

MP_1_0248_PCT_Sequence_Listing_as_Filed_20161109.txt
SEQUENCE LISTING

<110> Omeros Corporation
University of Leicester
Demopoulos, Gregory A.
Dudler, Thomas
Schwaebble, Hans-wilhelm

<120> METHODS FOR TREATING CONDITIONS ASSOCIATED WITH MASP-2 DEPENDENT
COMPLEMENT ACTIVATION

<130> MP.1.0248.PCT

<140> 62/406,726
<141> 2016-10-11

<140> 62/252,814
<141> 2015-11-09

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<170> PatentIn version 3.5

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Leu Cys Gly Ser Val Ala Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro
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Val Phe Gly Arg Leu Ala Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn
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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
Arg Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser His Leu Cys Glu
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Tyr Asp Phe Val Lys Leu Ser Ser Gly Ala Lys Val Leu Ala Thr Leu
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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

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Phe Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr
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Asp Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys Asp
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His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala
155 160 165

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Gly Tyr Val Leu His Arg Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu
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Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
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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
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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
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Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
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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
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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	
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Phe	Gly	Arg	Leu	Ala	Ser	Pro	Gly	Phe	Pro	Gly	Glu	Tyr	Ala	Asn	Asp	
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Gln	Glu	Arg	Arg	Trp	Thr	Leu	Thr	Ala	Pro	Pro	Gly	Tyr	Arg	Leu	Arg	
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Asp	Phe	Val	Lys	Leu	Ser	Ser	Gly	Ala	Lys	Val	Leu	Ala	Thr	Leu	Cys	
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Gly	Gln	Glu	Ser	Thr	Asp	Thr	Glu	Arg	Ala	Pro	Gly	Lys	Asp	Thr	Phe	
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Asn	Glu	Lys	Pro	Phe	Thr	Gly	Phe	Glu	Ala	Phe	Tyr	Ala	Ala	Glu	Asp	
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Ile	Asp	Glu	Cys	Gln	Val	Ala	Pro	Gly	Glu	Ala	Pro	Thr	Cys	Asp	His	
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Gln	Val	Phe	Thr	Gln	Arg	Ser	Gly	Glu	Leu	Ser	Ser	Pro	Glu	Tyr	Pro	
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Arg	Pro	Tyr	Pro	Lys	Leu	Ser	Ser	Cys	Thr	Tyr	Ser	Ile	Ser	Leu	Glu	
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Thr	His	Pro	Glu	Thr	Leu	Cys	Pro	Tyr	Asp	Phe	Leu	Lys	Ile	Gln	Thr	
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gac	aga	gaa	gaa	cat	ggc	cca	ttc	tgt	ggg	aag	aca	ttg	ccc	cac	agg	819
Asp	Arg	Glu	Glu	His	Gly	Pro	Phe	Cys	Gly	Lys	Thr	Leu	Pro	His	Arg	

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Arg Lys Glu Ala Glu Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala			
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Ser Gly Trp Gly Leu Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met			
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Glu Lys Pro Pro Tyr Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys			
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655 660 665			
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Gly Val Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile			
670 675 680			
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Ile Ser Asp Phe			
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Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
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Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
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Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
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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
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Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln Arg
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Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu
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Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val Ile
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Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
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Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
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Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
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Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
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Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro Met
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Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu Gln
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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
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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
450 455 460

Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu Thr
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Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu Asp
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Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln Ala
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Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala Gly
515 520 525

Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val Ile
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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
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MP_1_0248_PCT_Sequence_Listing_as_Filed_20161109.txt

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

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
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Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly
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Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro
355 360 365

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
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Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu
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Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly
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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
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Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu
545 550 555 560

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

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

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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
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Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
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Gly Phe Glu Ala Phe Tyr Ala Ala
130 135

<210> 9
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<212> PRT
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20 25 30

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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

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

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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
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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
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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
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
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Trp Lys Ile His Tyr
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20 25 30

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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
100 105 110

Glu Ala Glu Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly
Page 17

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
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Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser
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Gly Lys Asp Ser Cys Arg Gly Asp Ala Gly Gly Ala Leu Val Phe Leu
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Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe Asp
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Ile Asp Glu Cys Gln Val Ala Pro Gly
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<210> 19

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Arg Gly Asp Ser Gly Gly Ala Leu Val
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 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
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 Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly Asn Pro
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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
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 100 105 110

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

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
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Leu Ala Val Cys Glu Phe Pro Ile
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<222> (1)..(1)
<223> wherein X at position 1 represents hydroxyproline

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<400> 22

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<210> 23
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<400> 23

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<400> 24

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

<210> 25
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 <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

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<223> xaa can be any naturally occurring amino acid

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<222> (32)..(32)

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Asp Xaa Gly Lys Ser
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Pro Xaa Gly Pro Xaa Gly Lys Met Gly Pro Lys Gly Glu Xaa Gly Asp
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Xaa

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20 25 30

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

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<400> 29

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Asn Arg Pro Phe Leu Val Phe Ile
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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											

<210> 51
 <211> 685
 <212> PRT
 <213> Murine

<400> 51

Met	Arg	Leu	Leu	Ile	Phe	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			
Pro	Gly	Phe	Pro	Glu	Lys	Tyr	Ala	Asp	His	Gln	Asp	Arg	Ser	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	Tyr	Arg	Cys	Glu	Tyr	Asp	Phe	Val	Lys	Leu	Ser	
65					70					75					80	

MP_1_0248_PCT_Sequence_Listing_as_Filed_20161109.txt

Ser Gly Thr Lys Val₈₅ Leu Ala Thr Leu Cys₉₀ Gly Gln Glu Ser Thr Asp₉₅

Thr Glu Gln Ala₁₀₀ Pro Gly Asn Asp Thr₁₀₅ Phe Tyr Ser Leu Gly₁₁₀ Pro Ser

Leu Lys Val₁₁₅ Thr Phe His Ser Asp₁₂₀ Tyr Ser Asn Glu Lys₁₂₅ Pro Phe Thr

Gly Phe₁₃₀ Glu Ala Phe Tyr Ala₁₃₅ Ala Glu Asp Val Asp₁₄₀ Glu Cys Arg Val

Ser₁₄₅ Leu Gly Asp Ser Val₁₅₀ Pro Cys Asp His Tyr₁₅₅ Cys His Asn Tyr Leu₁₆₀

Gly Gly Tyr Tyr Cys₁₆₅ Ser Cys Arg Ala Gly₁₇₀ Tyr Ile Leu His Gln₁₇₅ Asn

Lys His Thr Cys₁₈₀ Ser Ala Leu Cys Ser₁₈₅ Gly Gln Val Phe Thr₁₉₀ Gly Arg

Ser Gly Tyr₁₉₅ Leu Ser Ser Pro Glu₂₀₀ Tyr Pro Gln Pro Tyr₂₀₅ Pro Lys Leu

Ser Ser₂₁₀ Cys Thr Tyr Ser Ile₂₁₅ Arg Leu Glu Asp Gly₂₂₀ Phe Ser Val Ile

Leu₂₂₅ Asp Phe Val Glu Ser₂₃₀ Phe Asp Val Glu Thr₂₃₅ His Pro Glu Ala Gln₂₄₀

Cys Pro Tyr Asp Ser₂₄₅ Leu Lys Ile Gln Thr₂₅₀ Asp Lys Gly Glu His₂₅₅ Gly

Pro Phe Cys Gly₂₆₀ Lys Thr Leu Pro Pro₂₆₅ Arg Ile Glu Thr Asp₂₇₀ Ser His

Lys Val Thr₂₇₅ Ile Thr Phe Ala Thr₂₈₀ Asp Glu Ser Gly Asn₂₈₅ His Thr Gly

Trp Lys₂₉₀ Ile His Tyr Thr Ser₂₉₅ Thr Ala Arg Pro Cys₃₀₀ Pro Asp Pro Thr

Ala₃₀₅ Pro Pro Asn Gly Ser₃₁₀ Ile Ser Pro Val Gln₃₁₅ Ala Thr Tyr Val Leu₃₂₀

Lys Asp Arg Phe Ser₃₂₅ Val Phe Cys Lys Thr₃₃₀ Gly Phe Glu Leu Leu₃₃₅ Gln

Gly Ser Val Pro₃₄₀ Leu Lys Ser Phe Thr₃₄₅ Ala Val Cys Gln Lys₃₅₀ Asp Gly

MP_1_0248_PCT_Sequence_Listing_as_Filed_20161109.txt

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

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

MP_1_0248_PCT_Sequence_Listing_as_Filed_20161109.txt

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

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

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

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

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

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

<400> 53
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MP_1_0248_PCT_Sequence_Listing_as_Filed_20161109.txt
Met Arg Leu Leu Ile Val Leu Gly Leu Leu Trp Ser Leu Val
1 5 10

gcc Ala 15	aca Thr	ctt Leu	tgt Leu	ggc Gly 20	tcc Ser 20	aag Lys	tgg Trp	cct Pro	gag Glu 25	cct Pro 25	gta Val	ttc Phe	ggg Gly	cgc Arg 30	ctg Leu 30	99
gtg Val	tcc Ser	ctg Leu	gcc Ala 35	ttc Phe 35	cca Pro	gag Glu	aag Lys	tat Tyr	ggc Gly 40	aac Asn	cat His	cag Gln	gat Asp 45	cga Arg 45	tcc Ser	147
tgg Trp	acg Thr	ctg Leu	act Thr 50	gca Ala	ccc Pro	cct Pro	ggc Gly 55	ttc Phe 55	cgc Arg	ctg Leu	cgc Arg	ctc Leu	tac Tyr 60	ttc Phe	acc Thr	195
cac His	ttc Phe 65	aac Asn 65	ctg Leu	gaa Glu	ctc Leu	tct Ser	tac Tyr 70	cgc Arg	tgc Cys	gag Glu	tat Tyr	gac Asp 75	ttt Phe	gtc Val	aag Lys	243
tgt Leu 80	acc Thr 80	tca Ser	ggg Gly	acc Thr	aag Lys	gtg Val 85	cta Leu	gcc Ala	acg Thr	ctg Leu	tgt Cys 90	ggg Gly	cag Gln	gag Glu	agt Ser	291
aca Thr 95	gat Asp	act Thr	gag Glu	cgg Arg	gca Ala 100	cct Pro	ggc Gly	aat Asn	gac Asp 105	acc Thr 105	ttc Phe	tac Tyr	tca Ser	ctg Leu	ggt Gly 110	339
ccc Pro	agc Ser	cta Leu	aag Lys	gtc Val 115	acc Thr	ttc Phe	cac His	tcc Ser	gac Asp 120	tac Tyr	tcc Ser	aat Asn	gag Glu	aag Lys 125	cca Pro	387
ttc Phe	aca Thr	gga Gly	ttt Phe 130	gag Glu	gcc Ala	ttc Phe	tat Tyr	gca Ala 135	gcg Ala	gag Glu	gat Asp	gtg Val 140	gat Asp 140	gaa Glu	tgc Cys	435
aga Arg	aca Thr	tcc Ser 145	ctg Leu	gga Gly	gac Asp	tca Ser	gtc Val 150	cct Pro	tgt Cys	gac Asp	cat His	tat Tyr 155	tgc Cys	cac His	aac Asn	483
tac Tyr 160	ctg Leu	ggc Gly	ggc Gly	tac Tyr	tac Tyr	tgc Cys 165	tcc Ser	tgc Cys	cga Arg	gtg Val	ggc Gly 170	tac Tyr	att Ile	ctg Leu	cac His	531
cag Gln 175	aac Asn	aag Lys	cat His	acc Thr	tgc Cys 180	tca Ser	gcc Ala	ctt Leu	tgt Cys	tca Ser 185	ggc Gly	cag Gln	gtg Val	ttc Phe	act Thr 190	579
ggg Gly	agg Arg	tct Ser	ggc Gly	ttt Phe 195	ctc Leu	agt Ser	agc Ser	cct Pro	gag Glu 200	tac Tyr	cca Pro	cag Gln	cca Pro	tac Tyr 205	ccc Pro	627
aaa Lys	ctc Leu	tcc Ser	agc Ser 210	tgc Cys	gcc Ala	tac Tyr	aac Asn	atc Ile 215	cgc Arg	ctg Leu	gag Glu	gaa Glu	ggc Gly 220	ttc Phe	agt Ser	675
atc Ile	acc Thr	ctg Leu 225	gac Asp	ttc Phe	gtg Val	gag Glu	tcc Ser 230	ttt Phe	gat Asp	gtg Val	gag Glu	atg Met 235	cac His	cct Pro	gaa Glu	723
gcc Ala 240	cag Gln	tgc Cys	ccc Pro	tac Tyr	gac Asp	tcc Ser 245	ctc Leu	aag Lys	att Ile	caa Gln	aca Thr 250	gac Asp	aag Lys	agg Arg	gaa Glu	771
tac Tyr 255	ggc Gly	ccg Pro	ttt Phe	tgt Cys	ggg Gly 260	aag Lys	acg Thr	ctg Leu	ccc Pro	ccc Pro 265	agg Arg	att Ile	gaa Glu	act Thr	gac Asp 270	819
agc	aac	aag	gtg	acc	att	acc	ttt	acc	acc	gac	gag	tca	ggg	aac	cac	867

MP_1_0248_PCT_Sequence_Listing_as_Filed_20161109.txt

Ser	Asn	Lys	Val	Thr 275	Ile	Thr	Phe	Thr 280	Thr	Asp	Glu	Ser	Gly	Asn 285	His	
aca Thr	ggc Gly	tgg Trp	aag Lys 290	ata Ile	cac His	tac Tyr	aca Thr	agc Ser 295	aca Thr	gca Ala	cag Gln	ccc Pro	tgc Cys 300	cct Pro	gat Asp	915
cca Pro	acg Thr	gcg Ala 305	cca Pro	cct Pro	aat Asn	ggg Gly	cac His 310	att Ile	tca Ser	cct Pro	gtg Val	caa Gln 315	gcc Ala	acg Thr	tat Tyr	963
gtc Val	ctg Leu 320	aag Lys	gac Asp	agc Ser	ttt Phe	tct Ser 325	gtc Val	ttc Phe	tgc Cys	aag Lys	act Thr 330	ggc Gly	ttc Phe	gag Glu	ctt Leu	1011
ctg Leu 335	caa Gln	ggg Gly	tct Ser	gtc Val	ccc Pro 340	ctg Leu	aag Lys	tca Ser	ttc Phe	act Thr 345	gct Ala	gtc Val	tgt Cys	cag Gln	aaa Lys 350	1059
gat Asp	gga Gly	tct Ser	tgg Trp	gac Asp 355	cgg Arg	ccg Pro	ata Ile	cca Pro	gag Glu 360	tgc Cys	agc Ser	att Ile	att Ile	gac Asp 365	tgt Cys	1107
ggc Gly	cct Pro	ccc Pro	gat Asp 370	gac Asp	cta Leu	ccc Pro	aat Asn	ggc Gly 375	cac His	gtg Val	gac Asp	tat Tyr	atc Ile 380	aca Thr	ggc Gly	1155
cct Pro	gaa Glu	gtg Val 385	acc Thr	acc Thr	tac Tyr	aaa Lys	gct Ala 390	gtg Val	att Ile	cag Gln	tac Tyr	agc Ser 395	tgt Cys	gaa Glu	gag Glu	1203
act Thr	ttc Phe 400	tac Tyr	aca Thr	atg Met	agc Ser	agc Ser 405	aat Asn	ggg Gly	aaa Lys	tat Tyr	gtg Val 410	tgt Cys	gag Glu	gct Ala	gat Asp	1251
gga Gly 415	ttc Phe	tgg Trp	acg Thr	agc Ser	tcc Ser 420	aaa Lys	gga Gly	gaa Glu	aaa Lys	tcc Ser 425	ctc Leu	ccg Pro	gtt Val	tgc Cys	aag Lys 430	1299
cct Pro	gtc Val	tgt Cys	gga Gly	ctg Leu 435	tcc Ser	aca Thr	cac His	act Thr	tca Ser 440	gga Gly	ggc Gly	cgt Arg	ata Ile	att Ile 445	gga Gly	1347
gga Gly	cag Gln	cct Pro	gca Ala 450	aag Lys	cct Pro	ggg Gly	gac Asp	ttt Phe 455	cct Pro	tgg Trp	caa Gln	gtc Val	ttg Leu 460	tta Leu	ctg Leu	1395
ggg Gly	gaa Glu	act Thr 465	aca Thr	gca Ala	gca Ala	ggg Gly	gct Ala 470	ctt Leu	ata Ile	cat His	gac Asp	gac Asp 475	tgg Trp	gtc Val	cta Leu	1443
aca Thr	gcg Ala 480	gct Ala	cat His	gct Ala	gta Val	tat Tyr 485	ggg Gly	aaa Lys	aca Thr	gag Glu	gca Ala 490	atg Met	tcc Ser	tcc Ser	ctg Leu	1491
gac Asp 495	atc Ile	cgc Arg	atg Met	ggc Gly	atc Ile 500	ctc Leu	aaa Lys	agg Arg	ctc Leu	tcc Ser 505	ctc Leu	att Ile	tac Tyr	act Thr	caa Gln 510	1539
gcc Ala	tgg Trp	cca Pro	gag Glu	gct Ala 515	gtc Val	ttt Phe	atc Ile	cat His	gaa Glu 520	ggc Gly	tac Tyr	act Thr	cac His	gga Gly 525	gct Ala	1587
ggg Gly	ttt Phe	gac Asp	aat Asn 530	gat Asp	ata Ile	gca Ala	ctg Leu	att Ile 535	aaa Lys	ctc Leu	aag Lys	aac Asn	aaa Lys 540	gtc Val	aca Thr	1635
atc	aac	aga	aac	atc	atg	ccg	att	tgt	cta	cca	aga	aaa	gaa	gct	gca	1683

MP_1_0248_PCT_Sequence_Listing_as_Filed_20161109.txt

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		
					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		
					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

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			

MP_1_0248_PCT_Sequence_Listing_as_Filed_20161109.txt

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

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

MP_1_0248_PCT_Sequence_Listing_as_Filed_20161109.txt

Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro Glu
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 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

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

MP_1_0248_PCT_Sequence_Listing_as_Filed_20161109.txt

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

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
 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
 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

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
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Thr Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe
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<220>
<223> Homo Sapiens

<400> 56
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28

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

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<220>
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23

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<220>
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23

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<211> 27
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<210> 61
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23

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 <220>
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 gaggtgacgc aggaggggca ttagtggtt 29

<210> 65
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 <400> 65
 ctagaaacac taatgccct cctgcgtcac ctctgca 37

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 acctgcaccg tctctgggtt ctactcagc aggggtaaaa tgggtgtgag ctggatccgt 120
 cagccccag ggaaggccct ggagtggctt gcacacattt tttcgagtga cgaaaaatcc 180
 tacaggacat cgctgaagag caggctcacc atctccaagg acacctcaa aaaccagggtg 240
 gtccttaca tgaccaacat ggaccctgtg gacacagcca cgtattactg tgcacggata 300
 cgacgtggag gaattgacta ctggggccag ggaaccctgg tcaactgtctc ctca 354

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 <212> PRT
 <213> Artificial sequence

 <220>
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 <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

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
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<211> 318
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cagtcccctg tgttggtcat gtatcaagat aaacagcggc cctcagggat ccctgagcga 180
ttctctggct ccaactctgg gaacacagcc actctgacca tcagcgggac ccaggctatg 240
gatgangctg actattactg tcaggcgtgg gacagcagca ctgcggtatt cggcggaggg 300
accaagctga ccgtccta 318

<210> 70
<211> 106
<212> PRT
<213> Artificial sequence

<220>
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<400> 70

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> 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

Ser Glu Gln Lys Leu Ile Ser Glu
 115 120