

SEQUENCE LISTING

<110> Eli Lilly and Company

<120> Variants of Human BMP7 Protein

<130> X21419

<150> US 62/490,910

<151> 2017-04-27

<160> 21

<170> PatentIn version 3.5

<210> 1

<211> 431

<212> PRT

<213> Homo sapiens

<400> 1

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

Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
20 25 30

Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
35 40 45

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
50 55 60

Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
65 70 75 80

Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
85 90 95

Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
100 105 110

Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
115 120 125

Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
130 135 140

Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
145 150 155 160

Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
165 170 175

Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
180 185 190

Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
195 200 205

Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
210 215 220

Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
225 230 235 240

His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
245 250 255

Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
260 265 270

Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
275 280 285

Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
290 295 300

Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
305 310 315 320

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

Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
340 345 350

Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
355 360 365

Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
370 375 380

Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
385 390 395 400

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
405 410 415

Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
420 425 430

<210> 2
<211> 139
<212> PRT
<213> Homo sapiens

<400> 2

Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1 5 10 15

Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
20 25 30

Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
35 40 45

Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala

50

55

60

Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
 65 70 75 80

Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
 85 90 95

Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
 100 105 110

Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
 115 120 125

Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 130 135

<210> 3
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<220>
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 <222> (33)..(33)
 <223> Xaa at position 33 = D or M

<220>
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 <222> (37)..(37)
 <223> Xaa at position 37 = A or P

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 <222> (60)..(60)
 <223> Xaa at position 60 = E or Q

<220>
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 <222> (65)..(65)

<223> Xaa at position 65 = Y, S, or G

<220>

<221> MISC_FEATURE

<222> (86)..(86)

<223> Xaa at position 86 = I, V, or L

<220>

<221> MISC_FEATURE

<222> (87)..(87)

<223> Xaa at position 87 = V or L

<220>

<221> MISC_FEATURE

<222> (89)..(89)

<223> Xaa at position 89 = T, S, or A

<220>

<221> MISC_FEATURE

<222> (91)..(91)

<223> Xaa at position 91 = V or M

<220>

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<222> (93)..(93)

<223> Xaa at position 93 = F or V

<220>

<221> MISC_FEATURE

<222> (94)..(94)

<223> Xaa at position 94 = I, F, or M

<220>

<221> MISC_FEATURE

<222> (110)..(110)

<223> Xaa at position 110 = N, A, S, or G

<220>

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<222> (114)..(114)

<223> Xaa at position 114 = V or M

<220>

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<222> (120)..(120)

<223> Xaa at position 120 = S or Q

<220>

<221> MISC_FEATURE

<222> (128)..(128)

<223> Xaa at position 128 = Y, F or W

<220>

<221> MISC_FEATURE

<222> (132)..(132)

<223> Xaa at position 132 = V, Q, or S

<220>

<221> MISC_FEATURE

<222> (134)..(134)

<223> Xaa at position 134 = R or K

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Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	Lys
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Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser	Ser
			20					25					30		

Xaa	Gln	Arg	Gln	Xaa	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg
			35				40					45			

Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Xaa	Gly	Tyr	Ala	Ala
	50					55					60				

Xaa	Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn
65					70					75					80

Ala	Thr	Asn	His	Ala	Xaa	Xaa	Gln	Xaa	Leu	Xaa	His	Xaa	Xaa	Asn	Pro
				85					90					95	

Glu	Thr	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Xaa	Ala	Ile
			100					105					110		

Ser	Xaa	Leu	Tyr	Phe	Asp	Asp	Xaa	Ser	Asn	Val	Ile	Leu	Lys	Lys	Xaa
		115					120					125			

Arg	Asn	Met	Xaa	Val	Xaa	Ala	Cys	Gly	Cys	His
	130					135				

<210> 4
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<400> 4

Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1 5 10 15

Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
20 25 30

Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
35 40 45

Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
50 55 60

Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
65 70 75 80

Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Val Ile Asn Pro
85 90 95

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

Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
115 120 125

Arg Asn Met Val Val Arg Ala Cys Gly Cys His
130 135

<210> 5
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<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 5

Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1 5 10 15

Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
20 25 30

Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
35 40 45

Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
50 55 60

Gly Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
65 70 75 80

Ala Thr Asn His Ala Leu Val Gln Ala Leu Val His Phe Ile Asn Pro
85 90 95

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

Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
115 120 125

Arg Asn Met Val Val Arg Ala Cys Gly Cys His
130 135

<210> 6

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<400> 6

Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1 5 10 15

Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
20 25 30

Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
35 40 45

Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
50 55 60

Gly Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
65 70 75 80

Ala Thr Asn His Ala Leu Val Gln Thr Leu Val His Phe Ile Asn Pro
85 90 95

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

Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Phe
115 120 125

Arg Asn Met Val Val Arg Ala Cys Gly Cys His
130 135

<210> 7

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<212> PRT

<213> Artificial Sequence

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<400> 7

Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1 5 10 15

Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
20 25 30

Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
35 40 45

Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
50 55 60

Gly Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
65 70 75 80

Ala Thr Asn His Ala Leu Val Gln Thr Leu Val His Phe Ile Asn Pro
85 90 95

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

Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Trp
115 120 125

Arg Asn Met Val Val Arg Ala Cys Gly Cys His
130 135

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<400> 8

Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1 5 10 15

Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
20 25 30

Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
35 40 45

Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
50 55 60

Gly Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
65 70 75 80

Ala Thr Asn His Ala Leu Val Gln Thr Leu Val His Val Ile Asn Pro
85 90 95

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

Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Trp
115 120 125

Arg Asn Met Val Val Arg Ala Cys Gly Cys His
130 135

<210> 9
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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 9

Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1 5 10 15

Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
20 25 30

Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
35 40 45

Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
50 55 60

Gly Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
65 70 75 80

Ala Thr Asn His Ala Ile Val Gln Ala Leu Val His Phe Ile Asn Pro
85 90 95

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

Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Phe
115 120 125

Arg Asn Met Val Val Arg Ala Cys Gly Cys His
130 135

<210> 10
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<400> 10

Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1 5 10 15

Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
20 25 30

Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
35 40 45

Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
50 55 60

Gly Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
65 70 75 80

Ala Thr Asn His Ala Leu Val Gln Thr Leu Val His Phe Ile Asn Pro
85 90 95

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

Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
115 120 125

Arg Asn Met Val Val Arg Ala Cys Gly Cys His
130 135

<210> 11
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 11

Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1 5 10 15

Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
20 25 30

Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
35 40 45

Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
50 55 60

Gly Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
65 70 75 80

Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
85 90 95

Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
100 105 110

Ser Met Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
115 120 125

Arg Asn Met Val Val Arg Ala Cys Gly Cys His
130 135

<210> 12
<211> 402
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 12

Asp Phe Ser Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg
1 5 10 15

Leu Arg Ser Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile
20 25 30

Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn
35 40 45

Ser Ala Pro Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu
50 55 60

Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala
65 70 75 80

Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His
85 90 95

Phe Leu Thr Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu
100 105 110

His Asp Lys Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg
115 120 125

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

Phe Arg Ile Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr
145 150 155 160

Phe Arg Ile Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu
165 170 175

Ser Asp Leu Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu
180 185 190

Gly Trp Leu Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val
195 200 205

Asn Pro Arg His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp
210 215 220

Gly Gln Ser Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly
225 230 235 240

Pro Gln Asn Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu
245 250 255

Val His Phe Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln
260 265 270

Asn Arg Ser Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn
275 280 285

Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His
290 295 300

Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile
305 310 315 320

Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe
325 330 335

Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr
340 345 350

Leu Val His Val Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala
355 360 365

Pro Thr Gln Leu Gly Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser
370 375 380

Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly
385 390 395 400

Cys His

<210> 13

<211> 402

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 13

Asp Phe Ser Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg
1 5 10 15

Leu Arg Ser Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile
20 25 30

Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn
35 40 45

Ser Ala Pro Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu
50 55 60

Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala
65 70 75 80

Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His
85 90 95

Phe Leu Thr Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu
100 105 110

His Asp Lys Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg
115 120 125

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

Phe Arg Ile Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr
145 150 155 160

Phe Arg Ile Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu
165 170 175

Ser Asp Leu Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu
180 185 190

Gly Trp Leu Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val
195 200 205

Asn Pro Arg His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp
210 215 220

Gly Gln Ser Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly
225 230 235 240

Pro Gln Asn Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu
245 250 255

Val His Phe Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln
260 265 270

Asn Arg Ser Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn
275 280 285

Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His
290 295 300

Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile
305 310 315 320

Ala Pro Glu Gly Tyr Ala Ala Gly Tyr Cys Glu Gly Glu Cys Ala Phe
325 330 335

Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His Ala Leu Val Gln Ala
340 345 350

Leu Val His Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala
355 360 365

Pro Thr Gln Leu Gly Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser
370 375 380

Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly
385 390 395 400

Cys His

<210> 14

<211> 402

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 14

Asp Phe Ser Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg
1 5 10 15

Leu Arg Ser Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile
20 25 30

Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn
35 40 45

Ser Ala Pro Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu
50 55 60

Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala
65 70 75 80

Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His
85 90 95

Phe Leu Thr Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu
100 105 110

His Asp Lys Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg
115 120 125

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

Phe Arg Ile Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr
145 150 155 160

Phe Arg Ile Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu
165 170 175

Ser Asp Leu Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu
180 185 190

Gly Trp Leu Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val
195 200 205

Asn Pro Arg His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp
210 215 220

Gly Gln Ser Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly
225 230 235 240

Pro Gln Asn Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu
245 250 255

Val His Phe Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln
260 265 270

Asn Arg Ser Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn
275 280 285

Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His
290 295 300

Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile
305 310 315 320

Ala Pro Glu Gly Tyr Ala Ala Gly Tyr Cys Glu Gly Glu Cys Ala Phe
325 330 335

Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His Ala Leu Val Gln Thr
340 345 350

Leu Val His Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala
355 360 365

Pro Thr Gln Leu Gly Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser
370 375 380

Asn Val Ile Leu Lys Lys Phe Arg Asn Met Val Val Arg Ala Cys Gly
385 390 395 400

Cys His

<210> 15
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<220>
<223> Synthetic construct

<400> 15

Asp Phe Ser Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg
1 5 10 15

Leu Arg Ser Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile
20 25 30

Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn
35 40 45

Ser Ala Pro Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu
50 55 60

Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala
65 70 75 80

Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His
85 90 95

Phe Leu Thr Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu
100 105 110

His Asp Lys Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg
115 120 125

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

Phe Arg Ile Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr
145 150 155 160

Phe Arg Ile Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu
165 170 175

Ser Asp Leu Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu
180 185 190

Gly Trp Leu Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val
195 200 205

Asn Pro Arg His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp
210 215 220

Gly Gln Ser Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly
225 230 235 240

Pro Gln Asn Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu
245 250 255

Val His Phe Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln
260 265 270

Asn Arg Ser Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn
275 280 285

Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His
290 295 300

Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile
305 310 315 320

Ala Pro Glu Gly Tyr Ala Ala Gly Tyr Cys Glu Gly Glu Cys Ala Phe
325 330 335

Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His Ala Leu Val Gln Thr
340 345 350

Leu Val His Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala
355 360 365

Pro Thr Gln Leu Gly Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser
370 375 380

Asn Val Ile Leu Lys Lys Trp Arg Asn Met Val Val Arg Ala Cys Gly
385 390 395 400

Cys His

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

<220>
<223> Synthetic construct

<400> 16

Asp Phe Ser Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg
1 5 10 15

Leu Arg Ser Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile
20 25 30

Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn
35 40 45

Ser Ala Pro Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu
50 55 60

Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala
65 70 75 80

Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His
85 90 95

Phe Leu Thr Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu
100 105 110

His Asp Lys Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg
115 120 125

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

Phe Arg Ile Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr
145 150 155 160

Phe Arg Ile Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu
165 170 175

Ser Asp Leu Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu
180 185 190

Gly Trp Leu Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val
195 200 205

Asn Pro Arg His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp
210 215 220

Gly Gln Ser Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly
225 230 235 240

Pro Gln Asn Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu
245 250 255

Val His Phe Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln
260 265 270

Asn Arg Ser Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn
275 280 285

Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His
290 295 300

Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile
305 310 315 320

Ala Pro Glu Gly Tyr Ala Ala Gly Tyr Cys Glu Gly Glu Cys Ala Phe
325 330 335

Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His Ala Leu Val Gln Thr
340 345 350

Leu Val His Val Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala
355 360 365

Pro Thr Gln Leu Gly Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser
370 375 380

Asn Val Ile Leu Lys Lys Trp Arg Asn Met Val Val Arg Ala Cys Gly
385 390 395 400

Cys His

<210> 17
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> MISC_FEATURE
<222> (33)..(33)

<223> Xaa at position 33 = D or M

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa at position 37 = A or P

<220>

<221> MISC_FEATURE

<222> (60)..(60)

<223> Xaa at position 60 = E or Q

<220>

<221> MISC_FEATURE

<222> (65)..(65)

<223> Xaa at position 65 = Y, S, or G

<220>

<221> MISC_FEATURE

<222> (86)..(86)

<223> Xaa at position 86 = I, V or L

<220>

<221> misc_feature

<222> (89)..(89)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> MISC_FEATURE

<222> (91)..(91)

<223> Xaa at position 91 = V or M

<220>

<221> MISC_FEATURE

<222> (93)..(93)

<223> Xaa at 93 = F or V

<220>

<221> MISC_FEATURE

<222> (94)..(94)

<223> Xaa at 94 = I, F or M

<220>

<221> MISC_FEATURE

<222> (110)..(110)

<223> Xaa at position 110 = N, A, S or G

<220>

<221> MISC_FEATURE

<222> (114)..(114)

<223> Xaa at position 114 = V or M

<220>

<221> MISC_FEATURE

<222> (128)..(128)

<223> Xaa at position 128 = Y, F or W

<400> 17

Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	Lys
1				5					10					15	

Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser	Ser
			20					25					30		

Xaa	Gln	Arg	Gln	Xaa	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg
			35				40					45			

Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Xaa	Gly	Tyr	Ala	Ala
	50					55					60				

Xaa	Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn
65					70					75					80

Ala	Thr	Asn	His	Ala	Xaa	Val	Gln	Xaa	Leu	Xaa	His	Xaa	Xaa	Asn	Pro
				85					90					95	

Glu	Thr	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Xaa	Ala	Ile
			100					105					110		

Ser	Xaa	Leu	Tyr	Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Xaa
		115					120					125			

Arg	Asn	Met	Val	Val	Arg	Ala	Cys	Gly	Cys	His
	130					135				

<210> 18

<211> 257

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 18

Asp Phe Ser Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg
1 5 10 15

Leu Arg Ser Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile
20 25 30

Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn
35 40 45

Ser Ala Pro Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu
50 55 60

Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala
65 70 75 80

Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His
85 90 95

Phe Leu Thr Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu
100 105 110

His Asp Lys Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg
115 120 125

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

Phe Arg Ile Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr
145 150 155 160

Phe Arg Ile Ser Val Tyr Gln Val Leu Gln Ser Asp Leu Phe Leu Leu
165 170 175

Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp

180

185

190

Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu
 195 200 205

Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro
 210 215 220

Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro
 225 230 235 240

Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile
 245 250 255

Arg

<210> 19
 <211> 1293
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 19
 atgcacgtgc gcagcctgcg cgccgccgcc cccacagct tcgtggccct gtgggcccc 60
 ctgttcctgc tgcgcagcgc cctggccgac ttcagcctgg acaacgaggt gcacagcagc 120
 ttcattccacc gccgcctgcg cagccaggag cgccgcgaga tgcagcgcga gatcctgagc 180
 atcctggggcc tgccccaccg cccccgcccc cacctgcagg gcaagcaca cagcgcccc 240
 atgttcatgc tggacctgta caacgccatg gccgtggagg agggcggcgg ccccggcggc 300
 cagggttca gctacccta caaggccgtg ttcagcacc agggcccccc cctggccagc 360
 ctgcaggaca gccacttctt gaccgacgcc gacatgggtga tgagcttcgt gaacctggtg 420
 gagcacgaca aggagtctt ccacccccgc taccaccacc gcgagttccg cttcgacctg 480
 agcaagatcc ccgagggcga ggccgtgacc gccgccgagt tccgcatcta caaggactac 540

atccgcgagc gcttcgacaa cgagaccttc cgcacagcgc tgtaccaggt gctgcaggag	600
cacctgggcc gcgagagcga cctgttcctg ctggacagcc gcaccctgtg ggccagcgag	660
gagggctggc tgggtgttcga catcaccgcc accagcaacc actgggtggg gaacccccgc	720
cacaacctgg gcctgcagct gagcgtggag accctggacg gccagagcat caacccaag	780
ctggccggcc tgatcggccg ccacggcccc cagaacaagc agcccttcat ggtggccttc	840
ttcaaggcca ccgaggtgca cttccgcagc atccgcagca ccggcagcaa gcagcgcagc	900
cagaaccgca gcaagacccc caagaaccag gaggccctgc gcatggccaa cgtggccgag	960
aacagcagca gcgaccagcg ccaggcctgc aagaagcacg agctgtacgt gagcttccgc	1020
gacctgggct ggaggactg gatcatcgcc cctgagggt acgccgccgg ctactgcgag	1080
ggcgagtgcg ctttccccct gaacagctac atgaacgcca ccaaccacgc cctggtgcag	1140
accctggtgc acttcatcaa ccccgagacc gtgcccgaagc cctgctgcgc cccacccag	1200
ctgggcgcca tcagcgtgct gtacttcgac gacagcagca acgtgatcct gaagaagtgg	1260
cgcaacatgg tgggtgcgcgc ctgaggctgc cac	1293

<210> 20
 <211> 1293
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 20	
atgcacgtgc gcagcctgcg cgccgccgcc cccacagct tcgtggccct gtgggcccc	60
ctgttcctgc tgcgcagcgc cctggccgac ttcagcctgg acaacgaggt gcacagcagc	120
ttcatccacc gccgcctgcg cagccaggag cgccgcgaga tgcagcgca gatcctgagc	180
atcctgggcc tgccccaccg ccccgcccc cacctgcagg gcaagcaca cagcgcccc	240
atgttcatgc tggacctgta caacgccatg gccgtggagg agggcggcgg ccccgcggc	300
cagggcttca gctaccccta caaggccgtg ttcagcacc agggcccccc cctggccagc	360
ctgcaggaca gccacttcct gaccgacgcc gacatggtga tgagcttcgt gaacctggtg	420

gagcacgaca aggagttctt ccacccccgc taccaccacc gcgagttccg cttcgacctg	480
agcaagatcc ccgagggcga ggccgtgacc gccgccgagt tccgcatcta caaggactac	540
atccgcgagc gcttcgacaa cgagaccttc cgcatcagcg tgtaccaggt gctgcaggag	600
cacctgggcc gcgagagcga cctgttcctg ctggacagcc gcaccctgtg ggccagcgag	660
gagggctggc tgggtgttca catcaccgcc accagcaacc actgggtggt gaacccccgc	720
cacaacctgg gcctgcagct gagcgtggag accctggacg gccagagcat caacccaag	780
ctggccggcc tgatcggccg ccacggcccc cagaacaagc agcccttcat ggtggccttc	840
ttcaaggcca ccgaggtgca cttccgcagc atccgcagca ccggcagcaa gcagcgcagc	900
cagaaccgca gcaagacccc caagaaccag gaggccctgc gcatggccaa cgtggccgag	960
aacagcagca gcgaccagcg ccaggcctgc aagaagcacg agctgtacgt gagcttccgc	1020
gacctgggct ggcaggactg gatcatcgcc cctgagggct acgccgccgg ctactgcgag	1080
ggcgagtgcg ctttccccct gaacagctac atgaacgcca ccaaccacgc cctggtgcag	1140
accctggtgc acgtgatcaa ccccgagacc gtgccaagc cctgctgcgc cccacccag	1200
ctgggcgcca tcagcgtgct gtacttcgac gacagcagca acgtgaccta gaagaagtgg	1260
cgcaacatgg tgggtgcgcgc ctgcggctgc cac	1293

<210> 21
 <211> 402
 <212> PRT
 <213> Homo sapiens

<400> 21

Asp	Phe	Ser	Leu	Asp	Asn	Glu	Val	His	Ser	Ser	Phe	Ile	His	Arg	Arg
1				5					10					15	

Leu	Arg	Ser	Gln	Glu	Arg	Arg	Glu	Met	Gln	Arg	Glu	Ile	Leu	Ser	Ile
			20					25					30		

Leu	Gly	Leu	Pro	His	Arg	Pro	Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn
		35					40					45			

Ser Ala Pro Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu
50 55 60

Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala
65 70 75 80

Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His
85 90 95

Phe Leu Thr Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu
100 105 110

His Asp Lys Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg
115 120 125

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

Phe Arg Ile Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr
145 150 155 160

Phe Arg Ile Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu
165 170 175

Ser Asp Leu Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu
180 185 190

Gly Trp Leu Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val
195 200 205

Asn Pro Arg His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp
210 215 220

Gly Gln Ser Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly
225 230 235 240

Pro Gln Asn Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu
245 250 255

Val His Phe Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln
260 265 270

Asn Arg Ser Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn
275 280 285

Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His
290 295 300

Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile
305 310 315 320

Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe
325 330 335

Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr
340 345 350

Leu Val His Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala
355 360 365

Pro Thr Gln Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser
370 375 380

Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly
385 390 395 400

Cys His