SEQUENCE LISTING

<110> CAMBRIDGE ENTERPRISE LIMITED
THE SYDNEY CHILDREN'S HOSPITALS NETWORK (RANDWICK AND WESTMEAD) (INCORPORATING THE ROYAL ALEXANDRA HOSPITAL FOR CHILDREN)

<120> Treatment of Complement-Mediated Disorders

<130> P/74985.WO01

<150> GB1608046.7
<151> 2016-05-09

<160> 12

<170> PatentIn version 3.5

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<212> DNA
<213> Homo sapiens

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Phe Cys Lys Val Thr Tyr Thr Ser Gln Glu Asp Leu Val Glu Lys Lys
20 25 30

Cys Leu Ala Lys Lys Tyr Thr His Leu Ser Cys Asp Lys Val Phe Cys
35 40 45

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Gln Pro Trp Gln Arg Cys Ile Glu Gly Thr Cys Val Cys Lys Leu Pro
    50                  55                  60

Tyr Gln Cys Pro Lys Asn Gly Thr Ala Val Cys Ala Thr Asn Arg Arg
65                  70                  75                  80

Ser Phe Pro Thr Tyr Cys Gln Gln Lys Ser Leu Glu Cys Leu His Pro
                85                  90                  95

Gly Thr Lys Phe Leu Asn Asn Gly Thr Cys Thr Ala Glu Gly Lys Phe
            100                 105                 110

Ser Val Ser Leu Lys His Gly Asn Thr Asp Ser Glu Gly Ile Val Glu
        115                 120                 125

Val Lys Leu Val Asp Gln Asp Lys Thr Met Phe Ile Cys Lys Ser Ser
    130                 135                 140

Trp Ser Met Arg Glu Ala Asn Val Ala Cys Leu Asp Leu Gly Phe Gln
145                 150                 155                 160

Gln Gly Ala Asp Thr Gln Arg Arg Phe Lys Leu Ser Asp Leu Ser Ile
                165                 170                 175

Asn Ser Thr Glu Cys Leu His Val His Cys Arg Gly Leu Glu Thr Ser
            180                 185                 190

Leu Ala Glu Cys Thr Phe Thr Lys Arg Arg Thr Met Gly Tyr Gln Asp
        195                 200                 205

Phe Ala Asp Val Val Cys Tyr Thr Gln Lys Ala Asp Ser Pro Met Asp
    210                 215                 220

Asp Phe Phe Gln Cys Val Asn Gly Lys Tyr Ile Ser Gln Met Lys Ala
225                 230                 235                 240

Cys Asp Gly Ile Asn Asp Cys Gly Asp Gln Ser Asp Glu Leu Cys Cys
                245                 250                 255
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Lys Ala Cys Gln Gly Lys Gly Phe His Cys Lys Ser Gly Val Cys Ile
            260                 265                 270

Pro Ser Gln Tyr Gln Cys Asn Gly Glu Val Asp Cys Ile Thr Gly Glu
        275                 280                 285

Asp Glu Val Gly Cys Ala Gly Phe Ala Ser Val Ala Gln Glu Glu Thr
    290                 295                 300

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

Leu Leu Pro Lys Leu Ser Cys Gly Val Lys Asn Arg Met His Ile Arg
                325                 330                 335

Arg Lys Arg Ile Val Gly Gly Lys Arg Ala Gln Leu Gly Asp Leu Pro
            340                 345                 350

Trp Gln Val Ala Ile Lys Asp Ala Ser Gly Ile Thr Cys Gly Gly Ile
        355                 360                 365

Tyr Ile Gly Gly Cys Trp Ile Leu Thr Ala Ala His Cys Leu Arg Ala
    370                 375                 380

Ser Lys Thr His Arg Tyr Gln Ile Trp Thr Thr Val Val Asp Trp Ile
385                 390                 395                 400

His Pro Asp Leu Lys Arg Ile Val Ile Glu Tyr Val Asp Arg Ile Ile
                405                 410                 415

Phe His Glu Asn Tyr Asn Ala Gly Thr Tyr Gln Asn Asp Ile Ala Leu
            420                 425                 430

Ile Glu Met Lys Lys Asp Gly Asn Lys Lys Asp Cys Glu Leu Pro Arg
        435                 440                 445

Ser Ile Pro Ala Cys Val Pro Trp Ser Pro Tyr Leu Phe Gln Pro Asn
    450                 455                 460
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Asp Thr Cys Ile Val Ser Gly Trp Gly Arg Glu Lys Asp Asn Glu Arg
465                 470                 475                 480


Val Phe Ser Leu Gln Trp Gly Glu Val Lys Leu Ile Ser Asn Cys Ser
                485                 490                 495


Lys Phe Tyr Gly Asn Arg Phe Tyr Glu Lys Glu Met Glu Cys Ala Gly
            500                 505                 510


Thr Tyr Asp Gly Ser Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro
        515                 520                 525


Leu Val Cys Met Asp Ala Asn Asn Val Thr Tyr Val Trp Gly Val Val
    530                 535                 540


Ser Trp Gly Glu Asn Cys Gly Lys Pro Glu Phe Pro Gly Val Tyr Thr
545                 550                 555                 560


Lys Val Ala Asn Tyr Phe Asp Trp Ile Ser Tyr His Val Gly Arg Pro
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Phe Ile Ser Gln Tyr Asn Val
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<210> 3
<211> 1698
<212> DNA
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<400> 3

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tgtgtttgta aactaccgta tcagtgccca aagaatggca ctgcagtgtg tgcaactaac      180

aggagaagct tcccaacata ctgtcaacaa aagagtttgg aatgtcttca tccagggaca      240

aagtttttaa ataacggaac atgcacagcc gaaggaaagt ttagtgtttc cttgaagcat      300

ggaaatacag attcagaggg aatagttgaa gtaaaacttg tggaccaaga taagacaatg      360

ttcatatgca aaagcagctg gagcatgagg gaagccaacg tggcctgcct tgaccttggg      420
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actaagagaa gaactatggg ttaccaggat ttcgctgatg tggtttgtta tacacagaaa 600

gcagattctc caatggatga cttctttcag tgtgtgaatg ggaaatacat ttctcagatg 660

aaagcctgtg atggtatcaa tgattgtgga gaccaaagtg atgaactgtg ttgtaaagca 720

tgccaaggca aaggcttcca ttgcaaatcg ggtgtttgca ttccaagcca gtatcaatgc 780

aatggtgagg tggactgcat tacaggggaa gatgaagttg gctgtgcagg ctttgcatct 840

gtggctcaag aagaaacaga aattttgact gctgacatgg atgcagaaag aagacggata 900

aaatcattat tacctaaact atcttgtgga gttaaaaaca gaatgcacat tcgaaggaaa 960

cgaattgtgg gaggaaagcg agcacaactg ggagacctcc catggcaggt ggcaattaag 1020

gatgccagtg gaatcacctg tgggggaatt tatattggtg gctgttggat tctgactgct 1080

gcacattgtc tcagagccag taaaactcat cgttaccaaa tatggacaac agtagtagac 1140

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gaaaactaca atgcaggcac ttaccaaaat gacatcgctt tgattgaaat gaaaaaagac 1260

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gaaagagtct tttcacttca gtggggtgaa gttaaactaa taagcaactg ctctaagttt 1440

tacggaaatc gtttctatga aaaagaaatg gaatgtgcag gtacatatga tggttccatc 1500

gatgcctgta aaggggactc tggaggcccc ttagtctgta tggatgccaa caatgtgact 1560

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<212> PRT
<213> Homo sapiens

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            20                  25                  30

Trp Gln Arg Cys Ile Glu Gly Thr Cys Val Cys Lys Leu Pro Tyr Gln
        35                  40                  45

Cys Pro Lys Asn Gly Thr Ala Val Cys Ala Thr Asn Arg Arg Ser Phe
    50                  55                  60

Pro Thr Tyr Cys Gln Gln Lys Ser Leu Glu Cys Leu His Pro Gly Thr
65                  70                  75                  80

Lys Phe Leu Asn Asn Gly Thr Cys Thr Ala Glu Gly Lys Phe Ser Val
                85                  90                  95

Ser Leu Lys His Gly Asn Thr Asp Ser Glu Gly Ile Val Glu Val Lys
            100                 105                 110

Leu Val Asp Gln Asp Lys Thr Met Phe Ile Cys Lys Ser Ser Trp Ser
        115                 120                 125

Met Arg Glu Ala Asn Val Ala Cys Leu Asp Leu Gly Phe Gln Gln Gly
    130                 135                 140

Ala Asp Thr Gln Arg Arg Phe Lys Leu Ser Asp Leu Ser Ile Asn Ser
145                 150                 155                 160

Thr Glu Cys Leu His Val His Cys Arg Gly Leu Glu Thr Ser Leu Ala
                165                 170                 175

Glu Cys Thr Phe Thr Lys Arg Arg Thr Met Gly Tyr Gln Asp Phe Ala
            180                 185                 190

Asp Val Val Cys Tyr Thr Gln Lys Ala Asp Ser Pro Met Asp Asp Phe
        195                 200                 205
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Phe Gln Cys Val Asn Gly Lys Tyr Ile Ser Gln Met Lys Ala Cys Asp
    210                 215                 220

Gly Ile Asn Asp Cys Gly Asp Gln Ser Asp Glu Leu Cys Cys Lys Ala
225                 230                 235                 240

Cys Gln Gly Lys Gly Phe His Cys Lys Ser Gly Val Cys Ile Pro Ser
                245                 250                 255

Gln Tyr Gln Cys Asn Gly Glu Val Asp Cys Ile Thr Gly Glu Asp Glu
            260                 265                 270

Val Gly Cys Ala Gly Phe Ala Ser Val Ala Gln Glu Glu Thr Glu Ile
        275                 280                 285

Leu Thr Ala Asp Met Asp Ala Glu Arg Arg Arg Ile Lys Ser Leu Leu
    290                 295                 300

Pro Lys Leu Ser Cys Gly Val Lys Asn Arg Met His Ile Arg Arg Lys
305                 310                 315                 320

Arg Ile Val Gly Gly Lys Arg Ala Gln Leu Gly Asp Leu Pro Trp Gln
                325                 330                 335

Val Ala Ile Lys Asp Ala Ser Gly Ile Thr Cys Gly Gly Ile Tyr Ile
            340                 345                 350

Gly Gly Cys Trp Ile Leu Thr Ala Ala His Cys Leu Arg Ala Ser Lys
        355                 360                 365

Thr His Arg Tyr Gln Ile Trp Thr Thr Val Val Asp Trp Ile His Pro
    370                 375                 380

Asp Leu Lys Arg Ile Val Ile Glu Tyr Val Asp Arg Ile Ile Phe His
385                 390                 395                 400

Glu Asn Tyr Asn Ala Gly Thr Tyr Gln Asn Asp Ile Ala Leu Ile Glu
                405                 410                 415
```

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Met Lys Lys Asp Gly Asn Lys Lys Asp Cys Glu Leu Pro Arg Ser Ile
            420                 425                 430

Pro Ala Cys Val Pro Trp Ser Pro Tyr Leu Phe Gln Pro Asn Asp Thr
        435                 440                 445

Cys Ile Val Ser Gly Trp Gly Arg Glu Lys Asp Asn Glu Arg Val Phe
    450                 455                 460

Ser Leu Gln Trp Gly Glu Val Lys Leu Ile Ser Asn Cys Ser Lys Phe
465                 470                 475                 480

Tyr Gly Asn Arg Phe Tyr Glu Lys Glu Met Glu Cys Ala Gly Thr Tyr
                485                 490                 495

Asp Gly Ser Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val
            500                 505                 510

Cys Met Asp Ala Asn Asn Val Thr Tyr Val Trp Gly Val Val Ser Trp
        515                 520                 525

Gly Glu Asn Cys Gly Lys Pro Glu Phe Pro Gly Val Tyr Thr Lys Val
    530                 535                 540

Ala Asn Tyr Phe Asp Trp Ile Ser Tyr His Val Gly Arg Pro Phe Ile
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Ser Gln Tyr Asn Val
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<210> 5
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<212> DNA
<213> Artificial

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<223> Primer sequence: FI-AAV-F

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<211> 47
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<223> Primer sequence: FI-AAV-R

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<211> 1752
<212> DNA
<213> Homo sapiens

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ctgagctgcg acaaggtgtt ctgtcagcct tggcagcggt gcatcgaggg cacctgcgtg 180

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tataatgtct aa 1752

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<211> 251
<212> DNA
<213> Artificial

<220>
<223> HLP liver-specific promoter sequence

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tggggtgacc ttggttaata ttcaccagca gcctcccccg ttgcccctct ggatccactg 180

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ggacagtgaa t 251

<210> 9
<211> 447
<212> DNA
<213> Artificial

<220>
<223> LP1 liver-specific promoter sequence

<400> 9
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cactcgaccc cttggaattt cggtggagag gagcagaggt tgtcctggcg tggtttaggt 180

agtgtgagag gggaatgact cctttcggta agtgcagtgg aagctgtaca ctgcccaggc 240

aaagcgtccg ggcagcgtag gcgggcgact cagatcccag ccagtggact tagcccctgt 300

ttgctcctcc gataactggg gtgaccttgg ttaatattca ccagcagcct cccccgttgc 360

ccctctggat ccactgctta aatacggacg aggacagggc cctgtctcct cagcttcagg 420

caccaccact gacctgggac agtgaat 447

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<212> DNA
<213> Artificial

<220>
<223> HLP2 liver-specific promoter sequence

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acacaggacg ctgtggtttc tgagccaggg ggcgactcag atcccagcca gtggacttag 180

cccctgtttg ctcctccgat aactggggtg accttggtta atattcacca gcagcctccc 240

ccgttgcccc tctggatcca ctgcttaaat acggacgagg acagggccct gtctcctcag 300

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<212> PRT
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Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
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Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

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

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415
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Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
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Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


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


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


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<212>  PRT
<213>  Artificial

<220>
<223>  LK03 capsid protein sequence

<400>  12

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Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
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50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145 150 155 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr

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            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

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

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
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465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

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

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735