

eolf-seql
SEQUENCE LISTING

<110> UCB Biopharma SPRL
<120> METHOD FOR TREATMENT OF NEUROLOGIC DISEASE
<130> PF0024-EP-EPA
<160> 15
<170> PatentIn version 3.5

<210> 1
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CA019_969 Ab sequences CDR-L1

<220>
<221> CDR-L1
<222> (1)..(11)

<400> 1

Leu Ala Ser Glu Asp Ile Tyr Asp Asn Leu Ala
1 5 10

<210> 2
<211> 7
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<223> CA019_969 Ab sequences CDRL2

<220>
<221> CDR-L2
<222> (1)..(7)

<400> 2

Tyr Ala Ser Ser Leu Gln Asp
1 5

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<210> 3
<211> 9
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<213> Artificial Sequence

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<223> CA019_969 Ab sequences CDR-L3

<220>
<221> CDR-L3
<222> (1)..(9)

<400> 3

Leu Gln Asp Ser Glu Tyr Pro Trp Thr
1 5

<210> 4
<211> 12
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<223> CA019_969 Ab sequences CDR-H1

<220>
<221> CDR-H1
<222> (1)..(12)

<400> 4

Gly Phe Ser Leu Thr Thr Tyr Gly Met Gly Val Gly
1 5 10

<210> 5
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<223> CA019_969 Ab sequences CDR-H2

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<220>

<221> CDR-H2

<222> (1)..(16)

<400> 5

Asn	Ile	Trp	Trp	Asp	Asp	Asp	Lys	Tyr	Tyr	Asn	Pro	Ser	Leu	Lys	Asn
1				5				10						15	

<210> 6

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> CA019_969 Ab sequences CDR-H3

<220>

<221> CDR-H3

<222> (1)..(16)

<400> 6

Ile	Gly	Pro	Ile	Lys	Tyr	Pro	Thr	Ala	Pro	Tyr	Arg	Tyr	Phe	Asp	Phe
1				5				10						15	

<210> 7

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 969 gL7 V-region

<220>

<221> 969 gL7 V-region

<222> (1)..(107)

<400> 7

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

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Asp Arg Val Thr Ile Thr Cys Leu Ala Ser Glu Asp Ile Tyr Asp Asn
20 25 30

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

Tyr Tyr Ala Ser Ser Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 8
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> 969 gL7 V-region

<220>
<221> 969 gL7 V-region
<222> (1)..(321)

<400> 8
gacatacaga tgactcagtc accctcaagc ctgagtgccg gtgtgggaga cagggtgaca 60
atcacctgtc tggcctccga ggatatctac gataacctgg catggtatca gcagaaacct 120
ggaaaggctc ccaagctcct gatttattat gcctcctctc tccaagacgg cgttccatct 180
cggttcagcg gaagcggctc cgggacggat tacacactga caattagctc tctgcaaccg 240
gaggattttg ctacttacta ctgcctgcaa gactccgaat acccatggac cttcgggtggt 300

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ggcaccaaag tggaaatcaa g

321

<210> 9
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> 969 gH2 V-region

<220>
<221> 969 gH2 V-region
<222> (1)..(125)

<400> 9

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Thr Thr Tyr
20 25 30

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

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Asn 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 Gly Pro Ile Lys Tyr Pro Thr Ala Pro Tyr Arg Tyr
100 105 110

Phe Asp Phe Trp Gly Gln Gly Thr Met Val Thr Val Ser

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115

120

125

<210> 10
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> 969 gH2 V-region

<220>
<221> 969 gH2 V-region
<222> (1)..(375)

<400> 10
gaagtgaac tcaaggagtc tggacccgct ctggtgaaac caacccaaac actcactttg 60
acatgtactt ttagtggctt ctcatgact acctatggaa tgggcgtggg atggatcaga 120
cagccacctg gcaaggctct ggaatggctg gccaacatct ggtgggatga cgacaagtac 180
tataaccctg ccctgaaaaa ccggctgacc attagcaagg atacttctaa aaatcaagtg 240
gtgctgacca tgacaaatat ggatcccggtt gacaccgcaa cctactactg cgcccgcat 300
gggtcccataa agtacacctac ggcaccttac cgatatttcg acttttgggg ccaagggaca 360
atggttactg tctcg 375

<210> 11
<211> 972
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for CSF-1R

<400> 11

Met Gly Pro Gly Val Leu Leu Leu Leu Leu Val Ala Thr Ala Trp His
1 5 10 15

Gly Gln Gly Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val
20 25 30

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Lys	Pro	Gly	Ala	Thr	Val	Thr	Leu	Arg	Cys	Val	Gly	Asn	Gly	Ser	Val	35	40	45	
Glu	Trp	Asp	Gly	Pro	Pro	Ser	Pro	His	Trp	Thr	Leu	Tyr	Ser	Asp	Gly	50	55	60	
Ser	Ser	Ser	Ile	Leu	Ser	Thr	Asn	Asn	Ala	Thr	Phe	Gln	Asn	Thr	Gly	65	70	75	80
Thr	Tyr	Arg	Cys	Thr	Glu	Pro	Gly	Asp	Pro	Leu	Gly	Gly	Ser	Ala	Ala	85	90	95	
Ile	His	Leu	Tyr	Val	Lys	Asp	Pro	Ala	Arg	Pro	Trp	Asn	Val	Leu	Ala	100	105	110	
Gln	Glu	Val	Val	Val	Phe	Glu	Asp	Gln	Asp	Ala	Leu	Leu	Pro	Cys	Leu	115	120	125	
Leu	Thr	Asp	Pro	Val	Leu	Glu	Ala	Gly	Val	Ser	Leu	Val	Arg	Val	Arg	130	135	140	
Gly	Arg	Pro	Leu	Met	Arg	His	Thr	Asn	Tyr	Ser	Phe	Ser	Pro	Trp	His	145	150	155	160
Gly	Phe	Thr	Ile	His	Arg	Ala	Lys	Phe	Ile	Gln	Ser	Gln	Asp	Tyr	Gln	165	170	175	
Cys	Ser	Ala	Leu	Met	Gly	Gly	Arg	Lys	Val	Met	Ser	Ile	Ser	Ile	Arg	180	185	190	
Leu	Lys	Val	Gln	Lys	Val	Ile	Pro	Gly	Pro	Pro	Ala	Leu	Thr	Leu	Val	195	200	205	
Pro	Ala	Glu	Leu	Val	Arg	Ile	Arg	Gly	Glu	Ala	Ala	Gln	Ile	Val	Cys	210	215	220	

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Ser Ala Ser Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn
225 230 235 240

Asn Thr Lys Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg
245 250 255

Tyr Gln Lys Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His
260 265 270

Ala Gly Asn Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser
275 280 285

Thr Ser Met Phe Phe Arg Val Val Glu Ser Ala Tyr Leu Asn Leu Ser
290 295 300

Ser Glu Gln Asn Leu Ile Gln Glu Val Thr Val Gly Glu Gly Leu Asn
305 310 315 320

Leu Lys Val Met Val Glu Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp
325 330 335

Thr Tyr Leu Gly Pro Phe Ser Asp His Gln Pro Glu Pro Lys Leu Ala
340 345 350

Asn Ala Thr Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu
355 360 365

Pro Arg Leu Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg
370 375 380

Asn Pro Gly Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr
385 390 395 400

Pro Pro Glu Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr
405 410 415

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Leu Leu Cys Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu
420 425 430

Gln Cys Ser Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln
435 440 445

Val Trp Asp Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His
450 455 460

Lys Val Thr Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn
465 470 475 480

Gln Thr Tyr Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp
485 490 495

Ala Phe Ile Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu
500 505 510

Phe Leu Phe Thr Pro Val Val Val Ala Cys Met Ser Ile Met Ala Leu
515 520 525

Leu Leu Leu Leu Leu Leu Leu Leu Leu Tyr Lys Tyr Lys Gln Lys Pro
530 535 540

Lys Tyr Gln Val Arg Trp Lys Ile Ile Glu Ser Tyr Glu Gly Asn Ser
545 550 555 560

Tyr Thr Phe Ile Asp Pro Thr Gln Leu Pro Tyr Asn Glu Lys Trp Glu
565 570 575

Phe Pro Arg Asn Asn Leu Gln Phe Gly Lys Thr Leu Gly Ala Gly Ala
580 585 590

Phe Gly Lys Val Val Glu Ala Thr Ala Phe Gly Leu Gly Lys Glu Asp
595 600 605

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Ala Val Leu Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala His Ala
610 615 620

Asp Glu Lys Glu Ala Leu Met Ser Glu Leu Lys Ile Met Ser His Leu
625 630 635 640

Gly Gln His Glu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr His Gly
645 650 655

Gly Pro Val Leu Val Ile Thr Glu Tyr Cys Cys Tyr Gly Asp Leu Leu
660 665 670

Asn Phe Leu Arg Arg Lys Ala Glu Ala Met Leu Gly Pro Ser Leu Ser
675 680 685

Pro Gly Gln Asp Pro Glu Gly Gly Val Asp Tyr Lys Asn Ile His Leu
690 695 700

Glu Lys Lys Tyr Val Arg Arg Asp Ser Gly Phe Ser Ser Gln Gly Val
705 710 715 720

Asp Thr Tyr Val Glu Met Arg Pro Val Ser Thr Ser Ser Asn Asp Ser
725 730 735

Phe Ser Glu Gln Asp Leu Asp Lys Glu Asp Gly Arg Pro Leu Glu Leu
740 745 750

Arg Asp Leu Leu His Phe Ser Ser Gln Val Ala Gln Gly Met Ala Phe
755 760 765

Leu Ala Ser Lys Asn Cys Ile His Arg Asp Val Ala Ala Arg Asn Val
770 775 780

Leu Leu Thr Asn Gly His Val Ala Lys Ile Gly Asp Phe Gly Leu Ala
785 790 795 800

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Arg Asp Ile Met Asn Asp Ser Asn Tyr Ile Val Lys Gly Asn Ala Arg
805 810 815

Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asp Cys Val Tyr
820 825 830

Thr Val Gln Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile
835 840 845

Phe Ser Leu Gly Leu Asn Pro Tyr Pro Gly Ile Leu Val Asn Ser Lys
850 855 860

Phe Tyr Lys Leu Val Lys Asp Gly Tyr Gln Met Ala Gln Pro Ala Phe
865 870 875 880

Ala Pro Lys Asn Ile Tyr Ser Ile Met Gln Ala Cys Trp Ala Leu Glu
885 890 895

Pro Thr His Arg Pro Thr Phe Gln Gln Ile Cys Ser Phe Leu Gln Glu
900 905 910

Gln Ala Gln Glu Asp Arg Arg Glu Arg Asp Tyr Thr Asn Leu Pro Ser
915 920 925

Ser Ser Arg Ser Gly Gly Ser Gly Ser Ser Ser Ser Glu Leu Glu Glu
930 935 940

Glu Ser Ser Ser Glu His Leu Thr Cys Cys Glu Gln Gly Asp Ile Ala
945 950 955 960

Gln Pro Leu Leu Gln Pro Asn Asn Tyr Gln Phe Cys
965 970

<210> 12
<211> 277

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<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence for CSF-1R

<400> 12

Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val Lys Pro Gly
1 5 10 15

Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val Glu Trp Asp
20 25 30

Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly Ser Ser Ser
35 40 45

Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly Thr Tyr Arg
50 55 60

Cys Thr Glu Pro Gly Asp Pro Leu Gly Gly Ser Ala Ala Ile His Leu
65 70 75 80

Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala Gln Glu Val
85 90 95

Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu Leu Thr Asp
100 105 110

Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg Gly Arg Pro
115 120 125

Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His Gly Phe Thr
130 135 140

Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln Cys Ser Ala
145 150 155 160

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Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg Leu Lys Val
165 170 175

Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val Pro Ala Glu
180 185 190

Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys Ser Ala Ser
195 200 205

Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn Asn Thr Lys
210 215 220

Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg Tyr Gln Lys
225 230 235 240

Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His Ala Gly Asn
245 250 255

Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser Thr Ser Met
260 265 270

Phe Phe Arg Val Val
275

<210> 13

<211> 49

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence for CSF-1R

<400> 13

Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His Gly Phe Thr Ile
1 5 10 15

His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln Cys Ser Ala Leu
20 25 30

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Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg Leu Lys Val Gln
 35 40 45

Lys

<210> 14
 <211> 493
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence for CSF-1R (SNP V32G, A245S, H247P, V279M,
 position underlined)

<400> 14

Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val Lys Pro Gly
 1 5 10 15

Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val Glu Trp Asp
 20 25 30

Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly Ser Ser Ser
 35 40 45

Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly Thr Tyr Arg
 50 55 60

Cys Thr Glu Pro Gly Asp Pro Leu Gly Gly Ser Ala Ala Ile His Leu
 65 70 75 80

Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala Gln Glu Val
 85 90 95

Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu Leu Thr Asp
 100 105 110

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Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg Gly Arg Pro
115 120 125

Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His Gly Phe Thr
130 135 140

Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln Cys Ser Ala
145 150 155 160

Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg Leu Lys Val
165 170 175

Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val Pro Ala Glu
180 185 190

Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys Ser Ala Ser
195 200 205

Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn Asn Thr Lys
210 215 220

Leu Ala Ile His Gln Gln Ser Asp Phe His Asn Asn Arg Tyr Gln Lys
225 230 235 240

Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His Ala Gly Asn
245 250 255

Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser Thr Ser Met
260 265 270

Phe Phe Arg Val Val Glu Ser Ala Tyr Leu Asn Leu Ser Ser Glu Gln
275 280 285

Asn Leu Ile Gln Glu Val Thr Val Gly Glu Gly Leu Asn Leu Lys Val
290 295 300

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Met Val Glu Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp Thr Tyr Leu
305 310 315 320

Gly Pro Phe Ser Asp His Gln Pro Glu Pro Lys Leu Ala Asn Ala Thr
325 330 335

Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu Pro Arg Leu
340 345 350

Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg Asn Pro Gly
355 360 365

Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr Pro Pro Glu
370 375 380

Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr Leu Leu Cys
385 390 395 400

Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu Gln Cys Ser
405 410 415

Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln Val Trp Asp
420 425 430

Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His Lys Val Thr
435 440 445

Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn Gln Thr Tyr
450 455 460

Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp Ala Phe Ile
465 470 475 480

Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu
485 490

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<210> 15

<211> 512

<212> PRT

<213> Artificial Sequence

<220>

<223> sequence of human CSF-1R extracellular domain

<400> 15

Met Gly Pro Gly Val Leu Leu Leu Leu Leu Val Ala Thr Ala Trp His
1 5 10 15

Gly Gln Gly Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val
20 25 30

Lys Pro Gly Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val
35 40 45

Glu Trp Asp Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly
50 55 60

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

Thr Tyr Arg Cys Thr Glu Pro Gly Asp Pro Leu Gly Gly Ser Ala Ala
85 90 95

Ile His Leu Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala
100 105 110

Gln Glu Val Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu
115 120 125

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

Gly Arg Pro Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His

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145						150						155						160
Gly	Phe	Thr	Ile	His	Arg	Ala	Lys	Phe	Ile	Gln	Ser	Gln	Asp	Tyr	Gln			
				165					170					175				
Cys	Ser	Ala	Leu	Met	Gly	Gly	Arg	Lys	Val	Met	Ser	Ile	Ser	Ile	Arg			
			180					185					190					
Leu	Lys	Val	Gln	Lys	Val	Ile	Pro	Gly	Pro	Pro	Ala	Leu	Thr	Leu	Val			
		195					200					205						
Pro	Ala	Glu	Leu	Val	Arg	Ile	Arg	Gly	Glu	Ala	Ala	Gln	Ile	Val	Cys			
	210					215					220							
Ser	Ala	Ser	Ser	Val	Asp	Val	Asn	Phe	Asp	Val	Phe	Leu	Gln	His	Asn			
225					230					235					240			
Asn	Thr	Lys	Leu	Ala	Ile	Pro	Gln	Gln	Ser	Asp	Phe	His	Asn	Asn	Arg			
				245					250					255				
Tyr	Gln	Lys	Val	Leu	Thr	Leu	Asn	Leu	Asp	Gln	Val	Asp	Phe	Gln	His			
			260					265					270					
Ala	Gly	Asn	Tyr	Ser	Cys	Val	Ala	Ser	Asn	Val	Gln	Gly	Lys	His	Ser			
		275					280					285						
Thr	Ser	Met	Phe	Phe	Arg	Val	Val	Glu	Ser	Ala	Tyr	Leu	Asn	Leu	Ser			
	290					295					300							
Ser	Glu	Gln	Asn	Leu	Ile	Gln	Glu	Val	Thr	Val	Gly	Glu	Gly	Leu	Asn			
305					310					315					320			
Leu	Lys	Val	Met	Val	Glu	Ala	Tyr	Pro	Gly	Leu	Gln	Gly	Phe	Asn	Trp			
				325					330					335				
Thr	Tyr	Leu	Gly	Pro	Phe	Ser	Asp	His	Gln	Pro	Glu	Pro	Lys	Leu	Ala			

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340

345

350

Asn Ala Thr Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu
355 360 365

Pro Arg Leu Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg
370 375 380

Asn Pro Gly Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr
385 390 395 400

Pro Pro Glu Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr
405 410 415

Leu Leu Cys Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu
420 425 430

Gln Cys Ser Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln
435 440 445

Val Trp Asp Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His
450 455 460

Lys Val Thr Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn
465 470 475 480

Gln Thr Tyr Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp
485 490 495

Ala Phe Ile Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu
500 505 510