
755 760 765

Leu Arg Asp Leu Leu Ser Glu Phe Asn Val Leu Lys Gln Val Asn His
770 775 780

Pro His Val Ile Lys Leu Tyr Gly Ala Cys Ser Gln Asp Gly Pro Leu
785 790 795 800

Leu Leu Ile Val Glu Tyr Ala Lys Tyr Gly Ser Leu Arg Gly Phe Leu
805 810 815

Arg Glu Ser Arg Lys Val Gly Pro Gly Tyr Leu Gly Ser Gly Gly Ser
820 825 830

Arg Asn Ser Ser Ser Leu Asp His Pro Asp Glu Arg Ala Leu Thr Met
835 840 845

Gly Asp Leu Ile Ser Phe Ala Trp Gln Ile Ser Gln Gly Met Gln Tyr
850 855 860

Leu Ala Glu Met Lys Leu Val His Arg Asp Leu Ala Ala Arg Asn Ile
865 870 875 880

Leu Val Ala Glu Gly Arg Lys Met Lys Ile Ser Asp Phe Gly Leu Ser
885 890 895

1020001191 - P17-158 Sequence Listing

Arg Asp Val Tyr Glu Glu Asp Ser Tyr Val Lys Arg Ser Gln Gly Arg
900 905 910

Ile Pro Val Lys Trp Met Ala Ile Glu Ser Leu Phe Asp His Ile Tyr
915 920 925

Thr Thr Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile
930 935 940

Val Thr Leu Gly Gly Asn Pro Tyr Pro Gly Ile Pro Pro Glu Arg Leu
945 950 955 960

Phe Asn Leu Leu Lys Thr Gly His Arg Met Glu Arg Pro Asp Asn Cys
965 970 975

Ser Glu Glu Met Tyr Arg Leu Met Leu Gln Cys Trp Lys Gln Glu Pro
980 985 990

Asp Lys Arg Pro Val Phe Ala Asp Ile Ser Lys Asp Leu Glu Lys Met
995 1000 1005

Met Val Lys Arg Arg Asp Tyr Leu Asp Leu Ala Ala Ser Thr Pro
1010 1015 1020

Ser Asp Ser Leu Ile Tyr Asp Asp Gly Leu Ser Glu Glu Glu Thr
1025 1030 1035

Pro Leu Val Asp Cys Asn Asn Ala Pro Leu Pro Arg Ala Leu Pro
1040 1045 1050

Ser Thr Trp Ile Glu Asn Lys Leu Tyr Gly Arg Ile Ser His Ala
1055 1060 1065

Phe Thr Arg Phe
1070

<210> 33
<211> 26
<212> DNA

1020001191 - P17-158 Sequence Listing

<213> Artificial Sequence

<220>

<223> primer

<400> 33

tgtccagctt tgtgcctgat tgatgt

26

<210> 34

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 34

gctgggcact gaagagaaag gaatgc

26

<210> 35

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 35

agcaggatga gtgcggaggc aagc

24

<210> 36

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 36

ttaactatca aacgtgtcca ttaattttgc cgc

33

<210> 37

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

1020001191 - P17-158 Sequence Listing

<400> 37
agtactgggg tggctggg 18

<210> 38
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 38
cactttggac aaggagatg 19

<210> 39
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 39
acagaactgg agctgcgg 18

<210> 40
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 40
ggactggtgt actcgctg 18

<210> 41
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 41
tcctagactg caggaaacac 20

1020001191 - P17-158 Sequence Listing

<210> 42
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 42
 catcgagaaa gtccagac 18

<210> 43
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 43
 gctgctggag acattgaa 18

<210> 44
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 44
 tcactgctgc tcagctca 18

<210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 45
 gaggatccaa agtgggaatt 20

<210> 46
 <211> 20
 <212> DNA

1020001191 - P17-158 Sequence Listing

<213> Artificial Sequence

<220>

<223> primer

<400> 46

agtatctggc cgagatgaag

20

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 47

gcaaagacct ggagaagatg

20

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 48

aggacgttga actctgacag

20

<210> 49

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 49

cctttgcttc atccagaatc

20

<210> 50

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

1020001191 - P17-158 Sequence Listing

<400> 50
gattttgtgt ttctccagct ct 22

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 51
cctgcttctc tgaggaagaa 20

<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 52
gggccttagt ctcagcaaac 20

<210> 53
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 53
gagcactctg cgtgaactta 20

<210> 54
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 54
cagcttggtc atgtactga t 21

1020001191 - P17-158 Sequence Listing

<210>	55	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	55	
	tggtgagtcc ttcaccag	18
<210>	56	
<211>	22	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	56	
	cctagagttt ttccaagaac ca	22
<210>	57	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	57	
	catttaactg gaatccgacc	20
<210>	58	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	58	
	gactctctcc aggccagttc	20
<210>	59	
<211>	22	
<212>	DNA	

1020001191 - P17-158 Sequence Listing

<213> Artificial Sequence

<220>

<223> primer

<400> 59

ggctatcaga agtaaaacca cc

22

<210> 60

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 60

cgagagctga tggcacta

18

<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 61

cttcatcaca agtgaagtac ttcc

24

<210> 62

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 62

cgtactccac gatgaggag

19

<210> 63

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

1020001191 - P17-158 Sequence Listing

<400> 63
gattctggat gaagcaaagg 20

<210> 64
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 64
ggaagtactt cacttgtgat gaag 24

<210> 65
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 65
cccagccacc ccagtact 18

<210> 66
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 66
gtaaaacgac ggccagt 17

<210> 67
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 67
gttttcccag tcacgac 17

1020001191 - P17-158 Sequence Listing

<210>	68	
<211>	17	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	68	
	caggaaacag ctatgac	17
<210>	69	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	69	
	ctggagccac agtaccact	20
<210>	70	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	70	
	tccaaattcg cttctccta	20
<210>	71	
<211>	25	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	71	
	ttcatcagcc ttcctcaggg aggat	25
<210>	72	
<211>	41	
<212>	DNA	

1020001191 - P17-158 Sequence Listing

<213> Artificial Sequence

<220>

<223> Primer

<400> 72

ggggacaagt ttgtacaaaa aagcaggctt cgccaccagc a

41

<210> 73

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 73

ggggaccact ttgtacaaga aagctggggtt ttaactatca aa

42

<210> 74

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> RET siRNA1

<220>

<221> misc_feature

<223> n stand for thymine

<220>

<221> misc_feature

<222> (20)..(21)

<223> n stand for thymine

<400> 74

cacaugucau caaauguan n

21

<210> 75

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> RET siRNA2

1020001191 - P17-158 Sequence Listing

```

<220>
<221> misc_feature
<222> (20)..(21)
<223> n stand for thymine

<400> 75
ggauugaaaa caaacucuan n
21

<210> 76
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> RET siRNA

<220>
<221> misc_feature
<222> (20)..(21)
<223> n stand for thymine

<400> 76
gcuugucccg agauguuuan n
21

<210> 77
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> RET siRNA3

<220>
<221> misc_feature
<222> (20)..(21)
<223> n stand for thymine

<400> 77
ccacugcuac cacaaguun n
21

```