

SEQUENCE LISTING

<110> MEDIMMUNE LIMITED
ASTRAZENECA PHARMACEUTICALS LP

<120> METHODS FOR TREATING HEPCIDIN-MEDIATED DISORDERS

<130> 32601-34392/PCT

<140> PCT/US2016/044528

<141> 2016-07-28

<150> 62/268,788

<151> 2015-12-17

<150> 62/199,434

<151> 2015-07-31

<160> 25

<170> PatentIn version 3.5

<210> 1

<211> 84

<212> PRT

<213> Homo sapiens

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Gln Leu Ala Glu Leu Gln Pro Gln Asp Arg Ala Gly Ala Arg Ala Ser
35 40 45

Trp Met Pro Met Phe Gln Arg Arg Arg Arg Arg Asp Thr His Phe Pro
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Ile Cys Ile Phe Cys Cys Gly Cys Cys His Arg Ser Lys Cys Gly Met
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Cys Cys Lys Thr

<210> 2

<211> 824

<212> PRT

<213> Homo sapiens

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Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	Thr	Ala	Lys	Ala	Gln	Lys	Met
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Pro	Gln	Thr 355	His	Cys	Ser	Trp	His 360	Leu	Thr	Val	Pro	Ser 365	Leu	Asp	Tyr
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Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	595	600	605	
Cys	Phe	Gln	Glu	Asp	Ser	Met	Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	610	615	620	
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Ala	Leu	Arg	Ala	Asp	Ala	Val	Ala	Leu	Phe	Tyr	Gly	Trp	Arg	Asn	Gln	705	710	715	720
Gly	Ser	Glu	Thr	Cys	Cys	Cys	Pro	Ile	Ser	Asn	Ala	Leu	Gln	Lys	Ala	725	730	735	
Asp	Val	Gln	Leu	Ile	Pro	Gln	Asp	Leu	Cys	Ser	Glu	Val	Tyr	Arg	Tyr	740	745	750	
Gln	Val	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	Tyr	Arg	Lys	Gly	Lys	Lys	755	760	765	
Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Lys	Ala	Leu	770	775	780	
Ser	Gly	Arg	Trp	Phe	Leu	Ala	Gly	Leu	Val	Ser	Trp	Gly	Leu	Gly	Cys	785	790	795	800

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Ser Trp Ile Gln Gln Val Val Thr
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<210> 3

<211> 824

<212> PRT

<213> Homo sapiens

<400> 3

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Asp Ser Lys Arg Lys Ala Arg Gly Tyr Leu Arg Leu Val Pro Leu Phe
35 40 45

Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly Val Leu Leu Trp
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Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val Ser Gln Val Tyr Ser
65 70 75 80

Gly Ser Leu Arg Val Leu Asn Arg His Phe Ser Gln Asp Leu Thr Arg
85 90 95

Arg Glu Ser Ser Ala Phe Arg Ser Glu Thr Ala Lys Ala Gln Lys Met
100 105 110

Leu Lys Glu Leu Ile Thr Ser Thr Arg Leu Gly Thr Tyr Tyr Asn Ser
115 120 125

Ser Ser Val Tyr Ser Phe Gly Glu Gly Pro Leu Thr Cys Phe Phe Trp
130 135 140

Phe Ile Leu Gln Ile Pro Glu His Arg Arg Leu Met Leu Ser Pro Glu
145 150 155 160

Val Val Gln Ala Leu Leu Val Glu Glu Leu Leu Ser Thr Val Asn Ser
165 170 175

Ser Ala Ala Val Pro Tyr Arg Ala Glu Tyr Glu Val Asp Pro Glu Gly
180 185 190

Leu Val Ile Leu Glu Ala Ser Val Lys Asp Ile Ala Ala Leu Asn Ser
 195 200 205

Thr Leu Gly Cys Tyr Arg Tyr Ser Tyr Val Gly Gln Gly Gln Val Leu
 210 215 220

Arg Leu Lys Gly Pro Asp His Leu Ala Ser Ser Cys Leu Trp His Leu
 225 230 235 240

Gln Gly Pro Lys Asp Leu Met Leu Lys Leu Arg Leu Glu Trp Thr Leu
 245 250 255

Ala Glu Cys Arg Asp Arg Leu Ala Met Tyr Asp Val Ala Gly Pro Leu
 260 265 270

Glu Lys Arg Leu Ile Thr Ser Val Tyr Gly Cys Ser Arg Gln Glu Pro
 275 280 285

Val Val Glu Val Leu Ala Ser Gly Ala Ile Met Ala Val Val Trp Lys
 290 295 300

Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val Leu Ser Val Gln Pro
 305 310 315 320

Val Val Phe Gln Ala Cys Glu Val Asn Leu Thr Leu Asp Asn Arg Leu
 325 330 335

Asp Ser Gln Gly Val Leu Ser Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser
 340 345 350

Pro Gln Thr His Cys Ser Trp His Leu Thr Val Pro Ser Leu Asp Tyr
 355 360 365

Gly Leu Ala Leu Trp Phe Asp Ala Tyr Ala Leu Arg Arg Gln Lys Tyr
 370 375 380

Asp Leu Pro Cys Thr Gln Gly Gln Trp Thr Ile Gln Asn Arg Arg Leu
 385 390 395 400

Cys Gly Leu Arg Ile Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val
 405 410 415

Ala Thr Ala Gly Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr
 420 425 430

Gly Pro Gly Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro
 435 440 445

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

Leu Pro Lys Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly Ser Asp
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Glu Glu Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe Thr Phe Gln
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Cys Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro Gln Cys Asp Gly
530 535 540

Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu His Cys Asp Cys Gly
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Leu Gln Gly Pro Ser Ser Arg Ile Val Gly Gly Ala Val Ser Ser Glu
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Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Val Arg Gly Arg His Ile
580 585 590

Cys Gly Gly Ala Leu Ile Ala Asp Arg Trp Val Ile Thr Ala Ala His
595 600 605

Cys Phe Gln Glu Asp Ser Met Ala Ser Thr Val Leu Trp Thr Val Phe
610 615 620

Leu Gly Lys Val Trp Gln Asn Ser Arg Trp Pro Gly Glu Val Ser Phe
625 630 635 640

Lys Val Ser Arg Leu Leu Leu His Pro Tyr His Glu Glu Asp Ser His
645 650 655

Asp Tyr Asp Val Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser
660 665 670

Ala Ala Val Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu
675 680 685

Pro Gly Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly
690 695 700

Ala Leu Arg Ala Asp Ala Val Ala Leu Phe Tyr Gly Trp Arg Asn Gln
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Gly Ser Glu Thr Cys Cys Cys Pro Ile Ser Asn Ala Leu Gln Lys Val
725 730 735

Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val Tyr Arg Tyr
740 745 750

Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys
755 760 765

Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu
770 775 780

Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys
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Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile
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Ser Trp Ile Gln Gln Val Val Thr
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<210> 4

<211> 3196

<212> DNA

<213> Homo sapiens

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agagcccagg	gcaactgcca	agcaggggga	caagtattct	ggcggggggg	gggggagaga	2640
gcaggccctg	tgggtggcagg	aggtggcatc	ttgtctcgtc	cctgatgtct	gctccagtga	2700
tggcaggagg	atggagaagt	gccagcagct	gggggtcaag	acgtcccctg	aggaccagg	2760
cccacaccca	gcccttctgc	ctcccatttc	tctctcctcc	gtccccttcc	tccactgctg	2820
cctaatagcaa	ggcagtggct	cagcagcaag	aatgctgggt	ctacatccc	aggagtgtct	2880
gaggtgcgcc	ccactctgta	cagaggctgt	ttgggcagcc	ttgcctccag	agagcagatt	2940
ccagcttcgg	aagcccctgg	tctaacttgg	gatctgggaa	tggaaagtgc	tcccatcgga	3000
ggggaccctc	agagccctgg	agactgccag	gtgggcctgc	tgccactgta	agccaaaagg	3060
tggggaagtc	ctgactccag	ggtccttgcc	ccaccctgc	ctgccacctg	ggccctcaca	3120

gcccagaccc tcactgggag gtgagctcag ctgccctttg gaataaagct gcctgatcca 3180

aaaaaaaaaa aaaaaa 3196

<210> 6

<211> 277

<212> PRT

<213> Homo sapiens

<400> 6

Met Cys Val Gly Ala Arg Arg Leu Gly Arg Gly Pro Cys Ala Ala Leu
1 5 10 15

Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly Leu His Cys Val
20 25 30

Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His Glu Cys Arg Pro
35 40 45

Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val Cys
50 55 60

Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro
65 70 75 80

Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly Ser Glu Arg Lys
85 90 95

Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly
100 105 110

Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp Cys Ala Pro Cys
115 120 125

Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp
130 135 140

Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn
145 150 155 160

Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro
165 170 175

Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr
180 185 190

Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu
195 200 205

Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val
 210 215 220

Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu
 225 230 235 240

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
 245 250 255

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
 260 265 270

Thr Leu Ala Lys Ile
 275

<210> 7
 <211> 1201
 <212> DNA
 <213> Homo sapiens

<400> 7
 aatattagag tctcaacccc caataaatat aggactggag atgtctgagg ctcatctctgc 60
 cctcgagccc accgggaacg aaagagaagc tctatctccc ctccaggagc ccagctatga 120
 actccttctc cacaagcgcc ttcgggtccag ttgccttctc cctggggctg ctcttggtgt 180
 tgccctgctgc cttccctgcc ccagtacccc caggagaaga ttccaaagat gtagccgccc 240
 cacacagaca gccactcacc tcttcagaac gaattgacaa acaaattcgg tacatcctcg 300
 acggcatctc agccctgaga aaggagacat gtaacaagag taacatgtgt gaaagcagca 360
 aagaggcact ggcagaaaac aacctgaacc ttccaaagat ggctgaaaaa gatggatgct 420
 tccaatctgg attcaatgag gagacttgcc tgggtgaaaat catcactggc cttttggagt 480
 ttgaggtata cctagagtac ctccagaaca gatttgagag tagtgaggaa caagccagag 540
 ctgtgcagat gagtacaaaa gtcctgatcc agttcctgca gaaaaaggca aagaatctag 600
 atgcaataac caccctgac ccaaccacaa atgccagcct gctgacgaag ctgcaggcac 660
 agaaccagtg gctgcaggac atgacaactc atctcattct gcgcagcttt aaggagttcc 720
 tgcagtccag cctgagggct cttcggcaaa tgtagcatgg gcacctcaga ttgttgttgt 780
 taatgggcat tccttcttct ggtcagaaac ctgtccactg ggcacagaac ttatgttgtt 840
 ctctatggag aactaaaagt atgagcgtaa ggacactatt ttaattattt ttaatttatt 900
 aatattttaa tatgtgaagc tgagttaatt tatgtaagtc atatttatat ttttaagaag 960
 taccacttga aacattttat gtattagttt tgaaataata atggaaagtg gctatgcagt 1020
 ttgaatatcc tttgtttcag agccagatca tttcttgga agtgtaggct tacctcaaat 1080
 aaatggctaa cttatacata tttttaaaga aatatttata ttgtatttat ataatgtata 1140

aatgggttttt ataccaataa atggcatttt aaaaaattca gcaaaaaaaaa aaaaaaaaaa 1200

a 1201

<210> 8

<211> 468

<212> PRT

<213> Homo sapiens

<400> 8

Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro
1 5 10 15

Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
20 25 30

Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
35 40 45

Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
50 55 60

Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
65 70 75 80

Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
85 90 95

Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
100 105 110

Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
115 120 125

Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
130 135 140

Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
145 150 155 160

Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
165 170 175

Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
180 185 190

Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
195 200 205

Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val

210

215

220

Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
 225 230 235 240

Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
 245 250 255

Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
 260 265 270

Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
 275 280 285

Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
 290 295 300

Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
 305 310 315 320

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

Asn Lys Asp Asp Asp Asn Ile Leu Phe Arg Asp Ser Ala Asn Ala Thr
 340 345 350

Ser Leu Pro Val Gln Asp Ser Ser Ser Val Pro Leu Pro Thr Phe Leu
 355 360 365

Val Ala Gly Gly Ser Leu Ala Phe Gly Thr Leu Leu Cys Ile Ala Ile
 370 375 380

Val Leu Arg Phe Lys Lys Thr Trp Lys Leu Arg Ala Leu Lys Glu Gly
 385 390 395 400

Lys Thr Ser Met His Pro Pro Tyr Ser Leu Gly Gln Leu Val Pro Glu
 405 410 415

Arg Pro Arg Pro Thr Pro Val Leu Val Pro Leu Ile Ser Pro Pro Val
 420 425 430

Ser Pro Ser Ser Leu Gly Ser Asp Asn Thr Ser Ser His Asn Arg Pro
 435 440 445

Asp Ala Arg Asp Pro Arg Ser Pro Tyr Asp Ile Ser Asn Thr Asp Tyr
 450 455 460

Phe Phe Pro Arg

<210> 9

<211> 918

<212> PRT

<213> Homo sapiens

<400> 9

Met Leu Thr Leu Gln Thr Trp Leu Val Gln Ala Leu Phe Ile Phe Leu
 1 5 10 15

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

Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
 35 40 45

Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
 50 55 60

Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
 65 70 75 80

Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
 85 90 95

Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
 100 105 110

Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
 115 120 125

Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
 130 135 140

Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
 145 150 155 160

Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
 165 170 175

Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
 180 185 190

Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
 195 200 205

Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
 210 215 220

Pro	His	Asn	Leu	Ser	Val	Ile	Asn	Ser	Glu	Glu	Leu	Ser	Ser	Ile	Leu	225	230	235	240
Lys	Leu	Thr	Trp	Thr	Asn	Pro	Ser	Ile	Lys	Ser	Val	Ile	Ile	Leu	Lys	245	250	255	
Tyr	Asn	Ile	Gln	Tyr	Arg	Thr	Lys	Asp	Ala	Ser	Thr	Trp	Ser	Gln	Ile	260	265	270	
Pro	Pro	Glu	Asp	Thr	Ala	Ser	Thr	Arg	Ser	Ser	Phe	Thr	Val	Gln	Asp	275	280	285	
Leu	Lys	Pro	Phe	Thr	Glu	Tyr	Val	Phe	Arg	Ile	Arg	Cys	Met	Lys	Glu	290	295	300	
Asp	Gly	Lys	Gly	Tyr	Trp	Ser	Asp	Trp	Ser	Glu	Glu	Ala	Ser	Gly	Ile	305	310	315	320
Thr	Tyr	Glu	Asp	Arg	Pro	Ser	Lys	Ala	Pro	Ser	Phe	Trp	Tyr	Lys	Ile	325	330	335	
Asp	Pro	Ser	His	Thr	Gln	Gly	Tyr	Arg	Thr	Val	Gln	Leu	Val	Trp	Lys	340	345	350	
Thr	Leu	Pro	Pro	Phe	Glu	Ala	Asn	Gly	Lys	Ile	Leu	Asp	Tyr	Glu	Val	355	360	365	
Thr	Leu	Thr	Arg	Trp	Lys	Ser	His	Leu	Gln	Asn	Tyr	Thr	Val	Asn	Ala	370	375	380	
Thr	Lys	Leu	Thr	Val	Asn	Leu	Thr	Asn	Asp	Arg	Tyr	Leu	Ala	Thr	Leu	385	390	395	400
Thr	Val	Arg	Asn	Leu	Val	Gly	Lys	Ser	Asp	Ala	Ala	Val	Leu	Thr	Ile	405	410	415	
Pro	Ala	Cys	Asp	Phe	Gln	Ala	Thr	His	Pro	Val	Met	Asp	Leu	Lys	Ala	420	425	430	
Phe	Pro	Lys	Asp	Asn	Met	Leu	Trp	Val	Glu	Trp	Thr	Thr	Pro	Arg	Glu	435	440	445	
Ser	Val	Lys	Lys	Tyr	Ile	Leu	Glu	Trp	Cys	Val	Leu	Ser	Asp	Lys	Ala	450	455	460	
Pro	Cys	Ile	Thr	Asp	Trp	Gln	Gln	Glu	Asp	Gly	Thr	Val	His	Arg	Thr	465	470	475	480

Tyr	Leu	Arg	Gly	Asn	Leu	Ala	Glu	Ser	Lys	Cys	Tyr	Leu	Ile	Thr	Val
				485					490					495	
Thr	Pro	Val	Tyr	Ala	Asp	Gly	Pro	Gly	Ser	Pro	Glu	Ser	Ile	Lys	Ala
			500					505					510		
Tyr	Leu	Lys	Gln	Ala	Pro	Pro	Ser	Lys	Gly	Pro	Thr	Val	Arg	Thr	Lys
		515					520					525			
Lys	Val	Gly	Lys	Asn	Glu	Ala	Val	Leu	Glu	Trp	Asp	Gln	Leu	Pro	Val
	530					535					540				
Asp	Val	Gln	Asn	Gly	Phe	Ile	Arg	Asn	Tyr	Thr	Ile	Phe	Tyr	Arg	Thr
545					550					555					560
Ile	Ile	Gly	Asn	Glu	Thr	Ala	Val	Asn	Val	Asp	Ser	Ser	His	Thr	Glu
			565						570					575	
Tyr	Thr	Leu	Ser	Ser	Leu	Thr	Ser	Asp	Thr	Leu	Tyr	Met	Val	Arg	Met
			580					585					590		
Ala	Ala	Tyr	Thr	Asp	Glu	Gly	Gly	Lys	Asp	Gly	Pro	Glu	Phe	Thr	Phe
		595					600					605			
Thr	Thr	Pro	Lys	Phe	Ala	Gln	Gly	Glu	Ile	Glu	Ala	Ile	Val	Val	Pro
	610					615					620				
Val	Cys	Leu	Ala	Phe	Leu	Leu	Thr	Thr	Leu	Leu	Gly	Val	Leu	Phe	Cys
625					630					635					640
Phe	Asn	Lys	Arg	Asp	Leu	Ile	Lys	Lys	His	Ile	Trp	Pro	Asn	Val	Pro
				645					650					655	
Asp	Pro	Ser	Lys	Ser	His	Ile	Ala	Gln	Trp	Ser	Pro	His	Thr	Pro	Pro
			660					665					670		
Arg	His	Asn	Phe	Asn	Ser	Lys	Asp	Gln	Met	Tyr	Ser	Asp	Gly	Asn	Phe
		675					680					685			
Thr	Asp	Val	Ser	Val	Val	Glu	Ile	Glu	Ala	Asn	Asp	Lys	Lys	Pro	Phe
	690					695					700				
Pro	Glu	Asp	Leu	Lys	Ser	Leu	Asp	Leu	Phe	Lys	Lys	Glu	Lys	Ile	Asn
705					710					715					720
Thr	Glu	Gly	His	Ser	Ser	Gly	Ile	Gly	Gly	Ser	Ser	Cys	Met	Ser	Ser
				725					730					735	

Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu Ser Ser Gln Asn
740 745 750

Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His Ser Gly Tyr Arg
755 760 765

His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser Glu Ser Thr Gln
770 775 780

Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu Asp Leu Gln Leu Val Asp
785 790 795 800

His Val Asp Gly Gly Asp Gly Ile Leu Pro Arg Gln Gln Tyr Phe Lys
805 810 815

Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile Ser His Phe Glu
820 825 830

Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp Phe Val Arg Leu
835 840 845

Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys Gly Ser Gly Gln
850 855 860

Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp Ala Phe Gly Pro Gly
865 870 875 880

Thr Glu Gly Gln Val Glu Arg Phe Glu Thr Val Gly Met Glu Ala Ala
885 890 895

Thr Asp Glu Gly Met Pro Lys Ser Tyr Leu Pro Gln Thr Val Arg Gln
900 905 910

Gly Gly Tyr Met Pro Gln
915

<210> 10
<211> 193
<212> PRT
<213> Homo sapiens

<400> 10
Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15

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

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu

35

40

45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Arg

<210> 11

<211> 224

<212> PRT

<213> Homo sapiens

<400> 11

Met Glu Lys Leu Leu Cys Phe Leu Val Leu Thr Ser Leu Ser His Ala
1 5 10 15

Phe Gly Gln Thr Asp Met Ser Arg Lys Ala Phe Val Phe Pro Lys Glu
20 25 30

Ser Asp Thr Ser Tyr Val Ser Leu Lys Ala Pro Leu Thr Lys Pro Leu
35 40 45

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

Arg Gly Tyr Ser Ile Phe Ser Tyr Ala Thr Lys Arg Gln Asp Asn Glu
65 70 75 80

Ile Leu Ile Phe Trp Ser Lys Asp Ile Gly Tyr Ser Phe Thr Val Gly
85 90 95

Gly Ser Glu Ile Leu Phe Glu Val Pro Glu Val Thr Val Ala Pro Val
100 105 110

His Ile Cys Thr Ser Trp Glu Ser Ala Ser Gly Ile Val Glu Phe Trp
115 120 125

Val Asp Gly Lys Pro Arg Val Arg Lys Ser Leu Lys Lys Gly Tyr Thr
130 135 140

Val Gly Ala Glu Ala Ser Ile Ile Leu Gly Gln Glu Gln Asp Ser Phe
145 150 155 160

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

Val Asn Met Trp Asp Phe Val Leu Ser Pro Asp Glu Ile Asn Thr Ile
180 185 190

Tyr Leu Gly Gly Pro Phe Ser Pro Asn Val Leu Asn Trp Arg Ala Leu
195 200 205

Lys Tyr Glu Val Gln Gly Glu Val Phe Thr Lys Pro Gln Leu Trp Pro
210 215 220

<210> 12

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 12

Ser Asn Tyr Met Ile

1 5

<210> 13

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 13
Asp Leu Tyr Tyr Tyr Ala Gly Asp Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 14
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 14
Trp Ala Asp Asp His Pro Pro Trp Ile Asp Leu
1 5 10

<210> 15
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 15
Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 16
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 16
Lys Ala Ser Thr Leu Glu Ser
1 5

<210> 17
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 17
Gln Gln Ser Trp Leu Gly Gly Ser
1 5

<210> 18
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 18
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Ser Asn
20 25 30

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

Ser Asp Leu Tyr Tyr Tyr Ala Gly Asp Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Met Ser Arg Asp Ile Ser Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Ala Asp Asp His Pro Pro Trp Ile Asp Leu Trp Gly Arg
100 105 110

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

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

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

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

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

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp

210

215

220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile
 245 250 255

Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335

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

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

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

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
 450

<210> 19

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

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 19

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

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

Tyr Lys Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Trp Leu Gly Gly Ser
85 90 95

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

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

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

Asn Arg Gly Glu Cys
210

<210> 20	
<211> 16	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic probe	
<400> 20	
cggtctgtgca gccttg	16
<210> 21	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide	
<400> 21	
cttccaggag cgagatcccg ctaa	24
<210> 22	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic primer	
<400> 22	
gcatgaggtc cttggggccc tgcag	25
<210> 23	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic primer	
<400> 23	
ctgcagggcc ccaaggacct catgc	25
<210> 24	
<211> 29	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic primer	
<400> 24	
cctggtagcg ataggcctcg ctgcacagg	29

<210> 25
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 25

cctgtgcagc gaggcctatc gctaccagg

29