

SEQUENCE LISTING

<110> Philogen SpA
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Neri, Dario

<120> Targeting of Bone Marrow Neovasculature

<130> HMK/FP6704019

<150> US 61/231,564

<151> 2009-08-05

<160> 42

<170> PatentIn version 3.3

<210> 1

<211> 348

<212> DNA

<213> Homo sapiens

<400> 1

gaggtgcagc	tggtggagtc	tgggggaggc	ttggtacagc	ctgggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	caccttttagc	cggtatggta	tgagctgggt	ccgccaggct	120
ccagggaagg	ggctggagtg	ggtctcagct	attagtggta	gtggtggtag	cacatactac	180
gcagactccg	tgaagggccg	gttcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggccgtat	attactgtgc	gaaagcgcac	300
aatgcttttg	actactgggg	ccagggaacc	ctggtcaccg	tgctcgaga		348

<210> 2
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 2

Glu Val Gln Leu Leu 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 Phe Ser Arg Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Ala His Asn Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Arg
 115

<210> 3
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 3
 tcttctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60
 acatgccaaag gagacagcct cagaagctat tatgcaagct ggtaccagca gaagccagga 120
 caggccccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga 180
 ttctctggct ccagctcagg aaacacagct tccttgacca tcaactggggc tcaggcggaa 240
 gatgaggctg actattactg taactcctct gtttatacta tgccgcccgt ggtattcggc 300
 ggagggacca agctgaccgt ccta 324

<210> 4
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 4

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

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

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
 50 55 60

4

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

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Ser Val Tyr Thr Met Pro Pro
85 90 95

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

<210> 5
<211> 5
<212> PRT
<213> Homo sapiens

<400> 5

Arg Tyr Gly Met Ser
1 5

<210> 6
<211> 17
<212> PRT
<213> Homo sapiens

<400> 6

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 7
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 7

Ala His Asn Ala Phe Asp Tyr
 1 5

<210> 8
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 8

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
 1 5 10

<210> 9
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 9

Gly Lys Asn Asn Arg Pro Ser
 1 5

<210> 10
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 10

Asn Ser Ser Val Tyr Thr Met Pro Pro Val Val
 1 5 10

<210> 11

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence: 4A1-F16 VH and VL domain peptide linker amino acid sequence

<400> 11

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

<210> 12

<211> 275

<212> DNA

<213> Homo sapiens

<400> 12

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttttagc ctgtttacga tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggc 275

<210> 13

<211> 118

<212> PRT

<213> Homo sapiens

<400> 13

Glu Val Gln Leu Leu 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 Phe Ser Leu Phe
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Ser Thr His Leu Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 14

<211> 324

<212> DNA

<213> Homo sapiens

<400> 14

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtggttagc atgccgtttt tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagatgcgtg gtcggccgcc gacgttcggc 300
 caagggacca aggtggaaat caaa 324

<210> 15

<211> 108

<212> PRT

<213> Homo sapiens

<400> 15

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Met Pro
 20 25 30

Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

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

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Met Arg Gly Arg Pro
 85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 16
<211> 3
<212> PRT
<213> Homo sapiens

<400> 16

Leu Phe Thr

1

<210> 17
<211> 6
<212> PRT
<213> Homo sapiens

<400> 17

Ser Gly Ser Gly Gly Ser

1 5

<210> 18
<211> 6
<212> PRT
<213> Homo sapiens

<400> 18

Ser Thr His Leu Tyr Leu

1 5

<210> 19
<211> 3
<212> PRT
<213> Homo sapiens

<400> 19

Met Pro Phe

1

<210> 20
<211> 7
<212> PRT
<213> Homo sapiens

<400> 20

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 21
<211> 6
<212> PRT
<213> Homo sapiens

<400> 21

Met Arg Gly Arg Pro Pro
1 5

<210> 22
<211> 14
<212> PRT
<213> Artificial sequence

<220>

<223> Synthetic sequence: F8 (V5L/K18R) VH and VL domain peptide linker
amino acid sequence

<400> 22

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

<210> 23

<211> 2

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence: 4A1-F16-SIP and F8-SIP (V5L/K18R) VL and CH4 domain peptide linker amino acid sequence

<400> 23

Ser Gly

1

<210> 24

<211> 119

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence: Amino acid sequence of CH4 dimerization domain of 4A1-F16-SIP and F8-SIP (V5L/K18R)

<400> 24

Gly	Ser	Gly	Gly	Pro	Arg	Ala	Ala	Pro	Glu	Val	Tyr	Ala	Phe	Ala	Thr
1				5					10					15	

Pro	Glu	Trp	Pro	Gly	Ser	Arg	Asp	Lys	Arg	Thr	Leu	Ala	Cys	Leu	Ile
			20					25					30		

Gln	Asn	Phe	Met	Pro	Glu	Asp	Ile	Ser	Val	Gln	Trp	Leu	His	Asn	Glu
			35					40					45		

Val	Gln	Leu	Pro	Asp	Ala	Arg	His	Ser	Thr	Thr	Gln	Pro	Arg	Lys	Thr
			50				55					60			

12

Lys Gly Ser Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala
65 70 75 80

Glu Trp Glu Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala
85 90 95

Ala Ser Pro Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Glu
100 105 110

Ser Ser Arg Arg Gly Gly Cys
115

<210> 25

<211> 355

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence: 4A1-F16-SIP amino acid sequence

<400> 25

Glu Val Gln Leu Leu 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 Phe Ser Arg Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu 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 Lys Ala His Asn Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ser
 115 120 125

Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val
 130 135 140

Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp
 145 150 155 160

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys
 165 170 175

Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser
 180 185 190

Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu
 195 200 205

Ala Asp Tyr Tyr Cys Asn Ser Ser Val Tyr Thr Met Pro Pro Val Val
 210 215 220

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gly Gly Ser Gly Gly
225 230 235 240

Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp Pro
245 250 255

Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe Met
260 265 270

Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu Pro
275 280 285

Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser Gly
290 295 300

Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu Gln
305 310 315 320

Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro Ser
325 330 335

Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Glu Ser Ser Arg Arg
340 345 350

Gly Gly Cys
355

<210> 26

<211> 361

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence: F8-SIP (V5L/K18R) amino acid sequence

<400> 26

Glu	Val	Gln	Leu	Leu	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	Phe	Ser	Leu	Phe
		20						25					30		

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

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

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	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	Lys	Ser	Thr	His	Leu	Tyr	Leu	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
			100					105						110	

Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly
		115						120						125	

Gly Gly Gly Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
 130 135 140

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 145 150 155 160

Val Ser Met Pro Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 165 170 175

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
 180 185 190

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 195 200 205

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Met
 210 215 220

Arg Gly Arg Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 225 230 235 240

Ser Gly Gly Ser Gly Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe
 245 250 255

Ala Thr Pro Glu Trp Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys
 260 265 270

Leu Ile Gln Asn Phe Met Pro Glu Asp Ile Ser Val Gln Trp Leu His
 275 280 285

17

Asn Glu Val Gln Leu Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg
290 295 300

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

Arg Ala Glu Trp Glu Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His
325 330 335

Glu Ala Ala Ser Pro Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn
340 345 350

Pro Glu Ser Ser Arg Arg Gly Gly Cys
355 360

<210> 27

<211> 153

<212> PRT

<213> Homo sapiens

<400> 27

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
20 25 30

Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
35 40 45

Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
50 55 60

18

Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
65 70 75 80

Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
85 90 95

Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
100 105 110

Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
115 120 125

Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
130 135 140

Cys Gln Ser Ile Ile Ser Thr Leu Thr
145 150

<210> 28

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence: IL-2 linker sequence

<400> 28

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

<210> 29
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: IL-2 linker sequence

<400> 29

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 30
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: IL-2 linker sequence

<400> 30

Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly
1 5 10 15

<210> 31
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: IL-2 linker sequence

<400> 31

Gly Ser Gly Ser Ala Gly Ser Gly Ser Ala Gly Ser Gly Ser Ala
1 5 10 15

<210> 32

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence: IL-2 linker sequence

<400> 32

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
1 5 10 15

<210> 33

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence: Linker motif

<400> 33

Gly Gly Gly Gly Ser
1 5

<210> 34

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence: Linker motif

<400> 34

Ser Ser Ser Ser Gly
1 5

<210> 35

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence: Linker motif

<400> 35

Gly Ser Gly Ser Ala

1 5

<210> 36

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence: Linker motif

<400> 36

Gly Gly Ser Gly Gly

1 5

<210> 37

<211> 2201

<212> PRT

<213> Homo sapiens

<400> 37

Met Gly Ala Met Thr Gln Leu Leu Ala Gly Val Phe Leu Ala Phe Leu

1 5 10 15

Ala Leu Ala Thr Glu Gly Gly Val Leu Lys Lys Val Ile Arg His Lys

20 25 30

Arg Gln Ser Gly Val Asn Ala Thr Leu Pro Glu Glu Asn Gln Pro Val
 35 40 45

Val Phe Asn His Val Tyr Asn Ile Lys Leu Pro Val Gly Ser Gln Cys
 50 55 60

Ser Val Asp Leu Glu Ser Ala Ser Gly Glu Lys Asp Leu Ala Pro Pro
 65 70 75 80

Ser Glu Pro Ser Glu Ser Phe Gln Glu His Thr Val Asp Gly Glu Asn
 85 90 95

Gln Ile Val Phe Thr His Arg Ile Asn Ile Pro Arg Arg Ala Cys Gly
 100 105 110

Cys Ala Ala Ala Pro Asp Val Lys Glu Leu Leu Ser Arg Leu Glu Glu
 115 120 125

Leu Glu Asn Leu Val Ser Ser Leu Arg Glu Gln Cys Thr Ala Gly Ala
 130 135 140

Gly Cys Cys Leu Gln Pro Ala Thr Gly Arg Leu Asp Thr Arg Pro Phe
 145 150 155 160

Cys Ser Gly Arg Gly Asn Phe Ser Thr Glu Gly Cys Gly Cys Val Cys
 165 170 175

Glu Pro Gly Trp Lys Gly Pro Asn Cys Ser Glu Pro Glu Cys Pro Gly
 180 185 190

Asn Cys His Leu Arg Gly Arg Cys Ile Asp Gly Gln Cys Ile Cys Asp
 195 200 205

Asp Gly Phe Thr Gly Glu Asp Cys Ser Gln Leu Ala Cys Pro Ser Asp
 210 215 220

Cys Asn Asp Gln Gly Lys Cys Val Asn Gly Val Cys Ile Cys Phe Glu
 225 230 235 240

Gly Tyr Ala Gly Ala Asp Cys Ser Arg Glu Ile Cys Pro Val Pro Cys
 245 250 255

Ser Glu Glu His Gly Thr Cys Val Asp Gly Leu Cys Val Cys His Asp
 260 265 270

Gly Phe Ala Gly Asp Asp Cys Asn Lys Pro Leu Cys Leu Asn Asn Cys
 275 280 285

Tyr Asn Arg Gly Arg Cys Val Glu Asn Glu Cys Val Cys Asp Glu Gly
 290 295 300

Phe Thr Gly Glu Asp Cys Ser Glu Leu Ile Cys Pro Asn Asp Cys Phe
 305 310 315 320

Asp Arg Gly Arg Cys Ile Asn Gly Thr Cys Tyr Cys Glu Glu Gly Phe
 325 330 335

Thr Gly Glu Asp Cys Gly Lys Pro Thr Cys Pro His Ala Cys His Thr
 340 345 350

Gln Gly Arg Cys Glu Glu Gly Gln Cys Val Cys Asp Glu Gly Phe Ala
 355 360 365

Gly Leu Asp Cys Ser Glu Lys Arg Cys Pro Ala Asp Cys His Asn Arg
 370 375 380

Gly Arg Cys Val Asp Gly Arg Cys Glu Cys Asp Asp Gly Phe Thr Gly
 385 390 395 400

Ala Asp Cys Gly Glu Leu Lys Cys Pro Asn Gly Cys Ser Gly His Gly
 405 410 415

Arg Cys Val Asn Gly Gln Cys Val Cys Asp Glu Gly Tyr Thr Gly Glu
 420 425 430

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

Cys Val Glu Gly Lys Cys Val Cys Glu Gln Gly Phe Lys Gly Tyr Asp
 450 455 460

Cys Ser Asp Met Ser Cys Pro Asn Asp Cys His Gln His Gly Arg Cys
 465 470 475 480

Val Asn Gly Met Cys Val Cys Asp Asp Gly Tyr Thr Gly Glu Asp Cys
 485 490 495

Arg Asp Arg Gln Cys Pro Arg Asp Cys Ser Asn Arg Gly Leu Cys Val
 500 505 510

Asp Gly Gln Cys Val Cys Glu Asp Gly Phe Thr Gly Pro Asp Cys Ala
 515 520 525

Glu Leu Ser Cys Pro Asn Asp Cys His Gly Gln Gly Arg Cys Val Asn
 530 535 540

Gly Gln Cys Val Cys His Glu Gly Phe Met Gly Lys Asp Cys Lys Glu
 545 550 555 560

Gln Arg Cys Pro Ser Asp Cys His Gly Gln Gly Arg Cys Val Asp Gly
 565 570 575

Gln Cys Ile Cys His Glu Gly Phe Thr Gly Leu Asp Cys Gly Gln His
 580 585 590

Ser Cys Pro Ser Asp Cys Asn Asn Leu Gly Gln Cys Val Ser Gly Arg
 595 600 605

Cys Ile Cys Asn Glu Gly Tyr Ser Gly Glu Asp Cys Ser Glu Val Ser
 610 615 620

Pro Pro Lys Asp Leu Val Val Thr Glu Val Thr Glu Glu Thr Val Asn
 625 630 635 640

Leu Ala Trp Asp Asn Glu Met Arg Val Thr Glu Tyr Leu Val Val Tyr
 645 650 655

Thr Pro Thr His Glu Gly Gly Leu Glu Met Gln Phe Arg Val Pro Gly
 660 665 670

Asp Gln Thr Ser Thr Ile Ile Gln Glu Leu Glu Pro Gly Val Glu Tyr
 675 680 685

Phe Ile Arg Val Phe Ala Ile Leu Glu Asn Lys Lys Ser Ile Pro Val
 690 695 700

Ser Ala Arg Val Ala Thr Tyr Leu Pro Ala Pro Glu Gly Leu Lys Phe
 705 710 715 720

Lys Ser Ile Lys Glu Thr Ser Val Glu Val Glu Trp Asp Pro Leu Asp
 725 730 735

Ile Ala Phe Glu Thr Trp Glu Ile Ile Phe Arg Asn Met Asn Lys Glu
 740 745 750

Asp Glu Gly Glu Ile Thr Lys Ser Leu Arg Arg Pro Glu Thr Ser Tyr
 755 760 765

Arg Gln Thr Gly Leu Ala Pro Gly Gln Glu Tyr Glu Ile Ser Leu His
 770 775 780

Ile Val Lys Asn Asn Thr Arg Gly Pro Gly Leu Lys Arg Val Thr Thr
 785 790 795 800

Thr Arg Leu Asp Ala Pro Ser Gln Ile Glu Val Lys Asp Val Thr Asp
 805 810 815

Thr Thr Ala Leu Ile Thr Trp Phe Lys Pro Leu Ala Glu Ile Asp Gly
 820 825 830

Ile Glu Leu Thr Tyr Gly Ile Lys Asp Val Pro Gly Asp Arg Thr Thr
 835 840 845

Ile Asp Leu Thr Glu Asp Glu Asn Gln Tyr Ser Ile Gly Asn Leu Lys
 850 855 860

Pro Asp Thr Glu Tyr Glu Val Ser Leu Ile Ser Arg Arg Gly Asp Met
 865 870 875 880

Ser Ser Asn Pro Ala Lys Glu Thr Phe Thr Thr Gly Leu Asp Ala Pro
 885 890 895

Arg Asn Leu Arg Arg Val Ser Gln Thr Asp Asn Ser Ile Thr Leu Glu
 900 905 910

Trp Arg Asn Gly Lys Ala Ala Ile Asp Ser Tyr Arg Ile Lys Tyr Ala
 915 920 925

Pro Ile Ser Gly Gly Asp His Ala Glu Val Asp Val Pro Lys Ser Gln
 930 935 940

Gln Ala Thr Thr Lys Thr Thr Leu Thr Gly Leu Arg Pro Gly Thr Glu
 945 950 955 960

Tyr Gly Ile Gly Val Ser Ala Val Lys Glu Asp Lys Glu Ser Asn Pro
 965 970 975

Ala Thr Ile Asn Ala Ala Thr Glu Leu Asp Thr Pro Lys Asp Leu Gln
 980 985 990

Val	Ser	Glu	Thr	Ala	Glu	Thr	Ser	Leu	Thr	Leu	Leu	Trp	Lys	Thr	Pro
		995					1000					1005			

Leu	Ala	Lys	Phe	Asp	Arg	Tyr	Arg	Leu	Asn	Tyr	Ser	Leu	Pro	Thr
	1010					1015					1020			

Gly	Gln	Trp	Val	Gly	Val	Gln	Leu	Pro	Arg	Asn	Thr	Thr	Ser	Tyr
	1025					1030					1035			

Val	Leu	Arg	Gly	Leu	Glu	Pro	Gly	Gln	Glu	Tyr	Asn	Val	Leu	Leu
	1040					1045					1050			

Thr	Ala	Glu	Lys	Gly	Arg	His	Lys	Ser	Lys	Pro	Ala	Arg	Val	Lys
	1055					1060					1065			

Ala	Ser	Thr	Glu	Gln	Ala	Pro	Glu	Leu	Glu	Asn	Leu	Thr	Val	Thr
	1070					1075					1080			

Glu	Val	Gly	Trp	Asp	Gly	Leu	Arg	Leu	Asn	Trp	Thr	Ala	Ala	Asp
	1085					1090					1095			

Gln	Ala	Tyr	Glu	His	Phe	Ile	Ile	Gln	Val	Gln	Glu	Ala	Asn	Lys
	1100					1105					1110			

Val	Glu	Ala	Ala	Arg	Asn	Leu	Thr	Val	Pro	Gly	Ser	Leu	Arg	Ala
	1115					1120					1125			

Val	Asp	Ile	Pro	Gly	Leu	Lys	Ala	Ala	Thr	Pro	Tyr	Thr	Val	Ser
	1130					1135					1140			

Ile	Tyr	Gly	Val	Ile	Gln	Gly	Tyr	Arg	Thr	Pro	Val	Leu	Ser	Ala
1145						1150					1155			

Glu	Ala	Ser	Thr	Gly	Glu	Thr	Pro	Asn	Leu	Gly	Glu	Val	Val	Val
1160						1165					1170			

Ala	Glu	Val	Gly	Trp	Asp	Ala	Leu	Lys	Leu	Asn	Trp	Thr	Ala	Pro
1175						1180					1185			

Glu	Gly	Ala	Tyr	Glu	Tyr	Phe	Phe	Ile	Gln	Val	Gln	Glu	Ala	Asp
1190						1195					1200			

Thr	Val	Glu	Ala	Ala	Gln	Asn	Leu	Thr	Val	Pro	Gly	Gly	Leu	Arg
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Ser Glu Pro Ser Glu Ser Phe Gln Glu His Thr Val Asp Gly Glu Asn
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Gln Ile Val Phe Thr His Arg Ile Asn Ile Pro Arg Arg Ala Cys Gly
 100 105 110

Cys Ala Ala Ala Pro Asp Val Lys Glu Leu Leu Ser Arg Leu Glu Glu
 115 120 125

Leu Glu Asn Leu Val Ser Ser Leu Arg Glu Gln Cys Thr Ala Gly Ala
 130 135 140

Gly Cys Cys Leu Gln Pro Ala Thr Gly Arg Leu Asp Thr Arg Pro Phe
 145 150 155 160

Cys Ser Gly Arg Gly Asn Phe Ser Thr Glu Gly Cys Gly Cys Val Cys
 165 170 175

Glu Pro Gly Trp Lys Gly Pro Asn Cys Ser Glu Pro Glu Cys Pro Gly
 180 185 190

Asn Cys His Leu Arg Gly Arg Cys Ile Asp Gly Gln Cys Ile Cys Asp
 195 200 205

Asp Gly Phe Thr Gly Glu Asp Cys Ser Gln Leu Ala Cys Pro Ser Asp
 210 215 220

Cys Asn Asp Gln Gly Lys Cys Val Asn Gly Val Cys Ile Cys Phe Glu
 225 230 235 240

Gly Tyr Ala Gly Ala Asp Cys Ser Arg Glu Ile Cys Pro Val Pro Cys
 245 250 255

Ser Glu Glu His Gly Thr Cys Val Asp Gly Leu Cys Val Cys His Asp
 260 265 270

Gly Phe Ala Gly Asp Asp Cys Asn Lys Pro Leu Cys Leu Asn Asn Cys
 275 280 285

Tyr Asn Arg Gly Arg Cys Val Glu Asn Glu Cys Val Cys Asp Glu Gly
 290 295 300

45

Phe Thr Gly Glu Asp Cys Ser Glu Leu Ile Cys Pro Asn Asp Cys Phe
305 310 315 320

Asp Arg Gly Arg Cys Ile Asn Gly Thr Cys Tyr Cys Glu Glu Gly Phe
325 330 335

Thr Gly Glu Asp Cys Gly Lys Pro Thr Cys Pro His Ala Cys His Thr
340 345 350

Gln Gly Arg Cys Glu Glu Gly Gln Cys Val Cys Asp Glu Gly Phe Ala
355 360 365

Gly Val Asp Cys Ser Glu Lys Arg Cys Pro Ala Asp Cys His Asn Arg
370 375 380

Gly Arg Cys Val Asp Gly Arg Cys Glu Cys Asp Asp Gly Phe Thr Gly
385 390 395 400

Ala Asp Cys Gly Glu Leu Lys Cys Pro Asn Gly Cys Ser Gly His Gly
405 410 415

Arg Cys Val Asn Gly Gln Cys Val Cys Asp Glu Gly Tyr Thr Gly Glu
420 425 430

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

Cys Val Glu Gly Lys Cys Val Cys Glu Gln Gly Phe Lys Gly Tyr Asp
450 455 460

46

Cys Ser Asp Met Ser Cys Pro Asn Asp Cys His Gln His Gly Arg Cys
465 470 475 480

Val Asn Gly Met Cys Val Cys Asp Asp Gly Tyr Thr Gly Glu Asp Cys
485 490 495

Arg Asp Arg Gln Cys Pro Arg Asp Cys Ser Asn Arg Gly Leu Cys Val
500 505 510

Asp Gly Gln Cys Val Cys Glu Asp Gly Phe Thr Gly Pro Asp Cys Ala
515 520 525

Glu Leu Ser Cys Pro Asn Asp Cys His Gly Gln Gly Arg Cys Val Asn
530 535 540

Gly Gln Cys Val Cys His Glu Gly Phe Met Gly Lys Asp Cys Lys Glu
545 550 555 560

Gln Arg Cys Pro Ser Asp Cys His Gly Gln Gly Arg Cys Val Asp Gly
565 570 575

Gln Cys Ile Cys His Glu Gly Phe Thr Gly Leu Asp Cys Gly Gln His
580 585 590

Ser Cys Pro Ser Asp Cys Asn Asn Leu Gly Gln Cys Val Ser Gly Arg
595 600 605

Cys Ile Cys Asn Glu Gly Tyr Ser Gly Glu Asp Cys Ser Glu Val Ser
610 615 620

Pro Pro Lys Asp Leu Val Val Thr Glu Val Thr Glu Glu Thr Val Asn
625 630 635 640

Leu Ala Trp Asp Asn Glu Met Arg Val Thr Glu Tyr Leu Val Val Tyr
645 650 655

Thr Pro Thr His Glu Gly Gly Leu Glu Met Gln Phe Arg Val Pro Gly
660 665 670

Asp Gln Thr Ser Thr Ile Ile Gln Glu Leu Glu Pro Gly Val Glu Tyr
675 680 685

Phe Ile Arg Val Phe Ala Ile Leu Glu Asn Lys Lys Ser Ile Pro Val
690 695 700

Ser Ala Arg Val Ala Thr Tyr Leu Pro Ala Pro Glu Gly Leu Lys Phe
705 710 715 720

Lys Ser Ile Lys Glu Thr Ser Val Glu Val Glu Trp Asp Pro Leu Asp
725 730 735

Ile Ala Phe Glu Thr Trp Glu Ile Ile Phe Arg Asn Met Asn Lys Glu
740 745 750

Asp Glu Gly Glu Ile Thr Lys Ser Leu Arg Arg Pro Glu Thr Ser Tyr
755 760 765

Arg Gln Thr Gly Leu Ala Pro Gly Gln Glu Tyr Glu Ile Ser Leu His
770 775 780

Ile Val Lys Asn Asn Thr Arg Gly Pro Gly Leu Lys Arg Val Thr Thr
 785 790 795 800

Thr Arg Leu Asp Ala Pro Ser Gln Ile Glu Val Lys Asp Val Thr Asp
 805 810 815

Thr Thr Ala Leu Ile Thr Trp Phe Lys Pro Leu Ala Glu Ile Asp Gly
 820 825 830

Ile Glu Leu Thr Tyr Gly Ile Lys Asp Val Pro Gly Asp Arg Thr Thr
 835 840 845

Ile Asp Leu Thr Glu Asp Glu Asn Gln Tyr Ser Ile Gly Asn Leu Lys
 850 855 860

Pro Asp Thr Glu Tyr Glu Val Ser Leu Ile Ser Arg Arg Gly Asp Met
 865 870 875 880

Ser Ser Asn Pro Ala Lys Glu Thr Phe Thr Thr Gly Leu Asp Ala Pro
 885 890 895

Arg Asn Leu Arg Arg Val Ser Gln Thr Asp Asn Ser Ile Thr Leu Glu
 900 905 910

Trp Arg Asn Gly Lys Ala Ala Ile Asp Ser Tyr Arg Ile Lys Tyr Ala
 915 920 925

Pro Ile Ser Gly Gly Asp His Ala Glu Val Asp Val Pro Lys Ser Gln
 930 935 940

Gln Ala Thr Thr Lys Thr Thr Leu Thr Gly Leu Arg Pro Gly Thr Glu
 945 950 955 960

Tyr Gly Ile Gly Val Ser Ala Val Lys Glu Asp Lys Glu Ser Asn Pro
 965 970 975

Ala Thr Ile Asn Ala Ala Thr Glu Leu Asp Thr Pro Lys Asp Leu Gln
 980 985 990

Val Ser Glu Thr Ala Glu Thr Ser Leu Thr Leu Leu Trp Lys Thr Pro
 995 1000 1005

Leu Ala Lys Phe Asp Arg Tyr Arg Leu Asn Tyr Ser Leu Pro Thr
 1010 1015 1020

Gly Gln Trp Val Gly Val Gln Leu Pro Arg Asn Thr Thr Ser Tyr
 1025 1030 1035

Val Leu Arg Gly Leu Glu Pro Gly Gln Glu Tyr Asn Val Leu Leu
 1040 1045 1050

Thr Ala Glu Lys Gly Arg His Lys Ser Lys Pro Ala Arg Val Lys
 1055 1060 1065

Ala Ser Thr Glu Gln Ala Pro Glu Leu Glu Asn Leu Thr Val Thr
 1070 1075 1080

Glu Val Gly Trp Asp Gly Leu Arg Leu Asn Trp Thr Ala Ala Asp
 1085 1090 1095

Gln Ala Tyr Glu His Phe Ile	Ile Gln Val Gln Glu	Ala Asn Lys
1100	1105	1110
Val Glu Ala Ala Arg Asn Leu	Thr Val Pro Gly Ser	Leu Arg Ala
1115	1120	1125
Val Asp Ile Pro Gly Leu Lys	Ala Ala Thr Pro Tyr	Thr Val Ser
1130	1135	1140
Ile Tyr Gly Val Ile Gln Gly	Tyr Arg Thr Pro Val	Leu Ser Ala
1145	1150	1155
Glu Ala Ser Thr Gly Glu Thr	Pro Asn Leu Gly Glu	Val Val Val
1160	1165	1170
Ala Glu Val Gly Trp Asp Ala	Leu Lys Leu Asn Trp	Thr Ala Pro
1175	1180	1185
Glu Gly Ala Tyr Glu Tyr Phe	Phe Ile Gln Val Gln	Glu Ala Asp
1190	1195	1200
Thr Val Glu Ala Ala Gln Asn	Leu Thr Val Pro Gly	Gly Leu Arg
1205	1210	1215
Ser Thr Asp Leu Pro Gly Leu	Lys Ala Ala Thr His	Tyr Thr Ile
1220	1225	1230
Thr Ile Arg Gly Val Thr Gln	Asp Phe Ser Thr Thr	Pro Leu Ser
1235	1240	1245

Val Glu	Val Leu Thr Glu Glu	Val Pro Asp Met Gly	Asn Leu Thr
1250	1255	1260	

Val Thr	Glu Val Ser Trp Asp	Ala Leu Arg Leu Asn	Trp Thr Thr
1265	1270	1275	

Pro Asp	Gly Thr Tyr Asp Gln	Phe Thr Ile Gln Val	Gln Glu Ala
1280	1285	1290	

Asp Gln	Val Glu Glu Ala His	Asn Leu Thr Val Pro	Gly Ser Leu
1295	1300	1305	

Arg Ser	Met Glu Ile Pro Gly	Leu Arg Ala Gly Thr	Pro Tyr Thr
1310	1315	1320	

Val Thr	Leu His Gly Glu Val	Arg Gly His Ser Thr	Arg Pro Leu
1325	1330	1335	

Ala Val	Glu Val Val Thr Glu	Asp Leu Pro Gln Leu	Gly Asp Leu
1340	1345	1350	

Ala Val	Ser Glu Val Gly Trp	Asp Gly Leu Arg Leu	Asn Trp Thr
1355	1360	1365	

Ala Ala	Asp Asn Ala Tyr Glu	His Phe Val Ile Gln	Val Gln Glu
1370	1375	1380	

Val Asn	Lys Val Glu Ala Ala	Gln Asn Leu Thr Leu	Pro Gly Ser
1385	1390	1395	

Leu Arg	Ala Val Asp Ile Pro	Gly Leu Glu Ala Ala	Thr Pro Tyr
1400	1405	1410	

Arg Val	Ser Ile Tyr Gly Val	Ile Arg Gly Tyr Arg	Thr Pro Val
1415	1420	1425	

Leu Ser	Ala Glu Ala Ser Thr	Ala Lys Glu Pro Glu	Ile Gly Asn
1430	1435	1440	

Leu Asn	Val Ser Asp Ile Thr	Pro Glu Ser Phe Asn	Leu Ser Trp
1445	1450	1455	

Met Ala	Thr Asp Gly Ile Phe	Glu Thr Phe Thr Ile	Glu Ile Ile
1460	1465	1470	

Asp Ser	Asn Arg Leu Leu Glu	Thr Val Glu Tyr Asn	Ile Ser Gly
1475	1480	1485	

Ala Glu	Arg Thr Ala His Ile	Ser Gly Leu Pro Pro	Ser Thr Asp
1490	1495	1500	

Phe Ile	Val Tyr Leu Ser Gly	Leu Ala Pro Ser Ile	Arg Thr Lys
1505	1510	1515	

Thr Ile	Ser Ala Thr Ala Thr	Thr Glu Ala Leu Pro	Leu Leu Glu
1520	1525	1530	

Asn Leu	Thr Ile Ser Asp Ile	Asn Pro Tyr Gly Phe	Thr Val Ser
1535	1540	1545	

Trp Met	Ala Ser Glu Asn Ala	Phe Asp Ser Phe Leu	Val Thr Val
1550	1555	1560	

Val Asp	Ser Gly Lys Leu Leu	Asp Pro Gln Glu Phe	Thr Leu Ser
1565	1570	1575	

Gly Thr	Gln Arg Lys Leu Glu	Leu Arg Gly Leu Ile	Thr Gly Ile
1580	1585	1590	

Gly Tyr	Glu Val Met Val Ser	Gly Phe Thr Gln Gly	His Gln Thr
1595	1600	1605	

Lys Pro	Leu Arg Ala Glu Ile	Val Thr Glu Ala Glu	Pro Glu Val
1610	1615	1620	

Asp Asn	Leu Leu Val Ser Asp	Ala Thr Pro Asp Gly	Phe Arg Leu
1625	1630	1635	

Ser Trp	Thr Ala Asp Glu Gly	Val Phe Asp Asn Phe	Val Leu Lys
1640	1645	1650	

Ile Arg	Asp Thr Lys Lys Gln	Ser Glu Pro Leu Glu	Ile Thr Leu
1655	1660	1665	

Leu Ala	Pro Glu Arg Thr Arg	Asp Ile Thr Gly Leu	Arg Glu Ala
1670	1675	1680	

Thr Glu	Tyr Glu Ile Glu Leu	Tyr Gly Ile Ser Lys	Gly Arg Arg
1685	1690	1695	

Ser	Gln	Thr	Val	Ser	Ala	Ile	Ala	Thr	Thr	Ala	Met	Gly	Ser	Pro
1700						1705					1710			

Lys	Glu	Val	Ile	Phe	Ser	Asp	Ile	Thr	Glu	Asn	Ser	Ala	Thr	Val
1715						1720					1725			

Ser	Trp	Arg	Ala	Pro	Thr	Ala	Gln	Val	Glu	Ser	Phe	Arg	Ile	Thr
1730						1735					1740			

Tyr	Val	Pro	Ile	Thr	Gly	Gly	Thr	Pro	Ser	Met	Val	Thr	Val	Asp
1745						1750					1755			

Gly	Thr	Lys	Thr	Gln	Thr	Arg	Leu	Val	Lys	Leu	Ile	Pro	Gly	Val
1760						1765					1770			

Glu	Tyr	Leu	Val	Ser	Ile	Ile	Ala	Met	Lys	Gly	Phe	Glu	Glu	Ser
1775						1780					1785			

Glu	Pro	Val	Ser	Gly	Ser	Phe	Thr	Thr	Ala	Leu	Asp	Gly	Pro	Ser
1790						1795					1800			

Gly	Leu	Val	Thr	Ala	Asn	Ile	Thr	Asp	Ser	Glu	Ala	Leu	Ala	Arg
1805						1810					1815			

Trp	Gln	Pro	Ala	Ile	Ala	Thr	Val	Asp	Ser	Tyr	Val	Ile	Ser	Tyr
1820						1825					1830			

Thr	Gly	Glu	Lys	Val	Pro	Glu	Ile	Thr	Arg	Thr	Val	Ser	Gly	Asn
1835						1840					1845			

Thr	Val	Glu	Tyr	Ala	Leu	Thr	Asp	Leu	Glu	Pro	Ala	Thr	Glu	Tyr
1850						1855					1860			

Thr	Leu	Arg	Ile	Phe	Ala	Glu	Lys	Gly	Pro	Gln	Lys	Ser	Ser	Thr
1865						1870					1875			

Ile	Thr	Ala	Lys	Phe	Thr	Thr	Asp	Leu	Asp	Ser	Pro	Arg	Asp	Leu
1880						1885					1890			

Thr	Ala	Thr	Glu	Val	Gln	Ser	Glu	Thr	Ala	Leu	Leu	Thr	Trp	Arg
1895						1900					1905			

Pro	Pro	Arg	Ala	Ser	Val	Thr	Gly	Tyr	Leu	Leu	Val	Tyr	Glu	Ser
1910						1915					1920			

Val	Asp	Gly	Thr	Val	Lys	Glu	Val	Ile	Val	Gly	Pro	Asp	Thr	Thr
1925						1930					1935			

Ser	Tyr	Ser	Leu	Ala	Asp	Leu	Ser	Pro	Ser	Thr	His	Tyr	Thr	Ala
1940						1945					1950			

Lys	Ile	Gln	Ala	Leu	Asn	Gly	Pro	Leu	Arg	Ser	Asn	Met	Ile	Gln
1955						1960					1965			

Thr	Ile	Phe	Thr	Thr	Ile	Gly	Leu	Leu	Tyr	Pro	Phe	Pro	Lys	Asp
1970						1975					1980			

Cys	Ser	Gln	Ala	Met	Leu	Asn	Gly	Asp	Thr	Thr	Ser	Gly	Leu	Tyr
1985						1990					1995			

Thr Ile Tyr Leu Asn Gly Asp Lys Ala Glu Ala Leu Glu Val Phe
2000 2005 2010

Cys Asp Met Thr Ser Asp Gly Gly Gly Trp Ile Val Phe Leu Arg
2015 2020 2025

Arg Lys Asn Gly Arg Glu Asn Phe Tyr Gln Asn Trp Lys Ala Tyr
2030 2035 2040

Ala Ala Gly Phe Gly Asp Arg Arg Glu Glu Phe Trp Leu Gly Leu
2045 2050 2055

Asp Asn Leu Asn Lys Ile Thr Ala Gln Gly Gln Tyr Glu Leu Arg
2060 2065 2070

Val Asp Leu Arg Asp His Gly Glu Thr Ala Phe Ala Val Tyr Asp
2075 2080 2085

Lys Phe Ser Val Gly Asp Ala Lys Thr Arg Tyr Lys Leu Lys Val
2090 2095 2100

Glu Gly Tyr Ser Gly Thr Ala Gly Asp Ser Met Ala Tyr His Asn
2105 2110 2115

Gly Arg Ser Phe Ser Thr Phe Asp Lys Asp Thr Asp Ser Ala Ile
2120 2125 2130

Thr Asn Cys Ala Leu Ser Tyr Lys Gly Ala Phe Trp Tyr Arg Asn
2135 2140 2145

Cys His Arg Val Asn Leu Met Gly Arg Tyr Gly Asp Asn Asn His
 2150 2155 2160

Ser Gln Gly Val Asn Trp Phe His Trp Lys Gly His Glu His Ser
 2165 2170 2175

Ile Gln Phe Ala Glu Met Lys Leu Arg Pro Ser Asn Phe Arg Asn
 2180 2185 2190

Leu Glu Gly Arg Arg Lys Arg Ala
 2195 2200

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 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 41

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Asp Gly Leu Arg Leu Asn Trp Thr Ala Ala Asp Gln Ala Tyr Glu His
 20 25 30

Phe Ile Ile Gln Val Gln Glu Ala Asn Lys Val Glu Ala Ala Arg Asn
 35 40 45

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

Ala Ala Thr Pro Tyr Thr Val Ser Ile Tyr Gly Val Ile Gln Gly Tyr
 65 70 75 80

Arg Thr Pro Val Leu Ser Ala Glu Ala Ser Thr

85

90

<210> 42

<211> 273

<212> DNA

<213> Homo sapiens

<400> 42

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ctcaactgga ccgcagctga ccaggcctat gagcacttta tcattcaggt gcaggaggcc 120

aacaaggtgg aggcagctcg gaacctcacc gtgcctggca gccttcgggc tgtggacata 180

ccgggcctca aggctgctac gccttataca gtctccatct atgggggtgat ccagggctat 240

agaacaccag tgctctctgc tgaggcctcc aca 273