

MP_1_0250_PCT_Sequence_Listing_20170104_ST25
SEQUENCE LISTING

<110> Omeros Corporation
University of Leicester
Brunskill, Nigel
Demopulos, Gregory A.
Dudler, Tom
Schwaeble, Hans-Wilhelm

<120> Methods for Inhibiting Fibrosis in a Subject in Need Thereof

<130> MP.1.0250.PCT

<150> 62/275,025

<151> 2016-01-05

<150> 62/407,979

<151> 2016-10-13

<160> 85

<170> PatentIn version 3.5

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (27)..(584)

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Leu Cys Gly Ser Val Ala Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro
10 15 20 25

gtg ttc ggg cgc ctg gca tcc ccc ggc ttt cca ggg gag tat gcc aat 149

Val Phe Gly Arg Leu Ala Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn
30 35 40

gac cag gag cgg cgc tgg acc ctg act gca ccc ccc ggc tac cgc ctg 197

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

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cgc ctc tac ttc acc cac ttc gac ctg gag ctc tcc cac ctc tgc gag			245
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tac gac ttc gtc aag ctg agc tcg ggg gcc aag gtg ctg gcc acg ctg			293
Tyr Asp Phe Val Lys Leu Ser Ser Gly Ala Lys Val Leu Ala Thr Leu			
75	80	85	
tgc ggg cag gag agc aca gac acg gag cgg gcc cct ggc aag gac act			341
Cys Gly Gln Glu Ser Thr Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr			
90	95	100	105
ttc tac tcg ctg ggc tcc agc ctg gac att acc ttc cgc tcc gac tac			389
Phe Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr			
110	115	120	
tcc aac gag aag ccg ttc acg ggg ttc gag gcc ttc tat gca gcc gag			437
Ser Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu			
125	130	135	
gac att gac gag tgc cag gtg gcc ccg gga gag gcg ccc acc tgc gac			485
Asp Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys Asp			
140	145	150	
cac cac tgc cac aac cac ctg ggc ggt ttc tac tgc tcc tgc cgc gca			533
His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala			
155	160	165	
ggc tac gtc ctg cac cgt aac aag cgc acc tgc tca gag cag agc ctc			581
Gly Tyr Val Leu His Arg Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu			
170	175	180	185
tag cctcccctgg agctccggcc tgcccagcag gtcagaagcc agagccagcc			634
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Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
20 25 30

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
130 135 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
145 150 155 160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
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Lys Arg Thr Cys Ser Glu Gln Ser Leu
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<212> PRT

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Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
35 40 45

Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
50 55 60

Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65 70 75 80

Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
85 90 95

Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
115 120 125

Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
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Cys Gly Ser Val Ala Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val
15 20 25

ttc ggg cgc ctg gca tcc ccc ggc ttt cca ggg gag tat gcc aat gac 147
Phe Gly Arg Leu Ala Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp
30 35 40

cag gag cgg cgc tgg acc ctg act gca ccc ccc ggc tac cgc ctg cgc 195
Gln Glu Arg Arg Trp Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg
45 50 55

ctc tac ttc acc cac ttc gac ctg gag ctc tcc cac ctc tgc gag tac 243
Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr
60 65 70

gac ttc gtc aag ctg agc tcg ggg gcc aag gtg ctg gcc acg ctg tgc 291
Asp Phe Val Lys Leu Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys
75 80 85 90

ggg cag gag agc aca gac acg gag cgg gcc cct ggc aag gac act ttc 339
Gly Gln Glu Ser Thr Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe
95 100 105

tac tcg ctg ggc tcc agc ctg gac att acc ttc cgc tcc gac tac tcc 387
Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser
110 115 120

aac gag aag ccg ttc acg ggg ttc gag gcc ttc tat gca gcc gag gac 435
Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp

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cac tgc cac aac cac ctg ggc ggt ttc tac tgc tcc tgc cgc gca ggc His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly 155 160 165 170			531
tac gtc ctg cac cgt aac aag cgc acc tgc tca gcc ctg tgc tcc ggc Tyr Val Leu His Arg Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly 175 180 185			579
cag gtc ttc acc cag agg tct ggg gag ctc agc agc cct gaa tac cca Gln Val Phe Thr Gln Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro 190 195 200			627
cgg ccg tat ccc aaa ctc tcc agt tgc act tac agc atc agc ctg gag Arg Pro Tyr Pro Lys Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu 205 210 215			675
gag ggg ttc agt gtc att ctg gac ttt gtg gag tcc ttc gat gtg gag Glu Gly Phe Ser Val Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu 220 225 230			723
aca cac cct gaa acc ctg tgt ccc tac gac ttt ctc aag att caa aca Thr His Pro Glu Thr Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr 235 240 245 250			771
gac aga gaa gaa cat ggc cca ttc tgt ggg aag aca ttg ccc cac agg Asp Arg Glu Glu His Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg 255 260 265			819
att gaa aca aaa agc aac acg gtg acc atc acc ttt gtc aca gat gaa Ile Glu Thr Lys Ser Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu 270 275 280			867
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cct tgc cct tat ccg atg gcg cca cct aat ggc cac gtt tca cct gtg Pro Cys Pro Tyr Pro Met Ala Pro Pro Asn Gly His Val Ser Pro Val 300 305 310			963
caa gcc aaa tac atc ctg aaa gac agc ttc tcc atc ttt tgc gag act Gln Ala Lys Tyr Ile Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr			1011

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Gly Tyr Glu Leu Leu Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala	335	340	345	
gtt tgt cag aaa gat gga tct tgg gac cgg cca atg ccc gcg tgc agc				1107
Val Cys Gln Lys Asp Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser	350	355	360	
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Ile Val Asp Cys Gly Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu	365	370	375	
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Tyr Ile Thr Gly Pro Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr	380	385	390	
agc tgt gaa gag acc ttc tac aca atg aaa gtg aat gat ggt aaa tat				1251
Ser Cys Glu Glu Thr Phe Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr	395	400	405	410
gtg tgt gag gct gat gga ttc tgg acg agc tcc aaa gga gaa aaa tca				1299
Val Cys Glu Ala Asp Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser	415	420	425	
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Leu Pro Val Cys Glu Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly	430	435	440	
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Gly Arg Ile Tyr Gly Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp	445	450	455	
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Gln Val Leu Ile Leu Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr	460	465	470	
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Asp Asn Trp Val Leu Thr Ala Ala His Ala Val Tyr Glu Gln Lys His	475	480	485	490
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Asp Ala Ser Ala Leu Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser	495	500	505	
cct cat tat aca caa gcc tgg tct gaa gct gtt ttt ata cat gaa ggt				1587
Pro His Tyr Thr Gln Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly				

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aat aac aaa gtt gta atc aat agc aac atc acg cct att tgt ctg cca Asn Asn Lys Val Val Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro 540 545 550			1683
aga aaa gaa gct gaa tcc ttt atg agg aca gat gac att gga act gca Arg Lys Glu Ala Glu Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala 555 560 565 570			1731
tct gga tgg gga tta acc caa agg ggt ttt ctt gct aga aat cta atg Ser Gly Trp Gly Leu Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met 575 580 585			1779
tat gtc gac ata ccg att gtt gac cat caa aaa tgt act gct gca tat Tyr Val Asp Ile Pro Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr 590 595 600			1827
gaa aag cca ccc tat cca agg gga agt gta act gct aac atg ctt tgt Glu Lys Pro Pro Tyr Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys 605 610 615			1875
gct ggc tta gaa agt ggg ggc aag gac agc tgc aga ggt gac agc gga Ala Gly Leu Glu Ser Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly 620 625 630			1923
ggg gca ctg gtg ttt cta gat agt gaa aca gag agg tgg ttt gtg gga Gly Ala Leu Val Phe Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly 635 640 645 650			1971
gga ata gtg tcc tgg ggt tcc atg aat tgt ggg gaa gca ggt cag tat Gly Ile Val Ser Trp Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr 655 660 665			2019
gga gtc tac aca aaa gtt att aac tat att ccc tgg atc gag aac ata Gly Val Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile 670 675 680			2067
att agt gat ttt taa cttgcgtgtc tgcagtcaag gattcttcat ttttagaaat Ile Ser Asp Phe 685			2122
gcctgtgaag accttggcag cgacgtggct cgagaagcat tcatcattac tgttgacatg			2182

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gtcatctttg	cccaccagtg	gtaatgtcac	tgctcaaatt	acatttcatt	accttaaaaa	2362
gccagtctct	tttcatactg	gctgtttggca	tttctgtaaa	ctgcctgtcc	atgctctttg	2422
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<213> Homo sapiens
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35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

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Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
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Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
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Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
 165 170 175

Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln Arg
 180 185 190

Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu
 195 200 205

Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val Ile
 210 215 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
 225 230 235 240

Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
 245 250 255

Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
 260 265 270

Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
 275 280 285

Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro Met
 290 295 300

Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile Leu
 305 310 315 320

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Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu Gln
325 330 335

Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
340 345 350

Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly Pro
355 360 365

Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro Gly
370 375 380

Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
385 390 395 400

Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp Gly
405 410 415

Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu Pro
420 425 430

Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly Gly
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Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu Gly
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Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu Thr
465 470 475 480

Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu Asp
485 490 495

Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln Ala
500 505 510

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Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala Gly
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Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val Ile
530 535 540

Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu Ser
545 550 555 560

Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu Thr
565 570 575

Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro Ile
580 585 590

Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr Pro
595 600 605

Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser Gly
610 615 620

Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
625 630 635 640

Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
645 650 655

Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val Tyr Thr Lys Val
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<213> Homo sapiens

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35 40 45

Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
50 55 60

Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65 70 75 80

Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
85 90 95

Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
115 120 125

Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
130 135 140

Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
145 150 155 160

Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln
165 170 175

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Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys
180 185 190

Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val
195 200 205

Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr
210 215 220

Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His
225 230 235 240

Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser
245 250 255

Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr
260 265 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro
275 280 285

Met Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile
290 295 300

Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu
305 310 315 320

Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
325 330 335

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340 345 350

Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro
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Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
370 375 380

Phe Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp
385 390 395 400

Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu
405 410 415

Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly
420 425 430

Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu
435 440 445

Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu
450 455 460

Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu
465 470 475 480

Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
485 490 495

Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala
500 505 510

Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val
515 520 525

Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu
530 535 540

Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu
545 550 555 560

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro
565 570 575

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580 585 590

Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser
595 600 605

Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe
610 615 620

Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp
625 630 635 640

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<212> DNA

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MP_1_0250_PCT_Sequence_Listing_20170104_ST25

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<210> 8
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 8

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

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

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
 35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
 50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
 65 70 75 80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
 85 90 95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
 100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
 115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

130

135

<210> 9

<211> 181

<212> PRT

<213> Homo sapiens

<400> 9

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

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

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
130 135 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
145 150 155 160

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
165 170 175

Lys Arg Thr Cys Ser
180

<210> 10
<211> 293
<212> PRT
<213> Homo sapiens

<400> 10

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

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

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

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Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
 130 135 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
 145 150 155 160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
 165 170 175

Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln Arg
 180 185 190

Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu
 195 200 205

Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val Ile
 210 215 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
 225 230 235 240

Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
 245 250 255

Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
 260 265 270

Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
 275 280 285

Trp Lys Ile His Tyr
 290

<210> 11
 <211> 41
 <212> PRT

<213> Homo sapiens

<400> 11

Glu Asp Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys
 1 5 10 15

Asp His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg
 20 25 30

Ala Gly Tyr Val Leu His Arg Asn Lys
 35 40

<210> 12

<211> 242

<212> PRT

<213> Homo sapiens

<400> 12

Ile Tyr Gly Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val
 1 5 10 15

Leu Ile Leu Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn
 20 25 30

Trp Val Leu Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala
 35 40 45

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

Tyr Thr Gln Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr
 65 70 75 80

His Asp Ala Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn
 85 90 95

Lys Val Val Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys

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100

105

110

Glu Ala Glu Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly
115 120 125

Trp Gly Leu Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val
130 135 140

Asp Ile Pro Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys
145 150 155 160

Pro Pro Tyr Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly
165 170 175

Leu Glu Ser Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala
180 185 190

Leu Val Phe Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile
195 200 205

Val Ser Trp Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val
210 215 220

Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser
225 230 235 240

Asp Phe

<210> 13

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 13

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

Gly Lys Asp Ser Cys Arg Gly Asp Ala Gly Gly Ala Leu Val Phe Leu
1 5 10 15

<210> 14
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 14

Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu
1 5 10 15

<210> 15
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 15

Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe Asp
1 5 10 15

Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser Ser
20 25 30

Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln
35 40

<210> 16
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

<400> 16

Thr Phe Arg Ser Asp Tyr Ser Asn
1 5

<210> 17

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 17

Phe Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr
1 5 10 15

Ser Asn Glu Lys Pro Phe Thr Gly Phe
20 25

<210> 18

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 18

Ile Asp Glu Cys Gln Val Ala Pro Gly
1 5

<210> 19

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 19

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

Ala Asn Met Leu Cys Ala Gly Leu Glu Ser Gly Gly Lys Asp Ser Cys
1 5 10 15

Arg Gly Asp Ser Gly Gly Ala Leu Val
20 25

<210> 20
<211> 960
<212> DNA
<213> Homo sapiens

<220>
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<222> (51)..(797)

<400> 20
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Met Ser
1

ctg ttt cca tca ctc cct ctc ctt ctc ctg agt atg gtg gca gcg tct 104
Leu Phe Pro Ser Leu Pro Leu Leu Leu Leu Ser Met Val Ala Ala Ser
5 10 15

tac tca gaa act gtg acc tgt gag gat gcc caa aag acc tgc cct gca 152
Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr Cys Pro Ala
20 25 30

gtg att gcc tgt agc tct cca ggc atc aac ggc ttc cca ggc aaa gat 200
Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly Lys Asp
35 40 45 50

ggg cgt gat ggc acc aag gga gaa aag ggg gaa cca ggc caa ggg ctc 248
Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln Gly Leu
55 60 65

aga ggc tta cag ggc ccc cct gga aag ttg ggg cct cca gga aat cca 296
Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly Asn Pro
70 75 80

ggg cct tct ggg tca cca gga cca aag ggc caa aaa gga gac cct gga 344
Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp Pro Gly
85 90 95

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aaa agt ccg gat ggt gat agt agc ctg gct gcc tca gaa aga aaa gct	392
Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg Lys Ala	
100 105 110	
ctg caa aca gaa atg gca cgt atc aaa aag tgg ctc acc ttc tct ctg	440
Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe Ser Leu	
115 120 125 130	
ggc aaa caa gtt ggg aac aag ttc ttc ctg acc aat ggt gaa ata atg	488
Gly Lys Gln Val Gly Asn Lys Phe Phe Leu Thr Asn Gly Glu Ile Met	
135 140 145	
acc ttt gaa aaa gtg aag gcc ttg tgt gtc aag ttc cag gcc tct gtg	536
Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala Ser Val	
150 155 160	
gcc acc ccc agg aat gct gca gag aat gga gcc att cag aat ctc atc	584
Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn Leu Ile	
165 170 175	
aag gag gaa gcc ttc ctg ggc atc act gat gag aag aca gaa ggg cag	632
Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu Gly Gln	
180 185 190	
ttt gtg gat ctg aca gga aat aga ctg acc tac aca aac tgg aac gag	680
Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp Asn Glu	
195 200 205 210	
ggt gaa ccc aac aat gct ggt tct gat gaa gat tgt gta ttg cta ctg	728
Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val Leu Leu Leu	
215 220 225	
aaa aat ggc cag tgg aat gac gtc ccc tgc tcc acc tcc cat ctg gcc	776
Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His Leu Ala	
230 235 240	
gtc tgt gag ttc cct atc tga agggatcatat cactcaggcc ctccttgtct	827
Val Cys Glu Phe Pro Ile	
245	
ttttactgca acccacaggc ccacagtatg cttgaaaaga taaattatat caatttcctc	887
atatccagta ttgttccttt tgtgggcaat cactaaaaat gatcactaac agcaccaaca	947
aagcaataat agt	960

<210> 21

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

<211> 248

<212> PRT

<213> Homo sapiens

<400> 21

Met Ser Leu Phe Pro Ser Leu Pro Leu Leu Leu Ser Met Val Ala
1 5 10 15

Ala Ser Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr Cys
20 25 30

Pro Ala Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly
35 40 45

Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln
50 55 60

Gly Leu Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly
65 70 75 80

Asn Pro Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp
85 90 95

Pro Gly Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg
100 105 110

Lys Ala Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe
115 120 125

Ser Leu Gly Lys Gln Val Gly Asn Lys Phe Phe Leu Thr Asn Gly Glu
130 135 140

Ile Met Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala
145 150 155 160

Ser Val Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn
165 170 175

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Leu Ile Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu
180 185 190

Gly Gln Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp
195 200 205

Asn Glu Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val Leu
210 215 220

Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His
225 230 235 240

Leu Ala Val Cys Glu Phe Pro Ile
245

<210> 22
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Wherein X at position 1 represents hydroxyproline

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Wherein X at position 4 represents hydrophobic residue

<400> 22

Xaa Gly Lys Xaa Gly Pro
1 5

<210> 23

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

<220>
 <223> Synthetic

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Wherein X represents hydroxyproline

<400> 23

Xaa Gly Lys Leu Gly
 1 5

<210> 24
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> MISC_FEATURE
 <222> (9)..(15)
 <223> Wherein X at positions 9 and 15 represents hydroxyproline

<400> 24

Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly Lys Leu Gly Pro Xaa Gly
 1 5 10 15

<210> 25
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

<220>

<221> MISC_FEATURE

<222> (3)..(27)

<223> Wherein X at positions 3, 6, 15, 21, 24, 27 represents hydroxyproline

<400> 25

Gly	Pro	Xaa	Gly	Pro	Xaa	Gly	Leu	Arg	Gly	Leu	Gln	Gly	Pro	Xaa	Gly
1				5				10						15	

Lys	Leu	Gly	Pro	Xaa	Gly	Pro	Xaa	Gly	Pro	Xaa
		20					25			

<210> 26

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (26)..(26)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (32)..(32)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (35)..(35)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (41)..(41)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (50)..(50)

<223> Xaa can be any naturally occurring amino acid

<400> 26

Gly Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly
1 5 10 15

Gln Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly Lys Leu Gly Pro Xaa
20 25 30

Gly Asn Xaa Gly Pro Ser Gly Ser Xaa Gly Pro Lys Gly Gln Lys Gly
35 40 45

Asp Xaa Gly Lys Ser
50

<210> 27

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (3)..(33)

<223> Wherein X at positions 3, 6, 12, 18, 21, 30, 33 represents
hydroxyproline

<400> 27

Gly Ala Xaa Gly Ser Xaa Gly Glu Lys Gly Ala Xaa Gly Pro Gln Gly
1 5 10 15

Pro Xaa Gly Pro Xaa Gly Lys Met Gly Pro Lys Gly Glu Xaa Gly Asp
20 25 30

Xaa

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<210> 28
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> MISC_FEATURE
 <222> (3)..(45)
 <223> Wherein X at positions 3, 6, 9, 27, 30, 36, 42, 45 represents
 hydroxyproline

<400> 28

Gly	Cys	Xaa	Gly	Leu	Xaa	Gly	Ala	Xaa	Gly	Asp	Lys	Gly	Glu	Ala	Gly
1				5					10					15	

Thr	Asn	Gly	Lys	Arg	Gly	Glu	Arg	Gly	Pro	Xaa	Gly	Pro	Xaa	Gly	Lys
			20					25					30		

Ala	Gly	Pro	Xaa	Gly	Pro	Asn	Gly	Ala	Xaa	Gly	Glu	Xaa
		35					40					45

<210> 29
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 29

Leu	Gln	Arg	Ala	Leu	Glu	Ile	Leu	Pro	Asn	Arg	Val	Thr	Ile	Lys	Ala
1				5					10					15	

Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile
				20			

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<210> 30
 <211> 559
 <212> DNA
 <213> Homo sapiens

<400> 30
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 aagtggcctg aacctgtgtt cgggcgcctg gcatcccccg gctttccagg ggagtatgcc 120
 aatgaccagg agcggcgctg gaccctgact gcaccccccg gctaccgcct gcgcctctac 180
 ttcaccact tcgacctgga gctctccac ctctgcgagt acgacttcgt caagctgagc 240
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aagacatgaa tccatgagga cagagtgtgg aagaggaagc agcagcctca aagttctgga 300
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acgacgcagg ggccgagggc cccatttaca gctgacaaag tggggccctg ccagcgggag	2520
cgctgccagg atgtttgatt tcagatccca gtccctgcag agaccaactg tgtgacctct	2580

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aaactccac tggtttaaca gaggtgatgt ttgcatcttt ctcccagcgc tgctgggagc	2760
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<220>
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gaa cct gta ttc ggg cgc ctg gtg tcc cct ggc ttc cca gag aag tat Glu Pro Val Phe Gly Arg Leu Val Ser Pro Gly Phe Pro Glu Lys Tyr 25 30 35	149
gct gac cat caa gat cga tcc tgg aca ctg act gca ccc cct ggc tac Ala Asp His Gln Asp Arg Ser Trp Thr Leu Thr Ala Pro Pro Gly Tyr 40 45 50 55	197
cgc ctg cgc ctc tac ttc acc cac ttt gac ctg gaa ctc tct tac cgc Arg Leu Arg Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser Tyr Arg 60 65 70	245
tgc gag tat gac ttt gtc aag ttg agc tca ggg acc aag gtg ctg gcc Cys Glu Tyr Asp Phe Val Lys Leu Ser Ser Gly Thr Lys Val Leu Ala 75 80 85	293
aca ctg tgt ggg cag gag agt aca gac act gag cag gca cct ggc aat Thr Leu Cys Gly Gln Glu Ser Thr Asp Thr Glu Gln Ala Pro Gly Asn 90 95 100	341
gac acc ttc tac tca ctg ggt ccc agc cta aag gtc acc ttc cac tcc Asp Thr Phe Tyr Ser Leu Gly Pro Ser Leu Lys Val Thr Phe His Ser 105 110 115	389
gac tac tcc aat gag aag ccg ttc aca ggg ttt gag gcc ttc tat gca Asp Tyr Ser Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala 120 125 130 135	437
gcg gag gat gtg gat gaa tgc aga gtg tct ctg gga gac tca gtc cct Ala Glu Asp Val Asp Glu Cys Arg Val Ser Leu Gly Asp Ser Val Pro 140 145 150	485
tgt gac cat tat tgc cac aac tac ttg ggc ggc tac tat tgc tcc tgc Cys Asp His Tyr Cys His Asn Tyr Leu Gly Gly Tyr Tyr Cys Ser Cys 155 160 165	533
aga gcg ggc tac att ctc cac cag aac aag cac acg tgc tca gcc ctt Arg Ala Gly Tyr Ile Leu His Gln Asn Lys His Thr Cys Ser Ala Leu 170 175 180	581
tgt tca ggc cag gtg ttc aca gga aga tct ggg tat ctc agt agc cct Cys Ser Gly Gln Val Phe Thr Gly Arg Ser Gly Tyr Leu Ser Ser Pro 185 190 195	629

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gag tac ccg cag cca tac ccc aag ctc tcc agc tgc acc tac agc atc Glu Tyr Pro Gln Pro Tyr Pro Lys Leu Ser Ser Cys Thr Tyr Ser Ile 200 205 210 215	677
cgc ctg gag gac ggc ttc agt gtc atc ctg gac ttc gtg gag tcc ttc Arg Leu Glu Asp Gly Phe Ser Val Ile Leu Asp Phe Val Glu Ser Phe 220 225 230	725
gat gtg gag acg cac cct gaa gcc cag tgc ccc tat gac tcc ctc aag Asp Val Glu Thr His Pro Glu Ala Gln Cys Pro Tyr Asp Ser Leu Lys 235 240 245	773
att caa aca gac aag ggg gaa cac ggc cca ttt tgt ggg aag acg ctg Ile Gln Thr Asp Lys Gly Glu His Gly Pro Phe Cys Gly Lys Thr Leu 250 255 260	821
cct ccc agg att gaa act gac agc cac aag gtg acc atc acc ttt gcc Pro Pro Arg Ile Glu Thr Asp Ser His Lys Val Thr Ile Thr Phe Ala 265 270 275	869
act gac gag tcg ggg aac cac aca ggc tgg aag ata cac tac aca agc Thr Asp Glu Ser Gly Asn His Thr Gly Trp Lys Ile His Tyr Thr Ser 280 285 290 295	917
aca gca cgg ccc tgc cct gat cca acg gcg cca cct aat ggc agc att Thr Ala Arg Pro Cys Pro Asp Pro Thr Ala Pro Pro Asn Gly Ser Ile 300 305 310	965
tca cct gtg caa gcc acg tat gtc ctg aag gac agg ttt tct gtc ttc Ser Pro Val Gln Ala Thr Tyr Val Leu Lys Asp Arg Phe Ser Val Phe 315 320 325	1013
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cat gtg gac tat atc aca ggc cct caa gtg act acc tac aaa gct gtg His Val Asp Tyr Ile Thr Gly Pro Gln Val Thr Thr Tyr Lys Ala Val 380 385 390	1205

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aaa tat gtg tgt gag gct gat gga ttc tgg acg agc tcc aaa gga gaa Lys Tyr Val Cys Glu Ala Asp Gly Phe Trp Thr Ser Ser Lys Gly Glu 410 415 420	1301
aaa ctc ccc ccg gtt tgt gag cct gtt tgt ggg ctg tcc aca cac act Lys Leu Pro Pro Val Cys Glu Pro Val Cys Gly Leu Ser Thr His Thr 425 430 435	1349
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cct tgg caa gtc ttg ttg ctg ggt caa act aca gca gca gca ggt gca Pro Trp Gln Val Leu Leu Gly Gln Thr Thr Ala Ala Ala Gly Ala 460 465 470	1445
ctt ata cat gac aat tgg gtc cta aca gcc gct cat gct gta tat gag Leu Ile His Asp Asn Trp Val Leu Thr Ala Ala His Ala Val Tyr Glu 475 480 485	1493
aaa aga atg gca gcg tcc tcc ctg aac atc cga atg ggc atc ctc aaa Lys Arg Met Ala Ala Ser Ser Leu Asn Ile Arg Met Gly Ile Leu Lys 490 495 500	1541
agg ctc tca cct cat tac act caa gcc tgg ccc gag gaa atc ttt ata Arg Leu Ser Pro His Tyr Thr Gln Ala Trp Pro Glu Glu Ile Phe Ile 505 510 515	1589
cat gaa ggc tac act cac ggt gct ggt ttt gac aat gat ata gca ttg His Glu Gly Tyr Thr His Gly Ala Gly Phe Asp Asn Asp Ile Ala Leu 520 525 530 535	1637
att aaa ctc aag aac aaa gtc aca atc aac gga agc atc atg cct gtt Ile Lys Leu Lys Asn Lys Val Thr Ile Asn Gly Ser Ile Met Pro Val 540 545 550	1685
tgc cta ccg cga aaa gaa gct gca tcc tta atg aga aca gac ttc act Cys Leu Pro Arg Lys Glu Ala Ala Ser Leu Met Arg Thr Asp Phe Thr 555 560 565	1733
gga act gtg gct ggc tgg ggg tta acc cag aag ggg ctt ctt gct aga Gly Thr Val Ala Gly Trp Gly Leu Thr Gln Lys Gly Leu Leu Ala Arg 570 575 580	1781

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aac cta atg ttt gtg gac ata cca att gct gac cac caa aaa tgt acc	1829
Asn Leu Met Phe Val Asp Ile Pro Ile Ala Asp His Gln Lys Cys Thr	
585 590 595	
acc gtg tat gaa aag ctc tat cca gga gta aga gta agc gct aac atg	1877
Thr Val Tyr Glu Lys Leu Tyr Pro Gly Val Arg Val Ser Ala Asn Met	
600 605 610 615	
ctc tgt gct ggc tta gag act ggt ggc aag gac agc tgc aga ggt gac	1925
Leu Cys Ala Gly Leu Glu Thr Gly Gly Lys Asp Ser Cys Arg Gly Asp	
620 625 630	
agt ggg ggg gca tta gtg ttt cta gat aat gag aca cag cga tgg ttt	1973
Ser Gly Gly Ala Leu Val Phe Leu Asp Asn Glu Thr Gln Arg Trp Phe	
635 640 645	
gtg gga gga ata gtt tcc tgg ggt tcc att aat tgt ggg gcg gca ggc	2021
Val Gly Gly Ile Val Ser Trp Gly Ser Ile Asn Cys Gly Ala Ala Gly	
650 655 660	
cag tat ggg gtc tac aca aaa gtc atc aac tat att ccc tgg aat gag	2069
Gln Tyr Gly Val Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Asn Glu	
665 670 675	
aac ata ata agt aat ttc taa	2090
Asn Ile Ile Ser Asn Phe	
680 685	

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<400> 51

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Pro Gly Phe Pro Glu Lys Tyr Ala Asp His Gln Asp Arg Ser Trp Thr
35 40 45

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Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Gln Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro Ser
100 105 110

Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg Val
130 135 140

Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr Leu
145 150 155 160

Gly Gly Tyr Tyr Cys Ser Cys Arg Ala Gly Tyr Ile Leu His Gln Asn
165 170 175

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

Ser Gly Tyr Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys Leu
195 200 205

Ser Ser Cys Thr Tyr Ser Ile Arg Leu Glu Asp Gly Phe Ser Val Ile
210 215 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Ala Gln
225 230 235 240

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Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Gly Glu His Gly
245 250 255

Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser His
260 265 270

Lys Val Thr Ile Thr Phe Ala Thr Asp Glu Ser Gly Asn His Thr Gly
275 280 285

Trp Lys Ile His Tyr Thr Ser Thr Ala Arg Pro Cys Pro Asp Pro Thr
290 295 300

Ala Pro Pro Asn Gly Ser Ile Ser Pro Val Gln Ala Thr Tyr Val Leu
305 310 315 320

Lys Asp Arg Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu Gln
325 330 335

Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
340 345 350

Ser Trp Asp Arg Pro Met Pro Glu Cys Ser Ile Ile Asp Cys Gly Pro
355 360 365

Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro Gln
370 375 380

Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
385 390 395 400

Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly Phe
405 410 415

Trp Thr Ser Ser Lys Gly Glu Lys Leu Pro Pro Val Cys Glu Pro Val
420 425 430

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Cys Gly Leu Ser Thr His Thr Ile Gly Gly Arg Ile Val Gly Gly Gln
435 440 445

Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly Gln
450 455 460

Thr Thr Ala Ala Ala Gly Ala Leu Ile His Asp Asn Trp Val Leu Thr
465 470 475 480

Ala Ala His Ala Val Tyr Glu Lys Arg Met Ala Ala Ser Ser Leu Asn
485 490 495

Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Pro His Tyr Thr Gln Ala
500 505 510

Trp Pro Glu Glu Ile Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly
515 520 525

Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile
530 535 540

Asn Gly Ser Ile Met Pro Val Cys Leu Pro Arg Lys Glu Ala Ala Ser
545 550 555 560

Leu Met Arg Thr Asp Phe Thr Gly Thr Val Ala Gly Trp Gly Leu Thr
565 570 575

Gln Lys Gly Leu Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile
580 585 590

Ala Asp His Gln Lys Cys Thr Thr Val Tyr Glu Lys Leu Tyr Pro Gly
595 600 605

Val Arg Val Ser Ala Asn Met Leu Cys Ala Gly Leu Glu Thr Gly Gly
610 615 620

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Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu Asp
625 630 635 640

Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly Ser
645 650 655

Ile Asn Cys Gly Ala Ala Gly Gln Tyr Gly Val Tyr Thr Lys Val Ile
660 665 670

Asn Tyr Ile Pro Trp Asn Glu Asn Ile Ile Ser Asn Phe
675 680 685

<210> 52
<211> 670
<212> PRT
<213> Murine

<400> 52

Thr Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val
1 5 10 15

Ser Pro Gly Phe Pro Glu Lys Tyr Ala Asp His Gln Asp Arg Ser Trp
20 25 30

Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
35 40 45

Phe Asp Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu
50 55 60

Ser Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65 70 75 80

Asp Thr Glu Gln Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro
85 90 95

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Ser Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe
100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg
115 120 125

Val Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr
130 135 140

Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Ala Gly Tyr Ile Leu His Gln
145 150 155 160

Asn Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly
165 170 175

Arg Ser Gly Tyr Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys
180 185 190

Leu Ser Ser Cys Thr Tyr Ser Ile Arg Leu Glu Asp Gly Phe Ser Val
195 200 205

Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Ala
210 215 220

Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Gly Glu His
225 230 235 240

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

His Lys Val Thr Ile Thr Phe Ala Thr Asp Glu Ser Gly Asn His Thr
260 265 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Arg Pro Cys Pro Asp Pro
275 280 285

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Thr Ala Pro Pro Asn Gly Ser Ile Ser Pro Val Gln Ala Thr Tyr Val
290 295 300

Leu Lys Asp Arg Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu
305 310 315 320

Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
325 330 335

Gly Ser Trp Asp Arg Pro Met Pro Glu Cys Ser Ile Ile Asp Cys Gly
340 345 350

Pro Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro
355 360 365

Gln Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
370 375 380

Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly
385 390 395 400

Phe Trp Thr Ser Ser Lys Gly Glu Lys Leu Pro Pro Val Cys Glu Pro
405 410 415

Val Cys Gly Leu Ser Thr His Thr Ile Gly Gly Arg Ile Val Gly Gly
420 425 430

Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly
435 440 445

Gln Thr Thr Ala Ala Ala Gly Ala Leu Ile His Asp Asn Trp Val Leu
450 455 460

Thr Ala Ala His Ala Val Tyr Glu Lys Arg Met Ala Ala Ser Ser Leu
465 470 475 480

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Asn Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
485 490 495

Ala Trp Pro Glu Glu Ile Phe Ile His Glu Gly Tyr Thr His Gly Ala
500 505 510

Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr
515 520 525

Ile Asn Gly Ser Ile Met Pro Val Cys Leu Pro Arg Lys Glu Ala Ala
530 535 540

Ser Leu Met Arg Thr Asp Phe Thr Gly Thr Val Ala Gly Trp Gly Leu
545 550 555 560

Thr Gln Lys Gly Leu Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro
565 570 575

Ile Ala Asp His Gln Lys Cys Thr Thr Val Tyr Glu Lys Leu Tyr Pro
580 585 590

Gly Val Arg Val Ser Ala Asn Met Leu Cys Ala Gly Leu Glu Thr Gly
595 600 605

Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
610 615 620

Asp Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
625 630 635 640

Ser Ile Asn Cys Gly Ala Ala Gly Gln Tyr Gly Val Tyr Thr Lys Val
645 650 655

Ile Asn Tyr Ile Pro Trp Asn Glu Asn Ile Ile Ser Asn Phe
660 665 670

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<210> 53
<211> 2091
<212> DNA
<213> Rat

<220>
<221> CDS
<222> (10)..(2067)

<400> 53
 tggcacaca atg agg cta ctg atc gtc ctg ggt ctg ctt tgg agt ttg gtg 51
 Met Arg Leu Leu Ile Val Leu Gly Leu Leu Trp Ser Leu Val
 1 5 10

 gcc aca ctt ttg ggc tcc aag tgg cct gag cct gta ttc ggg cgc ctg 99
 Ala Thr Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu
 15 20 25 30

 gtg tcc ctg gcc ttc cca gag aag tat ggc aac cat cag gat cga tcc 147
 Val Ser Leu Ala Phe Pro Glu Lys Tyr Gly Asn His Gln Asp Arg Ser
 35 40 45

 tgg acg ctg act gca ccc cct ggc ttc cgc ctg cgc ctc tac ttc acc 195
 Trp Thr Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr
 50 55 60

 cac ttc aac ctg gaa ctc tct tac cgc tgc gag tat gac ttt gtc aag 243
 His Phe Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys
 65 70 75

 ttg acc tca ggg acc aag gtg cta gcc acg ctg tgt ggg cag gag agt 291
 Leu Thr Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser
 80 85 90

 aca gat act gag cgg gca cct ggc aat gac acc ttc tac tca ctg ggt 339
 Thr Asp Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly
 95 100 105 110

 ccc agc cta aag gtc acc ttc cac tcc gac tac tcc aat gag aag cca 387
 Pro Ser Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro
 115 120 125

 ttc aca gga ttt gag gcc ttc tat gca gcg gag gat gtg gat gaa tgc 435
 Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys
 130 135 140

 aga aca tcc ctg gga gac tca gtc cct tgt gac cat tat tgc cac aac 483

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Arg	Thr	Ser	Leu	Gly	Asp	Ser	Val	Pro	Cys	Asp	His	Tyr	Cys	His	Asn	
		145					150					155				
tac	ctg	ggc	ggc	tac	tac	tgc	tcc	tgc	cga	gtg	ggc	tac	att	ctg	cac	531
Tyr	Leu	Gly	Gly	Tyr	Tyr	Cys	Ser	Cys	Arg	Val	Gly	Tyr	Ile	Leu	His	
	160					165					170					
cag	aac	aag	cat	acc	tgc	tca	gcc	ctt	tgt	tca	ggc	cag	gtg	ttc	act	579
Gln	Asn	Lys	His	Thr	Cys	Ser	Ala	Leu	Cys	Ser	Gly	Gln	Val	Phe	Thr	
175					180					185					190	
ggg	agg	tct	ggc	ttt	ctc	agt	agc	cct	gag	tac	cca	cag	cca	tac	ccc	627
Gly	Arg	Ser	Gly	Phe	Leu	Ser	Ser	Pro	Glu	Tyr	Pro	Gln	Pro	Tyr	Pro	
				195					200					205		
aaa	ctc	tcc	agc	tgc	gcc	tac	aac	atc	cgc	ctg	gag	gaa	ggc	ttc	agt	675
Lys	Leu	Ser	Ser	Cys	Ala	Tyr	Asn	Ile	Arg	Leu	Glu	Glu	Gly	Phe	Ser	
			210					215					220			
atc	acc	ctg	gac	ttc	gtg	gag	tcc	ttt	gat	gtg	gag	atg	cac	cct	gaa	723
Ile	Thr	Leu	Asp	Phe	Val	Glu	Ser	Phe	Asp	Val	Glu	Met	His	Pro	Glu	
		225					230					235				
gcc	cag	tgc	ccc	tac	gac	tcc	ctc	aag	att	caa	aca	gac	aag	agg	gaa	771
Ala	Gln	Cys	Pro	Tyr	Asp	Ser	Leu	Lys	Ile	Gln	Thr	Asp	Lys	Arg	Glu	
	240					245					250					
tac	ggc	ccg	ttt	tgt	ggg	aag	acg	ctg	ccc	ccc	agg	att	gaa	act	gac	819
Tyr	Gly	Pro	Phe	Cys	Gly	Lys	Thr	Leu	Pro	Pro	Arg	Ile	Glu	Thr	Asp	
255				260					265						270	
agc	aac	aag	gtg	acc	att	acc	ttt	acc	acc	gac	gag	tca	ggg	aac	cac	867
Ser	Asn	Lys	Val	Thr	Ile	Thr	Phe	Thr	Thr	Asp	Glu	Ser	Gly	Asn	His	
				275					280					285		
aca	ggc	tgg	aag	ata	cac	tac	aca	agc	aca	gca	cag	ccc	tgc	cct	gat	915
Thr	Gly	Trp	Lys	Ile	His	Tyr	Thr	Ser	Thr	Ala	Gln	Pro	Cys	Pro	Asp	
			290					295					300			
cca	acg	gcg	cca	cct	aat	ggc	cac	att	tca	cct	gtg	caa	gcc	acg	tat	963
Pro	Thr	Ala	Pro	Pro	Asn	Gly	His	Ile	Ser	Pro	Val	Gln	Ala	Thr	Tyr	
		305				310						315				
gtc	ctg	aag	gac	agc	ttt	tct	gtc	ttc	tgc	aag	act	ggc	ttc	gag	ctt	1011
Val	Leu	Lys	Asp	Ser	Phe	Ser	Val	Phe	Cys	Lys	Thr	Gly	Phe	Glu	Leu	
	320					325					330					
ctg	caa	ggc	tct	gtc	ccc	ctg	aag	tca	ttc	act	gct	gtc	tgt	cag	aaa	1059

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Leu	Gln	Gly	Ser	Val	Pro	Leu	Lys	Ser	Phe	Thr	Ala	Val	Cys	Gln	Lys		
335					340					345					350		
gat	gga	tct	tgg	gac	cgg	ccg	ata	cca	gag	tgc	agc	att	att	gac	tgt		1107
Asp	Gly	Ser	Trp	Asp	Arg	Pro	Ile	Pro	Glu	Cys	Ser	Ile	Ile	Asp	Cys		
				355					360					365			
ggc	cct	ccc	gat	gac	cta	ccc	aat	ggc	cac	gtg	gac	tat	atc	aca	ggc		1155
Gly	Pro	Pro	Asp	Asp	Leu	Pro	Asn	Gly	His	Val	Asp	Tyr	Ile	Thr	Gly		
			370					375					380				
cct	gaa	gtg	acc	acc	tac	aaa	gct	gtg	att	cag	tac	agc	tgt	gaa	gag		1203
Pro	Glu	Val	Thr	Thr	Tyr	Lys	Ala	Val	Ile	Gln	Tyr	Ser	Cys	Glu	Glu		
			385				390					395					
act	ttc	tac	aca	atg	agc	agc	aat	ggc	aaa	tat	gtg	tgt	gag	gct	gat		1251
Thr	Phe	Tyr	Thr	Met	Ser	Ser	Asn	Gly	Lys	Tyr	Val	Cys	Glu	Ala	Asp		
	400					405					410						
gga	ttc	tgg	acg	agc	tcc	aaa	gga	gaa	aaa	tcc	ctc	ccg	gtt	tgc	aag		1299
Gly	Phe	Trp	Thr	Ser	Ser	Lys	Gly	Glu	Lys	Ser	Leu	Pro	Val	Cys	Lys		
415					420				425						430		
cct	gtc	tgt	gga	ctg	tcc	aca	cac	act	tca	gga	ggc	cgt	ata	att	gga		1347
Pro	Val	Cys	Gly	Leu	Ser	Thr	His	Thr	Ser	Gly	Gly	Arg	Ile	Ile	Gly		
				435					440					445			
gga	cag	cct	gca	aag	cct	ggc	gac	ttt	cct	tgg	caa	gtc	ttg	tta	ctg		1395
Gly	Gln	Pro	Ala	Lys	Pro	Gly	Asp	Phe	Pro	Trp	Gln	Val	Leu	Leu	Leu		
			450				455						460				
ggc	gaa	act	aca	gca	gca	ggc	gct	ctt	ata	cat	gac	gac	tgg	gtc	cta		1443
Gly	Glu	Thr	Thr	Ala	Ala	Gly	Ala	Leu	Ile	His	Asp	Asp	Trp	Val	Leu		
		465				470						475					
aca	gcg	gct	cat	gct	gta	tat	ggg	aaa	aca	gag	gcg	atg	tcc	tcc	ctg		1491
Thr	Ala	Ala	His	Ala	Val	Tyr	Gly	Lys	Thr	Glu	Ala	Met	Ser	Ser	Leu		
	480					485				490							
gac	atc	cgc	atg	ggc	atc	ctc	aaa	agg	ctc	tcc	ctc	att	tac	act	caa		1539
Asp	Ile	Arg	Met	Gly	Ile	Leu	Lys	Arg	Leu	Ser	Leu	Ile	Tyr	Thr	Gln		
495					500				505						510		
gcc	tgg	cca	gag	gct	gtc	ttt	atc	cat	gaa	ggc	tac	act	cac	gga	gct		1587
Ala	Trp	Pro	Glu	Ala	Val	Phe	Ile	His	Glu	Gly	Tyr	Thr	His	Gly	Ala		
				515					520					525			
ggc	ttt	gac	aat	gat	ata	gca	ctg	att	aaa	ctc	aag	aac	aaa	gtc	aca		1635

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Gly	Phe	Asp	Asn	Asp	Ile	Ala	Leu	Ile	Lys	Leu	Lys	Asn	Lys	Val	Thr		
			530					535					540				
atc	aac	aga	aac	atc	atg	ccg	att	tgt	cta	cca	aga	aaa	gaa	gct	gca	1683	
Ile	Asn	Arg	Asn	Ile	Met	Pro	Ile	Cys	Leu	Pro	Arg	Lys	Glu	Ala	Ala		
			545				550					555					
tcc	tta	atg	aaa	aca	gac	ttc	gtt	gga	act	gtg	gct	ggc	tgg	ggg	tta	1731	
Ser	Leu	Met	Lys	Thr	Asp	Phe	Val	Gly	Thr	Val	Ala	Gly	Trp	Gly	Leu		
			560				565				570						
acc	cag	aag	ggg	ttt	ctt	gct	aga	aac	cta	atg	ttt	gtg	gac	ata	cca	1779	
Thr	Gln	Lys	Gly	Phe	Leu	Ala	Arg	Asn	Leu	Met	Phe	Val	Asp	Ile	Pro		
575					580				585						590		
att	gtt	gac	cac	caa	aaa	tgt	gct	act	gcg	tat	aca	aag	cag	ccc	tac	1827	
Ile	Val	Asp	His	Gln	Lys	Cys	Ala	Thr	Ala	Tyr	Thr	Lys	Gln	Pro	Tyr		
				595					600					605			
cca	gga	gca	aaa	gtg	act	gtt	aac	atg	ctc	tgt	gct	ggc	cta	gac	cgc	1875	
Pro	Gly	Ala	Lys	Val	Thr	Val	Asn	Met	Leu	Cys	Ala	Gly	Leu	Asp	Arg		
			610					615					620				
ggt	ggc	aag	gac	agc	tgc	aga	ggt	gac	agc	gga	ggg	gca	tta	gtg	ttt	1923	
Gly	Gly	Lys	Asp	Ser	Cys	Arg	Gly	Asp	Ser	Gly	Gly	Ala	Leu	Val	Phe		
			625				630					635					
cta	gac	aat	gaa	aca	cag	aga	tgg	ttt	gtg	gga	gga	ata	gtt	tcc	tgg	1971	
Leu	Asp	Asn	Glu	Thr	Gln	Arg	Trp	Phe	Val	Gly	Gly	Ile	Val	Ser	Trp		
			640				645					650					
ggt	tct	att	aac	tgt	ggg	ggg	tca	gaa	cag	tat	ggg	gtc	tac	acg	aaa	2019	
Gly	Ser	Ile	Asn	Cys	Gly	Gly	Ser	Glu	Gln	Tyr	Gly	Val	Tyr	Thr	Lys		
655					660					665					670		
gtc	acg	aac	tat	att	ccc	tgg	att	gag	aac	ata	ata	aat	aat	ttc	taa	2067	
Val	Thr	Asn	Tyr	Ile	Pro	Trp	Ile	Glu	Asn	Ile	Ile	Asn	Asn	Phe			
				675				680						685			
tttgcaaaaa	aaaaaaaaaa	aaaa														2091	

<210> 54
 <211> 685
 <212> PRT
 <213> Rat

<400> 54

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

Met Arg Leu Leu Ile Val Leu Gly Leu Leu Trp Ser Leu Val Ala Thr
1 5 10 15

Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val Ser
20 25 30

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

Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu Thr
65 70 75 80

Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro Ser
100 105 110

Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg Thr
130 135 140

Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr Leu
145 150 155 160

Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His Gln Asn
165 170 175

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

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys Leu
195 200 205

Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser Ile Thr
210 215 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu Ala Gln
225 230 235 240

Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu Tyr Gly
245 250 255

Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser Asn
260 265 270

Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His Thr Gly
275 280 285

Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp Pro Thr
290 295 300

Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr Val Leu
305 310 315 320

Lys Asp Ser Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu Gln
325 330 335

Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
340 345 350

Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys Gly Pro
355 360 365

Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro Glu
370 375 380

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Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
385 390 395 400

Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly Phe
405 410 415

Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Lys Pro Val
420 425 430

Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly Gly Gln
435 440 445

Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly Glu
450 455 460

Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu Thr Ala
465 470 475 480

Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu Asp Ile
485 490 495

Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln Ala Trp
500 505 510

Pro Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly Phe
515 520 525

Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile Asn
530 535 540

Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala Ser Leu
545 550 555 560

Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu Thr Gln
565 570 575

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

Lys Gly Phe Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile Val
580 585 590

Asp His Gln Lys Cys Ala Thr Ala Tyr Thr Lys Gln Pro Tyr Pro Gly
595 600 605

Ala Lys Val Thr Val Asn Met Leu Cys Ala Gly Leu Asp Arg Gly Gly
610 615 620

Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu Asp
625 630 635 640

Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly Ser
645 650 655

Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys Val Thr
660 665 670

Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe
675 680 685

<210> 55
<211> 670
<212> PRT
<213> Rat

<400> 55

Thr Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val
1 5 10 15

Ser Leu Ala Phe Pro Glu Lys Tyr Gly Asn His Gln Asp Arg Ser Trp
20 25 30

Thr Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr His
35 40 45

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

Phe Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu
50 55 60

Thr Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65 70 75 80

Asp Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro
85 90 95

Ser Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe
100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg
115 120 125

Thr Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr
130 135 140

Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His Gln
145 150 155 160

Asn Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly
165 170 175

Arg Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys
180 185 190

Leu Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser Ile
195 200 205

Thr Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu Ala
210 215 220

Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu Tyr
225 230 235 240

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

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

Asn Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His Thr
260 265 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp Pro
275 280 285

Thr Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr Val
290 295 300

Leu Lys Asp Ser Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu
305 310 315 320

Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
325 330 335

Gly Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys Gly
340 345 350

Pro Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro
355 360 365

Glu Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
370 375 380

Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly
385 390 395 400

Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Lys Pro
405 410 415

Val Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly Gly
420 425 430

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly
435 440 445

Glu Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu Thr
450 455 460

Ala Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu Asp
465 470 475 480

Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln Ala
485 490 495

Trp Pro Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly
500 505 510

Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile
515 520 525

Asn Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala Ser
530 535 540

Leu Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu Thr
545 550 555 560

Gln Lys Gly Phe Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile
565 570 575

Val Asp His Gln Lys Cys Ala Thr Ala Tyr Thr Lys Gln Pro Tyr Pro
580 585 590

Gly Ala Lys Val Thr Val Asn Met Leu Cys Ala Gly Leu Asp Arg Gly
595 600 605

Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
610 615 620

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Asp Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
625 630 635 640

Ser Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys Val
645 650 655

Thr Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe
660 665 670

<210> 56
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 56
atgaggctgc tgaccctcct gggccttc 28

<210> 57
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 57
gtgcccctcc tgcgtcacct ctg 23

<210> 58
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 58
cagaggtgac gcaggagggg cac 23

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<210>	59	
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<212>	DNA	
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<400>	59	
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<212>	DNA	
<213>	Artificial Sequence	
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<223>	Murine	
<400>	60	
	atgaggctac tcattcttcct gg	22
<210>	61	
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<212>	DNA	
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<220>		
<223>	Murine	
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	ctgcagaggt gacgcagggg ggg	23
<210>	62	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Murine	
<400>	62	
	ccccccctgc gtcacctctg cag	23

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<210> 63
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Murine

 <400> 63
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 <210> 64
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 <220>
 <223> Rat

 <400> 64
 gaggtgacgc aggaggggca ttagtgttt 29

 <210> 65
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Rat

 <400> 65
 ctgaaacac taatgcccct cctgcgtcac ctctgca 37

 <210> 66
 <211> 354
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 66
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 acctgcaccg tctctggggtt ctactcagc aggggtaaaa tgggtgtgag ctggatccgt 120

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cagccccccag ggaaggccct ggagtggctt gcacacattt tttcgagtga cgaaaaatcc 180
 tacaggacat cgctgaagag caggctcacc atctccaagg acacctccaa aaaccaggtg 240
 gtccttataa tgaccaacat ggaccctgtg gacacagcca cgtattactg tgcacggata 300
 cgacgtggag gaattgacta ctggggccag ggaaccctgg tcactgtctc ctca 354

<210> 67
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 67

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Gly
 20 25 30

Lys Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser
 50 55 60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

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Leu Val Thr Val Ser Ser
115

<210> 68
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 68

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Thr
20 25 30

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

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Asp Pro Phe Gly Val Pro Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 69
<211> 106

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 69

Gln Pro Val Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Glu Lys Leu Gly Asp Lys Tyr Ala
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr
35 40 45

Gln Asp Lys Gln Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Ala Val
85 90 95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 70

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 70

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acctgtgcgg gagacaacct tgggaagaaa cgtgtgcact ggtaccagca gaggccaggc 120

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

cagggcccctg tgttggtcat ctatgatgat agcgaccggc cctcagggat ccctgaccga 180
 ttctctgcct ccaactctgg gaacacggcc accctgacca tcactagggg cgaagccggg 240
 gatgaggccg actattattg tcaggtgtgg gacattgcta ctgatcatgt ggtcttcggc 300
 ggagggacca agctcaccgt ccta 324

<210> 71
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 71

Ser Tyr Glu Leu Ile Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1 5 10 15

Thr Ala Thr Ile Thr Cys Ala Gly Asp Asn Leu Gly Lys Lys Arg Val
 20 25 30

His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Ala Ser
 50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Gly Glu Ala Gly
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ile Ala Thr Asp His
 85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala Ala Ala Gly
 100 105 110

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Ser Glu Gln Lys Leu Ile Ser Glu
115 120

<210> 72
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 72

Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn
1 5 10 15

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

Trp Cys Asn Gln
35

<210> 73
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 73

Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn Thr Cys Arg
1 5 10 15

Cys Gly Ser Asp Gly Lys Ser Ala Val Cys Thr Lys Leu Trp Cys Asn
20 25 30

Gln

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<210> 74
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 74

Thr Cys Arg Cys Gly Ser Asp Gly Lys Ser Ala Val Cys Thr Lys Leu
 1 5 10 15

Trp Cys Asn Gln
 20

<210> 75
 <211> 491
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 75

Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn
 1 5 10 15

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

Trp Cys Asn Gln Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser Gln Val
 35 40 45

Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu Thr Leu
 50 55 60

Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Gly Lys Met
 65 70 75 80

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

Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser Leu Lys
100 105 110

Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu
115 120 125

Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
130 135 140

Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
145 150 155 160

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

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
180 185 190

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
195 200 205

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
210 215 220

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
225 230 235 240

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
245 250 255

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
260 265 270

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Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
275 280 285

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
290 295 300

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
305 310 315 320

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
325 330 335

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
340 345 350

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
355 360 365

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
370 375 380

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
385 390 395 400

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
405 410 415

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
420 425 430

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
435 440 445

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
450 455 460

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Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465 470 475 480

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
485 490

<210> 76
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 76

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Gly
20 25 30

Lys Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser
50 55 60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

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Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

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

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

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Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Ala Ala Gly
435 440 445

Gly Ser Gly Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp
450 455 460

Lys Cys Asn Thr Cys Arg Cys Gly Ser Asp Gly Lys Ser Ala Val Cys
465 470 475 480

Thr Lys Leu Trp Cys Asn Gln Gly Ser Gly Ala
485 490

<210> 77

<211> 258

MP_1_0250_PCT_Sequence_Listing_20170104_ST25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 77

Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn
1 5 10 15

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

Trp Cys Asn Gln Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser Gln Pro
35 40 45

Val Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln Thr Ala
50 55 60

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

Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr Gln Asp
85 90 95

Lys Gln Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser
100 105 110

Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu
115 120 125

Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Ala Val Phe Gly
130 135 140

Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser
145 150 155 160

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Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala
165 170 175

Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val
180 185 190

Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr
195 200 205

Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu
210 215 220

Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln
225 230 235 240

Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu
245 250 255

Cys Ser

<210> 78
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 78

Gln Pro Val Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Glu Lys Leu Gly Asp Lys Tyr Ala
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr
35 40 45

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Gln Asp Lys Gln Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Ala Val
85 90 95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala
100 105 110

Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
115 120 125

Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
130 135 140

Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
145 150 155 160

Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
165 170 175

Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
180 185 190

Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
195 200 205

Thr Glu Cys Ser Ala Ala Gly Gly Ser Gly Leu Glu Val Thr Cys Glu
210 215 220

Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn Thr Cys Arg Cys Gly Ser
225 230 235 240

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Asp Gly Lys Ser Ala Val Cys Thr Lys Leu Trp Cys Asn Gln Gly Ser
 245 250 255

Gly Ala

<210> 79
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 79

Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser
 1 5 10

<210> 80
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 80

Ala Ala Gly Gly Ser Gly
 1 5

<210> 81
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 81

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Gly Ser Gly Ala

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<210> 82

<211> 1533

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 82

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tcagatggga aatcggcggt ctgcacaaag ctctggtgta accagggcac cgggtggaggg	180
tcgggatcca gctcacaggt caccttgaag gagtctggtc ctgtgctggt gaaaccaca	240
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aaagccaaag ggcagccccg agagccacag gtgtacaccc tgcccccatc ccaggaggag	1260
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctaccc cagcgacatc	1320
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1380
ctggactccg acggctcctt cttcctctac agcaggctaa ccgtggacaa gagcagggtg	1440
caggagggga atgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacaca	1500
cagaagagcc tctccctgtc tctcgggaaa tga	1533

<210> 83
 <211> 1533
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 83	
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tgcaccgtct ctgggttctc actcagcagg ggtaaaatgg gtgtgagctg gatccgtcag	180
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cgtggaggaa ttgactactg gggccaggga accctgggtca ctgtctcctc agcctccacc	420
aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc	660

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cgagagccac aggtgtacac cctgccccca tcccaggagg agatgaccaa gaaccaggtc	1140
agcctgacct gcctgggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc	1200
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc	1260
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tcatgctccg tgatgcatga ggctctgcac aaccactaca cacagaagag cctctccctg	1380
tctctcggga aagccgctgg tggtagtggt ttggaagtga cgtgtgagcc cggaacgaca	1440
ttcaaagaca agtgcaatac ttgtcgggtc gggttcagatg ggaaatcggc ggtctgcaca	1500
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<210> 84

<211> 834

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 84

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