

7489616_1.txt
SEQUENCE LISTING

<110> Omeros Corporation
University of Leicester
Demopulos, Gregory A.
Schwaebler, Hans-Wilhelm
Dudler, Thomas
Tjoelker, Larry W.

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

<130> MP.1.0239.PCT

<150> US 62/315,857
<151> 2016-03-31

<160> 71

<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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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
Arg Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser His Leu Cys Glu
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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
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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

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

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Ser Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu
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gac att gac gag tgc cag gtg gcc ccg gga gag gcg ccc acc tgc gac 485

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 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
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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 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 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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Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
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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
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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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ttc ggg cgc ctg gca tcc ccc ggc ttt cca ggg gag tat gcc aat gac Phe Gly Arg Leu Ala Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp				30			35						40				147
cag gag cgg cgc tgg acc ctg act gca ccc ccc ggc tac cgc ctg cgc Gln Glu Arg Arg Trp Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg				45			50						55				195
ctc tac ttc acc cac ttc gac ctg gag ctc tcc cac ctc tgc gag tac Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr						65						70					243
gac ttc gtc aag ctg agc tcg ggg gcc aag gtg ctg gcc acg ctg tgc Asp Phe Val Lys Leu Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys					80				85								291
ggg cag gag agc aca gac acg gag cgg gcc cct ggc aag gac act ttc Gly Gln Glu Ser Thr Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe				95				100							105		339
tac tcg ctg ggc tcc agc ctg gac att acc ttc cgc tcc gac tac tcc Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser				110				115						120			387
aac gag aag ccg ttc acg ggg ttc gag gcc ttc tat gca gcc gag gac Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp				125			130						135				435
att gac gag tgc cag gtg gcc ccg gga gag gcg ccc acc tgc gac cac Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His					145						150						483
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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
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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						225						230					723
aca cac cct gaa acc ctg tgt ccc tac gag ttt ctc aag att caa aca Thr His Pro Glu Thr Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr					240					245							771
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cct Pro	tgc Cys 300	cct Pro	tat Tyr	ccg Pro	atg Met	gcg Ala 305	cca Pro	cct Pro	aat Asn	ggc Gly	cac His 310	gtt Val	tca Ser	cct Pro	gtg Val		963
caa Gln 315	gcc Ala	aaa Lys	tac Tyr	atc Ile	ctg Leu 320	aaa Lys	gac Asp	agc Ser	ttc Phe	tcc Ser 325	atc Ile	ttt Phe	tgc Cys	gag Glu	act Thr 330		1011
ggc Gly	tat Tyr	gag Glu	ctt Leu	ctg Leu 335	caa Gln	ggc Gly	cac His	ttg Leu	ccc Pro 340	ctg Leu	aaa Lys	tcc Ser	ttt Phe	act Thr 345	gca Ala		1059
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tac Tyr	atc Ile 380	aca Thr	ggc Gly	cct Pro	gga Gly	gtg Val 385	acc Thr	acc Thr	tac Tyr	aaa Lys	gct Ala 390	gtg Val	att Ile	cag Gln	tac Tyr		1203
agc Ser 395	tgt Cys	gaa Glu	gag Glu	acc Thr	ttc Phe 400	tac Tyr	aca Thr	atg Met	aaa Lys	gtg Val 405	aat Asn	gat Asp	ggc Gly	aaa Lys	tat Tyr 410		1251
gtg Val	tgt Cys	gag Glu	gct Ala	gat Asp 415	gga Gly	ttc Phe	tgg Trp	acg Thr	agc Ser 420	tcc Ser	aaa Lys	gga Gly	gaa Glu	aaa Lys 425	tca Ser		1299
ctc Leu	cca Pro	gtc Val	tgt Cys 430	gag Glu	cct Pro	gtt Val	tgt Cys	gga Gly 435	cta Leu	tca Ser	gcc Ala	cgc Arg	aca Thr 440	aca Thr	gga Gly		1347
ggg Gly	cgt Arg	ata Ile 445	tat Tyr	gga Gly	ggg Gly	caa Gln	aag Lys 450	gca Ala	aaa Lys	cct Pro	ggc Gly	gat Asp 455	ttt Phe	cct Pro	tgg Trp		1395
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gat Asp	gca Ala	tcc Ser	gcc Ala	ctg Leu 495	gac Asp	att Ile	cga Arg	atg Met	ggc Gly 500	acc Thr	ctg Leu	aaa Lys	aga Arg	cta Leu 505	tca Ser		1539
cct Pro	cat His	tat Tyr	aca Thr 510	caa Gln	gcc Ala	tgg Trp	tct Ser	gaa Glu 515	gct Ala	gtt Val	ttt Phe	ata Ile	cat His 520	gaa Glu	ggc Gly		1587
tat Tyr	act Thr	cat His 525	gat Asp	gct Ala	ggc Gly	ttt Phe	gac Asp 530	aat Asn	gac Asp	ata Ile	gca Ala	ctg Leu 535	att Ile	aaa Lys	ttg Leu		1635
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Ser	Gly	Trp	Gly	Leu	Thr	Gln	Arg	Gly	Phe	Leu	Ala	Arg	Asn	Leu	Met		
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gaa	aag	cca	ccc	tat	cca	agg	gga	agt	gta	act	gct	aac	atg	ctt	tgt	1875	
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Gly	Ala	Leu	Val	Phe	Leu	Asp	Ser	Glu	Thr	Glu	Arg	Trp	Phe	Val	Gly		
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gga	gtc	tac	aca	aaa	gtt	att	aac	tat	att	ccc	tgg	atc	gag	aac	ata	2067	
Gly	Val	Tyr	Thr	Lys	Val	Ile	Asn	Tyr	Ile	Pro	Trp	Ile	Glu	Asn	Ile		
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Ile	Ser	Asp	Phe														
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40

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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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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
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Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile Leu

305 310 315 320
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 Gly His Leu Pro₃₄₀ Leu Lys Ser Phe Thr₃₄₅ Ala Val Cys Gln Lys₃₅₀ Asp Gly
 Ser Trp Asp₃₅₅ Arg Pro Met Pro Ala₃₆₀ Cys Ser Ile Val Asp₃₆₅ Cys Gly Pro
 Pro Asp₃₇₀ Asp Leu Pro Ser Gly₃₇₅ Arg Val Glu Tyr Ile₃₈₀ Thr Gly Pro Gly
 Val₃₈₅ Thr Thr Tyr Lys Ala₃₉₀ Val Ile Gln Tyr Ser₃₉₅ Cys Glu Glu Thr Phe₄₀₀
 Tyr Thr Met Lys Val₄₀₅ Asn Asp Gly Lys Tyr₄₁₀ Val Cys Glu Ala Asp₄₁₅ Gly
 Phe Trp Thr Ser₄₂₀ Ser Lys Gly Glu Lys₄₂₅ Ser Leu Pro Val Cys₄₃₀ Glu Pro
 Val Cys Gly₄₃₅ Leu Ser Ala Arg Thr₄₄₀ Thr Gly Gly Arg Ile₄₄₅ Tyr Gly Gly
 Gln Lys₄₅₀ Ala Lys Pro Gly Asp₄₅₅ Phe Pro Trp Gln Val₄₆₀ Leu Ile Leu Gly
 Gly Thr Thr Ala Ala Gly₄₇₀ Ala Leu Leu Tyr Asp₄₇₅ Asn Trp Val Leu Thr₄₈₀
 Ala Ala His Ala Val₄₈₅ Tyr Glu Gln Lys His₄₉₀ Asp Ala Ser Ala Leu₄₉₅ Asp
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 Trp Ser Glu₅₁₅ Ala Val Phe Ile His₅₂₀ Glu Gly Tyr Thr His₅₂₅ Asp Ala Gly
 Phe Asp₅₃₀ Asn Asp Ile Ala Leu₅₃₅ Ile Lys Leu Asn Asn₅₄₀ Lys Val Val Ile
 Asn Ser Asn Ile Thr Pro₅₅₀ Ile Cys Leu Pro Arg₅₅₅ Lys Glu Ala Glu Ser₅₆₀
 Phe Met Arg Thr Asp₅₆₅ Asp Ile Gly Thr Ala₅₇₀ Ser Gly Trp Gly Leu₅₇₅ Thr
 Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro Ile

580

585

590

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Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
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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
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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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 180 185 190
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 195 200 205
 Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr
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 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
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 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
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 Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
 325 330 335
 Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly
 340 345 350
 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
 385 390 395 400
 Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu
 405 410 415

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Pro Val Cys Gly₄₂₀ Leu Ser Ala Arg Thr₄₂₅ Thr Gly Gly Arg Ile₄₃₀ Tyr Gly
 Gly Gln Lys₄₃₅ Ala Lys Pro Gly Asp₄₄₀ Phe Pro Trp Gln Val₄₄₅ Leu Ile Leu
 Gly Gly₄₅₀ Thr Thr Ala Ala Gly₄₅₅ Ala Leu Leu Tyr Asp₄₆₀ Asn Trp Val Leu
 Thr₄₆₅ Ala Ala His Ala Val₄₇₀ Tyr Glu Gln Lys His₄₇₅ Asp Ala Ser Ala Leu₄₈₀
 Asp Ile Arg Met Gly₄₈₅ Thr Leu Lys Arg Leu₄₉₀ Ser Pro His Tyr Thr₄₉₅ Gln
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 Gly Phe Asp₅₁₅ Asn Asp Ile Ala Leu₅₂₀ Ile Lys Leu Asn Asn₅₂₅ Lys Val Val
 Ile Asn₅₃₀ Ser Asn Ile Thr Pro₅₃₅ Ile Cys Leu Pro Arg₅₄₀ Lys Glu Ala Glu
 Ser₅₄₅ Phe Met Arg Thr Asp₅₅₀ Asp Ile Gly Thr Ala₅₅₅ Ser Gly Trp Gly Leu₅₆₀
 Thr Gln Arg Gly Phe₅₆₅ Leu Ala Arg Asn Leu₅₇₀ Met Tyr Val Asp Ile₅₇₅ Pro
 Ile Val Asp His₅₈₀ Gln Lys Cys Thr Ala₅₈₅ Ala Tyr Glu Lys Pro₅₉₀ Pro Tyr
 Pro Arg Gly₅₉₅ Ser Val Thr Ala Asn₆₀₀ Met Leu Cys Ala Gly₆₀₅ Leu Glu Ser
 Gly Gly₆₁₀ Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly₆₂₀ Ala Leu Val Phe
 Leu₆₂₅ Asp Ser Glu Thr Glu₆₃₀ Arg Trp Phe Val Gly₆₃₅ Gly Ile Val Ser Trp₆₄₀
 Gly Ser Met Asn Cys₆₄₅ Gly Glu Ala Gly Gln₆₅₀ Tyr Gly Val Tyr Thr₆₅₅ Lys
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Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
20          25          30

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Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg 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

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

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

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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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 <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

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
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Lys Arg Thr Cys Ser
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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
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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
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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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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
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Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
 275 280 285

Trp Lys Ile His Tyr
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 <213> Homo sapiens

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Glu Asp Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys
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Asp His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg
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Ala Gly Tyr Val Leu His Arg Asn Lys
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 <213> Homo sapiens

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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
 100 105 110

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

7489616_1.txt

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
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Asp Phe

<210> 13
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<220>
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<210> 14
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Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu
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<212> PRT
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<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
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Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln
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<210> 16

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<212> PRT

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Thr Phe Arg Ser Asp Tyr Ser Asn
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<210> 17

<211> 25

<212> PRT

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Phe Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr
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Ser Asn Glu Lys Pro Phe Thr Gly Phe
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<212> PRT

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Ile Asp Glu Cys Gln Val Ala Pro Gly
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<210> 19

<211> 25

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Ala Asn Met Leu Cys Ala Gly Leu Glu Ser Gly Gly Lys Asp Ser Cys
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Arg Gly Asp Ser Gly Gly Ala Leu Val
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<211> 960

<212> DNA

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 Leu Phe Pro Ser Leu Pro Leu Leu Leu Ser Met Val Ala Ala Ser
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 Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr Cys Pro Ala
 20 25 30

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 Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly Lys Asp
 35 40 45 50

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 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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 Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp Pro Gly
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 Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg Lys Ala
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 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

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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

ggg 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
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aaa aat ggc cag tgg aat gac gtc ccc tgc tcc acc tcc cat ctg gcc 776
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230 235 240

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Val Cys Glu Phe Pro Ile
245

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<213> Homo sapiens

<400> 21

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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

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
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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

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

<220>
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 <222> (4)..(4)
 <223> wherein X at position 4 represents hydrophobic residue

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Xaa Gly Lys Xaa Gly Pro
 1 5

<210> 23
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<223> wherein X represents hydroxyproline

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<210> 24

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<221> MISC_FEATURE

<222> (9)..(15)

<223> wherein X at positions 9 and 15 represents hydroxyproline

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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

<210> 26

<211> 53

<212> PRT

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<220>

<221> misc_feature

<222> (26)..(26)

<223> xaa can be any naturally occurring amino acid

<220>

<221> misc_feature
 <222> (32)..(32)
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 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
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Asp Xaa Gly Lys Ser
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 <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

<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

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

<400> 30
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 aatgaccagg agcggcgctg gaccctgact gcaccccccg gctaccgcct gcgcctctac 180
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tcagccctgt gctccggcc 559

<210> 31
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 31
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<210> 32
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 32
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<210> 33
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 33
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<210> 34
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 34
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<210> 35
 <211> 19
 <212> DNA
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<220>
 <223> Synthetic

<400> 35
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<210> 36
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<220>
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 <400> 36
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<210> 37
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<220>
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 <400> 37
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<210> 38
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 <212> DNA
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<220>
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 <400> 38
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<210> 39
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 <212> DNA
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<220>
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 <400> 39
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<210> 40
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<220>
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 <400> 40
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<210> 41
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 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 41
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<210> 42
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<220>
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<400> 42
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27

<210> 43
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<220>
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<400> 43
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28

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 <213> Artificial Sequence

<220>
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<400> 44
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37

<210> 45
 <211> 31
 <212> DNA
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<220>
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<400> 45
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31

<210> 46
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 <212> DNA
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<220>
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<400> 46
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36

<210> 47
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<220>
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<400> 47
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26

<210> 48
<211> 9
<212> PRT
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<220>
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<400> 48

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<210> 49
<211> 4960
<212> DNA
<213> Homo Sapiens

<400> 49
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Cys	Leu	Pro	Arg	Lys	Glu	Ala	Ala	Ser	Leu	Met	Arg	Thr	Asp	Phe	Thr					
			555					560					565							
gga	act	gtg	gct	ggc	tgg	ggg	tta	acc	cag	aag	ggg	ctt	ctt	gct	aga	1781				
Gly	Thr	Val	Ala	Gly	Trp	Gly	Leu	Thr	Gln	Lys	Gly	Leu	Leu	Ala	Arg					
		570					575					580								
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	ggg	ggc	aag	gac	agc	tgc	aga	ggg	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	ggg	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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 <212> PRT
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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

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

7489616_1.txt

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
 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

7489616_1.txt

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
 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

7489616_1.txt

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

7489616_1.txt

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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Met Arg Leu Leu Ile Val Leu Gly Leu Leu Trp Ser Leu Val
1 5 10

51

7489616_1.txt

gcc Ala 15	aca Thr	ctt Leu	ttg Leu	ggc Gly	tcc Ser 20	aag Lys	tgg Trp	cct Pro	gag Glu	cct Pro 25	gta Val	ttc Phe	ggg Gly	cgc Arg	ctg Leu 30	99
gtg Val	tcc Ser	ctg Leu	gcc Ala	ttc Phe 35	cca Pro	gag Glu	aag Lys	tat Tyr	ggc Gly 40	aac Asn	cat His	cag Gln	gat Asp	cga Arg 45	tcc Ser	147
tgg Trp	acg Thr	ctg Leu	act Thr 50	gca Ala	ccc Pro	cct Pro	ggc Gly	ttc Phe 55	cgc Arg	ctg Leu	cgc Arg	ctc Leu	tac Tyr 60	ttc Phe	acc Thr	195
cac His	ttc Phe	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
ttg Leu	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	acc Thr 105	ttc Phe	tac Tyr	tca Ser	ctg Leu	ggg 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	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	ctg Leu 160	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 Ser	aac Asn	aag Lys	gtg Val	acc Thr 275	att Ile	acc Thr	ttt Phe	acc Thr	acc Thr 280	gac Asp	gag Glu	tca Ser	ggg Gly	aac Asn 285	cac His	867

7489616_1.txt

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
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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	gcg 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 Ile	aac Asn	aga Arg 545	aac Asn	atc Ile	atg Met	ccg Pro	att Ile 550	tgt Cys	cta Leu	cca Pro	aga Arg	aaa Lys 555	gaa Glu	gct Ala	gca Ala	1683

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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	
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	
ggg 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	
ggg 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

Met Arg Leu Leu Ile Val Leu Gly Leu Leu Trp Ser Leu Val Ala Thr
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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

7489616_1.txt

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

7489616_1.txt

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

7489616_1.txt

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
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<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

7489616_1.txt

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

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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
645 650 655

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

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<220>
<223> Homo Sapiens

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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

<210> 59
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 59
ttaaaatcac taattatggt ctcgatc 27

<210> 60
<211> 22
<212> DNA
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<223> Murine

<400> 60
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<210> 61
<211> 23
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<220>
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<400> 61
ctgcagaggt gacgcagggg ggg 23

<210> 62
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<400> 62
ccccccctgc gtcacctctg cag 23

<210> 63
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ttagaaatta cttattatgt tctcaatcc

29

<210> 64

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Rat

<400> 64

gaggtgacgc aggaggggca ttagtgttt

29

<210> 65

<211> 37

<212> DNA

<213> Artificial Sequence

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<223> Rat

<400> 65

ctagaaacac taatgccct cctgcgtcac ctctgca

37

<210> 66

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 66

caggtcacct tgaaggagtc tggctctgtg ctggtgaaac ccacagagac cctcacgctg

60

acctgcaccg tctctgggtt ctcactcagc aggggtaaaa tgggtgtgag ctggatccgt

120

cagccccag ggaaggccct ggagtggctt gcacacattt tttcgagtga cgaaaaatcc

180

tacaggacat cgctgaagag caggctcacc atctccaagg acacctcaa aaaccaggtg

240

gtccttacia tgaccaacat ggaccctgtg gacacagcca cgtattactg tgcacggata

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<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

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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>
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<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
 <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
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 <212> DNA
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<400> 70

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acctgtgcgg gagacaacct tgggaagaaa cgtgtgcact ggtaccagca gaggccaggc	120
caggcccctg 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
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<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