

SEQUENCE LISTING

<110> Sementis Pty Ltd

<120> IMMUNE MODULATION

<130> 902409

<160> 12

<170> PatentIn version 3.5

<210> 1

<211> 228

<212> DNA

<213> Artificial Sequence

<220>

<223> Modified Ubiquitin C monomer

<400> 1

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gacacaatcg aaaatgtgaa agccaagatc caagataagg aaggcatccc tccagaccag 120

caacggctca tctttgcggg caaacaactg gaggatgggc gcactctcag tgattacaat 180

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<210> 2

<211> 76

<212> PRT

<213> Artificial Sequence

<220>

<223> Modified ubiquitin C monomer

<400> 2

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
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20 25 30Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
50 55 60Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Ala
65 70 75

<210> 3

<211> 1875
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Modified Ara h1

<400> 3
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<210>  4
<211> 625
<212> PRT
<213> Artificial Sequence

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<220>
<223> Modified Ara h1

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<400>  4

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Arg Gly Arg Val Ser Pro Leu Met Leu Leu Leu Gly Ile Leu Val Leu
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```

```

Ala Ser Val Ser Ala Thr His Ala Lys Ser Ser Pro Tyr Gln Lys Lys
          20          25          30

```

```

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

```

```

Pro Asp Asp Leu Lys Gln Lys Ala Cys Glu Ser Arg Cys Thr Lys Leu
          50          55          60

```

```

Glu Tyr Asp Pro Arg Cys Val Tyr Asp Pro Arg Gly His Thr Gly Thr
65              70              75              80

```

```

Thr Asn Gln Arg Ser Pro Pro Gly Glu Arg Thr Arg Gly Arg Gln Pro
          85          90          95

```

```

Gly Asp Tyr Asp Asp Asp Arg Arg Gln Pro Arg Arg Glu Glu Gly Gly
          100          105          110

```

```

Arg Trp Gly Pro Ala Gly Pro Arg Glu Arg Glu Arg Glu Glu Asp Trp
          115          120          125

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```

Arg Gln Pro Arg Glu Asp Trp Arg Arg Pro Ser His Gln Gln Pro Arg
          130          135          140

```

```

Lys Ile Arg Pro Glu Gly Arg Glu Gly Glu Gln Glu Trp Gly Thr Pro
145              150              155              160

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Gly Ser His Val Arg Glu Glu Thr Ser Arg Asn Asn Pro Phe Tyr Phe
 165 170 175

Pro Ser Arg Arg Phe Ser Thr Arg Tyr Gly Asn Gln Asn Gly Arg Ile
 180 185 190

Arg Val Leu Gln Arg Phe Asp Gln Arg Ser Arg Gln Phe Gln Asn Leu
 195 200 205

Gln Asn His Arg Ile Val Gln Ile Glu Ala Lys Pro Asn Thr Leu Val
 210 215 220

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

Gln Ala Thr Val Thr Val Ala Asn Gly Asn Asn Arg Lys Ser Phe Asn
 245 250 255

Leu Asp Glu Gly His Ala Leu Arg Ile Pro Ser Gly Phe Ile Ser Tyr
 260 265 270

Ile Leu Asn Arg His Asp Asn Gln Asn Leu Arg Val Ala Lys Ile Ser
 275 280 285

Met Pro Val Asn Thr Pro Gly Gln Phe Glu Asp Phe Phe Pro Ala Ser
 290 295 300

Ser Arg Asp Gln Ser Ser Tyr Leu Gln Gly Phe Ser Arg Asn Thr Leu
 305 310 315 320

Glu Ala Ala Phe Asn Ala Glu Phe Asn Glu Ile Arg Arg Val Leu Leu
 325 330 335

Glu Glu Asn Ala Gly Gly Glu Gln Glu Glu Arg Gly Gln Arg Arg Trp
 340 345 350

Ser Thr Arg Ser Ser Glu Asn Asn Glu Gly Val Ile Val Lys Val Ser
 355 360 365

Lys Glu His Val Glu Glu Leu Thr Lys His Ala Lys Ser Val Ser Lys
 370 375 380

Lys Gly Ser Glu Glu Glu Gly Asp Ile Thr Asn Pro Ile Asn Leu Arg
 385 390 395 400

Glu Gly Glu Pro Asp Leu Ser Asn Asn Phe Gly Lys Leu Phe Glu Val
 405 410 415

Lys Pro Asp Lys Lys Asn Pro Gln Leu Gln Asp Leu Asp Met Met Leu
 420 425 430

Thr Cys Val Glu Ile Lys Glu Gly Ala Leu Met Leu Pro His Phe Asn
 435 440 445

Ser Lys Ala Met Val Ile Val Val Val Asn Lys Gly Thr Gly Asn Leu
 450 455 460

Glu Leu Val Ala Val Arg Lys Glu Gln Gln Gln Arg Gly Arg Arg Glu
 465 470 475 480

Glu Glu Glu Asp Glu Asp Glu Glu Glu Glu Gly Ser Asn Arg Glu Val
 485 490 495

Arg Arg Tyr Thr Ala Arg Leu Lys Glu Gly Asp Val Phe Ile Met Pro
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Ala Ala His Pro Val Ala Ile Asn Ala Ser Ser Glu Leu His Leu Leu
 515 520 525

Gly Phe Gly Ile Asn Ala Glu Asn Asn His Arg Ile Phe Leu Ala Gly
 530 535 540

Asp Lys Asp Asn Val Ile Asp Gln Ile Glu Lys Gln Ala Lys Asp Leu
 545 550 555 560

Ala Phe Pro Gly Ser Gly Glu Gln Val Glu Lys Leu Ile Lys Asn Gln
 565 570 575

Lys Glu Ser His Phe Val Ser Ala Arg Pro Gln Ser Gln Ser Gln Ser
 580 585 590

Pro Ser Ser Pro Glu Lys Glu Ser Pro Glu Lys Glu Asp Gln Glu Glu
 595 600 605

Glu Asn Gln Gly Gly Lys Gly Pro Leu Leu Ser Ile Leu Lys Ala Phe
 610 615 620

Asn
 625

<210> 5

<211> 513
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Modified Ara h2

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 cgagatcctt acagtccttc ccaagatcca tatagcccggt ctcaagaccc agatcgcagg 240
 gacccatata gccccagccc ctatgatcga agaggtgccg gaagcagcca gcatcaggaa 300
 aggtgctgca atgagctgaa cgagttcgag aacaaccaga gatgtatgtg cgaggctctg 360
 cagcagatta tggaaaatca atctgaccgg ctgcaggggac ggcagcagga gcagcagttc 420
 aaaagggagc tccgcaacct tccacagcag tgcggtttgc gcgcacctca gcgtgcgac 480
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<210> 6
 <211> 171
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Modified Ara h2

<400> 6

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His Ala Ser Ala Arg Gln Gln Trp Glu Leu Gln Gly Asp Arg Arg Cys
 20 25 30

Gln Ser Gln Leu Glu Arg Ala Asn Leu Arg Pro Cys Glu Gln His Leu
 35 40 45

Met Gln Lys Ile Gln Arg Asp Glu Asp Ser Tyr Gly Arg Asp Pro Tyr
 50 55 60

Ser Pro Ser Gln Asp Pro Tyr Ser Pro Ser Gln Asp Pro Asp Arg Arg
 65 70 75 80

Asp Pro Tyr Ser Pro Ser Pro Tyr Asp Arg Arg Gly Ala Gly Ser Ser
 85 90 95

Gln His Gln Glu Arg Cys Cys Asn Glu Leu Asn Glu Phe Glu Asn Asn
 100 105 110

Gln Arg Cys Met Cys Glu Ala Leu Gln Gln Ile Met Glu Asn Gln Ser
 115 120 125

Asp Arg Leu Gln Gly Arg Gln Gln Glu Gln Gln Phe Lys Arg Glu Leu
 130 135 140

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

Leu Glu Val Glu Ser Gly Gly Arg Asp Arg Tyr
 165 170

<210> 7
 <211> 1587
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Modified Ara h3

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 tcttttaggc agcagccaga ggaaaatgcc tgccagtcc aacggctgaa cgctcagcga 120
 ccagacaata ggatcgaatc agaaggtgga tacatcgaga cttggaaccc gaataaccag 180
 gagttcgaat gtgcaggcgt ggcactgtct cgccttggtc tccgacgcaa tgcgctcagg 240
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 gggctgatct ttcccggctg tccccggcac tatgaggaac cccacacaca gggcagaagg 360
 agccagagcc agcggcctcc ccggagattg caaggggagg atcagagcca gcagcagaga 420
 gattctcatc agaaagtaca taggttcgat gagggtgacc tgatagctgt gccaaccggg 480
 gttgcctttt gggtgtataa tgaccacgac acagacgtgg tggctgtgtc tctgaccgat 540
 acaaacaaca atgacaatca gcttgatcag ttccctaggc gctttaacct ggctggcaac 600
 accgaacagg agttcttgag atatcagcag cagtctaggc agtctaggag gaggtccctg 660
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gagaacttcg agtacgttgc ctttaagacc gattccagac cctccattgc aaacctggcc      1440
ggagagaaca gtgttattga caatctgccg gaggaagtgg ttgctaacag ttatgggctt      1500
cagcgcgaac aggctcggca gctgaagaac aacaatccgt tcaagttttt cgtccctcca      1560
tcccagcagt caccagagc tgtggcc      1587

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<210> 8
<211> 529
<212> PRT
<213> Artificial Sequence

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<220>
<223> Modified Ara h3

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<400> 8

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Ala Lys Leu Leu Glu Leu Ser Phe Cys Phe Cys Phe Leu Val Leu Gly
1           5           10           15

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```

Ala Ser Ser Ile Ser Phe Arg Gln Gln Pro Glu Glu Asn Ala Cys Gln
20           25           30

```

```

Phe Gln Arg Leu Asn Ala Gln Arg Pro Asp Asn Arg Ile Glu Ser Glu
35           40           45

```

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Gly Gly Tyr Ile Glu Thr Trp Asn Pro Asn Asn Gln Glu Phe Glu Cys
50           55           60

```

```

Ala Gly Val Ala Leu Ser Arg Leu Val Leu Arg Arg Asn Ala Leu Arg
65           70           75           80

```

```

Arg Pro Phe Tyr Ser Asn Ala Pro Gln Glu Ile Phe Ile Gln Gln Gly
85           90           95

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Arg Gly Tyr Phe Gly Leu Ile Phe Pro Gly Cys Pro Arg His Tyr Glu
100          105          110

```

Glu Pro His Thr Gln Gly Arg Arg Ser Gln Ser Gln Arg Pro Pro Arg
 115 120 125

Arg Leu Gln Gly Glu Asp Gln Ser Gln Gln Gln Arg Asp Ser His Gln
 130 135 140

Lys Val His Arg Phe Asp Glu Gly Asp Leu Ile Ala Val Pro Thr Gly
 145 150 155 160

Val Ala Phe Trp Leu Tyr Asn Asp His Asp Thr Asp Val Val Ala Val
 165 170 175

Ser Leu Thr Asp Thr Asn Asn Asn Asp Asn Gln Leu Asp Gln Phe Pro
 180 185 190

Arg Arg Phe Asn Leu Ala Gly Asn Thr Glu Gln Glu Phe Leu Arg Tyr
 195 200 205

Gln Gln Gln Ser Arg Gln Ser Arg Arg Arg Ser Leu Pro Tyr Ser Pro
 210 215 220

Tyr Ser Pro Gln Ser Gln Pro Arg Gln Glu Glu Arg Glu Phe Ser Pro
 225 230 235 240

Arg Gly Gln His Ser Arg Arg Glu Arg Ala Gly Gln Glu Glu Glu Asn
 245 250 255

Glu Gly Gly Asn Ile Phe Ser Gly Phe Thr Pro Glu Phe Leu Glu Gln
 260 265 270

Ala Phe Gln Val Asp Asp Arg Gln Ile Val Gln Asn Leu Arg Gly Glu
 275 280 285

Thr Glu Ser Glu Glu Glu Gly Ala Ile Val Thr Val Arg Gly Gly Leu
 290 295 300

Arg Ile Leu Ser Pro Asp Arg Lys Arg Arg Ala Asp Glu Glu Glu Glu
 305 310 315 320

Tyr Asp Glu Asp Glu Tyr Glu Tyr Asp Glu Glu Asp Arg Arg Arg Gly
 325 330 335

Arg Gly Ser Arg Gly Arg Gly Asn Gly Ile Glu Glu Thr Ile Cys Thr
 340 345 350

Ala Ser Ala Lys Lys Asn Ile Gly Arg Asn Arg Ser Pro Asp Ile Tyr

355 360 365
 Asn Pro Gln Ala Gly Ser Leu Lys Thr Ala Asn Asp Leu Asn Leu Leu
 370 375 380

 Ile Leu Arg Trp Leu Gly Pro Ser Ala Glu Tyr Gly Asn Leu Tyr Arg
 385 390 395 400

 Asn Ala Leu Phe Val Ala His Tyr Asn Thr Asn Ala His Ser Ile Ile
 405 410 415

 Tyr Arg Leu Arg Gly Arg Ala His Val Gln Val Val Asp Ser Asn Gly
 420 425 430

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

 Pro Gln Asn Phe Ala Val Ala Gly Lys Ser Gln Ser Glu Asn Phe Glu
 450 455 460

 Tyr Val Ala Phe Lys Thr Asp Ser Arg Pro Ser Ile Ala Asn Leu Ala
 465 470 475 480
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 Gly Glu Asn Ser Val Ile Asp Asn Leu Pro Glu Glu Val Val Ala Asn
 485 490 495

 Ser Tyr Gly Leu Gln Arg Glu Gln Ala Arg Gln Leu Lys Asn Asn Asn
 500 505 510

 Pro Phe Lys Phe Phe Val Pro Pro Ser Gln Gln Ser Pro Arg Ala Val
 515 520 525

Ala

<210> 9
 <211> 435
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Modified Ara h6

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 gaactcaacg aaatggagaa tacgcagcgg tgcattgtgtg aggtctttca gcaaatacatg 300
 gaaaaccaat gcgatcggct ccaagatcga cagatgggtgc agcagtttaa gcgcgagctg 360
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 ggagggagat gctaa 435

<210> 10
 <211> 144
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Modified Ara h6

<400> 10

Ala Lys Ser Thr Ile Leu Val Ala Leu Leu Ala Leu Val Leu Val Ala
 1 5 10 15

His Ala Ser Ala Met Arg Arg Glu Arg Gly Arg Gln Gly Asp Ser Ser
 20 25 30

Ser Cys Glu Arg Gln Val Asp Arg Val Asn Leu Lys Pro Cys Glu Gln
 35 40 45

His Ile Met Gln Arg Ile Met Gly Glu Gln Glu Gln Tyr Asp Ser Tyr
 50 55 60

Asp Ile Arg Ser Thr Arg Ser Ser Asp Gln Gln Gln Arg Cys Cys Asp
 65 70 75 80

Glu Leu Asn Glu Met Glu Asn Thr Gln Arg Cys Met Cys Glu Ala Leu
 85 90 95

Gln Gln Ile Met Glu Asn Gln Cys Asp Arg Leu Gln Asp Arg Gln Met
 100 105 110

Val Gln Gln Phe Lys Arg Glu Leu Met Asn Leu Pro Gln Gln Cys Asn
 115 120 125

Phe Arg Ala Pro Gln Arg Cys Asp Leu Asp Val Ser Gly Gly Arg Cys
 130 135 140

<210> 11
 <211> 4638
 <212> DNA

<213> Artificial Sequence

<220>

<223> PHAVag sequence

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<220>
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<400> 12

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Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
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Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
20          25          30

```

```

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35          40          45

```

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
 50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Ala Arg Gly Arg Val
 65 70 75 80

Ser Pro Leu Met Leu Leu Leu Gly Ile Leu Val Leu Ala Ser Val Ser
 85 90 95

Ala Thr His Ala Lys Ser Ser Pro Tyr Gln Lys Lys Thr Glu Asn Pro
 100 105 110

Cys Ala Gln Arg Cys Leu Gln Ser Cys Gln Gln Glu Pro Asp Asp Leu
 115 120 125

Lys Gln Lys Ala Cys Glu Ser Arg Cys Thr Lys Leu Glu Tyr Asp Pro
 130 135 140

Arg Cys Val Tyr Asp Pro Arg Gly His Thr Gly Thr Thr Asn Gln Arg
 145 150 155 160

Ser Pro Pro Gly Glu Arg Thr Arg Gly Arg Gln Pro Gly Asp Tyr Asp
 165 170 175

Asp Asp Arg Arg Gln Pro Arg Arg Glu Glu Gly Gly Arg Trp Gly Pro
 180 185 190

Ala Gly Pro Arg Glu Arg Glu Arg Glu Glu Asp Trp Arg Gln Pro Arg
 195 200 205

Glu Asp Trp Arg Arg Pro Ser His Gln Gln Pro Arg Lys Ile Arg Pro
 210 215 220

Glu Gly Arg Glu Gly Glu Gln Glu Trp Gly Thr Pro Gly Ser His Val
 225 230 235 240

Arg Glu Glu Thr Ser Arg Asn Asn Pro Phe Tyr Phe Pro Ser Arg Arg
 245 250 255

Phe Ser Thr Arg Tyr Gly Asn Gln Asn Gly Arg Ile Arg Val Leu Gln
 260 265 270

Arg Phe Asp Gln Arg Ser Arg Gln Phe Gln Asn Leu Gln Asn His Arg
 275 280 285

Ile Val Gln Ile Glu Ala Lys Pro Asn Thr Leu Val Leu Pro Lys His
 290 295 300

Ala Asp Ala Asp Asn Ile Leu Val Ile Gln Gln Gly Gln Ala Thr Val
 305 310 315 320

Thr Val Ala Asn Gly Asn Asn Arg Lys Ser Phe Asn Leu Asp Glu Gly
 325 330 335

His Ala Leu Arg Ile Pro Ser Gly Phe Ile Ser Tyr Ile Leu Asn Arg
 340 345 350

His Asp Asn Gln Asn Leu Arg Val Ala Lys Ile Ser Met Pro Val Asn
 355 360 365

Thr Pro Gly Gln Phe Glu Asp Phe Phe Pro Ala Ser Ser Arg Asp Gln
 370 375 380

Ser Ser Tyr Leu Gln Gly Phe Ser Arg Asn Thr Leu Glu Ala Ala Phe
 385 390 395 400

Asn Ala Glu Phe Asn Glu Ile Arg Arg Val Leu Leu Glu Glu Asn Ala
 405 410 415

Gly Gly Glu Gln Glu Glu Arg Gly Gln Arg Arg Trp Ser Thr Arg Ser
 420 425 430

Ser Glu Asn Asn Glu Gly Val Ile Val Lys Val Ser Lys Glu His Val
 435 440 445

Glu Glu Leu Thr Lys His Ala Lys Ser Val Ser Lys Lys Gly Ser Glu
 450 455 460

Glu Glu Gly Asp Ile Thr Asn Pro Ile Asn Leu Arg Glu Gly Glu Pro
 465 470 475 480

Asp Leu Ser Asn Asn Phe Gly Lys Leu Phe Glu Val Lys Pro Asp Lys
 485 490 495

Lys Asn Pro Gln Leu Gln Asp Leu Asp Met Met Leu Thr Cys Val Glu
 500 505 510

Ile Lys Glu Gly Ala Leu Met Leu Pro His Phe Asn Ser Lys Ala Met
 515 520 525

Val Ile Val Val Val Asn Lys Gly Thr Gly Asn Leu Glu Leu Val Ala
 530 535 540

Val Arg Lys Glu Gln Gln Gln Arg Gly Arg Arg Glu Glu Glu Glu Asp
 545 550 555 560

Glu Asp Glu Glu Glu Glu Gly Ser Asn Arg Glu Val Arg Arg Tyr Thr
 565 570 575

Ala Arg Leu Lys Glu Gly Asp Val Phe Ile Met Pro Ala Ala His Pro
 580 585 590

Val Ala Ile Asn Ala Ser Ser Glu Leu His Leu Leu Gly Phe Gly Ile
 595 600 605

Asn Ala Glu Asn Asn His Arg Ile Phe Leu Ala Gly Asp Lys Asp Asn
 610 615 620

Val Ile Asp Gln Ile Glu Lys Gln Ala Lys Asp Leu Ala Phe Pro Gly
 625 630 635 640

Ser Gly Glu Gln Val Glu Lys Leu Ile Lys Asn Gln Lys Glu Ser His
 645 650 655

Phe Val Ser Ala Arg Pro Gln Ser Gln Ser Gln Ser Pro Ser Ser Pro
 660 665 670

Glu Lys Glu Ser Pro Glu Lys Glu Asp Gln Glu Glu Glu Asn Gln Gly
 675 680 685

Gly Lys Gly Pro Leu Leu Ser Ile Leu Lys Ala Phe Asn Ala Lys Leu
 690 695 700

Thr Ile Leu Val Ala Leu Ala Leu Phe Leu Leu Ala Ala His Ala Ser
 705 710 715 720

Ala Arg Gln Gln Trp Glu Leu Gln Gly Asp Arg Arg Cys Gln Ser Gln
 725 730 735

Leu Glu Arg Ala Asn Leu Arg Pro Cys Glu Gln His Leu Met Gln Lys
 740 745 750

Ile Gln Arg Asp Glu Asp Ser Tyr Gly Arg Asp Pro Tyr Ser Pro Ser
 755 760 765

Gln Asp Pro Tyr Ser Pro Ser Gln Asp Pro Asp Arg Arg Asp Pro Tyr

770						775										780
Ser	Pro	Ser	Pro	Tyr	Asp	Arg	Arg	Gly	Ala	Gly	Ser	Ser	Gln	His	Gln	
785					790					795					800	
Glu	Arg	Cys	Cys	Asn	Glu	Leu	Asn	Glu	Phe	Glu	Asn	Asn	Gln	Arg	Cys	
				805					810					815		
Met	Cys	Glu	Ala	Leu	Gln	Gln	Ile	Met	Glu	Asn	Gln	Ser	Asp	Arg	Leu	
			820					825					830			
Gln	Gly	Arg	Gln	Gln	Glu	Gln	Gln	Phe	Lys	Arg	Glu	Leu	Arg	Asn	Leu	
		835					840					845				
Pro	Gln	Gln	Cys	Gly	Leu	Arg	Ala	Pro	Gln	Arg	Cys	Asp	Leu	Glu	Val	
	850					855					860					
Glu	Ser	Gly	Gly	Arg	Asp	Arg	Tyr	Ala	Lys	Leu	Leu	Glu	Leu	Ser	Phe	
865					870					875					880	
Cys	Phe	Cys	Phe	Leu	Val	Leu	Gly	Ala	Ser	Ser	Ile	Ser	Phe	Arg	Gln	
				885					890					895		
Gln	Pro	Glu	Glu	Asn	Ala	Cys	Gln	Phe	Gln	Arg	Leu	Asn	Ala	Gln	Arg	
			900					905					910			
Pro	Asp	Asn	Arg	Ile	Glu	Ser	Glu	Gly	Gly	Tyr	Ile	Glu	Thr	Trp	Asn	
		915					920					925				
Pro	Asn	Asn	Gln	Glu	Phe	Glu	Cys	Ala	Gly	Val	Ala	Leu	Ser	Arg	Leu	
	930					935					940					
Val	Leu	Arg	Arg	Asn	Ala	Leu	Arg	Arg	Pro	Phe	Tyr	Ser	Asn	Ala	Pro	
945					950					955					960	
Gln	Glu	Ile	Phe	Ile	Gln	Gln	Gly	Arg	Gly	Tyr	Phe	Gly	Leu	Ile	Phe	
				965					970					975		
Pro	Gly	Cys	Pro	Arg	His	Tyr	Glu	Glu	Pro	His	Thr	Gln	Gly	Arg	Arg	
			980					985					990			
Ser	Gln	Ser	Gln	Arg	Pro	Pro	Arg	Arg	Leu	Gln	Gly	Glu	Asp	Gln	Ser	
		995					1000					1005				
Gln	Gln	Gln	Arg	Asp	Ser	His	Gln	Lys	Val	His	Arg	Phe	Asp	Glu		
	1010					1015					1020					

Gly Asp 1025	Leu Ile Ala Val	Pro Thr Gly Val Ala Phe 1030 1035	Trp Leu Tyr
Asn Asp 1040	His Asp Thr Asp Val	Val Ala Val Ser Leu Thr Asp Thr 1045 1050	
Asn Asn 1055	Asn Asp Asn Gln Leu	Asp Gln Phe Pro Arg Arg Phe Asn 1060 1065	
Leu Ala 1070	Gly Asn Thr Glu Gln	Glu Phe Leu Arg Tyr Gln Gln Gln 1075 1080	
Ser Arg 1085	Gln Ser Arg Arg Arg	Ser Leu Pro Tyr Ser Pro Tyr Ser 1090 1095	
Pro Gln 1100	Ser Gln Pro Arg Gln	Glu Glu Arg Glu Phe Ser Pro Arg 1105 1110	
Gly Gln 1115	His Ser Arg Arg Glu	Arg Ala Gly Gln Glu Glu Glu Asn 1120 1125	
Glu Gly 1130	Gly Asn Ile Phe Ser	Gly Phe Thr Pro Glu Phe Leu Glu 1135 1140	
Gln Ala 1145	Phe Gln Val Asp Asp	Arg Gln Ile Val Gln Asn Leu Arg 1150 1155	
Gly Glu 1160	Thr Glu Ser Glu Glu	Glu Gly Ala Ile Val Thr Val Arg 1165 1170	
Gly Gly 1175	Leu Arg Ile Leu Ser	Pro Asp Arg Lys Arg Arg Ala Asp 1180 1185	
Glu Glu 1190	Glu Glu Tyr Asp Glu	Asp Glu Tyr Glu Tyr Asp Glu Glu 1195 1200	
Asp Arg 1205	Arg Arg Gly Arg Gly	Ser Arg Gly Arg Gly Asn Gly Ile 1210 1215	
Glu Glu 1220	Thr Ile Cys Thr Ala	Ser Ala Lys Lys Asn Ile Gly Arg 1225 1230	
Asn Arg 1235	Ser Pro Asp Ile Tyr	Asn Pro Gln Ala Gly Ser Leu Lys 1240 1245	

Thr	Ala	Asn	Asp	Leu	Asn	Leu	Leu	Ile	Leu	Arg	Trp	Leu	Gly	Pro
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Ser	Ala	Glu	Tyr	Gly	Asn	Leu	Tyr	Arg	Asn	Ala	Leu	Phe	Val	Ala
1265						1270					1275			
His	Tyr	Asn	Thr	Asn	Ala	His	Ser	Ile	Ile	Tyr	Arg	Leu	Arg	Gly
1280						1285					1290			
Arg	Ala	His	Val	Gln	Val	Val	Asp	Ser	Asn	Gly	Asn	Arg	Val	Tyr
1295						1300					1305			
Asp	Glu	Glu	Leu	Gln	Glu	Gly	His	Val	Leu	Val	Val	Pro	Gln	Asn
1310						1315					1320			
Phe	Ala	Val	Ala	Gly	Lys	Ser	Gln	Ser	Glu	Asn	Phe	Glu	Tyr	Val
1325						1330					1335			
Ala	Phe	Lys	Thr	Asp	Ser	Arg	Pro	Ser	Ile	Ala	Asn	Leu	Ala	Gly
1340						1345					1350			
Glu	Asn	Ser	Val	Ile	Asp	Asn	Leu	Pro	Glu	Glu	Val	Val	Ala	Asn
1355						1360					1365			
Ser	Tyr	Gly	Leu	Gln	Arg	Glu	Gln	Ala	Arg	Gln	Leu	Lys	Asn	Asn
1370						1375					1380			
Asn	Pro	Phe	Lys	Phe	Phe	Val	Pro	Pro	Ser	Gln	Gln	Ser	Pro	Arg
1385						1390					1395			
Ala	Val	Ala	Ala	Lys	Ser	Thr	Ile	Leu	Val	Ala	Leu	Leu	Ala	Leu
1400						1405					1410			
Val	Leu	Val	Ala	His	Ala	Ser	Ala	Met	Arg	Arg	Glu	Arg	Gly	Arg
1415						1420					1425			
Gln	Gly	Asp	Ser	Ser	Ser	Cys	Glu	Arg	Gln	Val	Asp	Arg	Val	Asn
1430						1435					1440			
Leu	Lys	Pro	Cys	Glu	Gln	His	Ile	Met	Gln	Arg	Ile	Met	Gly	Glu
1445						1450					1455			
Gln	Glu	Gln	Tyr	Asp	Ser	Tyr	Asp	Ile	Arg	Ser	Thr	Arg	Ser	Ser
1460						1465					1470			

Asp Gln Gln Gln Arg Cys Cys Asp Glu Leu Asn Glu Met Glu Asn
1475 1480 1485

Thr Gln Arg Cys Met Cys Glu Ala Leu Gln Gln Ile Met Glu Asn
1490 1495 1500

Gln Cys Asp Arg Leu Gln Asp Arg Gln Met Val Gln Gln Phe Lys
1505 1510 1515

Arg Glu Leu Met Asn Leu Pro Gln Gln Cys Asn Phe Arg Ala Pro
1520 1525 1530

Gln Arg Cys Asp Leu Asp Val Ser Gly Gly Arg Cys
1535 1540 1545