

# SEQUENCE LISTING

<110> Tenaya Therapeutics, Inc.

<120> GENE THERAPY VECTORS FOR TREATING HEART DISEASE

<130> TENA-015/02WO 334682-2115

<150> 62/976,160

<151> 2020-02-13

<150> 63/047,633

<151> 2020-07-02

<160> 201

<170> PatentIn version 3.5

<210> 1

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<212> DNA

<213> Homo sapiens

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| acttatggag tgtcttggag gttgccttct gcccccaac cctgctcca gctggccctc   | 240 |
| ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat | 300 |
| gttgcatgac tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg | 360 |
| aggaccacat gggcttatat ggcgtgggg acatgttcct gtagccttgt ccctggcacc  | 420 |
| tgccaaaata gcagccaaca cccccaccc ccaccgcat ccccctgccc caccgtccc    | 480 |
| ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagccca catgcctgct      | 540 |
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|                                                                   |     |
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| tgccaaaata gcagccaaca cccccaccc ccaccgccat cccctgccc caccgtccc    | 180 |
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| ggagcagcac ataactcttg ccctctgcct tccaagattc tggctgag acttatggag   | 180 |
| tgtcttggag gttgccttct gcccccaac cctgctcca gctggccctc ccaggcctgg   | 240 |
| gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat gttgcatgac | 300 |
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| gcagccaaca cccccaccc ccaccgccat cccctgccc caccgtccc ctgtcgcaca    | 480 |
| ttctccctc cgcagggtg gtcaccagg cccagccca catgcctgct taaagccctc     | 540 |
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| ataactcttg ccctctgcct tccaagattc tggctgag acttatggag tgtcttggag   | 180 |
| gttgcttct gcccccaac cctgctcca gctggccctc ccaggcctgg gttgctggcc    | 240 |
| tctgctttat caggattctc aagagggaca gctggtttat gttgcatgac tgttccctgc | 300 |

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atatctgctc | tggttttaaa | tagcttatct | gagcagctgg  | aggaccacat | gggcttatat | 360 |
| ggcgtggggg | acatgttcct | gtagccttgt | ccctggcacc  | tgccaaaata | gcagccaaca | 420 |
| ccccccaccc | ccaccgccat | ccccctgccc | caccctgtccc | ctgtcgcaca | ttcctccctc | 480 |
| cgcagggtg  | gctcaccagg | ccccagccca | catgcctgct  | taaagccctc | tccatcctct | 540 |
| gcctcaccca | gtccccgctg | agactgagca | gacgcctcca  |            |            | 580 |

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| ctcactgggg | ctggcagagc | cggcaacctg  | cctaaggctg | ctcagtccat | taggagccag | 60  |
| tagcctggaa | gatgtcttta | ccccagcat   | cagttcaagt | ggagcagcac | ataactcttg | 120 |
| ccctctgcct | tccaagattc | tggtgctgag  | acttatggag | tgtcttggag | gttgctttct | 180 |
| gccccccaac | cctgctccca | gctggccctc  | ccaggcctgg | gttgctggcc | tctgctttat | 240 |
| caggattctc | aagagggaca | gctggtttat  | gttgcatgac | tgttccctgc | atatctgctc | 300 |
| tggttttaaa | tagcttatct | gagcagctgg  | aggaccacat | gggcttatat | ggcgtggggg | 360 |
| acatgttcct | gtagccttgt | ccctggcacc  | tgccaaaata | gcagccaaca | ccccccaccc | 420 |
| ccaccgccat | ccccctgccc | caccctgtccc | ctgtcgcaca | ttcctccctc | cgcagggtg  | 480 |
| gctcaccagg | ccccagccca | catgcctgct  | taaagccctc | tccatcctct | gcctcaccca | 540 |
| gtccccgctg | agactgagca | gacgcctcca  |            |            |            | 570 |

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| gatgtcttta | ccccagcat  | cagttcaagt | ggagcagcac | ataactcttg | ccctctgcct | 120 |
| tccaagattc | tggtgctgag | acttatggag | tgtcttggag | gttgctttct | gccccccaac | 180 |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cctgctccca gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc  | 240 |
| aagagggaca gctggtttat gttgcatgac tgttccctgc atatctgctc tggttttaaa  | 300 |
| tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct | 360 |
| gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat    | 420 |
| ccccctgccc caccgtccc ctgtcgaca ttctccctc cgcagggtg gtcaccagg       | 480 |
| ccccagccca catgcctgct taaagccctc tccatcctct gcctcaccca gtccccgctg  | 540 |
| agactgagca gacgcctcca                                              | 560 |

<210> 9  
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 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
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| ccccagcat cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc   | 120 |
| tgggtgctgag acttatggag tgtcttggag gttgccttct gcccccaac cctgctccca  | 180 |
| gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca  | 240 |
| gctggtttat gttgcatgac tgttccctgc atatctgctc tggttttaaa tagcttatct  | 300 |
| gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct gtagccttgt | 360 |
| ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat cccccctgccc   | 420 |
| caccgtccc ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagccca        | 480 |
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|                                                                    |     |
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| cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc tggctgctgag | 120 |
| acttatggag tgtcttggag gttgccttct gcccccaac cctgctcca gctggccctc    | 180 |
| ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat  | 240 |
| gttgcacgac tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg  | 300 |
| aggaccacat gggcttatat ggcgtggggt acatgttcct gtagccttgt ccctggcacc  | 360 |
| tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc      | 420 |
| ctgtcgaca ttctccctc cgcagggtg gctcaccagg cccagccca catgcctgct      | 480 |
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<210> 11  
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|                                                                    |     |
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| ggagcagcac ataactcttg ccctctgcct tccaagattc tggctgctgag acttatggag | 120 |
| tgtcttggag gttgccttct gcccccaac cctgctcca gctggccctc ccaggcctgg    | 180 |
| gttgcctggc tctgctttat caggattctc aagagggaca gctggtttat gttgcacgac  | 240 |
| tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat  | 300 |
| gggcttatat ggcgtggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata  | 360 |
| gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc ctgtcgaca       | 420 |
| ttctccctc cgcagggtg gctcaccagg cccagccca catgcctgct taaagccctc     | 480 |
| tccatcctct gcctcaccca gtccccgtg agactgagca gacgcctcca              | 530 |

<210> 12  
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 <212> DNA  
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|                                                                   |    |
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|                                                                    |     |
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| ataactcttg ccctctgcct tccaagattc tggctgctgag acttatggag tgtcttggag | 120 |
| gttgcccttct gccccccaac cctgctccca gctggccctc ccaggcctgg gttgctggcc | 180 |
| tctgctttat caggattctc aagagggaca gctggtttat gttgcatgac tgttccctgc  | 240 |
| atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat  | 300 |
| ggcgtggggg acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca  | 360 |
| ccccccaccc ccaccgcat cccctgccc caccgtccc ctgtcgaca ttctccctc       | 420 |
| cgcagggtg gctcaccagg cccagccca catgcctgct taaagccctc tccatcctct    | 480 |
| gcctcaccca gtccccgtg agactgagca gacgcctcca                         | 520 |

<210> 13  
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 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
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| ccctctgcct tccaagattc tggctgctgag acttatggag tgtcttggag gttgccttct | 120 |
| gccccccaac cctgctccca gctggccctc ccaggcctgg gttgctggcc tctgctttat  | 180 |
| caggattctc aagagggaca gctggtttat gttgcatgac tgttccctgc atatctgctc  | 240 |
| tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtggggg  | 300 |
| acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc   | 360 |
| ccaccgcat cccctgccc caccgtccc ctgtcgaca ttctccctc cgcagggtg        | 420 |
| gctcaccagg cccagccca catgcctgct taaagccctc tccatcctct gcctcaccca   | 480 |
| gtccccgtg agactgagca gacgcctcca                                    | 510 |

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|                                                                    |     |
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| gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca  | 180 |
| gctggtttat gttgcatgac tgttccctgc atatctgctc tggttttaaa tagcttatct  | 240 |
| gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct gtagccttgt | 300 |
| ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc     | 360 |
| caccgtccc ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagccca        | 420 |
| catgcctgct taaagccctc tccatcctct gcctcaccca gtccccgtg agactgagca   | 480 |
| gacgcctcca                                                         | 490 |

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|                                                                    |     |
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| acttatggag tgtcttggag gttgccttct gccccccaac cctgctccca gctggccctc  | 120 |
| ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat  | 180 |
| gttgcattgac tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg | 240 |
| aggaccacat gggcttatat ggcgtgggggt acatgttcct gtagccttgt ccctggcacc | 300 |
| tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc      | 360 |
| ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagccca catgcctgct       | 420 |
| taaagccctc tccatcctct gcctcaccca gtccccgtg agactgagca gacgcctcca   | 480 |

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|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat gttgcatgac  | 180 |
| tggtccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat  | 240 |
| gggcttatat ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata | 300 |
| gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc ctgtcgaca       | 360 |
| ttcctccctc cgcagggtg gtcaccagg cccagccca catgcctgct taaagccctc     | 420 |
| tccatcctct gcctcaccca gtccccgctg agactgagca gacgcctcca             | 470 |

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 <213> Homo sapiens

|                                                                                |     |
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| gttgctttct gcccccaac cctgctccca gctggccctc ccaggcctgg gttgctggcc               | 120 |
| tctgctttat caggattctc aagagggaca gctggtttat gttgcatgac tggtccctgc              | 180 |
| atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat              | 240 |
| ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca             | 300 |
| ccccccaccc ccaccgcat cccctgccc caccgtccc ctgtcgaca ttcctccctc                  | 360 |
| cgcagggtg gtcaccagg cccagccca catgcctgct taaagccctc tccatcctct                 | 420 |
| gcctcaccca gtccccgctg agactgagca gacgcctcca                                    | 460 |

<210> 18  
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|                                                                                |     |
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| gcccccaac cctgctccca gctggccctc ccaggcctgg gttgctggcc tctgctttat               | 120 |
| caggattctc aagagggaca gctggtttat gttgcatgac tggtccctgc atatctgctc              | 180 |
| tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt             | 240 |

|                                                                  |     |
|------------------------------------------------------------------|-----|
| acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc | 300 |
| ccaccgccat cccctgccc caccgctccc ctgtcgcaca ttcctccctc cgcagggtg  | 360 |
| gctcaccagg cccagccca catgcctgct taaagccctc tccatcctct gcctcaccca | 420 |
| gtccccgctg agactgagca gacgcctcca                                 | 450 |

<210> 19  
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 <212> DNA  
 <213> Homo sapiens

|                                                                   |     |
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| aagagggaca gctggtttat gttgcatgac tgttccctgc atatctgctc tggttttaaa | 180 |
| tagcttatct gagcagctgg aggaccacat gggcttatat ggctgtgggt acatgttcct | 240 |
| gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgccat  | 300 |
| ccctgccc caccgctccc ctgtcgcaca ttcctccctc cgcagggtg gctcaccagg    | 360 |
| cccagccca catgcctgct taaagccctc tccatcctct gcctcaccca gtccccgctg  | 420 |
| agactgagca gacgcctcca                                             | 440 |

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 <212> DNA  
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|                                                                   |     |
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| gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca | 120 |
| gctggtttat gttgcatgac tgttccctgc atatctgctc tggttttaaa tagcttatct | 180 |
| gagcagctgg aggaccacat gggcttatat ggctgtgggt acatgttcct gtagccttgt | 240 |
| ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgccat cccctgccc   | 300 |
| caccgctccc ctgtcgcaca ttcctccctc cgcagggtg gctcaccagg cccagccca   | 360 |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
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| gacgcctcca                                                        | 430 |

<210> 21  
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|                                                                   |     |
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| ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat | 120 |
| gttgcacgac tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg | 180 |
| aggaccacat gggcttatat ggcgtggggc acatgttcct gtagccttgt ccctggcacc | 240 |
| tgccaaaata gcagccaaca cccccaccc ccaccgccat cccctgccc caccgtccc    | 300 |
| ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagccca catgcctgct      | 360 |
| taaagccctc tccatcctct gcctcaccca gtccccgctg agactgagca gacgcctcca | 420 |

<210> 22  
 <211> 410  
 <212> DNA  
 <213> Homo sapiens

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 22                                                          |     |
| tgtcttggag gttgccttct gcccccaac cctgctcca gctggccctc ccaggcctgg   | 60  |
| gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat gttgcacgac | 120 |
| tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat | 180 |
| gggcttatat ggcgtggggc acatgttcct gtagccttgt ccctggcacc tgccaaaata | 240 |
| gcagccaaca cccccaccc ccaccgccat cccctgccc caccgtccc ctgtcgaca     | 300 |
| ttctccctc cgcagggtg gtcaccagg cccagccca catgcctgct taaagccctc     | 360 |
| tccatcctct gcctcaccca gtccccgctg agactgagca gacgcctcca            | 410 |

<210> 23  
 <211> 390

<212> DNA

<213> Homo sapiens

<400> 23

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gccccccaac cctgctccca gctggccctc ccaggcctgg gttgctggcc tctgctttat  | 60  |
| caggattctc aagagggaca gctggtttat gttgcatgac tggtccctgc atatctgctc  | 120 |
| tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt | 180 |
| acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc   | 240 |
| ccaccgcat cccctgccc caccgtccc ctgtcgaca ttctccctc cgcagggtg        | 300 |
| gctcaccagg cccagccca catgcctgct taaagccctc tccatcctct gcctcaccca   | 360 |
| gtccccgctg agactgagca gacgcctcca                                   | 390 |

<210> 24

<211> 380

<212> DNA

<213> Homo sapiens

<400> 24

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cctgctccca gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc  | 60  |
| aagagggaca gctggtttat gttgcatgac tggtccctgc atatctgctc tggttttaaa  | 120 |
| tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct | 180 |
| gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat    | 240 |
| ccccctgccc caccgtccc ctgtcgaca ttctccctc cgcagggtg gctcaccagg      | 300 |
| cccagccca catgcctgct taaagccctc tccatcctct gcctcaccca gtccccgctg   | 360 |
| agactgagca gacgcctcca                                              | 380 |

<210> 25

<211> 370

<212> DNA

<213> Homo sapiens

<400> 25

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca | 60  |
| gctggtttat gttgcatgac tggtccctgc atatctgctc tggttttaaa tagcttatct | 120 |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct gtagccttgt | 180 |
| ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc     | 240 |
| caccgtccc ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagccca        | 300 |
| catgcctgct taaagccctc tccatcctct gcctcaccca gtccccgctg agactgagca  | 360 |
| gacgcctcca                                                         | 370 |

<210> 26  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 26                                                           |     |
| ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat  | 60  |
| gttgcacgac tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg  | 120 |
| aggaccacat gggcttatat ggcgtgggggt acatgttcct gtagccttgt ccctggcacc | 180 |
| tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc      | 240 |
| ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagccca catgcctgct       | 300 |
| taaagccctc tccatcctct gcctcaccca gtccccgctg agactgagca gacgcctcca  | 360 |

<210> 27  
 <211> 350  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 27                                                           |     |
| gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat gttgcacgac  | 60  |
| tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat  | 120 |
| gggcttatat ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata | 180 |
| gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc ctgtcgaca       | 240 |
| ttctccctc cgcagggtg gtcaccagg cccagccca catgcctgct taaagccctc      | 300 |
| tccatcctct gcctcaccca gtccccgctg agactgagca gacgcctcca             | 350 |

<210> 28

<211> 340  
<212> DNA  
<213> Homo sapiens

<400> 28  
tctgctttat caggattctc aagaggggaca gctggtttat gttgcatgac tgttccctgc 60  
atatctgctc tggtttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat 120  
ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca 180  
ccccccaccc ccaccgccat ccccctgccc caccctgccc ctgtcgcaca ttctccctc 240  
cgcagggtg gctcaccagg cccagccca catgcctgct taaagccctc tccatcctct 300  
gcctcaccca gtccccgctg agactgagca gacgcctcca 340

<210> 29  
<211> 330  
<212> DNA  
<213> Homo sapiens

<400> 29  
caggattctc aagaggggaca gctggtttat gttgcatgac tgttccctgc atatctgctc 60  
tggtttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt 120  
acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc 180  
ccaccgccat ccccctgccc caccctgccc ctgtcgcaca ttctccctc cgcagggtg 240  
gctcaccagg cccagccca catgcctgct taaagccctc tccatcctct gcctcaccca 300  
gtccccgctg agactgagca gacgcctcca 330

<210> 30  
<211> 320  
<212> DNA  
<213> Homo sapiens

<400> 30  
aagaggggaca gctggtttat gttgcatgac tgttccctgc atatctgctc tggtttttaaa 60  
tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct 120  
gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgccat 180  
ccccctgccc caccctgccc ctgtcgcaca ttctccctc cgcagggtg gctcaccagg 240

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ccccagccca catgcctgct taaagccctc tccatcctct gcctcaccca gtccccgctg | 300 |
| agactgagca gacgcctcca                                             | 320 |

<210> 31  
 <211> 310  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 31                                                           |     |
| gctggtttat gttgcatgac tggtccctgc atatctgctc tggttttaaa tagcttatct  | 60  |
| gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct gtagccttgt | 120 |
| ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc     | 180 |
| caccgtccc ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagccca        | 240 |
| catgcctgct taaagccctc tccatcctct gcctcaccca gtccccgctg agactgagca  | 300 |
| gacgcctcca                                                         | 310 |

<210> 32  
 <211> 290  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 32                                                           |     |
| tggtccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat  | 60  |
| gggcttatat ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata | 120 |
| gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc ctgtcgaca       | 180 |
| ttctccctc cgcagggtg gtcaccagg cccagccca catgcctgct taaagccctc      | 240 |
| tccatcctct gcctcaccca gtccccgctg agactgagca gacgcctcca             | 290 |

<210> 33  
 <211> 280  
 <212> DNA  
 <213> Homo sapiens

|                                                                   |    |
|-------------------------------------------------------------------|----|
| <400> 33                                                          |    |
| atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat | 60 |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca | 120 |
| ccccccaccc ccaccgcat cccctgccc caccgtccc ctgtcgaca ttctccctc       | 180 |
| cgcagggtg gtcaccagg cccagccca catgcctgct taaagccctc tccatcctct     | 240 |
| gcctcaccca gtccccgctg agactgagca gacgcctcca                        | 280 |

<210> 34  
 <211> 270  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 34                                                           |     |
| tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt | 60  |
| acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc   | 120 |
| ccaccgcat cccctgccc caccgtccc ctgtcgaca ttctccctc cgcagggtg        | 180 |
| gtcaccagg cccagccca catgcctgct taaagccctc tccatcctct gcctcaccca    | 240 |
| gtccccgctg agactgagca gacgcctcca                                   | 270 |

<210> 35  
 <211> 260  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 35                                                           |     |
| tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct | 60  |
| gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat    | 120 |
| ccccctgccc caccgtccc ctgtcgaca ttctccctc cgcagggtg gtcaccagg       | 180 |
| cccagccca catgcctgct taaagccctc tccatcctct gcctcaccca gtccccgctg   | 240 |
| agactgagca gacgcctcca                                              | 260 |

<210> 36  
 <211> 250  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |    |
|--------------------------------------------------------------------|----|
| <400> 36                                                           |    |
| gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct gtagccttgt | 60 |



|                                                                  |     |
|------------------------------------------------------------------|-----|
| ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc   | 120 |
| caccgtccc ctgtgcaca ttctccctc cgcagggtg gtcaccagg cccagccca      | 180 |
| catgcctgct taaagccctc tccatcctct gcctcaccca gtcccgctg agactgagca | 240 |
| gacgcctcca                                                       | 250 |

<210> 37  
 <211> 240  
 <212> DNA  
 <213> Homo sapiens

|                                                                  |     |
|------------------------------------------------------------------|-----|
| <400> 37                                                         |     |
| aggaccacat gggcttatat ggcgtgggt acatgttct gtagccttgt ccctggcacc  | 60  |
| tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc    | 120 |
| ctgtgcaca ttctccctc cgcagggtg gtcaccagg cccagccca catgcctgct     | 180 |
| taaagccctc tccatcctct gcctcaccca gtcccgctg agactgagca gacgcctcca | 240 |

<210> 38  
 <211> 230  
 <212> DNA  
 <213> Homo sapiens

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| <400> 38                                                        |     |
| gggcttatat ggcgtgggt acatgttct gtagccttgt ccctggcacc tgccaaaata | 60  |
| gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc ctgtgcaca    | 120 |
| ttctccctc cgcagggtg gtcaccagg cccagccca catgcctgct taaagccctc   | 180 |
| tccatcctct gcctcaccca gtcccgctg agactgagca gacgcctcca           | 230 |

<210> 39  
 <211> 220  
 <212> DNA  
 <213> Homo sapiens

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| <400> 39                                                        |     |
| ggcgtgggt acatgttct gtagccttgt ccctggcacc tgccaaaata gcagccaaca | 60  |
| ccccaccc ccaccgcat cccctgccc caccgtccc ctgtgcaca ttctccctc      | 120 |

|                                                                  |     |
|------------------------------------------------------------------|-----|
| cgcagggctg gctcaccagg cccagccca catgcctgct taaagccctc tccatcctct | 180 |
| gcctcaccca gtccccgctg agactgagca gacgcctcca                      | 220 |

<210> 40  
 <211> 210  
 <212> DNA  
 <213> Homo sapiens

|                                                                  |     |
|------------------------------------------------------------------|-----|
| <400> 40                                                         |     |
| acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc | 60  |
| ccaccgcat cccctgccc caccgtccc ctgtgcaca ttctccctc cgcagggctg     | 120 |
| gctcaccagg cccagccca catgcctgct taaagccctc tccatcctct gcctcaccca | 180 |
| gtccccgctg agactgagca gacgcctcca                                 | 210 |

<210> 41  
 <211> 200  
 <212> DNA  
 <213> Homo sapiens

|                                                                  |     |
|------------------------------------------------------------------|-----|
| <400> 41                                                         |     |
| gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat  | 60  |
| ccccctgccc caccgtccc ctgtgcaca ttctccctc cgcagggctg gctcaccagg   | 120 |
| cccagccca catgcctgct taaagccctc tccatcctct gcctcaccca gtccccgctg | 180 |
| agactgagca gacgcctcca                                            | 200 |

<210> 42  
 <211> 550  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 42                                                           |     |
| gtcatggaga agaccacct tgcagatgtc ctactgggg ctggcagagc cggcaacctg    | 60  |
| cctaaggctg ctcatccat taggagccag tagcctggaa gatgtcttta ccccagcat    | 120 |
| cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc tgggtgctgag | 180 |
| acttatggag tgtcttggag gttgccttct gcccccaac cctgtccca gctggccctc    | 240 |
| ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat  | 300 |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gttgcatgac tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg | 360 |
| aggaccacat gggcttatat ggcgtggggg acatgttcct gtagccttgt ccctggcacc | 420 |
| tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc     | 480 |
| ctgtcgaca ttctccctc cgcagggtg gctcaccagg cccagccca catgcctgct     | 540 |
| taaagccctc                                                        | 550 |

<210> 43  
 <211> 540  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 43                                                           |     |
| agaccacct tgcagatgtc ctactgggg ctggcagagc cggcaacctg cctaaggctg    | 60  |
| ctcagtccat taggagccag tagcctggaa gatgtcttta ccccgagcat cagttcaagt  | 120 |
| ggagcagcac ataactcttg ccctctgcct tccaagattc tggctgctgag acttatggag | 180 |
| tgtcttggag gttgccttct gcccccaac cctgctcca gctggccctc ccaggcctgg    | 240 |
| gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat gttgcatgac  | 300 |
| tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat  | 360 |
| gggcttatat ggcgtggggg acatgttcct gtagccttgt ccctggcacc tgccaaaata  | 420 |
| gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc ctgtcgaca       | 480 |
| ttctccctc cgcagggtg gctcaccagg cccagccca catgcctgct taaagccctc     | 540 |

<210> 44  
 <211> 530  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 44                                                           |     |
| tgcagatgtc ctactgggg ctggcagagc cggcaacctg cctaaggctg ctcagtccat   | 60  |
| taggagccag tagcctggaa gatgtcttta ccccgagcat cagttcaagt ggagcagcac  | 120 |
| ataactcttg ccctctgcct tccaagattc tggctgctgag acttatggag tgtcttggag | 180 |
| gttgcttct gcccccaac cctgctcca gctggccctc ccaggcctgg gttgctggcc     | 240 |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tctgctttat caggattctc aagagggaca gctggtttat gttgcatgac tgttccctgc  | 300 |
| atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat  | 360 |
| ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca | 420 |
| ccccccaccc ccaccgccat cccctgccc caccgtccc ctgtcgaca ttcctccctc     | 480 |
| cgcagggtg gctcaccagg cccagccca catgcctgct taaagccctc               | 530 |

<210> 45  
 <211> 520  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 45                                                           |     |
| ctcactgggg ctggcagagc cggcaacctg cctaaggctg ctcagtccat taggagccag  | 60  |
| tagcctggaa gatgtcttta cccccagcat cagttcaagt ggagcagcac ataactcttg  | 120 |
| ccctctgcct tccaagattc tgggtctgag acttatggag tgtcttggag gttgccttct  | 180 |
| gcccccaac cctgctcca gctggccctc ccaggcctgg gttgctggcc tctgctttat    | 240 |
| caggattctc aagagggaca gctggtttat gttgcatgac tgttccctgc atatctgctc  | 300 |
| tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt | 360 |
| acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc   | 420 |
| ccaccgccat cccctgccc caccgtccc ctgtcgaca ttcctccctc cgcagggtg      | 480 |
| gctcaccagg cccagccca catgcctgct taaagccctc                         | 520 |

<210> 46  
 <211> 510  
 <212> DNA  
 <213> Homo sapiens

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 46                                                          |     |
| ctggcagagc cggcaacctg cctaaggctg ctcagtccat taggagccag tagcctggaa | 60  |
| gatgtcttta cccccagcat cagttcaagt ggagcagcac ataactcttg ccctctgcct | 120 |
| tccaagattc tgggtctgag acttatggag tgtcttggag gttgccttct gcccccaac  | 180 |
| cctgctcca gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc  | 240 |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aagagggaca gctggtttat gttgcatgac tgttccctgc atatctgctc tggttttaaa  | 300 |
| tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct | 360 |
| gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat    | 420 |
| ccccctgccc caccgtccc ctgtcgaca ttctccctc cgcagggtg gctcaccagg      | 480 |
| ccccagccca catgcctgct taaagccctc                                   | 510 |

<210> 47  
 <211> 500  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 47                                                           |     |
| cggcaacctg cctaaggctg ctgagtcctat taggagccag tagcctggaa gatgtcttta | 60  |
| ccccagcat cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc   | 120 |
| tggctgctgag acttatggag tgtcttggag gttgccttct gcccccaac cctgctcca   | 180 |
| gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca  | 240 |
| gctggtttat gttgcatgac tgttccctgc atatctgctc tggttttaaa tagcttatct  | 300 |
| gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct gtagccttgt | 360 |
| ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat cccccctgccc   | 420 |
| caccgtccc ctgtcgaca ttctccctc cgcagggtg gctcaccagg ccccagccca      | 480 |
| catgcctgct taaagccctc                                              | 500 |

<210> 48  
 <211> 490  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 48                                                           |     |
| cctaaggctg ctgagtcctat taggagccag tagcctggaa gatgtcttta cccccagcat | 60  |
| cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc tggctgctgag | 120 |
| acttatggag tgtcttggag gttgccttct gcccccaac cctgctcca gctggccctc    | 180 |
| ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat  | 240 |

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| gttgcacgac  | tggtccctgc | atatctgctc | tggttttaaa | tagcttatct | gagcagctgg | 300 |
| aggaccacat  | gggcttatat | ggcgtggggg | acatgttcct | gtagccttgt | ccctggcacc | 360 |
| tgccaaaata  | gcagccaaca | ccccccaccc | ccaccgccat | ccccctgccc | cacccgtccc | 420 |
| ctgtcgcaca  | ttcctccctc | cgcagggctg | gctcaccagg | ccccagccca | catgcctgct | 480 |
| ttaaagccctc |            |            |            |            |            | 490 |

<210> 49  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| ctcagtcacat | taggagccag  | tagcctggaa | gatgtcttta | ccccagcat  | cagttcaagt  | 60  |
| ggagcagcac  | ataactcttg  | ccctctgcct | tccaagattc | tggtgctgag | acttatggag  | 120 |
| tgtcttggag  | gttgcccttct | gccccccaac | cctgctccca | gctggccctc | ccaggcctgg  | 180 |
| gttgctggcc  | tctgctttat  | caggattctc | aagagggaca | gctggtttat | gttgcacgac  | 240 |
| tggtccctgc  | atatctgctc  | tggttttaaa | tagcttatct | gagcagctgg | aggaccacat  | 300 |
| gggcttatat  | ggcgtggggg  | acatgttcct | gtagccttgt | ccctggcacc | tgccaaaata  | 360 |
| gcagccaaca  | ccccccaccc  | ccaccgccat | ccccctgccc | cacccgtccc | ctgtcgcaca  | 420 |
| ttcctccctc  | cgcagggctg  | gctcaccagg | ccccagccca | catgcctgct | ttaaagccctc | 480 |

<210> 50  
 <211> 470  
 <212> DNA  
 <213> Homo sapiens

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| taggagccag  | tagcctggaa | gatgtcttta | ccccagcat  | cagttcaagt | ggagcagcac | 60  |
| ataactcttg  | ccctctgcct | tccaagattc | tggtgctgag | acttatggag | tgtcttggag | 120 |
| gttgcccttct | gccccccaac | cctgctccca | gctggccctc | ccaggcctgg | gttgctggcc | 180 |
| tctgctttat  | caggattctc | aagagggaca | gctggtttat | gttgcacgac | tggtccctgc | 240 |
| atatctgctc  | tggttttaaa | tagcttatct | gagcagctgg | aggaccacat | gggcttatat | 300 |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca | 360 |
| ccccccaccc ccaccgccat cccctgccc caccgtccc ctgtcgaca ttcctccctc     | 420 |
| cgcagggctg gtcaccagg cccagccca catgcctgct taaagccctc               | 470 |

<210> 51  
 <211> 460  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 51                                                           |     |
| tagcctggaa gatgtcttta ccccagcat cagttcaagt ggagcagcac ataactcttg   | 60  |
| ccctctgcct tccaagattc tggctgtag acttatggag tgtcttggag gttgccttct   | 120 |
| gcccccaac cctgctcca gctggccctc ccaggcctgg gttgctggcc tctgctttat    | 180 |
| caggattctc aagagggaca gctggtttat gttgcatgac tgttccctgc atatctgctc  | 240 |
| tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt | 300 |
| acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc   | 360 |
| ccaccgccat cccctgccc caccgtccc ctgtcgaca ttcctccctc cgcagggctg     | 420 |
| gtcaccagg cccagccca catgcctgct taaagccctc                          | 460 |

<210> 52  
 <211> 450  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 52                                                           |     |
| gatgtcttta ccccagcat cagttcaagt ggagcagcac ataactcttg ccctctgcct   | 60  |
| tccaagattc tggctgtag acttatggag tgtcttggag gttgccttct gcccccaac    | 120 |
| cctgctcca gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc   | 180 |
| aagagggaca gctggtttat gttgcatgac tgttccctgc atatctgctc tggttttaaa  | 240 |
| tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct | 300 |
| gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgccat   | 360 |
| ccctgccc caccgtccc ctgtcgaca ttcctccctc cgcagggctg gtcaccagg       | 420 |

ccccagccca catgcctgct taaagccctc 450

<210> 53  
<211> 440  
<212> DNA  
<213> Homo sapiens

<400> 53  
ccccagcat cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc 60  
tggtgctgag acttatggag tgtcttggag gttgccttct gcccccaac cctgctccca 120  
gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca 180  
gctggtttat gttgcatgac tggtccctgc atatctgctc tggttttaaa tagcttatct 240  
gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct gtagccttgt 300  
ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc 360  
caccgtccc ctgtcgaca ttcctccctc cgcagggtg gtcaccagg cccagccca 420  
catgcctgct taaagccctc 440

<210> 54  
<211> 430  
<212> DNA  
<213> Homo sapiens

<400> 54  
cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc tggtgctgag 60  
acttatggag tgtcttggag gttgccttct gcccccaac cctgctccca gctggccctc 120  
ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat 180  
gttgcattgac tggtccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg 240  
aggaccacat gggcttatat ggcgtgggggt acatgttcct gtagccttgt ccctggcacc 300  
tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc 360  
ctgtcgaca ttcctccctc cgcagggtg gtcaccagg cccagccca catgcctgct 420  
taaagccctc 430



<210> 55  
<211> 420  
<212> DNA  
<213> Homo sapiens

<400> 55  
ggagcagcac ataactcttg ccctctgcct tccaagattc tggctgctgag acttatggag 60  
tgtcttggag gttgccttct gcccccaac cctgctcca gctggccctc ccaggcctgg 120  
gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat gttgcatgac 180  
tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat 240  
gggcttatat ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata 300  
gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc ctgtcgaca 360  
ttcctccctc cgcagggtg gtcaccagg cccagccca catgcctgct taaagccctc 420

<210> 56  
<211> 410  
<212> DNA  
<213> Homo sapiens

<400> 56  
ataactcttg ccctctgcct tccaagattc tggctgctgag acttatggag tgtcttggag 60  
gttgccttct gcccccaac cctgctcca gctggccctc ccaggcctgg gttgctggcc 120  
tctgctttat caggattctc aagagggaca gctggtttat gttgcatgac tgttccctgc 180  
atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat 240  
ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca 300  
ccccccaccc ccaccgcat cccctgccc caccgtccc ctgtcgaca ttcctccctc 360  
cgcagggtg gtcaccagg cccagccca catgcctgct taaagccctc 410

<210> 57  
<211> 400  
<212> DNA  
<213> Homo sapiens

<400> 57  
ccctctgcct tccaagattc tggctgctgag acttatggag tgtcttggag gttgccttct 60

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gccccccaac cctgctccca gctggccctc ccaggcctgg gttgctggcc tctgctttat  | 120 |
| caggattctc aagagggaca gctggtttat gttgcatgac tgttccctgc atatctgctc  | 180 |
| tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt | 240 |
| acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc   | 300 |
| ccaccgcat cccctgccc caccgtccc ctgtcgaca ttctccctc cgcagggtg        | 360 |
| gctcaccagg cccagccca catgcctgct taaagccctc                         | 400 |

<210> 58  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 58                                                           |     |
| tccaagattc tgggtgctgag acttatggag tgtcttggag gttgccttct gcccccaac  | 60  |
| cctgctccca gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc  | 120 |
| aagagggaca gctggtttat gttgcatgac tgttccctgc atatctgctc tggttttaaa  | 180 |
| tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct | 240 |
| gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat    | 300 |
| ccccctgccc caccgtccc ctgtcgaca ttctccctc cgcagggtg gctcaccagg      | 360 |
| ccccagccca catgcctgct taaagccctc                                   | 390 |

<210> 59  
 <211> 380  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 59                                                           |     |
| tgggtgctgag acttatggag tgtcttggag gttgccttct gcccccaac cctgctccca  | 60  |
| gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca  | 120 |
| gctggtttat gttgcatgac tgttccctgc atatctgctc tggttttaaa tagcttatct  | 180 |
| gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct gtagccttgt | 240 |
| ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc     | 300 |

|                                                                |     |
|----------------------------------------------------------------|-----|
| cacccgtccc ctgtcgaca ttcctccctc cgcagggtg gctcaccagg cccagccca | 360 |
| catgcctgct taaagccctc                                          | 380 |

<210> 60  
 <211> 370  
 <212> DNA  
 <213> Homo sapiens

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 60                                                          |     |
| acttatggag tgtcttggag gttgccttct gcccccaac cctgctcca gctggccctc   | 60  |
| ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat | 120 |
| gttgcacgac tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg | 180 |
| aggaccacat gggcttatat ggcgtggggc acatgttcct gtagccttgt ccctggcacc | 240 |
| tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc     | 300 |
| ctgtcgaca ttcctccctc cgcagggtg gctcaccagg cccagccca catgcctgct    | 360 |
| taaagccctc                                                        | 370 |

<210> 61  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 61                                                          |     |
| tgtcttggag gttgccttct gcccccaac cctgctcca gctggccctc ccaggcctgg   | 60  |
| gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat gttgcacgac | 120 |
| tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat | 180 |
| gggcttatat ggcgtggggc acatgttcct gtagccttgt ccctggcacc tgccaaaata | 240 |
| gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc ctgtcgaca      | 300 |
| ttcctccctc cgcagggtg gctcaccagg cccagccca catgcctgct taaagccctc   | 360 |

<210> 62  
 <211> 350  
 <212> DNA  
 <213> Homo sapiens

<400> 62  
gttgcttctt gccccccaac cctgctccca gctggccctc ccaggcctgg gttgctggcc 60  
tctgctttat caggattctc aagagggaca gctggtttat gttgcatgac tgttccctgc 120  
atatctgctc tggtttttaa tagcttatct gagcagctgg aggaccacat gggcttatat 180  
ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca 240  
ccccccaccc ccaccgcat cccctgccc caccgtccc ctgtcgaca ttcctccctc 300  
cgcagggtg gctcaccagg cccagccca catgcctgct taaagccctc 350

<210> 63  
<211> 340  
<212> DNA  
<213> Homo sapiens

<400> 63  
gccccccaac cctgctccca gctggccctc ccaggcctgg gttgctggcc tctgctttat 60  
caggattctc aagagggaca gctggtttat gttgcatgac tgttccctgc atatctgctc 120  
tggtttttaa tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt 180  
acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc 240  
ccaccgcat cccctgccc caccgtccc ctgtcgaca ttcctccctc cgcagggtg 300  
gctcaccagg cccagccca catgcctgct taaagccctc 340

<210> 64  
<211> 330  
<212> DNA  
<213> Homo sapiens

<400> 64  
cctgctccca gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc 60  
aagagggaca gctggtttat gttgcatgac tgttccctgc atatctgctc tggtttttaa 120  
tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct 180  
gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat 240  
ccccctgccc caccgtccc ctgtcgaca ttcctccctc cgcagggtg gctcaccagg 300  
cccagccca catgcctgct taaagccctc 330

<210> 65  
<211> 320  
<212> DNA  
<213> Homo sapiens

<400> 65  
gctggccctc ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca 60  
gctggtttat gttgcatgac tgttccctgc atatctgctc tggttttaaa tagcttatct 120  
gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct gtagccttgt 180  
ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc 240  
caccgtccc ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagccca 300  
catgcctgct taaagccctc 320

<210> 66  
<211> 310  
<212> DNA  
<213> Homo sapiens

<400> 66  
ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat 60  
gttgcacatgac tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg 120  
aggaccacat gggcttatat ggcgtgggggt acatgttcct gtagccttgt ccctggcacc 180  
tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc 240  
ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagccca catgcctgct 300  
taaagccctc 310

<210> 67  
<211> 300  
<212> DNA  
<213> Homo sapiens

<400> 67  
gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat gttgcatgac 60  
tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat 120

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gggcttatat ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata | 180 |
| gcagccaaca cccccacccc ccaccgcat cccctgccc caccgtccc ctgtcgaca      | 240 |
| ttcctccctc cgcagggtg gctcaccagg cccagccca catgcctgct taaagccctc    | 300 |

<210> 68  
 <211> 290  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 68                                                           |     |
| tctgctttat caggattctc aagagggaca gctggtttat gttgcatgac tgttccctgc  | 60  |
| atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat  | 120 |
| ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca | 180 |
| ccccccacccc ccaccgcat cccctgccc caccgtccc ctgtcgaca ttcctccctc     | 240 |
| cgcagggtg gctcaccagg cccagccca catgcctgct taaagccctc               | 290 |

<210> 69  
 <211> 280  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 69                                                           |     |
| caggattctc aagagggaca gctggtttat gttgcatgac tgttccctgc atatctgctc  | 60  |
| tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt | 120 |
| acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccacccc  | 180 |
| ccaccgcat cccctgccc caccgtccc ctgtcgaca ttcctccctc cgcagggtg       | 240 |
| gctcaccagg cccagccca catgcctgct taaagccctc                         | 280 |

<210> 70  
 <211> 270  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 70                                                           |     |
| aagagggaca gctggtttat gttgcatgac tgttccctgc atatctgctc tggttttaaa  | 60  |
| tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct | 120 |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat | 180 |
| ccccctgccc caccgtccc ctgtcgaca ttctccctc cgcagggtg gtcaccagg    | 240 |
| ccccagcca catgcctgct taaagccctc                                 | 270 |

<210> 71  
 <211> 260  
 <212> DNA  
 <213> Homo sapiens

|                                                                  |     |
|------------------------------------------------------------------|-----|
| <400> 71                                                         |     |
| gctggttat gttgcatgac tttccctgc atatctgctc tggttttaa tagcttatct   | 60  |
| gagcagctgg aggaccacat gggcttatat ggcgtgggt acatgttcct gtagccttgt | 120 |
| ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat cccccctgccc | 180 |
| caccgtccc ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagcca       | 240 |
| catgcctgct taaagccctc                                            | 260 |

<210> 72  
 <211> 250  
 <212> DNA  
 <213> Homo sapiens

|                                                                  |     |
|------------------------------------------------------------------|-----|
| <400> 72                                                         |     |
| gttgcacgac tttccctgc atatctgctc tggttttaa tagcttatct gagcagctgg  | 60  |
| aggaccacat gggcttatat ggcgtgggt acatgttcct gtagccttgt ccctggcacc | 120 |
| tgccaaaata gcagccaaca cccccaccc ccaccgcat cccccctgccc caccgtccc  | 180 |
| ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagcca catgcctgct      | 240 |
| taaagccctc                                                       | 250 |

<210> 73  
 <211> 240  
 <212> DNA  
 <213> Homo sapiens

|                                                                  |    |
|------------------------------------------------------------------|----|
| <400> 73                                                         |    |
| gtttccctgc atatctgctc tggttttaa tagcttatct gagcagctgg aggaccacat | 60 |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gggcttatat ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata | 120 |
| gcagccaaca cccccacccc ccaccgccat cccctgccc caccgtccc ctgtcgaca     | 180 |
| ttcctccctc cgcagggtg gctcaccagg cccagccca catgcctgct taaagccctc    | 240 |

<210> 74  
 <211> 230  
 <212> DNA  
 <213> Homo sapiens

|                                                                               |     |
|-------------------------------------------------------------------------------|-----|
| <400> 74<br>atatctgctc tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat | 60  |
| ggcgtgggggt acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca            | 120 |
| ccccccacccc ccaccgccat cccctgccc caccgtccc ctgtcgaca ttcctccctc               | 180 |
| cgcagggtg gctcaccagg cccagccca catgcctgct taaagccctc                          | 230 |

<210> 75  
 <211> 220  
 <212> DNA  
 <213> Homo sapiens

|                                                                                |     |
|--------------------------------------------------------------------------------|-----|
| <400> 75<br>tggttttaaa tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt | 60  |
| acatgttcct gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccacccc              | 120 |
| ccaccgccat cccctgccc caccgtccc ctgtcgaca ttcctccctc cgcagggtg                  | 180 |
| gctcaccagg cccagccca catgcctgct taaagccctc                                     | 220 |

<210> 76  
 <211> 210  
 <212> DNA  
 <213> Homo sapiens

|                                                                                |     |
|--------------------------------------------------------------------------------|-----|
| <400> 76<br>tagcttatct gagcagctgg aggaccacat gggcttatat ggcgtgggggt acatgttcct | 60  |
| gtagccttgt ccctggcacc tgccaaaata gcagccaaca cccccacccc ccaccgccat              | 120 |
| ccccctgccc caccgtccc ctgtcgaca ttcctccctc cgcagggtg gctcaccagg                 | 180 |
| ccccagccca catgcctgct taaagccctc                                               | 210 |



<210> 77  
<211> 200  
<212> DNA  
<213> Homo sapiens

<400> 77  
gagcagctgg aggaccacat gggcttatat ggcgtggggg acatgttcct gtagccttgt 60  
ccctggcacc tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc 120  
caccgtccc ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagccca 180  
catgcctgct taaagccctc 200

<210> 78  
<211> 550  
<212> DNA  
<213> Homo sapiens

<400> 78  
gtcatggaga agaccacat tgcagatgtc ctactgggg ctggcagagc cggcaacctg 60  
cctaaggctg ctcatccat taggagccag tagcctggaa gatgtcttta ccccagcat 120  
cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc tggctgtgag 180  
acttatggag tgtcttggag gttgccttct gcccccaac cctgctcca gctggccctc 240  
ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat 300  
gttgcattgac tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg 360  
aggaccacat gggcttatat ggcgtggggg acatgttcct gtagccttgt ccctggcacc 420  
tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc 480  
ctgtcgaca ttctccctc cgcagggtg gtcaccagg cccagccca catgcctgct 540  
taaagccctc 550

<210> 79  
<211> 500  
<212> DNA  
<213> Homo sapiens

<400> 79

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gtcatggaga agacccacct tgcagatgtc ctactgggg ctggcagagc cggcaacctg   | 60  |
| cctaaggctg ctcagtccat taggagccag tagcctggaa gatgtcttta cccccagcat  | 120 |
| cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc tggtgctgag  | 180 |
| acttatggag tgtcttggag gttgccttct gcccccaac cctgctcca gctggccctc    | 240 |
| ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat  | 300 |
| gttgcattgac tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg | 360 |
| aggaccacat gggcttatat ggcgtgggg acatgttcct gtagccttgt ccctggcacc   | 420 |
| tgccaaaata gcagccaaca cccccaccc ccaccgcat cccctgccc caccgtccc      | 480 |
| ctgtcgaca ttcctccctc                                               | 500 |

<210> 80  
 <211> 450  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 80                                                           |     |
| gtcatggaga agacccacct tgcagatgtc ctactgggg ctggcagagc cggcaacctg   | 60  |
| cctaaggctg ctcagtccat taggagccag tagcctggaa gatgtcttta cccccagcat  | 120 |
| cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc tggtgctgag  | 180 |
| acttatggag tgtcttggag gttgccttct gcccccaac cctgctcca gctggccctc    | 240 |
| ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat  | 300 |
| gttgcattgac tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg | 360 |
| aggaccacat gggcttatat ggcgtgggg acatgttcct gtagccttgt ccctggcacc   | 420 |
| tgccaaaata gcagccaaca cccccaccc                                    | 450 |

<210> 81  
 <211> 400  
 <212> DNA  
 <213> Homo sapiens

|                                                                  |    |
|------------------------------------------------------------------|----|
| <400> 81                                                         |    |
| gtcatggaga agacccacct tgcagatgtc ctactgggg ctggcagagc cggcaacctg | 60 |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cctaaggctg ctcagtccat taggagccag tagcctggaa gatgtcttta cccccagcat  | 120 |
| cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc tggctgctgag | 180 |
| acttatggag tgtcttggag gttgccttct gccccccaac cctgctccca gctggccctc  | 240 |
| ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat  | 300 |
| gttgcattgac tgttccctgc atatctgctc tggttttaaa tagcttatct gagcagctgg | 360 |
| aggaccacat gggcttatat ggcgtggggg acatgttcct                        | 400 |

<210> 82  
 <211> 350  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 82                                                           |     |
| gtcatggaga agaccacct tgcagatgtc ctactgggg ctggcagagc cggcaacctg    | 60  |
| cctaaggctg ctcagtccat taggagccag tagcctggaa gatgtcttta cccccagcat  | 120 |
| cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc tggctgctgag | 180 |
| acttatggag tgtcttggag gttgccttct gccccccaac cctgctccca gctggccctc  | 240 |
| ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat  | 300 |
| gttgcattgac tgttccctgc atatctgctc tggttttaaa tagcttatct            | 350 |

<210> 83  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 83                                                           |     |
| gtcatggaga agaccacct tgcagatgtc ctactgggg ctggcagagc cggcaacctg    | 60  |
| cctaaggctg ctcagtccat taggagccag tagcctggaa gatgtcttta cccccagcat  | 120 |
| cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc tggctgctgag | 180 |
| acttatggag tgtcttggag gttgccttct gccccccaac cctgctccca gctggccctc  | 240 |
| ccaggcctgg gttgctggcc tctgctttat caggattctc aagagggaca gctggtttat  | 300 |

<210> 84

<211> 250  
<212> DNA  
<213> Homo sapiens

<400> 84  
gtcatggaga agacccacct tgcagatgtc ctactgggg ctggcagagc cggcaacctg 60  
cctaaggctg ctcagtccat taggagccag tagcctggaa gatgtcttta cccccagcat 120  
cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc tggtgctgag 180  
acttatggag tgtcttggag gttgccttct gccccccaac cctgctccca gctggccctc 240  
ccaggcctgg 250

<210> 85  
<211> 200  
<212> DNA  
<213> Homo sapiens

<400> 85  
gtcatggaga agacccacct tgcagatgtc ctactgggg ctggcagagc cggcaacctg 60  
cctaaggctg ctcagtccat taggagccag tagcctggaa gatgtcttta cccccagcat 120  
cagttcaagt ggagcagcac ataactcttg ccctctgcct tccaagattc tggtgctgag 180  
acttatggag tgtcttggag 200

<210> 86  
<211> 3825  
<212> DNA  
<213> Homo sapiens

<400> 86  
atgcctgagc cggggaagaa gccagtctca gcttttagca agaagccacg gtcagtggaa 60  
gtggccgcag gcagccctgc cgtgttcgag gccgagacag agcgggcagg agtgaagggtg 120  
cgctggcagc gcggaggcag tgacatcagc gccagcaaca agtacggcct ggccacagag 180  
ggcacacggc atacgtgac agtgcgggaa gtgggccctg ccgaccaggg atcttacgca 240  
gtcattgctg gtcctccaa ggtcaagttc gacctcaagg tcatagaggc agagaaggca 300  
gagcccatgc tggcccctgc ccctgcccct gctgaggcca ctggagcccc tggagaagcc 360  
ccggccccag ccgctgagct gggagaaagt gcccgaagtc ccaaagggtc aagctcagca 420

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gctctcaatg gtcctacccc tggagcccc gatgaccca ttggcctctt cgtgatgcgg    | 480  |
| ccacaggatg gcgaggtgac cgtgggtggc agcatcacct tctcagcccg cgtggccggc  | 540  |
| gccagcctcc tgaagccgcc tgtggtcaag tggttcaagg gcaaatgggt ggacctgagc  | 600  |
| agcaagggtg gccagcacct gcagctgcac gacagctacg accgcgccag caaggcttat  | 660  |
| ctgttcgagc tgcacatcac cgatgcccg cctgccttca ctggcagcta ccgctgtgag   | 720  |
| gtgtccacca aggacaaatt tgactgctcc aacttcaatc tcaactgtcca cgaggccatg | 780  |
| ggcaccggag acctggacct cctatcagcc ttccgccga cgagcctggc tggagggtgt   | 840  |
| cggcggatca gtgatagcca tgaggacact gggattcttg acttcagctc actgctgaaa  | 900  |
| aagagagaca gtttccggac cccgagggac tcgaagctgg aggcaccagc agaggaggac  | 960  |
| gtgtgggaga tcctacggca ggcaccccca tctgagtacg agcgcacgc cttccagtac   | 1020 |
| ggcgtcactg acctgcgcgg catgctaaag aggctcaagg gcatgaggcg cgatgagaag  | 1080 |
| aagagcacag cttttcagaa gaagctggag ccggcctacc aggtgagcaa aggccacaag  | 1140 |
| atccggctga ccgtggaact ggctgaccat gacgctgagg tcaaatggct caagaatggc  | 1200 |
| caggagatcc agatgagcgg cagcaagtac atctttgagt ccatcggtgc caagcgtaac  | 1260 |
| ctgaccatca gccagtgtc attggcggac gacgcagcct accagtgcgt ggtgggtggc   | 1320 |
| gagaagtgtg gcacggagct ctttgtgaaa gagccccctg tgctcatcac gcgccccttg  | 1380 |
| gaggaccagc tggatgatgtt ggggcagcgg gtggagtttg agtgtgaagt atcggaggag | 1440 |
| ggggcgcaag tcaaatggct gaaggacggg gtggagctga cccgggagga gaccttcaaa  | 1500 |
| taccggttca agaaggacgg gcagagacac cacctgatca tcaacgaggc catgctggag  | 1560 |
| gacgcggggc actatgcact gtgcactagc gggggccagg cgctggctga gctcattgtg  | 1620 |
| caggaaaaga agctggaggt gtaccagagc atcgagacc tgatggtggg cgcaaaggac   | 1680 |
| caggcgggtg tcaaatgtga ggtctcagat gagaatgttc ggggtgtgtg gctgaagaat  | 1740 |
| gggaaggagc tgggtccccg cagccgcata aagggtgtcc acatcgggcg ggtccacaaa  | 1800 |
| ctgaccattg acgacgtcac acctgccgac gaggctgact acagctttgt gcccgagggc  | 1860 |
| ttgcctgca acctgtcagc caagctccac ttcatggagg tcaagattga cttcgtaccc   | 1920 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| aggcaggaac ctcccaagat ccacctggac tgcccaggcc gcataccaga caccattgtg  | 1980 |
| gttgtagctg gaaataagct acgtctggac gtccctatct ctggggaccc cgctcccact  | 2040 |
| gtgatctggc agaaggctat cacgcagggg aataaggccc cagccaggcc agccccagat  | 2100 |
| gccccagagg acacagggtga cagcgatgag tgggtgtttg acaagaagct gctgtgtgag | 2160 |
| accgagggcc ggggtccgct ggagaccacc aaggaccgca gcatcttcac ggtcgagggg  | 2220 |
| gcagagaagg aagatgaggg cgtctacacg gtcacagtga agaaccctgt gggcgaggac  | 2280 |
| cagggtcaacc tcacagtcaa ggtcatcgac gtgccagacg cacctgcggc cccaagatc  | 2340 |
| agcaacgtgg gagaggactc ctgcacagta cagtgggagc cgcctgccta cgatggcggg  | 2400 |
| cagccccatcc tgggctacat cctggagcgc aagaagaaga agagctaccg gtggatgcgg | 2460 |
| ctgaacttcg acctgattca ggagctgagt catgaagcgc ggcgcatgat cgagggcgtg  | 2520 |
| gtgtacgaga tgcgcgtcta cgcggtcaac gccatcggca tgtccaggcc cagccctgcc  | 2580 |
| tcccagccct tcatgcctat cgggtcccccc agcgaacca cccacctggc agtagaggac  | 2640 |
| gtctctgaca ccacggtctc cctcaagtgg cggccccccag agcgcgtggg agcaggaggc | 2700 |
| ctggatggct acagcgtgga gtactgcccag gagggtgct cagagtgggt ggctgccctg  | 2760 |
| caggggctga cagagcacac atcgatactg gtgaaggacc tgcccacggg ggcccggctg  | 2820 |
| cttttccgag tgcgggcaca caatatggca gggcctggag cccctgttac caccacggag  | 2880 |
| ccggtgacag tgcaggagat cctgcaacgg ccacggcttc agctgcccag gcacctgcgc  | 2940 |
| cagaccattc agaagaaggt cggggagcct gtgaaccttc tcatcccttt ccagggaag   | 3000 |
| ccccggcctc aggtgacctg gaccaaagag gggcagcccc tggcaggcga ggaggtgagc  | 3060 |
| atccgcaaca gccccacaga caccatcctg ttcacccggg ccgctcgccg cgtgcattca  | 3120 |
| ggcacttacc aggtgacggg gcgcattgag aacatggagg acaaggccac gctgggtgctg | 3180 |
| caggttggtg acaagccaag tcctccccag gatctccggg tgactgacgc ctggggcttt  | 3240 |
| aatgtggctc tggagtggaa gccaccccag gatgtcggca acacggaact ctgggggtac  | 3300 |
| acagtgcaga aagccgacaa gaagaccatg gagtgggttca ccgtcttgga gcattaccgc | 3360 |
| cgcacccact gcgtggtgcc agagctcatc attggcaatg gctactactt ccgcgtcttc  | 3420 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| agccagaata tggttggctt tagtgacaga gcggccacca ccaaggagcc cgtctttatc | 3480 |
| cccagaccag gcatcaccta tgagccaccc aactataagg ccctggactt ctccgaggcc | 3540 |
| ccaagcttca cccagcccct ggtgaaccgc tcggtcatcg cgggctacac tgctatgctc | 3600 |
| tgctgtgctg tccggggtag cccaagccc aagatttcct ggttcaagaa tggcctggac  | 3660 |
| ctgggagaag acgcccgtt ccgcatgttc agcaagcagg gagtggtgac tctggagatt  | 3720 |
| agaaagccct gcccctttga cgggggcatc tatgtctgca gggccaccaa cttacagggc | 3780 |
| gaggcacggt gtgagtgccg cctggagggtg cgagtgcctc agtaa                | 3825 |

<210> 87  
 <211> 3546  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 87                                                           |     |
| atgcctgagc cggggaagaa gccagtctca gcttttagca agaagccacg gtcagtggaa  | 60  |
| gtggccgcag gcagccctgc cgtgttcgag gccgagacag agcgggcagg agtgaagggtg | 120 |
| cgctggcagc gcggaggcag tgacatcagc gccagcaaca agtacggcct ggccacagag  | 180 |
| ggcacacggc atacgtgac agtgcgggaa gtgggccctg ccgaccaggg atcttacgca   | 240 |
| gtcattgctg gtcctccaa ggtcaagttc gacctcaagg tcatagaggc agagaaggca   | 300 |
| gagcccatgc tggcccctgc ccctgcccct gctgaggcca ctggagcccc tggagaagcc  | 360 |
| ccggccccag ccgctgagct gggagaaagt gcccgaagtc ccaaagggtc aagctcagca  | 420 |
| gctctcaatg gtcctacccc tggagcccc gatgaccca ttggcctctt cgtgatgcgg    | 480 |
| ccacaggatg gcgagggtgac cgtgggtggc agcatcacct tctcagcccc cgtggccggc | 540 |
| gccagcctcc tgaagccgcc tgttgtcaag tggttcaagg gcaaatgggt ggacctgagc  | 600 |
| agcaagggtg gccagcacct gcagctgcac gacagctacg accgcgccag caaggtctat  | 660 |
| ctgttcgagc tgcacatcac cgatgcccag cctgccttca ctggcagcta ccgctgtgag  | 720 |
| gtgtccacca aggacaaaatt tgactgtcc aacttcaatc tcaactgtcca cgaggccatg | 780 |
| ggcaccggag acctggacct cctatcagcc ttccgccgca cgagcctggc tggagggtggt | 840 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cggcggatca gtgatagcca tgaggacact gggattctgg acttcagctc actgctgaaa  | 900  |
| aagagagaca gtttccggac cccgagggac tcgaagctgg aggaccagc agaggaggac   | 960  |
| gtgtgggaga tcctacggca ggcacccccca tctgagtacg agcgcacgc cttccagtac  | 1020 |
| ggcgtcactg acctgcgcgg catgctaaag aggctcaagg gcatgaggcg cgatgagaag  | 1080 |
| aagagcacag cttttcagaa gaagctggag ccggcctacc aggtgagcaa aggccacaag  | 1140 |
| atccggctga ccgtggaact ggctgaccat gacgctgagg tcaaatggct caagaatggc  | 1200 |
| caggagatcc agatgagcgg cagcaagtac atctttgagt ccatcggcgc caagcgtacc  | 1260 |
| ctgaccatca gccagtgtc attggcggac gacgcagcct accagtgcgt ggtgggtggc   | 1320 |
| gagaagtgtg gcacggagct ctttgtgaaa gagccccctg tgtaccagag catcgcagac  | 1380 |
| ctgatgggtg gcgcaaagga ccaggcgggtg ttcaaatgtg aggtctcaga tgagaatgtt | 1440 |
| cgggggtgtg ggctgaagaa tgggaaggag ctgggtgccc acagccgcgc aaaggtgtcc  | 1500 |
| cacatcgggc ggggtccacaa actgaccatt gacgacgtca cacctgccga cgaggctgac | 1560 |
| tacagctttg tgcccagagg cttcgcctgc aacctgtcag ccaagctcca cttcatggag  | 1620 |
| gtcaagattg acttcgtacc caggcaggaa cctcccaaga tccacctgga ctgcccaggc  | 1680 |
| cgcataccag acaccattgt ggttgtagct ggaaataagc tacgtctgga cgtccctatc  | 1740 |
| tctggggacc ccgctcccac tgtgatctgg cagaaggcta tcacgcaggg gaataaggcc  | 1800 |
| ccagccaggc cagccccaga tgccccagag gacacagggt acagcgatga gtgggtgttt  | 1860 |
| gacaagaagc tgctgtgtga gaccgagggc cgggtccgcg tggagaccac caaggaccgc  | 1920 |
| agcatcttca cggtcgaggg ggcagagaag gaagatgagg gcgtctacac ggtcacagtg  | 1980 |
| aagaaccctg tgggcgagga ccaggctaac ctcacagtca aggtcatcga cgtgccagac  | 2040 |
| gcacctgcgg cccccaagat cagcaacgtg ggagaggact cctgcacagt acagtgggag  | 2100 |
| ccgcctgcct acgatggcgg gcagcccatc ctgggctaca tcctggagcg caagaagaag  | 2160 |
| aagagctacc ggtggatgcg gctgaacttc gacctgattc aggagctgag tcatgaagcg  | 2220 |
| cggcgcacga tcgagggcgt ggtgtacgag atgcgcgtct acgcgggtcaa cgccatcggc | 2280 |
| atgtccaggc ccagccctgc ctcccagccc ttcatgccta tcgggtcccc cagcgaaccc  | 2340 |



|                                                                     |      |
|---------------------------------------------------------------------|------|
| accacactgg cagtagagga cgtctctgac accacgggtct ccctcaagtg gcggccccc   | 2400 |
| gagcgcgtgg gagcaggagg cctggatggc tacagcgtgg agtactgccc agagggctgc   | 2460 |
| tcagagtggg tggctgccct gcaggggctg acagagcaca catcgatact ggtgaaggac   | 2520 |
| ctgcccacgg gggcccggct gcttttccga gtgcgggcac acaatatggc agggcctgga   | 2580 |
| gcccctgtta ccaccacgga gccggtgaca gtgcaggaga tcctgcaacg gccacggctt   | 2640 |
| cagctgcccc ggcacctgcg ccagaccatt cagaagaagg tcggggagcc tgtgaacctt   | 2700 |
| ctcatccctt tccaggga caa gccccggcct caggtgacct ggaccaaaga ggggcagccc | 2760 |
| ctggcaggcg aggaggtgag catccgcaac agccccacag acaccatcct gttcatccgg   | 2820 |
| gccgctcgcc gcgtgcattc aggcacttac caggtgacgg tgcgcattga gaacatggag   | 2880 |
| gacaaggcca cgctgggtgct gcaggttggt gacaagccaa gtcctcccca ggatctccgg  | 2940 |
| gtgactgacg cctgggggtct taatgtggct ctggagtgga agccaccca ggatgtcggc   | 3000 |
| aacacggaac tctgggggta cacagtgcag aaagccgaca agaagaccat ggagtgggtc   | 3060 |
| accgtcttgg agcattaccg ccgcacccac tgcgtgggtgc cagagctcat cattggcaat  | 3120 |
| ggctactact tccgcgtctt cagccagaat atggttggct ttagtgacag agcggccacc   | 3180 |
| accaaggagc ccgtctttat cccagacca ggcatcacct atgagccacc caactataag    | 3240 |
| gccctggact tctccgaggc cccaagcttc acccagcccc tggatgaaccg ctcggtcac   | 3300 |
| gcgggctaca ctgctatgct ctgctgtgct gtccggggta gcccgaagcc caagatttcc   | 3360 |
| tggttcaaga atggcctgga cctgggagaa gacgcccgt tccgcatgtt cagcaagcag    | 3420 |
| ggagtgttga ctctggagat tagaaagccc tgcccctttg acgggggcat ctatgtctgc   | 3480 |
| agggccacca acttacaggg cgaggcacgg tgtgagtgcc gcctggagggt gcgagtgcct  | 3540 |
| cagtaa                                                              | 3546 |

<210> 88  
 <211> 3534  
 <212> DNA  
 <213> Homo sapiens

|                                                                   |    |
|-------------------------------------------------------------------|----|
| <400> 88                                                          |    |
| atgcctgagc cggggaagaa gccagtctca gcttttagca agaagccacg gtcagtggaa | 60 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gtggccgcag gcagccctgc cgtgttcgag gccgagacag agcgggcagg agtgaagggtg | 120  |
| cgctggcagc gcggaggcag tgacatcagc gccagcaaca agtacggcct ggccacagag  | 180  |
| ggcacacggc atacgctgac agtgcgggaa gtgggcccctg ccgaccaggg atcttacgca | 240  |
| gtcattgctg gtcctccaa ggtcaagttc gacctcaagg tcatagaggc agagaaggca   | 300  |
| gagcccatgc tggcccctgc ccctgcccct gctgaggcca ctggagcccc tggagaagcc  | 360  |
| ccggccccag ccgctgagct gggagaaaagt gcccgaagtc ccaaagggtc aagctcagca | 420  |
| gctctcaatg gtcctacccc tggagcccc gatgaccca ttggcctctt cgtgatgcgg    | 480  |
| ccacaggatg gcgagggtgac cgtgggtggc agcatcacct tctcagcccc cgtggccggc | 540  |
| gccagcctcc tgaagccgcc tgtgttcaag tggttcaagg gcaaatgggt ggacctgagc  | 600  |
| agcaagggtg gccagcacct gcagctgcac gacagctacg accgcgccag caaggcttat  | 660  |
| ctgttcgagc tgcacatcac cgatgccag cctgccttca ctggcagcta ccgctgtgag   | 720  |
| gtgtccacca aggacaaatt tgactgctcc aacttcaatc tcaactgtcca cgaggccatg | 780  |
| ggcaccggag acctggacct cctatcagcc ttccgccga cgagcctggc tggagggtgt   | 840  |
| cggcggatca gtgatagcca tgaggacact gggattctgg acttcagctc actgctgaaa  | 900  |
| aagagagaca gtttccggac cccgagggaac tcgaagctgg aggcaccagc agaggaggac | 960  |
| gtgtgggaga tcctacggca ggcccccca tctgagtacg agcgcacgc cttccagtac    | 1020 |
| ggcgtcactg acctgcgcgg catgctaaag aggctcaagg gcatgaggcg cgatgagaag  | 1080 |
| aagagcacag cttttcagaa gaagctggag ccggcctacc aggtgagcaa aggccacaag  | 1140 |
| atccggctga ccgtggaact ggctgaccat gacgctgagg tcaaatggct caagaatggc  | 1200 |
| caggagatcc agatgagcgg cagcaagtac atctttgagt ccatcgggtgc caagcgtacc | 1260 |
| ctgaccatca gccagtgtc attggcggac gacgcagcct accagtgcgt ggtgggtggc   | 1320 |
| gagaagtgtg gcacggagct ctttgtgaaa gagccccctg tgctcatcac gcgccccttg  | 1380 |
| gaggaccagc tggatgtgtt ggggcagcgg gtggagtgtt agtgtgaagt atcggaggag  | 1440 |
| ggggcgcaag tcaaatggct gaaggacggg gtggagctga cccgggagga gaccttcaaa  | 1500 |
| taccggttca agaaggacgg gcagagacac cacctgatca tcaacgaggc catgctggag  | 1560 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| gacgcggggc actatgcact gtgcactagc gggggccagg cgctggctga gctcattgtg | 1620 |
| caggaaaaga agctggagcc tcccaagatc cacctggact gcccaggccg cataccagac | 1680 |
| accattgtgg ttgtagctgg aaataagcta cgtctggacg tccctatctc tggggacccc | 1740 |
| gctcccactg tgatctggca gaaggctatc acgcagggga ataaggcccc agccaggcca | 1800 |
| gccccagatg ccccagagga cacaggtgac agcgatgagt ggggtgttga caagaagctg | 1860 |
| ctgtgtgaga ccgagggccg ggtccgcgtg gagaccacca aggaccgcag catcttcacg | 1920 |
| gtcgaggggg cagagaagga agatgagggc gtctacacgg tcacagtga gaacctgtg   | 1980 |
| ggcgaggacc aggtcaacct cacagtcaag gtcatcgacg tgccagacgc acctgcggcc | 2040 |
| cccaagatca gcaacgtggg agaggactcc tgcacagtac agtgggagcc gcctgcctac | 2100 |
| gatggcgggc agcccatcct gggctacatc ctggagcgca agaagaagaa gagctaccgg | 2160 |
| tggatgcggc tgaacttcga cctgattcag gagctgagtc atgaagcgcg gcgcatgac  | 2220 |
| gagggcgtgg tgtacgagat gcgcgtctac gcggtcaacg ccatcggcac gtccaggccc | 2280 |
| agccctgcct cccagccctt catgcctatc ggtcccccca gcgaaccac ccacctggca  | 2340 |
| gtagaggacg tctctgacac cacggtctcc ctcaagtggc ggccccaga gcgcgtggga  | 2400 |
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| gcccggctgc ttttccgagt gcgggcacac aatatggcag ggcctggagc ccctgttacc | 2580 |
| accacggagc cggtgacagt gcaggagatc ctgcaacggc cacggcttca gctgcccagg | 2640 |
| cacctgcgcc agaccattca gaagaaggc ggggagcctg tgaaccttct catccctttc  | 2700 |
| cagggcaagc cccggcctca ggtgacctg accaaagagg ggcagcccct ggcaggcgag  | 2760 |
| gaggtgagca tccgcaacag cccacagac accatcctgt tcatccgggc cgctcgccgc  | 2820 |
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| ctgggtgctg aggttgttga caagccaagt cctccccagg atctccgggt gactgacgcc | 2940 |
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| tgggggtaca cagtgcagaa agccgacaag aagaccatgg agtggttcac cgtcttggag | 3060 |

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| gtcttttatcc ccagaccagg catcacctat gagccaccca actataaggc cctggacttc  | 3240 |
| tccgaggccc caagcttcac ccagcccctg gtgaaccgct cggtcatcgc gggctacact   | 3300 |
| gctatgctct gctgtgctgt ccggggtagc cccaagccca agatttcctg gttcaagaat   | 3360 |
| ggcctggacc tgggagaaga cggccgcttc cgcatgttca gcaagcaggg agtgttgact   | 3420 |
| ctggagatta gaaagccctg cccctttgac gggggcatct atgtctgcag ggccaccaac   | 3480 |
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<210> 89  
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 <212> DNA  
 <213> Homo sapiens

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| cgctggcagc gcggaggcag tgacatcagc gccagcaaca agtacggcct ggccacagag  | 180 |
| ggcacacggc atacgtgac agtgccggaa gtgggccctg ccgaccaggg atcttacgca   | 240 |
| gtcattgctg gtcctccaa ggtcaagttc gacctcaagg tcatagaggc agagaaggca   | 300 |
| gagcccatgc tggcccctgc ccctgcccct gctgaggcca ctggagcccc tggagaagcc  | 360 |
| ccggccccag ccgctgagct gggagaaaagt gcccgaagtc ccaaagggtc aagctcagca | 420 |
| gctctcaatg gtcctacccc tggagcccc gatgaccca ttggcctctt cgtgatgcgg    | 480 |
| ccacaggatg gcgagggtgac cgtgggtggc agcatcacct tctcagcccc cgtggccggc | 540 |
| gccagcctcc tgaagccgcc tgttgtcaag tggttcaagg gcaaatgggt ggacctgagc  | 600 |
| agcaagggtg gccagcacct gcagctgcac gacagctacg accgcgccag caaggcttat  | 660 |
| ctgttcgagc tgcacatcac cgatgcccag cctgccttca ctggcagcta ccgctgtgag  | 720 |
| gtgtccacca aggacaaatt tgactgctcc aacttcaatc tactgtcca cgaggccatg   | 780 |

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| aagagagaca gtttccggac cccgagggac tcgaagctgg aggcaccagc agaggaggac  | 960  |
| gtgtgggaga tcctacggca ggcacccccca tctgagtacg agcgcacgc cttccagtac  | 1020 |
| ggcgtcactg acctgcgcgg catgctaaag aggctcaagg gcatgaggcg cgatgagaag  | 1080 |
| aagagcacag cttttcagaa gaagctggag ccggcctacc aggtgagcaa aggccacaag  | 1140 |
| atccggctga ccgtggaact ggctgaccat gacgctgagg tcaaatggct caagaatggc  | 1200 |
| caggagatcc agatgagcgg cagcaagtac atctttgagt ccatcgggtgc caagcgtaac | 1260 |
| ctgaccatca gccagtgtc attggcggac gacgcagcct accagtgcgt ggtgggtggc   | 1320 |
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| gaggaccagc tgggtgatggt ggggcagcgg gtggagtttg agtgtgaagt atcggaggag | 1440 |
| ggggcgcaag tcaaatggct gaaggacggg gtggagctga cccgggagga gaccttcaaa  | 1500 |
| taccggttca agaaggacgg gcagagacac cacctgatca tcaacgaggc catgctggag  | 1560 |
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| ccagccaggc cagccccaga tgccccagag gacacagggtg acagcgatga gtgggtgttt | 1860 |
| gacaagaagc tgctgtgtga gaccgagggc cgggtccgcg tggagaccac caaggaccgc  | 1920 |
| agcatcttca cggtcgaggg ggacagagaag gaagatgagg gcgtctacac ggtcacagtg | 1980 |
| aagaaccctg tgggcgagga ccagggtcaac ctcacagtca aggtcatcga cgtgccagac | 2040 |
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| ccgcctgcct acgatggcgg gcagcccatc ctgggctaca tcctggagcg caagaagaag  | 2160 |
| aagagctacc ggtggatgcg gctgaacttc gacctgattc aggagctgag tcatgaagcg  | 2220 |
| cggcgcacga tcgagggcgt ggtgtacgag atgcgcgtct acgcgggtcaa cgccatcggc | 2280 |

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| ctgcccacgg gggcccggct gcttttccga gtgcgggcac acaatatggc agggcctgga   | 2580 |
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| cagctgccc                                                           | 2700 |
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| aacacggaac tctgggggta cacagtgcag aaagccgaca agaagaccat ggagtggttc   | 3060 |
| accgtcttgg agcattaccg ccgcacccac tgcgtgggtgc cagagctcat cattggcaat  | 3120 |
| ggctactact tccgcgtctt cagccagaat atggttggct ttagtgacag agcggccacc   | 3180 |
| accaaggagc ccgtctttat ccccagacca ggcatcacct atgagccacc caactataag   | 3240 |
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| gcgggctaca ctgctatgct ctgctgtgct gtccggggta gcccgaagcc caagatttcc   | 3360 |
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 <220>  
 <223> pCard1 promoter

<400> 91  
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<213> Artificial Sequence

<220>  
<223> pCard1 polyA signal

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<223> pCard1 5' segment

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<210> 94

<211> 148

<212> DNA

<213> Artificial Sequence

<220>

<223> pCard1 3' segment

<400> 94

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tagcatggcg ggtaaatcat taactaca 148

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<212> DNA

<213> Artificial Sequence

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<223> pCard1 with MYBPC3 no ITR

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acatgggctt atatggcgtg gggtagatgt tcctgtagcc ttgtccctgg cacctgccaa 300

aatagcagcc aacaccccc accccaccg ccatccccct gccccaccg tcccctgtcg 360

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| gagcccatgc tggcccctgc ccctgcccct gctgaggcca ctggagcccc tggagaagcc  | 840  |
| ccggccccag ccgctgagct gggagaaaagt gcccgaagtc ccaaagggtc aagctcagca | 900  |
| gctctcaatg gtcctacccc tggagcccc gatgaccca ttggcctctt cgtgatgcgg    | 960  |
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| gaggaccagc tggatgatggg ggggcagcgg gtggagtttg agtgtgaagt atcgaggag  | 1920 |
| ggggcgcaag tcaaattggct gaaggacggg gtggagctga cccgggagga gaccttcaaa | 1980 |
| taccggttca agaaggacgg gcagagacac cacctgatca tcaacgaggc catgctggag  | 2040 |
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| caggcgggtgt tcaaattgtga ggtctcagat gagaatgttc ggggtgtgtg gctgaagaat  | 2220 |
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| acagtgcaga aagccgacaa gaagaccatg gagtggttca ccgtcttgga gcattaccgc  | 3840 |
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| gaggcacggt gtgagtgccg cctggagggtg cgagtgcctc agtaaagctt aataaaagat | 4320 |
| ctttattttc attagatctg tgtgttggtt ttttgtgtgc tggggactcg agttaagggc  | 4380 |
| gaattcccg taaggatctt cctagagcat ggctacgtag ataagtagca tggcgggtta   | 4440 |
| atcattaact aca                                                     | 4453 |

<210> 96  
 <211> 130  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 5' ITR

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 96                                                          |     |
| ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgtcg ggcgaccttt | 60  |
| ggtcgcccgg cctcagtgag cgagcgagcg cgcagagagg gagtggccaa ctccatcact | 120 |
| aggggttcct                                                        | 130 |

<210> 97  
 <211> 130  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> 3' ITR

<400> 97

aggaacccct agtgatggag ttggccactc cctctctgcg cgctcgctcg ctactgagg 60

ccgggcgacc aaaggctgcc cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc 120

gagcgcgcag 130

<210> 98

<211> 1089

<212> DNA

<213> Artificial Sequence

<220>

<223> pCard0 viral genome

<400> 98

ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgctcg ggcgaccttt 60

ggtcgccccg cctcagttag cgagcgagcg cgagagagg gagtggccaa ctccatcact 120

aggggttcct tgtagttaat gattaacccg ccatgctact tatctacgta gccatgctct 180

aggaagatcg gaattcgccc ttaagtcagtg gagaagaccc accttgcaga tgcctcact 240

ggggctggca gagccggcaa cctgcccgaag gctgctcagt ccattaggag ccagtagcct 300

ggaagatgtc tttaacccca gcatcagttc aagtggagca gcacataact cttgccctct 360

gccttccaag attctgggtg tgagacttat ggagtgtcct ggaggttgcc ttctgcccc 420

caaccctgct ccagctggc cctcccaggc ctgggttgct ggctctgct ttatcaggat 480

tctcaagagg gacagctggg ttatgttgca tgactgttcc ctgcatatct gctctggttt 540

taaatagctt atctgagcag ctggaggacc acatgggctt atatggcgtg gggtagatgt 600

tcctgtagcc ttgtccctgg cacctgcaa aatagcagcc aacaccccc accccaccg 660

ccatccccct gcccacccg tcccctgtcg cacattcctc cctccgcagg gctggctcac 720

caggccccag cccacatgcc tgcttaaagc cctctccatc ctctgcctca ccagtcccc 780

gctgagactg agcagacgcc tccagccacc aagcttaata aaagatcttt attttcatta 840

gatctgtgtg ttggtttttt gtgtgctggg gactcgagtt aaggcgcaat tccgataag 900

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gatcttccta gagcatggct acgtagataa gtagcatggc gggttaatca ttaactacaa  | 960  |
| ggaacccccta gtgatggagt tggccactcc ctctctgcgc gctcgctcgc tcactgaggc | 1020 |
| cgggcgacca aaggtcgccc gacgcccggg ctttgcccgg gcggcctcag tgagcgagcg  | 1080 |
| agcgcgcag                                                          | 1089 |

<210> 99  
 <211> 830  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pCard0 expression cassette

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 99                                                          |     |
| tgtagttaat gattaacccg ccatgctact tatctacgta gccatgctct aggaagatcg | 60  |
| gaattcgccc ttaagtcattg gagaagaccc accttcgaga tgcctcact ggggctggca | 120 |
| gagccggcaa cctgcccag gctgctcagt ccattaggag ccagtagcct ggaagatgtc  | 180 |
| tttaccacca gcatcagttc aagtggagca gcacataact cttgccctct gccttccaag | 240 |
| attctggtgc tgagacttat ggagtgtctt ggagggtgcc ttctgcccc caaccctgct  | 300 |
| cccagctggc cctcccaggc ctgggttgct ggctctgct ttatcaggat tctcaagagg  | 360 |
| gacagctggg ttatgttgca tgactgttcc ctgcatatct gctctggttt taaatagctt | 420 |
| atctgagcag ctggaggacc acatgggctt atatggcgtg gggtagatgt tcctgtagcc | 480 |
| ttgtccctgg cacctgcaa aatagcagcc aacaccccc accccaccg ccatccccct    | 540 |
| gccccacccg tcccctgtcg cacattcctc cctccgcagg gctggctcac caggccccag | 600 |
| cccacatgcc tgcttaaagc cctctccatc ctctgcctca ccagtcctcc gctgagactg | 660 |
| agcagacgcc tccagccacc aagcttaata aaagatcttt attttcatta gatctgtgtg | 720 |
| ttggtttttt gtgtgctggg gactcgagtt aagggcgaat tcccataag gatcttccta  | 780 |
| gagcatggct acgtagataa gtagcatggc gggttaatca ttaactacaa            | 830 |

<210> 100  
 <211> 889

<212> DNA  
<213> Artificial Sequence

<220>  
<223> pCard1 viral genome

<400> 100  
ctgcgcgctc gctcgtcac tgaggccgcc cgggcaaagc ccgggcgtcg ggcgaccttt 60  
ggtcgccccg cctcagttag cgagcgagcg cgagagagg gagtggccaa ctccatcact 120  
aggggttcct tgtagttaat gattaacccg ccatgctact tatctacgta gccatgctct 180  
aggaagatcg gaattcgccc ttaagttgcc ttctgcccc caaccctgct cccagctggc 240  
cctcccaggc ctgggttgct ggccctctgct ttatcaggat tctcaagagg gacagctggc 300  
ttatgttgca tgactgttcc ctgcatatct gctctgggtt taaatagctt atctgagcag 360  
ctggaggacc acatgggctt atatggcgtg gggtagatgt tcctgtagcc ttgtccctgg 420  
cacctgcaa aatagcagcc aacaccccc accccaccg ccatccccct gccccaccg 480  
tcccctgtcg cacattcctc cctccgcagg gctggctcac caggccccag cccacatgcc 540  
tgcttaaagc cctctccatc ctctgcctca cccagtcccc gctgagactg agcagacgcc 600  
tccagccacc aagcttaata aaagatcttt attttcatta gatctgtgtg ttggtttttt 660  
gtgtgctggg gactcgagtt aaggcggaat tcccataag gatcttccta gagcatggct 720  
acgtagataa gtagcatggc gggttaatca ttaactacaa ggaacccta gtgatggagt 780  
tggccactcc ctctctgcgc gctcgtcgc tctagaggc cgggcgacca aaggtcgccc 840  
gacgccggg ctttgcccg gcggcctcag tgagcgagcg agcgcgcag 889

<210> 101  
<211> 629  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> pCard1 expression cassette

<400> 101  
tgtagttaat gattaacccg ccatgctact tatctacgta gccatgctct aggaagatcg 60  
gaattcgccc ttaagttgcc ttctgcccc caaccctgct cccagctggc cctcccaggc 120

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ctgggttgct ggcctctgct ttatcaggat tctcaagagg gacagctggt ttatgttgca | 180 |
| tgactgttcc ctgcatatct gctctggttt taaatagctt atctgagcag ctggaggacc | 240 |
| acatgggctt atatggcgtg gggtagatgt tcctgtagcc ttgtccctgg cacctgccaa | 300 |
| aatagcagcc aacaccccc accccaccg ccatccccct gccccaccg tcccctgtcg    | 360 |
| cacattcctc cctccgcagg gctggctcac caggccccag cccacatgcc tgcttaaagc | 420 |
| cctctccatc ctctgcctca cccagtcccc gctgagactg agcagacgcc tccagccacc | 480 |
| aagcttaata aaagatcttt attttcatta gatctgtgtg ttggtttttt gtgtgctggg | 540 |
| gactcgagtt aagggcgaat tcccataag gatcttccta gagcatggct acgtagataa  | 600 |
| gtagcatggc gggttaatca ttaactaca                                   | 629 |

<210> 102  
 <211> 4713  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pCard1 viral genome with MYBPC3

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 102                                                         |     |
| ctgcgcgctc gctcgtcac tgaggccgcc cgggcaaagc ccgggcgtcg ggcgaccttt  | 60  |
| ggtcgccccg cctcagttag cgagcgagcg cgcagagagg gaggggccaa ctccatcact | 120 |
| aggggttcct ttagttaat gattaacccg ccatgctact tatctacgta gccatgctct  | 180 |
| aggaagatcg gaattcgccc ttaagttgcc ttctgcccc caaccctgct cccagctggc  | 240 |
| cctcccaggc ctgggttgct ggcctctgct ttatcaggat tctcaagagg gacagctggt | 300 |
| ttatgttgca tgactgttcc ctgcatatct gctctggttt taaatagctt atctgagcag | 360 |
| ctggaggacc acatgggctt atatggcgtg gggtagatgt tcctgtagcc ttgtccctgg | 420 |
| cacctgccaa aatagcagcc aacaccccc accccaccg ccatccccct gccccaccg    | 480 |
| tcccctgtcg cacattcctc cctccgcagg gctggctcac caggccccag cccacatgcc | 540 |
| tgcttaaagc cctctccatc ctctgcctca cccagtcccc gctgagactg agcagacgcc | 600 |
| tccagccacc atgcctgagc cggggaagaa gccagtctca gcttttagca agaagccacg | 660 |



|                                                                    |      |
|--------------------------------------------------------------------|------|
| gtcagtggaa gtggccgcag gcagccctgc cgtgttcgag gccgagacag agcgggcagg  | 720  |
| agtgaaggtg cgctggcagc gcggaggcag tgacatcagc gccagcaaca agtacggcct  | 780  |
| ggccacagag ggcacacggc atacgctgac agtgcgggaa gtgggcccctg ccgaccaggg | 840  |
| atcttacgca gtcattgctg gtcctccaa ggtcaagttc gacctcaagg tcatagaggc   | 900  |
| agagaaggca gagcccatgc tggcccctgc ccctgcccct gctgaggcca ctggagcccc  | 960  |
| tggagaagcc ccggccccag ccgctgagct gggagaaagt gcccgaagtc ccaaagggtc  | 1020 |
| aagctcagca gctctcaatg gtcctacccc tggagcccc gatgaccca ttggcctctt    | 1080 |
| cgtgatgcgg ccacaggatg gcgagggtgac cgtgggtggc agcatcacct tctcagcccc | 1140 |
| cgtggccggc gccagcctcc tgaagccgcc tgtggtcaag tggttcaagg gcaaattgggt | 1200 |
| ggacctgagc agcaagggtg gccagcacct gcagctgcac gacagctacg accgcgccag  | 1260 |
| caaggtctat ctgttcgagc tgcacatcac cgatgccag cctgccttca ctggcagcta   | 1320 |
| ccgctgtgag gtgtccacca aggacaaatt tgactgctcc aacttcaatc tactgtcca   | 1380 |
| cgaggccatg ggcaccggag acctggacct cctatcagcc ttccgccgca cgagcctggc  | 1440 |
| tggagggtggc cggcggatca gtgatagcca tgaggacact gggattctgg acttcagctc | 1500 |
| actgctgaaa aagagagaca gtttccggac cccgagggac tcgaagctgg aggcaccagc  | 1560 |
| agaggaggac gtgtgggaga tcctacggca ggcaccccca tctgagtacg agcgcatcgc  | 1620 |
| cttccagtac ggcgctactg acctgcgcgg catgctaaag aggctcaagg gcatgaggcg  | 1680 |
| cgatgagaag aagagcacag cttttcagaa gaagctggag ccggcctacc aggtgagcaa  | 1740 |
| aggccacaag atccggctga ccgtggaact ggctgaccat gacgctgagg tcaaatggct  | 1800 |
| caagaatggc caggagatcc agatgagcgg cagcaagtac atctttgagt ccatcggtgc  | 1860 |
| caagcgtacc ctgaccatca gccagtgctc attggcggac gacgcagcct accagtgcgt  | 1920 |
| ggtgggtggc gagaagtgtg gcacggagct ctttgtgaaa gagccccctg tgctcatcac  | 1980 |
| gcgccccctg gaggaccagc tggatggtt ggggcagcgg gtggagtttg agtgtgaagt   | 2040 |
| atcggaggag ggggcgcaag tcaaatggct gaaggacggg gtggagctga cccgggagga  | 2100 |
| gaccttcaaa taccggttca agaaggacgg gcagagacac cacctgatca tcaacgaggc  | 2160 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| catgctggag gacgcggggc actatgcact gtgcactagc gggggccagg cgctggctga  | 2220 |
| gctcattgtg caggaaaaga agctggaggt gtaccagagc atcgagacc tgatgggtggg  | 2280 |
| cgcaaaggac caggcgggtgt tcaaatgtga ggtctcagat gagaatgttc ggggtgtgtg | 2340 |
| gctgaagaat gggaaggagc tgggtcccga cagccgcata aagggtgtccc acatcgggcg | 2400 |
| ggtccacaaa ctgaccattg acgacgtcac acctgccgac gaggctgact acagctttgt  | 2460 |
| gcccagaggc ttgcctgca acctgtcagc caagctccac ttcatggagg tcaagattga   | 2520 |
| cttcgtaccc aggcaggaac ctccaagat ccacctggac tgcccaggcc gcataccaga   | 2580 |
| caccattgtg gttgtagctg gaaataagct acgtctggac gtccctatct ctggggaccc  | 2640 |
| cgctcccact gtgatctggc agaaggctat cacgcagggg aataaggccc cagccaggcc  | 2700 |
| agccccagat gccccagagg acacaggtga cagcgatgag tgggtgtttg acaagaagct  | 2760 |
| gctgtgtgag accgagggcc ggggtccgct ggagaccacc aaggaccgca gcatcttcac  | 2820 |
| ggtcgagggg gcagagaagg aagatgaggg cgtctacacg gtcacagtga agaaccctgt  | 2880 |
| gggcgaggac caggtcaacc tcacagtcaa ggtcatcgac gtgccagacg cacctgcggc  | 2940 |
| ccccaagatc agcaacgtgg gagaggactc ctgcacagta cagtgggagc cgctgccta   | 3000 |
| cgatggcggg cagcccatcc tgggctacat cctggagcgc aagaagaaga agagctaccg  | 3060 |
| gtggatgcgg ctgaacttcg acctgattca ggagctgagt catgaagcgc ggcgcatgat  | 3120 |
| cgagggcgtg gtgtacgaga tgcgctcta cgcggtcaac gccatcggca tgtccaggcc   | 3180 |
| cagccctgcc tcccagccct tcatgcctat cgggtcccc agcgaacca cccacctggc    | 3240 |
| agtagaggac gtctctgaca ccacgggtctc cctcaagtgg cggccccag agcgcgtggg  | 3300 |
| agcaggaggc ctggatggct acagcgtgga gtactgcca gagggctgct cagagtgggt   | 3360 |
| ggctgccctg caggggctga cagagcacac atcgatactg gtgaaggacc tgcccacggg  | 3420 |
| ggcccggctg cttttccgag tgcgggcaca caatatggca gggcctggag cccctgttac  | 3480 |
| caccacggag ccggtgacag tgcaggagat cctgcaacgg ccacggcttc agctgcccag  | 3540 |
| gcacctgcgc cagaccattc agaagaaggt cgggggagcct gtgaaccttc tcatcccttt | 3600 |
| ccagggaag ccccgccctc aggtgacctg gaccaaagag gggcagcccc tggcaggcga   | 3660 |

ggaggtgagc atccgcaaca gccccacaga caccatcctg ttcatccggg ccgctcgccg 3720  
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 gctggtgctg caggttggtg acaagccaag tcctccccag gatctccggg tgactgacgc 3840  
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 ccgcgtcttc agccagaata tggttggctt tagtgacaga gcggccacca ccaaggagcc 4080  
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 tctggagatt agaaaagccct gcccctttga cgggggcatc tatgtctgca gggccaccaa 4380  
 cttacagggc gaggcacggt gtgagtgccg cctggagggtg cgagtgcctc agtaaagctt 4440  
 aataaaagat ctttatcttc attagatctg tgtgttggtt ttttgtgtgc tggggactcg 4500  
 agttaagggc gaattcccga taaggatctt cctagagcat ggctacgtag ataagtagca 4560  
 tggcgggtta atcattaact acaaggaacc cctagtgatg gagttggcca ctccctctct 4620  
 gcgcgctcgc tcgctcactg aggccgggcg accaaaggtc gcccgacgcc cgggctttgc 4680  
 ccgggcggcc tcagtgagcg agcgagcgcg cag 4713

<210> 103  
 <211> 1274  
 <212> PRT  
 <213> Homo sapiens

<400> 103

Met Pro Glu Pro Gly Lys Lys Pro Val Ser Ala Phe Ser Lys Lys Pro  
 1 5 10 15

Arg Ser Val Glu Val Ala Ala Gly Ser Pro Ala Val Phe Glu Ala Glu

20

25

30

Thr Glu Arg Ala Gly Val Lys Val Arg Trp Gln Arg Gly Gly Ser Asp  
 35 40 45

Ile Ser Ala Ser Asn Lys Tyr Gly Leu Ala Thr Glu Gly Thr Arg His  
 50 55 60

Thr Leu Thr Val Arg Glu Val Gly Pro Ala Asp Gln Gly Ser Tyr Ala  
 65 70 75 80

Val Ile Ala Gly Ser Ser Lys Val Lys Phe Asp Leu Lys Val Ile Glu  
 85 90 95

Ala Glu Lys Ala Glu Pro Met Leu Ala Pro Ala Pro Ala Pro Ala Glu  
 100 105 110

Ala Thr Gly Ala Pro Gly Glu Ala Pro Ala Pro Ala Ala Glu Leu Gly  
 115 120 125

Glu Ser Ala Pro Ser Pro Lys Gly Ser Ser Ser Ala Ala Leu Asn Gly  
 130 135 140

Pro Thr Pro Gly Ala Pro Asp Asp Pro Ile Gly Leu Phe Val Met Arg  
 145 150 155 160

Pro Gln Asp Gly Glu Val Thr Val Gly Gly Ser Ile Thr Phe Ser Ala  
 165 170 175

Arg Val Ala Gly Ala Ser Leu Leu Lys Pro Pro Val Val Lys Trp Phe  
 180 185 190

Lys Gly Lys Trp Val Asp Leu Ser Ser Lys Val Gly Gln His Leu Gln  
 195 200 205

Leu His Asp Ser Tyr Asp Arg Ala Ser Lys Val Tyr Leu Phe Glu Leu  
 210 215 220

His Ile Thr Asp Ala Gln Pro Ala Phe Thr Gly Ser Tyr Arg Cys Glu  
225 230 235 240

Val Ser Thr Lys Asp Lys Phe Asp Cys Ser Asn Phe Asn Leu Thr Val  
245 250 255

His Glu Ala Met Gly Thr Gly Asp Leu Asp Leu Leu Ser Ala Phe Arg  
260 265 270

Arg Thr Ser Leu Ala Gly Gly Gly Arg Arg Ile Ser Asp Ser His Glu  
275 280 285

Asp Thr Gly Ile Leu Asp Phe Ser Ser Leu Leu Lys Lys Arg Asp Ser  
290 295 300

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

Val Trp Glu Ile Leu Arg Gln Ala Pro Pro Ser Glu Tyr Glu Arg Ile  
325 330 335

Ala Phe Gln Tyr Gly Val Thr Asp Leu Arg Gly Met Leu Lys Arg Leu  
340 345 350

Lys Gly Met Arg Arg Asp Glu Lys Lys Ser Thr Ala Phe Gln Lys Lys  
355 360 365

Leu Glu Pro Ala Tyr Gln Val Ser Lys Gly His Lys Ile Arg Leu Thr  
370 375 380

Val Glu Leu Ala Asp His Asp Ala Glu Val Lys Trp Leu Lys Asn Gly  
385 390 395 400

Gln Glu Ile Gln Met Ser Gly Ser Lys Tyr Ile Phe Glu Ser Ile Gly  
405 410 415

Ala Lys Arg Thr Leu Thr Ile Ser Gln Cys Ser Leu Ala Asp Asp Ala

420

425

430

Ala Tyr Gln Cys Val Val Gly Gly Glu Lys Cys Ser Thr Glu Leu Phe  
435 440 445

Val Lys Glu Pro Pro Val Leu Ile Thr Arg Pro Leu Glu Asp Gln Leu  
450 455 460

Val Met Val Gly Gln Arg Val Glu Phe Glu Cys Glu Val Ser Glu Glu  
465 470 475 480

Gly Ala Gln Val Lys Trp Leu Lys Asp Gly Val Glu Leu Thr Arg Glu  
485 490 495

Glu Thr Phe Lys Tyr Arg Phe Lys Lys Asp Gly Gln Arg His His Leu  
500 505 510

Ile Ile Asn Glu Ala Met Leu Glu Asp Ala Gly His Tyr Ala Leu Cys  
515 520 525

Thr Ser Gly Gly Gln Ala Leu Ala Glu Leu Ile Val Gln Glu Lys Lys  
530 535 540

Leu Glu Val Tyr Gln Ser Ile Ala Asp Leu Met Val Gly Ala Lys Asp  
545 550 555 560

Gln Ala Val Phe Lys Cys Glu Val Ser Asp Glu Asn Val Arg Gly Val  
565 570 575

Trp Leu Lys Asn Gly Lys Glu Leu Val Pro Asp Ser Arg Ile Lys Val  
580 585 590

Ser His Ile Gly Arg Val His Lys Leu Thr Ile Asp Asp Val Thr Pro  
595 600 605

Ala Asp Glu Ala Asp Tyr Ser Phe Val Pro Glu Gly Phe Ala Cys Asn  
610 615 620

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

Arg Gln Glu Pro Pro Lys Ile His Leu Asp Cys Pro Gly Arg Ile Pro  
645 650 655

Asp Thr Ile Val Val Val Ala Gly Asn Lys Leu Arg Leu Asp Val Pro  
660 665 670

Ile Ser Gly Asp Pro Ala Pro Thr Val Ile Trp Gln Lys Ala Ile Thr  
675 680 685

Gln Gly Asn Lys Ala Pro Ala Arg Pro Ala Pro Asp Ala Pro Glu Asp  
690 695 700

Thr Gly Asp Ser Asp Glu Trp Val Phe Asp Lys Lys Leu Leu Cys Glu  
705 710 715 720

Thr Glu Gly Arg Val Arg Val Glu Thr Thr Lys Asp Arg Ser Ile Phe  
725 730 735

Thr Val Glu Gly Ala Glu Lys Glu Asp Glu Gly Val Tyr Thr Val Thr  
740 745 750

Val Lys Asn Pro Val Gly Glu Asp Gln Val Asn Leu Thr Val Lys Val  
755 760 765

Ile Asp Val Pro Asp Ala Pro Ala Ala Pro Lys Ile Ser Asn Val Gly  
770 775 780

Glu Asp Ser Cys Thr Val Gln Trp Glu Pro Pro Ala Tyr Asp Gly Gly  
785 790 795 800

Gln Pro Ile Leu Gly Tyr Ile Leu Glu Arg Lys Lys Lys Lys Ser Tyr  
805 810 815

Arg Trp Met Arg Leu Asn Phe Asp Leu Ile Gln Glu Leu Ser His Glu

820

825

830

Ala Arg Arg Met Ile Glu Gly Val Val Tyr Glu Met Arg Val Tyr Ala  
 835 840 845

Val Asn Ala Ile Gly Met Ser Arg Pro Ser Pro Ala Ser Gln Pro Phe  
 850 855 860

Met Pro Ile Gly Pro Pro Ser Glu Pro Thr His Leu Ala Val Glu Asp  
 865 870 875 880

Val Ser Asp Thr Thr Val Ser Leu Lys Trp Arg Pro Pro Glu Arg Val  
 885 890 895

Gly Ala Gly Gly Leu Asp Gly Tyr Ser Val Glu Tyr Cys Pro Glu Gly  
 900 905 910

Cys Ser Glu Trp Val Ala Ala Leu Gln Gly Leu Thr Glu His Thr Ser  
 915 920 925

Ile Leu Val Lys Asp Leu Pro Thr Gly Ala Arg Leu Leu Phe Arg Val  
 930 935 940

Arg Ala His Asn Met Ala Gly Pro Gly Ala Pro Val Thr Thr Thr Glu  
 945 950 955 960

Pro Val Thr Val Gln Glu Ile Leu Gln Arg Pro Arg Leu Gln Leu Pro  
 965 970 975

Arg His Leu Arg Gln Thr Ile Gln Lys Lys Val Gly Glu Pro Val Asn  
 980 985 990

Leu Leu Ile Pro Phe Gln Gly Lys Pro Arg Pro Gln Val Thr Trp Thr  
 995 1000 1005

Lys Glu Gly Gln Pro Leu Ala Gly Glu Glu Val Ser Ile Arg Asn  
 1010 1015 1020



Ser Pro Thr Asp Thr Ile Leu Phe Ile Arg Ala Ala Arg Arg Val  
1025 1030 1035

His Ser Gly Thr Tyr Gln Val Thr Val Arg Ile Glu Asn Met Glu  
1040 1045 1050

Asp Lys Ala Thr Leu Val Leu Gln Val Val Asp Lys Pro Ser Pro  
1055 1060 1065

Pro Gln Asp Leu Arg Val Thr Asp Ala Trp Gly Leu Asn Val Ala  
1070 1075 1080

Leu Glu Trp Lys Pro Pro Gln Asp Val Gly Asn Thr Glu Leu Trp  
1085 1090 1095

Gly Tyr Thr Val Gln Lys Ala Asp Lys Lys Thr Met Glu Trp Phe  
1100 1105 1110

Thr Val Leu Glu His Tyr Arg Arg Thr His Cys Val Val Pro Glu  
1115 1120 1125

Leu Ile Ile Gly Asn Gly Tyr Tyr Phe Arg Val Phe Ser Gln Asn  
1130 1135 1140

Met Val Gly Phe Ser Asp Arg Ala Ala Thr Thr Lys Glu Pro Val  
1145 1150 1155

Phe Ile Pro Arg Pro Gly Ile Thr Tyr Glu Pro Pro Asn Tyr Lys  
1160 1165 1170

Ala Leu Asp Phe Ser Glu Ala Pro Ser Phe Thr Gln Pro Leu Val  
1175 1180 1185

Asn Arg Ser Val Ile Ala Gly Tyr Thr Ala Met Leu Cys Cys Ala  
1190 1195 1200

Val Arg Gly Ser Pro Lys Pro Lys Ile Ser Trp Phe Lys Asn Gly

1205

1210

1215

Leu Asp Leu Gly Glu Asp Ala Arg Phe Arg Met Phe Ser Lys Gln  
 1220 1225 1230

Gly Val Leu Thr Leu Glu Ile Arg Lys Pro Cys Pro Phe Asp Gly  
 1235 1240 1245

Gly Ile Tyr Val Cys Arg Ala Thr Asn Leu Gln Gly Glu Ala Arg  
 1250 1255 1260

Cys Glu Cys Arg Leu Glu Val Arg Val Pro Gln  
 1265 1270

<210> 104  
 <211> 1181  
 <212> PRT  
 <213> Homo sapiens

<400> 104

Met Pro Glu Pro Gly Lys Lys Pro Val Ser Ala Phe Ser Lys Lys Pro  
 1 5 10 15

Arg Ser Val Glu Val Ala Ala Gly Ser Pro Ala Val Phe Glu Ala Glu  
 20 25 30

Thr Glu Arg Ala Gly Val Lys Val Arg Trp Gln Arg Gly Gly Ser Asp  
 35 40 45

Ile Ser Ala Ser Asn Lys Tyr Gly Leu Ala Thr Glu Gly Thr Arg His  
 50 55 60

Thr Leu Thr Val Arg Glu Val Gly Pro Ala Asp Gln Gly Ser Tyr Ala  
 65 70 75 80

Val Ile Ala Gly Ser Ser Lys Val Lys Phe Asp Leu Lys Val Ile Glu  
 85 90 95

Ala Glu Lys Ala Glu Pro Met Leu Ala Pro Ala Pro Ala Pro Ala Glu  
100 105 110

Ala Thr Gly Ala Pro Gly Glu Ala Pro Ala Pro Ala Ala Glu Leu Gly  
115 120 125

Glu Ser Ala Pro Ser Pro Lys Gly Ser Ser Ser Ala Ala Leu Asn Gly  
130 135 140

Pro Thr Pro Gly Ala Pro Asp Asp Pro Ile Gly Leu Phe Val Met Arg  
145 150 155 160

Pro Gln Asp Gly Glu Val Thr Val Gly Gly Ser Ile Thr Phe Ser Ala  
165 170 175

Arg Val Ala Gly Ala Ser Leu Leu Lys Pro Pro Val Val Lys Trp Phe  
180 185 190

Lys Gly Lys Trp Val Asp Leu Ser Ser Lys Val Gly Gln His Leu Gln  
195 200 205

Leu His Asp Ser Tyr Asp Arg Ala Ser Lys Val Tyr Leu Phe Glu Leu  
210 215 220

His Ile Thr Asp Ala Gln Pro Ala Phe Thr Gly Ser Tyr Arg Cys Glu  
225 230 235 240

Val Ser Thr Lys Asp Lys Phe Asp Cys Ser Asn Phe Asn Leu Thr Val  
245 250 255

His Glu Ala Met Gly Thr Gly Asp Leu Asp Leu Leu Ser Ala Phe Arg  
260 265 270

Arg Thr Ser Leu Ala Gly Gly Gly Arg Arg Ile Ser Asp Ser His Glu  
275 280 285

Asp Thr Gly Ile Leu Asp Phe Ser Ser Leu Leu Lys Lys Arg Asp Ser  
290 295 300

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

Val Trp Glu Ile Leu Arg Gln Ala Pro Pro Ser Glu Tyr Glu Arg Ile  
325 330 335

Ala Phe Gln Tyr Gly Val Thr Asp Leu Arg Gly Met Leu Lys Arg Leu  
340 345 350

Lys Gly Met Arg Arg Asp Glu Lys Lys Ser Thr Ala Phe Gln Lys Lys  
355 360 365

Leu Glu Pro Ala Tyr Gln Val Ser Lys Gly His Lys Ile Arg Leu Thr  
370 375 380

Val Glu Leu Ala Asp His Asp Ala Glu Val Lys Trp Leu Lys Asn Gly  
385 390 395 400

Gln Glu Ile Gln Met Ser Gly Ser Lys Tyr Ile Phe Glu Ser Ile Gly  
405 410 415

Ala Lys Arg Thr Leu Thr Ile Ser Gln Cys Ser Leu Ala Asp Asp Ala  
420 425 430

Ala Tyr Gln Cys Val Val Gly Gly Glu Lys Cys Ser Thr Glu Leu Phe  
435 440 445

Val Lys Glu Pro Pro Val Tyr Gln Ser Ile Ala Asp Leu Met Val Gly  
450 455 460

Ala Lys Asp Gln Ala Val Phe Lys Cys Glu Val Ser Asp Glu Asn Val  
465 470 475 480

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

Ile Lys Val Ser His Ile Gly Arg Val His Lys Leu Thr Ile Asp Asp  
500 505 510

Val Thr Pro Ala Asp Glu Ala Asp Tyr Ser Phe Val Pro Glu Gly Phe  
515 520 525

Ala Cys Asn Leu Ser Ala Lys Leu His Phe Met Glu Val Lys Ile Asp  
530 535 540

Phe Val Pro Arg Gln Glu Pro Pro Lys Ile His Leu Asp Cys Pro Gly  
545 550 555 560

Arg Ile Pro Asp Thr Ile Val Val Val Ala Gly Asn Lys Leu Arg Leu  
565 570 575

Asp Val Pro Ile Ser Gly Asp Pro Ala Pro Thr Val Ile Trp Gln Lys  
580 585 590

Ala Ile Thr Gln Gly Asn Lys Ala Pro Ala Arg Pro Ala Pro Asp Ala  
595 600 605

Pro Glu Asp Thr Gly Asp Ser Asp Glu Trp Val Phe Asp Lys Lys Leu  
610 615 620

Leu Cys Glu Thr Glu Gly Arg Val Arg Val Glu Thr Thr Lys Asp Arg  
625 630 635 640

Ser Ile Phe Thr Val Glu Gly Ala Glu Lys Glu Asp Glu Gly Val Tyr  
645 650 655

Thr Val Thr Val Lys Asn Pro Val Gly Glu Asp Gln Val Asn Leu Thr  
660 665 670

Val Lys Val Ile Asp Val Pro Asp Ala Pro Ala Ala Pro Lys Ile Ser  
675 680 685

Asn Val Gly Glu Asp Ser Cys Thr Val Gln Trp Glu Pro Pro Ala Tyr  
690 695 700

Asp Gly Gly Gln Pro Ile Leu Gly Tyr Ile Leu Glu Arg Lys Lys Lys  
705 710 715 720

Lys Ser Tyr Arg Trp Met Arg Leu Asn Phe Asp Leu Ile Gln Glu Leu  
725 730 735

Ser His Glu Ala Arg Arg Met Ile Glu Gly Val Val Tyr Glu Met Arg  
740 745 750

Val Tyr Ala Val Asn Ala Ile Gly Met Ser Arg Pro Ser Pro Ala Ser  
755 760 765

Gln Pro Phe Met Pro Ile Gly Pro Pro Ser Glu Pro Thr His Leu Ala  
770 775 780

Val Glu Asp Val Ser Asp Thr Thr Val Ser Leu Lys Trp Arg Pro Pro  
785 790 795 800

Glu Arg Val Gly Ala Gly Gly Leu Asp Gly Tyr Ser Val Glu Tyr Cys  
805 810 815

Pro Glu Gly Cys Ser Glu Trp Val Ala Ala Leu Gln Gly Leu Thr Glu  
820 825 830

His Thr Ser Ile Leu Val Lys Asp Leu Pro Thr Gly Ala Arg Leu Leu  
835 840 845

Phe Arg Val Arg Ala His Asn Met Ala Gly Pro Gly Ala Pro Val Thr  
850 855 860

Thr Thr Glu Pro Val Thr Val Gln Glu Ile Leu Gln Arg Pro Arg Leu  
865 870 875 880

Gln Leu Pro Arg His Leu Arg Gln Thr Ile Gln Lys Lys Val Gly Glu  
885 890 895

Pro Val Asn Leu Leu Ile Pro Phe Gln Gly Lys Pro Arg Pro Gln Val  
900 905 910

Thr Trp Thr Lys Glu Gly Gln Pro Leu Ala Gly Glu Glu Val Ser Ile  
915 920 925

Arg Asn Ser Pro Thr Asp Thr Ile Leu Phe Ile Arg Ala Ala Arg Arg  
930 935 940

Val His Ser Gly Thr Tyr Gln Val Thr Val Arg Ile Glu Asn Met Glu  
945 950 955 960

Asp Lys Ala Thr Leu Val Leu Gln Val Val Asp Lys Pro Ser Pro Pro  
965 970 975

Gln Asp Leu Arg Val Thr Asp Ala Trp Gly Leu Asn Val Ala Leu Glu  
980 985 990

Trp Lys Pro Pro Gln Asp Val Gly Asn Thr Glu Leu Trp Gly Tyr Thr  
995 1000 1005

Val Gln Lys Ala Asp Lys Lys Thr Met Glu Trp Phe Thr Val Leu  
1010 1015 1020

Glu His Tyr Arg Arg Thr His Cys Val Val Pro Glu Leu Ile Ile  
1025 1030 1035

Gly Asn Gly Tyr Tyr Phe Arg Val Phe Ser Gln Asn Met Val Gly  
1040 1045 1050

Phe Ser Asp Arg Ala Ala Thr Thr Lys Glu Pro Val Phe Ile Pro  
1055 1060 1065

Arg Pro Gly Ile Thr Tyr Glu Pro Pro Asn Tyr Lys Ala Leu Asp  
1070 1075 1080

Phe Ser Glu Ala Pro Ser Phe Thr Gln Pro Leu Val Asn Arg Ser  
1085 1090 1095

Val Ile Ala Gly Tyr Thr Ala Met Leu Cys Cys Ala Val Arg Gly  
1100 1105 1110

Ser Pro Lys Pro Lys Ile Ser Trp Phe Lys Asn Gly Leu Asp Leu  
1115 1120 1125

Gly Glu Asp Ala Arg Phe Arg Met Phe Ser Lys Gln Gly Val Leu  
1130 1135 1140

Thr Leu Glu Ile Arg Lys Pro Cys Pro Phe Asp Gly Gly Ile Tyr  
1145 1150 1155

Val Cys Arg Ala Thr Asn Leu Gln Gly Glu Ala Arg Cys Glu Cys  
1160 1165 1170

Arg Leu Glu Val Arg Val Pro Gln  
1175 1180

<210> 105  
<211> 1177  
<212> PRT  
<213> Homo sapiens

<400> 105

Met Pro Glu Pro Gly Lys Lys Pro Val Ser Ala Phe Ser Lys Lys Pro  
1 5 10 15

Arg Ser Val Glu Val Ala Ala Gly Ser Pro Ala Val Phe Glu Ala Glu  
20 25 30

Thr Glu Arg Ala Gly Val Lys Val Arg Trp Gln Arg Gly Gly Ser Asp  
35 40 45

Ile Ser Ala Ser Asn Lys Tyr Gly Leu Ala Thr Glu Gly Thr Arg His  
50 55 60

Thr Leu Thr Val Arg Glu Val Gly Pro Ala Asp Gln Gly Ser Tyr Ala



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |     |
| Val | Ile | Ala | Gly | Ser | Ser | Lys | Val | Lys | Phe | Asp | Leu | Lys | Val | Ile | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Glu | Lys | Ala | Glu | Pro | Met | Leu | Ala | Pro | Ala | Pro | Ala | Pro | Ala | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Thr | Gly | Ala | Pro | Gly | Glu | Ala | Pro | Ala | Pro | Ala | Ala | Glu | Leu | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Ser | Ala | Pro | Ser | Pro | Lys | Gly | Ser | Ser | Ser | Ala | Ala | Leu | Asn | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Thr | Pro | Gly | Ala | Pro | Asp | Asp | Pro | Ile | Gly | Leu | Phe | Val | Met | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Gln | Asp | Gly | Glu | Val | Thr | Val | Gly | Gly | Ser | Ile | Thr | Phe | Ser | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Val | Ala | Gly | Ala | Ser | Leu | Leu | Lys | Pro | Pro | Val | Val | Lys | Trp | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Gly | Lys | Trp | Val | Asp | Leu | Ser | Ser | Lys | Val | Gly | Gln | His | Leu | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | His | Asp | Ser | Tyr | Asp | Arg | Ala | Ser | Lys | Val | Tyr | Leu | Phe | Glu | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| His | Ile | Thr | Asp | Ala | Gln | Pro | Ala | Phe | Thr | Gly | Ser | Tyr | Arg | Cys | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Val | Ser | Thr | Lys | Asp | Lys | Phe | Asp | Cys | Ser | Asn | Phe | Asn | Leu | Thr | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| His | Glu | Ala | Met | Gly | Thr | Gly | Asp | Leu | Asp | Leu | Leu | Ser | Ala | Phe | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |

Arg Thr Ser Leu Ala Gly Gly Gly Arg Arg Ile Ser Asp Ser His Glu  
275 280 285

Asp Thr Gly Ile Leu Asp Phe Ser Ser Leu Leu Lys Lys Arg Asp Ser  
290 295 300

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

Val Trp Glu Ile Leu Arg Gln Ala Pro Pro Ser Glu Tyr Glu Arg Ile  
325 330 335

Ala Phe Gln Tyr Gly Val Thr Asp Leu Arg Gly Met Leu Lys Arg Leu  
340 345 350

Lys Gly Met Arg Arg Asp Glu Lys Lys Ser Thr Ala Phe Gln Lys Lys  
355 360 365

Leu Glu Pro Ala Tyr Gln Val Ser Lys Gly His Lys Ile Arg Leu Thr  
370 375 380

Val Glu Leu Ala Asp His Asp Ala Glu Val Lys Trp Leu Lys Asn Gly  
385 390 395 400

Gln Glu Ile Gln Met Ser Gly Ser Lys Tyr Ile Phe Glu Ser Ile Gly  
405 410 415

Ala Lys Arg Thr Leu Thr Ile Ser Gln Cys Ser Leu Ala Asp Asp Ala  
420 425 430

Ala Tyr Gln Cys Val Val Gly Gly Glu Lys Cys Ser Thr Glu Leu Phe  
435 440 445

Val Lys Glu Pro Pro Val Leu Ile Thr Arg Pro Leu Glu Asp Gln Leu  
450 455 460

Val Met Val Gly Gln Arg Val Glu Phe Glu Cys Glu Val Ser Glu Glu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 465 |     | 470 |     | 475 |     | 480 |     |     |     |     |     |     |     |     |     |
| Gly | Ala | Gln | Val | Lys | Trp | Leu | Lys | Asp | Gly | Val | Glu | Leu | Thr | Arg | Glu |
|     |     |     | 485 |     |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Glu | Thr | Phe | Lys | Tyr | Arg | Phe | Lys | Lys | Asp | Gly | Gln | Arg | His | His | Leu |
|     |     | 500 |     |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Ile | Ile | Asn | Glu | Ala | Met | Leu | Glu | Asp | Ala | Gly | His | Tyr | Ala | Leu | Cys |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Thr | Ser | Gly | Gly | Gln | Ala | Leu | Ala | Glu | Leu | Ile | Val | Gln | Glu | Lys | Lys |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Leu | Glu | Pro | Pro | Lys | Ile | His | Leu | Asp | Cys | Pro | Gly | Arg | Ile | Pro | Asp |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Thr | Ile | Val | Val | Val | Ala | Gly | Asn | Lys | Leu | Arg | Leu | Asp | Val | Pro | Ile |
|     |     |     | 565 |     |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Ser | Gly | Asp | Pro | Ala | Pro | Thr | Val | Ile | Trp | Gln | Lys | Ala | Ile | Thr | Gln |
|     |     | 580 |     |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Gly | Asn | Lys | Ala | Pro | Ala | Arg | Pro | Ala | Pro | Asp | Ala | Pro | Glu | Asp | Thr |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Gly | Asp | Ser | Asp | Glu | Trp | Val | Phe | Asp | Lys | Lys | Leu | Leu | Cys | Glu | Thr |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Glu | Gly | Arg | Val | Arg | Val | Glu | Thr | Thr | Lys | Asp | Arg | Ser | Ile | Phe | Thr |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |
| Val | Glu | Gly | Ala | Glu | Lys | Glu | Asp | Glu | Gly | Val | Tyr | Thr | Val | Thr | Val |
|     |     |     | 645 |     |     |     |     |     | 650 |     |     |     |     | 655 |     |
| Lys | Asn | Pro | Val | Gly | Glu | Asp | Gln | Val | Asn | Leu | Thr | Val | Lys | Val | Ile |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |

Asp Val Pro Asp Ala Pro Ala Ala Pro Lys Ile Ser Asn Val Gly Glu  
675 680 685

Asp Ser Cys Thr Val Gln Trp Glu Pro Pro Ala Tyr Asp Gly Gly Gln  
690 695 700

Pro Ile Leu Gly Tyr Ile Leu Glu Arg Lys Lys Lys Lys Ser Tyr Arg  
705 710 715 720

Trp Met Arg Leu Asn Phe Asp Leu Ile Gln Glu Leu Ser His Glu Ala  
725 730 735

Arg Arg Met Ile Glu Gly Val Val Tyr Glu Met Arg Val Tyr Ala Val  
740 745 750

Asn Ala Ile Gly Met Ser Arg Pro Ser Pro Ala Ser Gln Pro Phe Met  
755 760 765

Pro Ile Gly Pro Pro Ser Glu Pro Thr His Leu Ala Val Glu Asp Val  
770 775 780

Ser Asp Thr Thr Val Ser Leu Lys Trp Arg Pro Pro Glu Arg Val Gly  
785 790 795 800

Ala Gly Gly Leu Asp Gly Tyr Ser Val Glu Tyr Cys Pro Glu Gly Cys  
805 810 815

Ser Glu Trp Val Ala Ala Leu Gln Gly Leu Thr Glu His Thr Ser Ile  
820 825 830

Leu Val Lys Asp Leu Pro Thr Gly Ala Arg Leu Leu Phe Arg Val Arg  
835 840 845

Ala His Asn Met Ala Gly Pro Gly Ala Pro Val Thr Thr Thr Glu Pro  
850 855 860

Val Thr Val Gln Glu Ile Leu Gln Arg Pro Arg Leu Gln Leu Pro Arg

|     |      |     |     |     |     |      |      |     |     |     |      |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|------|-----|-----|-----|------|------|-----|-----|-----|
| 865 |      | 870 |     | 875 |     | 880  |      |     |     |     |      |      |     |     |     |
| His | Leu  | Arg | Gln | Thr | Ile | Gln  | Lys  | Lys | Val | Gly | Glu  | Pro  | Val | Asn | Leu |
|     |      |     | 885 |     |     |      |      |     | 890 |     |      |      |     | 895 |     |
| Leu | Ile  | Pro | Phe | Gln | Gly | Lys  | Pro  | Arg | Pro | Gln | Val  | Thr  | Trp | Thr | Lys |
|     |      |     | 900 |     |     |      |      | 905 |     |     |      |      | 910 |     |     |
| Glu | Gly  | Gln | Pro | Leu | Ala | Gly  | Glu  | Glu | Val | Ser | Ile  | Arg  | Asn | Ser | Pro |
|     |      | 915 |     |     |     |      | 920  |     |     |     |      | 925  |     |     |     |
| Thr | Asp  | Thr | Ile | Leu | Phe | Ile  | Arg  | Ala | Ala | Arg | Arg  | Val  | His | Ser | Gly |
|     | 930  |     |     |     |     | 935  |      |     |     |     | 940  |      |     |     |     |
| Thr | Tyr  | Gln | Val | Thr | Val | Arg  | Ile  | Glu | Asn | Met | Glu  | Asp  | Lys | Ala | Thr |
| 945 |      |     |     |     | 950 |      |      |     |     | 955 |      |      |     |     | 960 |
| Leu | Val  | Leu | Gln | Val | Val | Asp  | Lys  | Pro | Ser | Pro | Pro  | Gln  | Asp | Leu | Arg |
|     |      |     | 965 |     |     |      |      | 970 |     |     |      |      |     | 975 |     |
| Val | Thr  | Asp | Ala | Trp | Gly | Leu  | Asn  | Val | Ala | Leu | Glu  | Trp  | Lys | Pro | Pro |
|     |      | 980 |     |     |     |      | 985  |     |     |     |      |      | 990 |     |     |
| Gln | Asp  | Val | Gly | Asn | Thr | Glu  | Leu  | Trp | Gly | Tyr | Thr  | Val  | Gln | Lys | Ala |
|     | 995  |     |     |     |     |      | 1000 |     |     |     |      | 1005 |     |     |     |
| Asp | Lys  | Lys | Thr | Met | Glu | Trp  | Phe  | Thr | Val | Leu | Glu  | His  | Tyr | Arg |     |
|     | 1010 |     |     |     |     | 1015 |      |     |     |     | 1020 |      |     |     |     |
| Arg | Thr  | His | Cys | Val | Val | Pro  | Glu  | Leu | Ile | Ile | Gly  | Asn  | Gly | Tyr |     |
|     | 1025 |     |     |     |     | 1030 |      |     |     |     | 1035 |      |     |     |     |
| Tyr | Phe  | Arg | Val | Phe | Ser | Gln  | Asn  | Met | Val | Gly | Phe  | Ser  | Asp | Arg |     |
|     | 1040 |     |     |     |     | 1045 |      |     |     |     | 1050 |      |     |     |     |
| Ala | Ala  | Thr | Thr | Lys | Glu | Pro  | Val  | Phe | Ile | Pro | Arg  | Pro  | Gly | Ile |     |
|     | 1055 |     |     |     |     | 1060 |      |     |     |     | 1065 |      |     |     |     |

Thr Tyr Glu Pro Pro Asn Tyr Lys Ala Leu Asp Phe Ser Glu Ala  
1070 1075 1080

Pro Ser Phe Thr Gln Pro Leu Val Asn Arg Ser Val Ile Ala Gly  
1085 1090 1095

Tyr Thr Ala Met Leu Cys Cys Ala Val Arg Gly Ser Pro Lys Pro  
1100 1105 1110

Lys Ile Ser Trp Phe Lys Asn Gly Leu Asp Leu Gly Glu Asp Ala  
1115 1120 1125

Arg Phe Arg Met Phe Ser Lys Gln Gly Val Leu Thr Leu Glu Ile  
1130 1135 1140

Arg Lys Pro Cys Pro Phe Asp Gly Gly Ile Tyr Val Cys Arg Ala  
1145 1150 1155

Thr Asn Leu Gln Gly Glu Ala Arg Cys Glu Cys Arg Leu Glu Val  
1160 1165 1170

Arg Val Pro Gln  
1175

<210> 106  
<211> 1181  
<212> PRT  
<213> Homo sapiens

<400> 106

Met Pro Glu Pro Gly Lys Lys Pro Val Ser Ala Phe Ser Lys Lys Pro  
1 5 10 15

Arg Ser Val Glu Val Ala Ala Gly Ser Pro Ala Val Phe Glu Ala Glu  
20 25 30

Thr Glu Arg Ala Gly Val Lys Val Arg Trp Gln Arg Gly Gly Ser Asp  
35 40 45

Ile Ser Ala Ser Asn Lys Tyr Gly Leu Ala Thr Glu Gly Thr Arg His  
50 55 60

Thr Leu Thr Val Arg Glu Val Gly Pro Ala Asp Gln Gly Ser Tyr Ala  
65 70 75 80

Val Ile Ala Gly Ser Ser Lys Val Lys Phe Asp Leu Lys Val Ile Glu  
85 90 95

Ala Glu Lys Ala Glu Pro Met Leu Ala Pro Ala Pro Ala Pro Ala Glu  
100 105 110

Ala Thr Gly Ala Pro Gly Glu Ala Pro Ala Pro Ala Ala Glu Leu Gly  
115 120 125

Glu Ser Ala Pro Ser Pro Lys Gly Ser Ser Ser Ala Ala Leu Asn Gly  
130 135 140

Pro Thr Pro Gly Ala Pro Asp Asp Pro Ile Gly Leu Phe Val Met Arg  
145 150 155 160

Pro Gln Asp Gly Glu Val Thr Val Gly Gly Ser Ile Thr Phe Ser Ala  
165 170 175

Arg Val Ala Gly Ala Ser Leu Leu Lys Pro Pro Val Val Lys Trp Phe  
180 185 190

Lys Gly Lys Trp Val Asp Leu Ser Ser Lys Val Gly Gln His Leu Gln  
195 200 205

Leu His Asp Ser Tyr Asp Arg Ala Ser Lys Val Tyr Leu Phe Glu Leu  
210 215 220

His Ile Thr Asp Ala Gln Pro Ala Phe Thr Gly Ser Tyr Arg Cys Glu  
225 230 235 240

Val Ser Thr Lys Asp Lys Phe Asp Cys Ser Asn Phe Asn Leu Thr Val  
245 250 255

His Glu Ala Met Gly Thr Gly Asp Leu Asp Leu Leu Ser Ala Phe Arg  
260 265 270

Arg Thr Ser Leu Ala Gly Gly Gly Arg Arg Ile Ser Asp Ser His Glu  
275 280 285

Asp Thr Gly Ile Leu Asp Phe Ser Ser Leu Leu Lys Lys Arg Asp Ser  
290 295 300

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

Val Trp Glu Ile Leu Arg Gln Ala Pro Pro Ser Glu Tyr Glu Arg Ile  
325 330 335

Ala Phe Gln Tyr Gly Val Thr Asp Leu Arg Gly Met Leu Lys Arg Leu  
340 345 350

Lys Gly Met Arg Arg Asp Glu Lys Lys Ser Thr Ala Phe Gln Lys Lys  
355 360 365

Leu Glu Pro Ala Tyr Gln Val Ser Lys Gly His Lys Ile Arg Leu Thr  
370 375 380

Val Glu Leu Ala Asp His Asp Ala Glu Val Lys Trp Leu Lys Asn Gly  
385 390 395 400

Gln Glu Ile Gln Met Ser Gly Ser Lys Tyr Ile Phe Glu Ser Ile Gly  
405 410 415

Ala Lys Arg Thr Leu Thr Ile Ser Gln Cys Ser Leu Ala Asp Asp Ala  
420 425 430

Ala Tyr Gln Cys Val Val Gly Gly Glu Lys Cys Ser Thr Glu Leu Phe  
435 440 445



Val Lys Glu Pro Pro Val Leu Ile Thr Arg Pro Leu Glu Asp Gln Leu  
450 455 460

Val Met Val Gly Gln Arg Val Glu Phe Glu Cys Glu Val Ser Glu Glu  
465 470 475 480

Gly Ala Gln Val Lys Trp Leu Lys Asp Gly Val Glu Leu Thr Arg Glu  
485 490 495

Glu Thr Phe Lys Tyr Arg Phe Lys Lys Asp Gly Gln Arg His His Leu  
500 505 510

Ile Ile Asn Glu Ala Met Leu Glu Asp Ala Gly His Tyr Ala Leu Cys  
515 520 525

Thr Ser Gly Gly Gln Ala Leu Ala Glu Leu Ile Val Gln Glu Lys Lys  
530 535 540

Leu Glu Pro Arg Gln Glu Pro Pro Lys Ile His Leu Asp Cys Pro Gly  
545 550 555 560

Arg Ile Pro Asp Thr Ile Val Val Val Ala Gly Asn Lys Leu Arg Leu  
565 570 575

Asp Val Pro Ile Ser Gly Asp Pro Ala Pro Thr Val Ile Trp Gln Lys  
580 585 590

Ala Ile Thr Gln Gly Asn Lys Ala Pro Ala Arg Pro Ala Pro Asp Ala  
595 600 605

Pro Glu Asp Thr Gly Asp Ser Asp Glu Trp Val Phe Asp Lys Lys Leu  
610 615 620

Leu Cys Glu Thr Glu Gly Arg Val Arg Val Glu Thr Thr Lys Asp Arg  
625 630 635 640

Ser Ile Phe Thr Val Glu Gly Ala Glu Lys Glu Asp Glu Gly Val Tyr  
645 650 655

Thr Val Thr Val Lys Asn Pro Val Gly Glu Asp Gln Val Asn Leu Thr  
660 665 670

Val Lys Val Ile Asp Val Pro Asp Ala Pro Ala Ala Pro Lys Ile Ser  
675 680 685

Asn Val Gly Glu Asp Ser Cys Thr Val Gln Trp Glu Pro Pro Ala Tyr  
690 695 700

Asp Gly Gly Gln Pro Ile Leu Gly Tyr Ile Leu Glu Arg Lys Lys Lys  
705 710 715 720

Lys Ser Tyr Arg Trp Met Arg Leu Asn Phe Asp Leu Ile Gln Glu Leu  
725 730 735

Ser His Glu Ala Arg Arg Met Ile Glu Gly Val Val Tyr Glu Met Arg  
740 745 750

Val Tyr Ala Val Asn Ala Ile Gly Met Ser Arg Pro Ser Pro Ala Ser  
755 760 765

Gln Pro Phe Met Pro Ile Gly Pro Pro Ser Glu Pro Thr His Leu Ala  
770 775 780

Val Glu Asp Val Ser Asp Thr Thr Val Ser Leu Lys Trp Arg Pro Pro  
785 790 795 800

Glu Arg Val Gly Ala Gly Gly Leu Asp Gly Tyr Ser Val Glu Tyr Cys  
805 810 815

Pro Glu Gly Cys Ser Glu Trp Val Ala Ala Leu Gln Gly Leu Thr Glu  
820 825 830

His Thr Ser Ile Leu Val Lys Asp Leu Pro Thr Gly Ala Arg Leu Leu  
835 840 845

Phe Arg Val Arg Ala His Asn Met Ala Gly Pro Gly Ala Pro Val Thr  
850 855 860

Thr Thr Glu Pro Val Thr Val Gln Glu Ile Leu Gln Arg Pro Arg Leu  
865 870 875 880

Gln Leu Pro Arg His Leu Arg Gln Thr Ile Gln Lys Lys Val Gly Glu  
885 890 895

Pro Val Asn Leu Leu Ile Pro Phe Gln Gly Lys Pro Arg Pro Gln Val  
900 905 910

Thr Trp Thr Lys Glu Gly Gln Pro Leu Ala Gly Glu Glu Val Ser Ile  
915 920 925

Arg Asn Ser Pro Thr Asp Thr Ile Leu Phe Ile Arg Ala Ala Arg Arg  
930 935 940

Val His Ser Gly Thr Tyr Gln Val Thr Val Arg Ile Glu Asn Met Glu  
945 950 955 960

Asp Lys Ala Thr Leu Val Leu Gln Val Val Asp Lys Pro Ser Pro Pro  
965 970 975

Gln Asp Leu Arg Val Thr Asp Ala Trp Gly Leu Asn Val Ala Leu Glu  
980 985 990

Trp Lys Pro Pro Gln Asp Val Gly Asn Thr Glu Leu Trp Gly Tyr Thr  
995 1000 1005

Val Gln Lys Ala Asp Lys Lys Thr Met Glu Trp Phe Thr Val Leu  
1010 1015 1020

Glu His Tyr Arg Arg Thr His Cys Val Val Pro Glu Leu Ile Ile  
1025 1030 1035

Gly Asn Gly Tyr Tyr Phe Arg Val Phe Ser Gln Asn Met Val Gly  
1040 1045 1050

Phe Ser Asp Arg Ala Ala Thr Thr Lys Glu Pro Val Phe Ile Pro  
1055 1060 1065

Arg Pro Gly Ile Thr Tyr Glu Pro Pro Asn Tyr Lys Ala Leu Asp  
1070 1075 1080

Phe Ser Glu Ala Pro Ser Phe Thr Gln Pro Leu Val Asn Arg Ser  
1085 1090 1095

Val Ile Ala Gly Tyr Thr Ala Met Leu Cys Cys Ala Val Arg Gly  
1100 1105 1110

Ser Pro Lys Pro Lys Ile Ser Trp Phe Lys Asn Gly Leu Asp Leu  
1115 1120 1125

Gly Glu Asp Ala Arg Phe Arg Met Phe Ser Lys Gln Gly Val Leu  
1130 1135 1140

Thr Leu Glu Ile Arg Lys Pro Cys Pro Phe Asp Gly Gly Ile Tyr  
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| cagcgaccct gcacctgcga cttcctgcac gggccgcgca cgacgcgccg cgctgccgcg  | 240  |
| cagatcgcg caggcactgct gggcgccgag gagcgcaaag tggaaatcgc cttctaccgg  | 300  |
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| gctgtcatca tgttcatcct caatttcgag gtggtgatgg agaaggacat ggtgggggtcc | 420  |
| ccggctcatg acaccaacca ccggggcccc cccaccagct ggctggcccc aggccgcgcc  | 480  |
| aagaccttcc gcctgaagct gcccgcgctg ctggcgctga cggcccggga gtcgtcggtg  | 540  |
| cggtcgggcg gcgcgggcgg cgcgggcgcc ccgggggccc tgggtggtgga cgtggacctg | 600  |
| acgcccgcgg caccagcag cgagtcgctg gccctggacg aagtgcagc catggacaac    | 660  |
| cacgtggcag ggctcgggcc cgcgaggag cggcgtgcgc tgggtgggtcc cggctctccg  | 720  |
| ccccgcagcg cgccggcca gctcccatcg ccccgggcgc acagcctcaa ccccgacgcc   | 780  |
| tcgggctcca gctgcagcct ggcccggacg cgctcccag aaagctgcgc cagcgtgcgc   | 840  |
| cgcgctcgt cgcccgacga catcgaggcc atgcgcgccg gggctgctgcc cccgccaccg  | 900  |
| cgccacgcca gcaccggggc catgcacca ctgcgcagcg gcttgctcaa ctccacctcg   | 960  |
| gactccgacc tcgtgcgcta ccgcaccatt agcaagattc cccaaatcac cctcaacttt  | 1020 |
| gtggacctca agggcgaccc cttcttggt tcgcccacca gtgacctga gatcatagca    | 1080 |
| cctaagataa aggagcgaac ccacaatgtc actgagaagg tcacccaggt cctgtccctg  | 1140 |
| ggcgccgacg tgctgcctga gtacaagctg caggcaccgc gcatccaccg ctggaccatc  | 1200 |
| ctgcattaca gccccttcaa ggccgtgtgg gactggctca tcctgctgct ggtcatctac  | 1260 |
| acggctgtct tcacacccta ctcggctgcc ttcctgctga aggagacgga agaaggccccg | 1320 |
| cctgctaccg agtgtggcta cgcctgccag ccgctggctg tgggtggacct catcgtggac | 1380 |
| atcatgttca ttgtggacat cctcatcaac ttccgcacca cctacgtcaa tgccaacgag  | 1440 |
| gagggtgtca gccaccccgg ccgcatcgcc gtccactact tcaagggtg gttcctcatc   | 1500 |
| gacatggtgg ccgccatccc cttcgacctg ctcatcttcg gctctggctc tgaggagctg  | 1560 |
| atcgggctgc tgaagactgc gcggctgctg cggctggtgc gcgtggcgcg gaagctggat  | 1620 |

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| ggcctgggcg gcccctccat caaggacaag tatgtgacgg cgctctactt caccttcagc  | 1860 |
| agcctcacca gtgtgggctt cggcaacgtc tctcccaaca ccaactcaga gaagatcttc  | 1920 |
| tccatctgcg tcatgctcat tggctccctc atgtatgcta gcatcttcgg caacgtgtcg  | 1980 |
| gccatcatcc agcggctgta ctcgggcaca gcccgtacc acacacagat gctgcgggtg   | 2040 |
| cgggagttca tccgcttcca ccagatcccc aatcccctgc gccagcgcct cgaggagtac  | 2100 |
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| aaacccttcc gaggggccac caagggtgc cttcgggccc tggccatgaa gttcaagacc   | 2280 |
| acacatgcac cgccagggga cacactgggtg catgctgggg acctgctcac cgccctgtac | 2340 |
| ttcatctccc ggggctccat cgagatcctg cggggcgacg tcgtcgtggc catcctgggg  | 2400 |
| aagaatgaca tctttgggga gcctctgaac ctgtatgcaa ggccctggcaa gtcgaacggg | 2460 |
| gatgtgcggg ccctcaccta ctgtgaccta cacaagatcc atcgggacga cctgctggag  | 2520 |
| gtgctggaca tgtaccctga gttctccgac cacttctggt ccagcctgga gatcaccttc  | 2580 |
| aacctgcgag ataccaacat gatcccgggc tccccggca gtacggagtt agagggtggc   | 2640 |
| ttcagtcggc aacgcaagcg caagtgtcc ttccgcaggc gcacggacaa ggacacggag   | 2700 |
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| ggccggccgg gggggccgtg gggggagagc ccgtccagtg gcccctccag ccctgagagc  | 2820 |
| agtgaggatg agggcccagg ccgcagctcc agccccctcc gcctggtgcc cttctccagc  | 2880 |
| cccaggcccc ccggagagcc gccgggtggg gagcccctga tggaggactg cgagaagagc  | 2940 |
| agcgacactt gcaaccccc tgcaggcgcc ttctcaggag tgtccaacat tttcagcttc   | 3000 |
| tggggggaca gtcggggccg ccagtaccag gagctccctc gatgccccgc cccaccccc   | 3060 |
| agcctcctca acatccccct ctccagcccc ggctcggcggc cccggggcga cgtggagagc | 3120 |

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<400> 108

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Asn Ala Arg Val Glu Asn Cys Ala Val Ile Tyr Cys Asn Asp Gly Phe  
35 40 45

Cys Glu Leu Cys Gly Tyr Ser Arg Ala Glu Val Met Gln Arg Pro Cys  
50 55 60

Thr Cys Asp Phe Leu His Gly Pro Arg Thr Gln Arg Arg Ala Ala Ala  
65 70 75 80

Gln Ile Ala Gln Ala Leu Leu Gly Ala Glu Glu Arg Lys Val Glu Ile  
85 90 95

Ala Phe Tyr Arg Lys Asp Gly Ser Cys Phe Leu Cys Leu Val Asp Val  
100 105 110

Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn  
115 120 125

Phe Glu Val Val Met Glu Lys Asp Met Val Gly Ser Pro Ala His Asp  
130 135 140

Thr Asn His Arg Gly Pro Pro Thr Ser Trp Leu Ala Pro Gly Arg Ala  
145 150 155 160

Lys Thr Phe Arg Leu Lys Leu Pro Ala Leu Leu Ala Leu Thr Ala Arg  
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Glu Ser Ser Val Arg Ser Gly Gly Ala Gly Gly Ala Gly Ala Pro Gly  
180 185 190

Ala Val Val Val Asp Val Asp Leu Thr Pro Ala Ala Pro Ser Ser Glu  
195 200 205

Ser Leu Ala Leu Asp Glu Val Thr Ala Met Asp Asn His Val Ala Gly  
210 215 220

Leu Gly Pro Ala Glu Glu Arg Arg Ala Leu Val Gly Pro Gly Ser Pro  
225 230 235 240

Pro Arg Ser Ala Pro Gly Gln Leu Pro Ser Pro Arg Ala His Ser Leu  
245 250 255

Asn Pro Asp Ala Ser Gly Ser Ser Cys Ser Leu Ala Arg Thr Arg Ser  
260 265 270

Arg Glu Ser Cys Ala Ser Val Arg Arg Ala Ser Ser Ala Asp Asp Ile  
275 280 285

Glu Ala Met Arg Ala Gly Val Leu Pro Pro Pro Pro Arg His Ala Ser  
290 295 300

Thr Gly Ala Met His Pro Leu Arg Ser Gly Leu Leu Asn Ser Thr Ser  
305 310 315 320



Asp Ser Asp Leu Val Arg Tyr Arg Thr Ile Ser Lys Ile Pro Gln Ile  
325 330 335

Thr Leu Asn Phe Val Asp Leu Lys Gly Asp Pro Phe Leu Ala Ser Pro  
340 345 350

Thr Ser Asp Arg Glu Ile Ile Ala Pro Lys Ile Lys Glu Arg Thr His  
355 360 365

Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp Val  
370 375 380

Leu Pro Glu Tyr Lys Leu Gln Ala Pro Arg Ile His Arg Trp Thr Ile  
385 390 395 400

Leu His Tyr Ser Pro Phe Lys Ala Val Trp Asp Trp Leu Ile Leu Leu  
405 410 415

Leu Val Ile Tyr Thr Ala Val Phe Thr Pro Tyr Ser Ala Ala Phe Leu  
420 425 430

Leu Lys Glu Thr Glu Glu Gly Pro Pro Ala Thr Glu Cys Gly Tyr Ala  
435 440 445

Cys Gln Pro Leu Ala Val Val Asp Leu Ile Val Asp Ile Met Phe Ile  
450 455 460

Val Asp Ile Leu Ile Asn Phe Arg Thr Thr Tyr Val Asn Ala Asn Glu  
465 470 475 480

Glu Val Val Ser His Pro Gly Arg Ile Ala Val His Tyr Phe Lys Gly  
485 490 495

Trp Phe Leu Ile Asp Met Val Ala Ala Ile Pro Phe Asp Leu Leu Ile  
500 505 510

Phe Gly Ser Gly Ser Glu Glu Leu Ile Gly Leu Leu Lys Thr Ala Arg  
515 520 525

Leu Leu Arg Leu Val Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser Glu  
530 535 540

Tyr Gly Ala Ala Val Leu Phe Leu Leu Met Cys Thr Phe Ala Leu Ile  
545 550 555 560

Ala His Trp Leu Ala Cys Ile Trp Tyr Ala Ile Gly Asn Met Glu Gln  
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Pro His Met Asp Ser Arg Ile Gly Trp Leu His Asn Leu Gly Asp Gln  
580 585 590

Ile Gly Lys Pro Tyr Asn Ser Ser Gly Leu Gly Gly Pro Ser Ile Lys  
595 600 605

Asp Lys Tyr Val Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser  
610 615 620

Val Gly Phe Gly Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Ile Phe  
625 630 635 640

Ser Ile Cys Val Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile Phe  
645 650 655

Gly Asn Val Ser Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala Arg  
660 665 670

Tyr His Thr Gln Met Leu Arg Val Arg Glu Phe Ile Arg Phe His Gln  
675 680 685

Ile Pro Asn Pro Leu Arg Gln Arg Leu Glu Glu Tyr Phe Gln His Ala  
690 695 700

Trp Ser Tyr Thr Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly Phe  
705 710 715 720

Pro Glu Cys Leu Gln Ala Asp Ile Cys Leu His Leu Asn Arg Ser Leu  
725 730 735

Leu Gln His Cys Lys Pro Phe Arg Gly Ala Thr Lys Gly Cys Leu Arg  
740 745 750

Ala Leu Ala Met Lys Phe Lys Thr Thr His Ala Pro Pro Gly Asp Thr  
755 760 765

Leu Val His Ala Gly Asp Leu Leu Thr Ala Leu Tyr Phe Ile Ser Arg  
770 775 780

Gly Ser Ile Glu Ile Leu Arg Gly Asp Val Val Val Ala Ile Leu Gly  
785 790 795 800

Lys Asn Asp Ile Phe Gly Glu Pro Leu Asn Leu Tyr Ala Arg Pro Gly  
805 810 815

Lys Ser Asn Gly Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His Lys  
820 825 830

Ile His Arg Asp Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Glu Phe  
835 840 845

Ser Asp His Phe Trp Ser Ser Leu Glu Ile Thr Phe Asn Leu Arg Asp  
850 855 860

Thr Asn Met Ile Pro Gly Ser Pro Gly Ser Thr Glu Leu Glu Gly Gly  
865 870 875 880

Phe Ser Arg Gln Arg Lys Arg Lys Leu Ser Phe Arg Arg Arg Thr Asp  
885 890 895

Lys Asp Thr Glu Gln Pro Gly Glu Val Ser Ala Leu Gly Pro Gly Arg  
900 905 910

Ala Gly Ala Gly Pro Ser Ser Arg Gly Arg Pro Gly Gly Pro Trp Gly  
915 920 925

Glu Ser Pro Ser Ser Gly Pro Ser Ser Pro Glu Ser Ser Glu Asp Glu  
930 935 940

Gly Pro Gly Arg Ser Ser Ser Pro Leu Arg Leu Val Pro Phe Ser Ser  
945 950 955 960

Pro Arg Pro Pro Gly Glu Pro Pro Gly Gly Glu Pro Leu Met Glu Asp  
965 970 975

Cys Glu Lys Ser Ser Asp Thr Cys Asn Pro Leu Ser Gly Ala Phe Ser  
980 985 990

Gly Val Ser Asn Ile Phe Ser Phe Trp Gly Asp Ser Arg Gly Arg Gln  
995 1000 1005

Tyr Gln Glu Leu Pro Arg Cys Pro Ala Pro Thr Pro Ser Leu Leu  
1010 1015 1020

Asn Ile Pro Leu Ser Ser Pro Gly Arg Arg Pro Arg Gly Asp Val  
1025 1030 1035

Glu Ser Arg Leu Asp Ala Leu Gln Arg Gln Leu Asn Arg Leu Glu  
1040 1045 1050

Thr Arg Leu Ser Ala Asp Met Ala Thr Val Leu Gln Leu Leu Gln  
1055 1060 1065

Arg Gln Met Thr Leu Val Pro Pro Ala Tyr Ser Ala Val Thr Thr  
1070 1075 1080

Pro Gly Pro Gly Pro Thr Ser Thr Ser Pro Leu Leu Pro Val Ser  
1085 1090 1095

Pro Leu Pro Thr Leu Thr Leu Asp Ser Leu Ser Gln Val Ser Gln  
1100 1105 1110

Phe Met Ala Cys Glu Glu Leu Pro Pro Gly Ala Pro Glu Leu Pro  
 1115 1120 1125

Gln Glu Gly Pro Thr Arg Arg Leu Ser Leu Pro Gly Gln Leu Gly  
 1130 1135 1140

Ala Leu Thr Ser Gln Pro Leu His Arg His Gly Ser Asp Pro Gly  
 1145 1150 1155

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 <211> 3645  
 <212> DNA  
 <213> Homo sapiens

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| ccagggagtg ggggagccag gcaaggcgaa gcccagatc gaatcaggcg tttctttccc   | 1020 |
| aaaggggacc ttgaggtcct gcaggcccag gtggagagga ttatgacccg gaaggagctc  | 1080 |
| ctgacagtct attcttctga ggatgggtct gaggaattcg agaccatagt tttgaaggcc  | 1140 |
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| gtggcttgga accgcgtgga cattgcccag agtgaactct ttcgggggga catccaatgg  | 1260 |
| cggtccttcc atctcgaagc ttccctcatg gacgccctgc tgaatgaccg gcctgagttc  | 1320 |
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| atgggttcca atgcagtttc ctcagctctt ggggcctgtt tgctgctccg ggtgatggca  | 1800 |
| cgcttgagc ctgacgctga ggaggcagca cggaggaaaag acctggcggt caagtttgag  | 1860 |
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| ctcctcctcc gtcgctgccc gctctggggg gatgccactt gcctccagct ggccatgcaa  | 1980 |
| gctgacgccc gtgccttctt tgcccaggat ggggtacagt ctctgctgac acagaagtgg  | 2040 |
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| ccactcatct acaccgcct catcaccttc aggaaatcag aagaggagcc cacacgggag   | 2160 |
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| ccagccgaga agacgccgct ggggggtccc cgccagtcgg gccgtccggg ttgctgcggg  | 2280 |
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| gctttcacgc tgctgtgcga ggaactgcgc cagggcctga gcggaggcgg gggcagcctc   | 2520 |
| gccagcgggg gccccgggccc tggccatgcc tctactgagcc agcgcctgcg cctctacctc | 2580 |
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| gcacaccctc ctggggccca ggcgggcacc tgcgtctccc agtatgcaa ctggctggtg    | 3060 |
| tgctgtctcc tcgtcatctt cctgctcgtg gccaacatcc tgctgggtcaa cttgctcatt  | 3120 |
| gccatgttca gttacacatt cggcaaagta cagggaaca gcgatctcta ctggaaggcg    | 3180 |
| cagcgttacc gcctcatccg ggaattccac tctcggcccg cgctggcccc gccctttatc   | 3240 |
| gtcatctccc acttgccct cctgctcagg caattgtgca ggcgaccccc gagccccag     | 3300 |
| ccgtcctccc cggccctcga gcatttccgg gtttaccttt ctaaggaagc cgagcgggaag  | 3360 |
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| cagctgggac acatccgcga gtacgaacag cgcctgaaaag tgctggagcg ggaggtccag  | 3540 |
| cagtgtagcc gcgtcctggg gtgggtggcc gaggccctga gccgctctgc cttgctgccc   | 3600 |
| ccagggtgggc cgccaccccc tgacctgcct ggggtccaaag actga                 | 3645 |

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 <211> 1214  
 <212> PRT  
 <213> Homo sapiens

<400> 110

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35 40 45

Met Glu Asp Ala Phe Gly Ala Ala Val Val Thr Val Trp Asp Ser Asp  
50 55 60

Ala His Thr Thr Glu Lys Pro Thr Asp Ala Tyr Gly Glu Leu Asp Phe  
65 70 75 80

Thr Gly Ala Gly Arg Lys His Ser Asn Phe Leu Arg Leu Ser Asp Arg  
85 90 95

Thr Asp Pro Ala Ala Val Tyr Ser Leu Val Thr Arg Thr Trp Gly Phe  
100 105 110

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

Val Leu Gln Thr Trp Leu Gln Asp Leu Leu Arg Arg Gly Leu Val Arg  
130 135 140

Ala Ala Gln Ser Thr Gly Ala Trp Ile Val Thr Gly Gly Leu His Thr  
145 150 155 160

Gly Ile Gly Arg His Val Gly Val Ala Val Arg Asp His Gln Met Ala  
165 170 175

Ser Thr Gly Gly Thr Lys Val Val Ala Met Gly Val Ala Pro Trp Gly  
180 185 190



Val Val Arg Asn Arg Asp Thr Leu Ile Asn Pro Lys Gly Ser Phe Pro  
195 200 205

Ala Arg Tyr Arg Trp Arg Gly Asp Pro Glu Asp Gly Val Gln Phe Pro  
210 215 220

Leu Asp Tyr Asn Tyr Ser Ala Phe Phe Leu Val Asp Asp Gly Thr His  
225 230 235 240

Gly Cys Leu Gly Gly Glu Asn Arg Phe Arg Leu Arg Leu Glu Ser Tyr  
245 250 255

Ile Ser Gln Gln Lys Thr Gly Val Gly Gly Thr Gly Ile Asp Ile Pro  
260 265 270

Val Leu Leu Leu Leu Ile Asp Gly Asp Glu Lys Met Leu Thr Arg Ile  
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Glu Asn Ala Thr Gln Ala Gln Leu Pro Cys Leu Leu Val Ala Gly Ser  
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Gly Gly Ala Ala Asp Cys Leu Ala Glu Thr Leu Glu Asp Thr Leu Ala  
305 310 315 320

Pro Gly Ser Gly Gly Ala Arg Gln Gly Glu Ala Arg Asp Arg Ile Arg  
325 330 335

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

Arg Ile Met Thr Arg Lys Glu Leu Leu Thr Val Tyr Ser Ser Glu Asp  
355 360 365

Gly Ser Glu Glu Phe Glu Thr Ile Val Leu Lys Ala Leu Val Lys Ala  
370 375 380

Cys Gly Ser Ser Glu Ala Ser Ala Tyr Leu Asp Glu Leu Arg Leu Ala  
385 390 395 400

Val Ala Trp Asn Arg Val Asp Ile Ala Gln Ser Glu Leu Phe Arg Gly  
405 410 415

Asp Ile Gln Trp Arg Ser Phe His Leu Glu Ala Ser Leu Met Asp Ala  
420 425 430

Leu Leu Asn Asp Arg Pro Glu Phe Val Arg Leu Leu Ile Ser His Gly  
435 440 445

Leu Ser Leu Gly His Phe Leu Thr Pro Met Arg Leu Ala Gln Leu Tyr  
450 455 460

Ser Ala Ala Pro Ser Asn Ser Leu Ile Arg Asn Leu Leu Asp Gln Ala  
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Ser His Ser Ala Gly Thr Lys Ala Pro Ala Leu Lys Gly Gly Ala Ala  
485 490 495

Glu Leu Arg Pro Pro Asp Val Gly His Val Leu Arg Met Leu Leu Gly  
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Lys Met Cys Ala Pro Arg Tyr Pro Ser Gly Gly Ala Trp Asp Pro His  
515 520 525

Pro Gly Gln Gly Phe Gly Glu Ser Met Tyr Leu Leu Ser Asp Lys Ala  
530 535 540

Thr Ser Pro Leu Ser Leu Asp Ala Gly Leu Gly Gln Ala Pro Trp Ser  
545 550 555 560

Asp Leu Leu Leu Trp Ala Leu Leu Leu Asn Arg Ala Gln Met Ala Met  
565 570 575

Tyr Phe Trp Glu Met Gly Ser Asn Ala Val Ser Ser Ala Leu Gly Ala  
580 585 590

Cys Leu Leu Leu Arg Val Met Ala Arg Leu Glu Pro Asp Ala Glu Glu  
595 600 605

Ala Ala Arg Arg Lys Asp Leu Ala Phe Lys Phe Glu Gly Met Gly Val  
610 615 620

Asp Leu Phe Gly Glu Cys Tyr Arg Ser Ser Glu Val Arg Ala Ala Arg  
625 630 635 640

Leu Leu Leu Arg Arg Cys Pro Leu Trp Gly Asp Ala Thr Cys Leu Gln  
645 650 655

Leu Ala Met Gln Ala Asp Ala Arg Ala Phe Phe Ala Gln Asp Gly Val  
660 665 670

Gln Ser Leu Leu Thr Gln Lys Trp Trp Gly Asp Met Ala Ser Thr Thr  
675 680 685

Pro Ile Trp Ala Leu Val Leu Ala Phe Phe Cys Pro Pro Leu Ile Tyr  
690 695 700

Thr Arg Leu Ile Thr Phe Arg Lys Ser Glu Glu Glu Pro Thr Arg Glu  
705 710 715 720

Glu Leu Glu Phe Asp Met Asp Ser Val Ile Asn Gly Glu Gly Pro Val  
725 730 735

Gly Thr Ala Asp Pro Ala Glu Lys Thr Pro Leu Gly Val Pro Arg Gln  
740 745 750

Ser Gly Arg Pro Gly Cys Cys Gly Gly Arg Cys Gly Gly Arg Arg Cys  
755 760 765

Leu Arg Arg Trp Phe His Phe Trp Gly Ala Pro Val Thr Ile Phe Met  
770 775 780

Gly Asn Val Val Ser Tyr Leu Leu Phe Leu Leu Leu Phe Ser Arg Val  
785 790 795 800

Leu Leu Val Asp Phe Gln Pro Ala Pro Pro Gly Ser Leu Glu Leu Leu  
805 810 815

Leu Tyr Phe Trp Ala Phe Thr Leu Leu Cys Glu Glu Leu Arg Gln Gly  
820 825 830

Leu Ser Gly Gly Gly Gly Ser Leu Ala Ser Gly Gly Pro Gly Pro Gly  
835 840 845

His Ala Ser Leu Ser Gln Arg Leu Arg Leu Tyr Leu Ala Asp Ser Trp  
850 855 860

Asn Gln Cys Asp Leu Val Ala Leu Thr Cys Phe Leu Leu Gly Val Gly  
865 870 875 880

Cys Arg Leu Thr Pro Gly Leu Tyr His Leu Gly Arg Thr Val Leu Cys  
885 890 895

Ile Asp Phe Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val  
900 905 910

Asn Lys Gln Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys  
915 920 925

Asp Val Phe Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr  
930 935 940

Gly Val Ala Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro  
945 950 955 960

Ser Ile Leu Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly  
965 970 975

Gln Ile Pro Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn  
980 985 990

Cys Ser Ser Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala  
995 1000 1005

Gly Thr Cys Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu  
1010 1015 1020

Leu Val Ile Phe Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu  
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Leu Ile Ala Met Phe Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn  
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Ser Asp Leu Tyr Trp Lys Ala Gln Arg Tyr Arg Leu Ile Arg Glu  
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Phe His Ser Arg Pro Ala Leu Ala Pro Pro Phe Ile Val Ile Ser  
1070 1075 1080

His Leu Arg Leu Leu Leu Arg Gln Leu Cys Arg Arg Pro Arg Ser  
1085 1090 1095

Pro Gln Pro Ser Ser Pro Ala Leu Glu His Phe Arg Val Tyr Leu  
1100 1105 1110

Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr Trp Glu Ser Val His  
1115 1120 1125

Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp Lys Arg Glu Ser  
1130 1135 1140

Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val Asp Leu Ala  
1145 1150 1155

Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg Leu Lys  
1160 1165 1170

Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly Trp  
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Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly  
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Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp  
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 gttgaagaaa atcaagtcaa cgtagaagtt acgcgcataa aagtgttcga tgcagatgaa 900  
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| atggatagat caagcaaagg ccaaataatt ggaaattttc aagcttttga tgaggacact  | 1260 |
| ggactaccag cccatgcaag atatgtaaaa ttagaagata gagataattg gatctctgtg  | 1320 |
| gattctgtca catctgaaat taaacttgca aaacttcctg attttgaatc tagatatgtt  | 1380 |
| caaaatggca catacactgt aaagattgtg gccatatcag aagattatcc tagaaaaacc  | 1440 |
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| gatggacacc caaacagtgg ccctttcagt ttctccgtca ttgacaaaacc acctggcatg | 1620 |
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| aaaaagcttg ggagaagtga aattcagttc ctgatttcag acaatcaggg ttttagttgt  | 1740 |
| cctgaaaagc aggtccttac actcacagtt tgtgagtgtc tgcattggcag cggctgcagg | 1800 |
| gaagcacagc atgactccta tgtgggcctg ggacccgcag caattgcgct catgattttg  | 1860 |
| gcctttctgc tcctgctatt ggtaccactt ttactgctga tgtgccattg cggaaagggc  | 1920 |
| gccaaaggct ttaccccat acctggcacc atagagatgc tgcattcctg gaataatgaa   | 1980 |
| ggagcaccac ctgaagacaa ggtggtgcca tcatttctgc cagtggatca agggggcagt  | 2040 |
| ctagtaggaa gaaatggagt aggaggatat gccaaaggaag ccacgatgaa aggaagtagc | 2100 |
| tctgcttcca ttgtcaaagg gcaacatgag atgtccgaga tggatggaag gtgggaagaa  | 2160 |
| cacagaagcc tgctttctgg tagagctacc cagtttacag gggccacagg cgctatcatg  | 2220 |
| accactgaaa ccacgaagac cgcaagggcc acaggggctt ccagagacat ggccggagct  | 2280 |
| caggcagctg ctgttgcaact gaacgaagaa ttcttaagaa attatttcac tgataaagcg | 2340 |
| gcctcttaca ctgaggaaga tgaaaaatcac acagccaaag attgccttct ggtttattct | 2400 |
| caggaagaaa ctgaatcgct gaatgcttct attgggtgtt gcagttttat tgaaggagag  | 2460 |
| ctagatgacc gcttcttaga tgatttggga cttaaattca agacactagc tgaagtttgc  | 2520 |

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| acctactcct ctggcagtag cttcccagtt ccaaaatctt tgcaagaagc caatgcagag  | 2700 |
| aaagtaactc aggaaatagt cactgaaaga tctgtgtctt ctaggcaggc gcaaaaggta  | 2760 |
| gctacacctc ttcctgaccc aatggcttct agaaatgtga tagcaacaga aacttcctat  | 2820 |
| gtcacagggt ccactatgcc accaaccact gtgacctgg gtcctagcca gccacagagc   | 2880 |
| cttattgtga cagagagggt gtatgctcca gcttctacct tggtagatca gccttatgct  | 2940 |
| aatgaaggta cagttgtggt cactgaaaga gtaatacagc ctcattggggg tggatcgaat | 3000 |
| cctctggaag gcactcagca tcttcaagat gtaccttacg tcatgggtgag ggaaagagag | 3060 |
| agcttccttg ccccccagctc aggtgtgcag cctactctgg ccatgcctaa tatagcagta | 3120 |
| ggacagaatg tgacagtgc agaaagagtt ctagcacctg cttccactct gcaatccagt   | 3180 |
| taccagattc ccactgaaaa ttctatgacg gctaggaaca ccacggtgtc tggagctgga  | 3240 |
| gtccctggcc ctctgccaga ttttggttta gaggaatctg gtcattctaa ttctaccata  | 3300 |
| accacatctt ccaccagagt taccaagcat agcactgtac agcattctta ctcctaa     | 3357 |

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 <212> PRT  
 <213> Homo sapiens

<400> 112

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| Met | Ala | Arg | Ser | Pro | Gly | Arg | Ala | Tyr | Ala | Leu | Leu | Leu | Leu | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Phe | Asn | Val | Gly | Ser | Gly | Leu | His | Leu | Gln | Val | Leu | Ser | Thr | Arg |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Glu | Asn | Lys | Leu | Leu | Pro | Lys | His | Pro | His | Leu | Val | Arg | Gln | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Trp | Ile | Thr | Ala | Pro | Val | Ala | Leu | Arg | Glu | Gly | Glu | Asp | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |



Ser Lys Lys Asn Pro Ile Ala Lys Ile His Ser Asp Leu Ala Glu Glu  
65 70 75 80

Arg Gly Leu Lys Ile Thr Tyr Lys Tyr Thr Gly Lys Gly Ile Thr Glu  
85 90 95

Pro Pro Phe Gly Ile Phe Val Phe Asn Lys Asp Thr Gly Glu Leu Asn  
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Val Thr Ser Ile Leu Asp Arg Glu Glu Thr Pro Phe Phe Leu Leu Thr  
115 120 125

Gly Tyr Ala Leu Asp Ala Arg Gly Asn Asn Val Glu Lys Pro Leu Glu  
130 135 140

Leu Arg Ile Lys Val Leu Asp Ile Asn Asp Asn Glu Pro Val Phe Thr  
145 150 155 160

Gln Asp Val Phe Val Gly Ser Val Glu Glu Leu Ser Ala Ala His Thr  
165 170 175

Leu Val Met Lys Ile Asn Ala Thr Asp Ala Asp Glu Pro Asn Thr Leu  
180 185 190

Asn Ser Lys Ile Ser Tyr Arg Ile Val Ser Leu Glu Pro Ala Tyr Pro  
195 200 205

Pro Val Phe Tyr Leu Asn Lys Asp Thr Gly Glu Ile Tyr Thr Thr Ser  
210 215 220

Val Thr Leu Asp Arg Glu Glu His Ser Ser Tyr Thr Leu Thr Val Glu  
225 230 235 240

Ala Arg Asp Gly Asn Gly Glu Val Thr Asp Lys Pro Val Lys Gln Ala  
245 250 255

Gln Val Gln Ile Arg Ile Leu Asp Val Asn Asp Asn Ile Pro Val Val  
260 265 270

Glu Asn Lys Val Leu Glu Gly Met Val Glu Glu Asn Gln Val Asn Val  
275 280 285

Glu Val Thr Arg Ile Lys Val Phe Asp Ala Asp Glu Ile Gly Ser Asp  
290 295 300

Asn Trp Leu Ala Asn Phe Thr Phe Ala Ser Gly Asn Glu Gly Gly Tyr  
305 310 315 320

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

Ile Lys Glu Val Asp Tyr Glu Glu Met Lys Asn Leu Asp Phe Ser Val  
340 345 350

Ile Val Ala Asn Lys Ala Ala Phe His Lys Ser Ile Arg Ser Lys Tyr  
355 360 365

Lys Pro Thr Pro Ile Pro Ile Lys Val Lys Val Lys Asn Val Lys Glu  
370 375 380

Gly Ile His Phe Lys Ser Ser Val Ile Ser Ile Tyr Val Ser Glu Ser  
385 390 395 400

Met Asp Arg Ser Ser Lys Gly Gln Ile Ile Gly Asn Phe Gln Ala Phe  
405 410 415

Asp Glu Asp Thr Gly Leu Pro Ala His Ala Arg Tyr Val Lys Leu Glu  
420 425 430

Asp Arg Asp Asn Trp Ile Ser Val Asp Ser Val Thr Ser Glu Ile Lys  
435 440 445

Leu Ala Lys Leu Pro Asp Phe Glu Ser Arg Tyr Val Gln Asn Gly Thr  
450 455 460

Tyr Thr Val Lys Ile Val Ala Ile Ser Glu Asp Tyr Pro Arg Lys Thr  
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Ile Thr Gly Thr Val Leu Ile Asn Val Glu Asp Ile Asn Asp Asn Cys  
485 490 495

Pro Thr Leu Ile Glu Pro Val Gln Thr Ile Cys His Asp Ala Glu Tyr  
500 505 510

Val Asn Val Thr Ala Glu Asp Leu Asp Gly His Pro Asn Ser Gly Pro  
515 520 525

Phe Ser Phe Ser Val Ile Asp Lys Pro Pro Gly Met Ala Glu Lys Trp  
530 535 540

Lys Ile Ala Arg Gln Glu Ser Thr Ser Val Leu Leu Gln Gln Ser Glu  
545 550 555 560

Lys Lys Leu Gly Arg Ser Glu Ile Gln Phe Leu Ile Ser Asp Asn Gln  
565 570 575

Gly Phe Ser Cys Pro Glu Lys Gln Val Leu Thr Leu Thr Val Cys Glu  
580 585 590

Cys Leu His Gly Ser Gly Cys Arg Glu Ala Gln His Asp Ser Tyr Val  
595 600 605

Gly Leu Gly Pro Ala Ala Ile Ala Leu Met Ile Leu Ala Phe Leu Leu  
610 615 620

Leu Leu Leu Val Pro Leu Leu Leu Leu Met Cys His Cys Gly Lys Gly  
625 630 635 640

Ala Lys Gly Phe Thr Pro Ile Pro Gly Thr Ile Glu Met Leu His Pro  
645 650 655

Trp Asn Asn Glu Gly Ala Pro Pro Glu Asp Lys Val Val Pro Ser Phe  
660 665 670

Leu Pro Val Asp Gln Gly Gly Ser Leu Val Gly Arg Asn Gly Val Gly  
675 680 685

Gly Met Ala Lys Glu Ala Thr Met Lys Gly Ser Ser Ser Ala Ser Ile  
690 695 700

Val Lys Gly Gln His Glu Met Ser Glu Met Asp Gly Arg Trp Glu Glu  
705 710 715 720

His Arg Ser Leu Leu Ser Gly Arg Ala Thr Gln Phe Thr Gly Ala Thr  
725 730 735

Gly Ala Ile Met Thr Thr Glu Thr Thr Lys Thr Ala Arg Ala Thr Gly  
740 745 750

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

Glu Glu Phe Leu Arg Asn Tyr Phe Thr Asp Lys Ala Ala Ser Tyr Thr  
770 775 780

Glu Glu Asp Glu Asn His Thr Ala Lys Asp Cys Leu Leu Val Tyr Ser  
785 790 795 800

Gln Glu Glu Thr Glu Ser Leu Asn Ala Ser Ile Gly Cys Cys Ser Phe  
805 810 815

Ile Glu Gly Glu Leu Asp Asp Arg Phe Leu Asp Asp Leu Gly Leu Lys  
820 825 830

Phe Lys Thr Leu Ala Glu Val Cys Leu Gly Gln Lys Ile Asp Ile Asn  
835 840 845

Lys Glu Ile Glu Gln Arg Gln Lys Pro Ala Thr Glu Thr Ser Met Asn  
850 855 860

Thr Ala Ser His Ser Leu Cys Glu Gln Thr Met Val Asn Ser Glu Asn  
865 870 875 880

Thr Tyr Ser Ser Gly Ser Ser Phe Pro Val Pro Lys Ser Leu Gln Glu  
885 890 895

Ala Asn Ala Glu Lys Val Thr Gln Glu Ile Val Thr Glu Arg Ser Val  
900 905 910

Ser Ser Arg Gln Ala Gln Lys Val Ala Thr Pro Leu Pro Asp Pro Met  
915 920 925

Ala Ser Arg Asn Val Ile Ala Thr Glu Thr Ser Tyr Val Thr Gly Ser  
930 935 940

Thr Met Pro Pro Thr Thr Val Ile Leu Gly Pro Ser Gln Pro Gln Ser  
945 950 955 960

Leu Ile Val Thr Glu Arg Val Tyr Ala Pro Ala Ser Thr Leu Val Asp  
965 970 975

Gln Pro Tyr Ala Asn Glu Gly Thr Val Val Val Thr Glu Arg Val Ile  
980 985 990

Gln Pro His Gly Gly Gly Ser Asn Pro Leu Glu Gly Thr Gln His Leu  
995 1000 1005

Gln Asp Val Pro Tyr Val Met Val Arg Glu Arg Glu Ser Phe Leu  
1010 1015 1020

Ala Pro Ser Ser Gly Val Gln Pro Thr Leu Ala Met Pro Asn Ile  
1025 1030 1035

Ala Val Gly Gln Asn Val Thr Val Thr Glu Arg Val Leu Ala Pro  
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Ala Ser Thr Leu Gln Ser Ser Tyr Gln Ile Pro Thr Glu Asn Ser  
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Met Thr Ala Arg Asn Thr Thr Val Ser Gly Ala Gly Val Pro Gly  
1070 1075 1080

Pro Leu Pro Asp Phe Gly Leu Glu Glu Ser Gly His Ser Asn Ser  
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Thr Ile Thr Thr Ser Ser Thr Arg Val Thr Lys His Ser Thr Val  
1100 1105 1110

Gln His Ser Tyr Ser  
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ctagttagga ttttattact ggcagcatgt atatcttttg ttttggcttg gtttgaagaa 240  
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gaatatgagc ctgaaatggg caaagtgtat cgacaggaca gaaagagtgt gcagcggatt 420  
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| gacccgggtc atggaggggtc ctggatcaga ggtgctatctt actactttaa aattgcagtg | 900  |
| gccctggctg tagcagccat tcctgaagggt ctgcctgcag tcatcaccac ctgcctggct  | 960  |
| cttggaaactc gcagaatggc aaagaaaaat gccattgttc gaagcctccc gtctgtggaa  | 1020 |
| acccttgggtt gtacttctgt tatctgctca gacaagactg gtacacttac aacaaaccag  | 1080 |
| atgtcagtct gcaggatgtt cattctggac agagtgggaag gtgatacttg ttcccttaat  | 1140 |
| gagtttacca taactggatc aacttatgca cctattggag aagtgcataa agatgataaa   | 1200 |
| ccagtgaatt gtcaccagta tgatgggtctg gtagaattag caacaatttg tgctctttgt  | 1260 |
| aatgactctg ctttggatta caatgaggca aagggtgtgt atgaaaaagt tggagaagct   | 1320 |
| acagagactg ctctcacttg cctagtagag aagatgaatg tatttgatac cgaattgaag   | 1380 |
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| aaggaattca ctctagagtt ttcacgtgac agaaagtcaa tgtcggttta ctgtacacca   | 1500 |
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|                                                                    |      |
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| ggatttcccc aggctttgat tcctgttcag ctgctctggg tcaatctggt gacagatggc  | 2400 |
| ctgcctgcca ctgcactggg gttcaaccct cctgatctgg acatcatgaa taaacctccc  | 2460 |
| cggaaaccaa aggaaccatt gatcagcggg tggctctttt tccgttactt ggctattggc  | 2520 |
| tgttacgtcg gcgctgctac cgtgggtgct gctgcatggt gggtcattgc tgctgacggt  | 2580 |
| ggccaagag tgtccttcta ccagctgagt catttcctac agtgtaaaga ggacaacccg   | 2640 |
| gactttgaag gcgtggattg tgcaatcttt gaatccccat acccgatgac aatggcgctc  | 2700 |
| tctgttctag taactataga aatgtgtaac gccctcaaca gcttgtccga aaaccagtcc  | 2760 |
| ttgctgagga tgccccctg ggagaacatc tggctcgtgg gctccatctg cctgtccatg   | 2820 |
| tcactccact tcctgatcct ctatgtcgaa cccttgccac tcactttcca gatcacaccg  | 2880 |
| ctgaacgtga cccagtggct gatgggtgctg aaaatctcct tgcccgtgat tctcatggat | 2940 |
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<400> 114

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Ala | His | Thr | Lys | Thr | Val | Glu | Glu | Val | Leu | Gly | His | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | Asn | Glu | Ser | Thr | Gly | Leu | Ser | Leu | Glu | Gln | Val | Lys | Lys | Leu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Glu | Arg | Trp | Gly | Ser | Asn | Glu | Leu | Pro | Ala | Glu | Glu | Gly | Lys | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Glu | Leu | Val | Ile | Glu | Gln | Phe | Glu | Asp | Leu | Leu | Val | Arg | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |



Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu Glu  
65 70 75 80

Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu Leu  
85 90 95

Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn Ala  
100 105 110

Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly Lys  
115 120 125

Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys Asp  
130 135 140

Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val Pro  
145 150 155 160

Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val Asp  
165 170 175

Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr Asp  
180 185 190

Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met Leu  
195 200 205

Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val Val  
210 215 220

Ala Thr Gly Val Asn Thr Glu Ile Gly Lys Ile Arg Asp Glu Met Val  
225 230 235 240

Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu Phe  
245 250 255

Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val Trp  
260 265 270

Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser Trp  
275 280 285

Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala Val  
290 295 300

Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu Ala  
305 310 315 320

Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser Leu  
325 330 335

Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp Lys  
340 345 350

Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Arg Met Phe Ile  
355 360 365

Leu Asp Arg Val Glu Gly Asp Thr Cys Ser Leu Asn Glu Phe Thr Ile  
370 375 380

Thr Gly Ser Thr Tyr Ala Pro Ile Gly Glu Val His Lys Asp Asp Lys  
385 390 395 400

Pro Val Asn Cys His Gln Tyr Asp Gly Leu Val Glu Leu Ala Thr Ile  
405 410 415

Cys Ala Leu Cys Asn Asp Ser Ala Leu Asp Tyr Asn Glu Ala Lys Gly  
420 425 430

Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Cys Leu  
435 440 445

Val Glu Lys Met Asn Val Phe Asp Thr Glu Leu Lys Gly Leu Ser Lys  
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Ile Glu Arg Ala Asn Ala Cys Asn Ser Val Ile Lys Gln Leu Met Lys  
465 470 475 480

Lys Glu Phe Thr Leu Glu Phe Ser Arg Asp Arg Lys Ser Met Ser Val  
485 490 495

Tyr Cys Thr Pro Asn Lys Pro Ser Arg Thr Ser Met Ser Lys Met Phe  
500 505 510

Val Lys Gly Ala Pro Glu Gly Val Ile Asp Arg Cys Thr His Ile Arg  
515 520 525

Val Gly Ser Thr Lys Val Pro Met Thr Ser Gly Val Lys Gln Lys Ile  
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Met Ser Val Ile Arg Glu Trp Gly Ser Gly Ser Asp Thr Leu Arg Cys  
545 550 555 560

Leu Ala Leu Ala Thr His Asp Asn Pro Leu Arg Arg Glu Glu Met His  
565 570 575

Leu Glu Asp Ser Ala Asn Phe Ile Lys Tyr Glu Thr Asn Leu Thr Phe  
580 585 590

Val Gly Cys Val Gly Met Leu Asp Pro Pro Arg Ile Glu Val Ala Ser  
595 600 605

Ser Val Lys Leu Cys Arg Gln Ala Gly Ile Arg Val Ile Met Ile Thr  
610 615 620

Gly Asp Asn Lys Gly Thr Ala Val Ala Ile Cys Arg Arg Ile Gly Ile  
625 630 635 640

Phe Gly Gln Asp Glu Asp Val Thr Ser Lys Ala Phe Thr Gly Arg Glu  
645 650 655

Phe Asp Glu Leu Asn Pro Ser Ala Gln Arg Asp Ala Cys Leu Asn Ala  
660 665 670

Arg Cys Phe Ala Arg Val Glu Pro Ser His Lys Ser Lys Ile Val Glu  
675 680 685

Phe Leu Gln Ser Phe Asp Glu Ile Thr Ala Met Thr Gly Asp Gly Val  
690 695 700

Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met Gly  
705 710 715 720

Ser Gly Thr Ala Val Ala Lys Thr Ala Ser Glu Met Val Leu Ala Asp  
725 730 735

Asp Asn Phe Ser Thr Ile Val Ala Ala Val Glu Glu Gly Arg Ala Ile  
740 745 750

Tyr Asn Asn Met Lys Gln Phe Ile Arg Tyr Leu Ile Ser Ser Asn Val  
755 760 765

Gly Glu Val Val Cys Ile Phe Leu Thr Ala Ala Leu Gly Phe Pro Glu  
770 775 780

Ala Leu Ile Pro Val Gln Leu Leu Trp Val Asn Leu Val Thr Asp Gly  
785 790 795 800

Leu Pro Ala Thr Ala Leu Gly Phe Asn Pro Pro Asp Leu Asp Ile Met  
805 810 815

Asn Lys Pro Pro Arg Asn Pro Lys Glu Pro Leu Ile Ser Gly Trp Leu  
820 825 830

Phe Phe Arg Tyr Leu Ala Ile Gly Cys Tyr Val Gly Ala Ala Thr Val  
835 840 845

Gly Ala Ala Ala Trp Trp Phe Ile Ala Ala Asp Gly Gly Pro Arg Val  
850 855 860

Ser Phe Tyr Gln Leu Ser His Phe Leu Gln Cys Lys Glu Asp Asn Pro  
 865 870 875 880

Asp Phe Glu Gly Val Asp Cys Ala Ile Phe Glu Ser Pro Tyr Pro Met  
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Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala Leu  
 900 905 910

Asn Ser Leu Ser Glu Asn Gln Ser Leu Leu Arg Met Pro Pro Trp Glu  
 915 920 925

Asn Ile Trp Leu Val Gly Ser Ile Cys Leu Ser Met Ser Leu His Phe  
 930 935 940

Leu Ile Leu Tyr Val Glu Pro Leu Pro Leu Ile Phe Gln Ile Thr Pro  
 945 950 955 960

Leu Asn Val Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro Val  
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Pro Ala Ile Leu Glu  
 995

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 gagcacatcc ccaccccggg ggctgccctg tcgtggcagg cggccatcga cgcagcccgg 180  
 caggctaagc tgatgggcag cgctggcaat gcgaccatct ccacagtcag ctccacgcag 240

|                                                                    |      |
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| cggaagcggc agcaatatgg gaaacccaag aagcagggca gcaccacggc cacacgcccg  | 300  |
| ccccgagccc tgctctgcct gacctgaag aaccccatcc ggagggcctg catcagcatt   | 360  |
| gtcgaatgga aaccatttga aataattatt ttactgacta tttttgcaa ttgtgtggcc   | 420  |
| ttagcgatct atattccctt tccagaagat gattccaacg ccaccaattc caacctggaa  | 480  |
| cgagtggaat atctctttct cataattttt acggtggaag cgtttttaaa agtaatcgcc  | 540  |
| tatggactcc tctttcaccc caatgcctac ctccgcaacg gctggaacct actagatttt  | 600  |
| ataattgtgg ttgtggggct ttttagtgca attttagaac aagcaaccaa agcagatggg  | 660  |
| gcaaacgctc tcggagggaag aggggccgga tttgatgtga aggcgctgag ggccttccgc | 720  |
| gtgctgcgcc ccctgcggct ggtgtccgga gtcccaagtc tccagggtgt cctgaattcc  | 780  |
| atcatcaagg ccatggctcc cctgctgcac atcgccctgc ttgtgctgtt tgtcatcatc  | 840  |
| atctacgcca tcatcggctt ggagctcttc atggggaaga tgcacaagac ctgctacaac  | 900  |
| caggagggca tagcagatgt tccagcagaa gatgaccctt ccccttgtgc gctggaaacg  | 960  |
| ggccacgggc ggagtgcca gaacggcacg gtgtgcaagc ccggctggga tgggtccaag   | 1020 |
| cacggcatca ccaactttga caactttgcc ttcgccatgc tcacgggtgtt ccagtgcac  | 1080 |
| accatggagg gctggacgga cgtgctgtac tgggtcaatg atgccgtagg aagggactgg  | 1140 |
| ccctggatct attttgttac actaatcatc atagggtcat tttttgtact taacttggtt  | 1200 |
| ctcgggtgtc ttagcggaga gttttccaaa gagagggaga aggccaaggc ccggggagat  | 1260 |
| ttccagaagc tgcgggagaa gcagcagcta gaagaggatc tcaaaggcta cctggattgg  | 1320 |
| atcactcagg ccgaagacat cgatcctgag aatgaggacg aaggcatgga tgaggagaag  | 1380 |
| ccccgaaaca tgagcatgcc caccagtga accgagtccg tcaacaccga aaacgtggct   | 1440 |
| ggagggtgaca tcgagggaga aaactgcggg gccaggctgg cccaccggat ctccaagtca | 1500 |
| aagttcagcc gctactggcg ccggtggaat cggttctgca gaaggaagtg ccgcgccgca  | 1560 |
| gtcaagtcta atgtcttcta ctggctgggtg attttcctgg tgttcctcaa cacgctcacc | 1620 |
| attgcctctg agcactacaa ccagcccaac tggctcacag aagtccaaga cacggcaaac  | 1680 |
| aaggccctgc tggccctgtt cacggcagag atgctcctga agatgtacag cctgggcctg  | 1740 |

|                                                                    |      |
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| ctggagacca tcctggtgga gaccaagatc atgtcccccac tgggcatctc cgtgctcaga | 1860 |
| tgcgtccggc tgctgaggat tttcaagatc acgagggtact ggaactcctt gagcaacctg | 1920 |
| gtggcatcct tgctgaactc tgtgcgctcc atcgccctccc tgctccttct cctcttcctc | 1980 |
| ttcatcatca tcttctccct cctgggggatg cagctctttg gaggaaagtt caactttgat | 2040 |
| gagatgcaga cccggaggag cacattcgat aacttcccc agtccctcct cactgtgttt   | 2100 |
| cagatcctga ccggggagga ctggaattcg gtgatgtatg atgggatcat ggcttatggc  | 2160 |
| ggccccctctt ttccagggat gttagtctgt atttacttca tcatcctctt catctgtgga | 2220 |
| aactatatcc tactgaatgt gttcttggcc attgctgtgg acaacctggc tgatgctgag  | 2280 |
| agcctcacat ctgccccaaa ggaggaggaa gaggagaagg agagaaagaa gctggccagg  | 2340 |
| actgccagcc cagagaagaa acaagagttg gtggagaagc cggcagtggg ggaatccaag  | 2400 |
| gaggagaaga ttgagctgaa atccatcacg gctgacggag agtctccacc cgccaccaag  | 2460 |
| atcaacatgg atgacctcca gccaatgaa aatgaggata agagccccta cccaaccca    | 2520 |
| gaaactacag gagaagagga tgaggaggag ccagagatgc ctgtcggccc tcgcccacga  | 2580 |
| ccactctctg agcttcacct taaggaaaag gcagtgccca tgccagaagc cagcgcgttt  | 2640 |
| ttcatcttca gctctaacaa caggtttcgc ctccagtgcc accgcattgt caatgacacg  | 2700 |
| atcttcacca acctgacct cttcttcatt ctgctcagca gcatttcctt ggctgctgag   | 2760 |
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| ctcatctcct ttggcatcca gtccagtgca atcaatgtcg tgaagatctt gcgagtcctg  | 3060 |
| cgagtactca ggccccctgag ggccatcaac agggccaagg ggctaaagca tgtggttcag | 3120 |
| tgtgtgtttg tcgccatccg gaccatcggg aacatcgtga ttgtcaccac cctgctgcag  | 3180 |
| ttcatgtttg cctgcatcgg ggtccagctc ttcaagggaag agctgtacac ctgttcagac | 3240 |

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| aggtacatcc ccaagaacca gcaccagtac aaagtgtggt acgtggtcaa ctccacctac   | 3720 |
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| ccagagtccg agcccagcaa cagcacggag ggtgaaacac cctgtggtag cagctttgct   | 4500 |
| gtcttctact tcatcagctt ctacatgctc tgtgccttcc tgatcatcaa cctctttgta   | 4560 |
| gctgtcatca tggacaactt tgactacctg acaagggact ggtccatcct tgggtcccccac | 4620 |
| cacctggatg agtttaaaag aatctgggca gagtatgacc ctgaagccaa gggtcgtatc   | 4680 |
| aaacacctgg atgtggtgac cctcctccgg cggattcagc cgccactagg ttttgggaag   | 4740 |



|                                                                    |      |
|--------------------------------------------------------------------|------|
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| gcgggcagca gccagggcga cactgagtcg ccatcccacg agaagctggg ggactccacc  | 5400 |
| ttcaccccga gcagctactc gtccaccggc tccaacgcca acatcaacaa cgccaacaac  | 5460 |
| accgccctgg gtcgcctccc tcgccccgcc ggctacccca gcacggtcag cactgtggag  | 5520 |
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| gaagtgaaga tgaaccatga cacggaggcc tgcagtgagc ccagcctgct ctccacagag  | 5820 |
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| gacatccggc aatctccgaa gaggggtttc ctccgctctg cctcactagg tcgaagggcc  | 5940 |
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| acagtcttgc ctttgcattc ggttcatcat caggcattgg cagtggcagg cctgagcccc  | 6060 |
| ctcctccaga gaagccattc ccctgcctca ttccctaggc cttttgccac cccaccagcc  | 6120 |
| acacctggca gccgaggctg gccccacag cccgtcccca ccctgcggct tgagggggtc   | 6180 |
| gagtccagtg agaaactcaa cagcagcttc ccatccatcc actgcggctc ctgggctgag  | 6240 |

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ctgtag                                                                    6666

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<212> PRT
<213> Homo sapiens

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Gly Ser Asn Tyr Gly Ser Pro Arg Pro Ala His Ala Asn Met Asn Ala
20              25              30

```

```

Asn Ala Ala Ala Gly Leu Ala Pro Glu His Ile Pro Thr Pro Gly Ala
35              40              45

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Ala Leu Ser Trp Gln Ala Ala Ile Asp Ala Ala Arg Gln Ala Lys Leu
50              55              60

```

```

Met Gly Ser Ala Gly Asn Ala Thr Ile Ser Thr Val Ser Ser Thr Gln
65              70              75              80

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```

Arg Lys Arg Gln Gln Tyr Gly Lys Pro Lys Lys Gln Gly Ser Thr Thr
85              90              95

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```

Ala Thr Arg Pro Pro Arg Ala Leu Leu Cys Leu Thr Leu Lys Asn Pro
100             105             110

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Ile Arg Arg Ala Cys Ile Ser Ile Val Glu Trp Lys Pro Phe Glu Ile  
115 120 125

Ile Ile Leu Leu Thr Ile Phe Ala Asn Cys Val Ala Leu Ala Ile Tyr  
130 135 140

Ile Pro Phe Pro Glu Asp Asp Ser Asn Ala Thr Asn Ser Asn Leu Glu  
145 150 155 160

Arg Val Glu Tyr Leu Phe Leu Ile Ile Phe Thr Val Glu Ala Phe Leu  
165 170 175

Lys Val Ile Ala Tyr Gly Leu Leu Phe His Pro Asn Ala Tyr Leu Arg  
180 185 190

Asn Gly Trp Asn Leu Leu Asp Phe Ile Ile Val Val Val Gly Leu Phe  
195 200 205

Ser Ala Ile Leu Glu Gln Ala Thr Lys Ala Asp Gly Ala Asn Ala Leu  
210 215 220

Gly Gly Lys Gly Ala Gly Phe Asp Val Lys Ala Leu Arg Ala Phe Arg  
225 230 235 240

Val Leu Arg Pro Leu Arg Leu Val Ser Gly Val Pro Ser Leu Gln Val  
245 250 255

Val Leu Asn Ser Ile Ile Lys Ala Met Val Pro Leu Leu His Ile Ala  
260 265 270

Leu Leu Val Leu Phe Val Ile Ile Ile Tyr Ala Ile Ile Gly Leu Glu  
275 280 285

Leu Phe Met Gly Lys Met His Lys Thr Cys Tyr Asn Gln Glu Gly Ile  
290 295 300

Ala Asp Val Pro Ala Glu Asp Asp Pro Ser Pro Cys Ala Leu Glu Thr  
305 310 315 320

Gly His Gly Arg Gln Cys Gln Asn Gly Thr Val Cys Lys Pro Gly Trp  
325 330 335

Asp Gly Pro Lys His Gly Ile Thr Asn Phe Asp Asn Phe Ala Phe Ala  
340 345 350

Met Leu Thr Val Phe Gln Cys Ile Thr Met Glu Gly Trp Thr Asp Val  
355 360 365

Leu Tyr Trp Val Asn Asp Ala Val Gly Arg Asp Trp Pro Trp Ile Tyr  
370 375 380

Phe Val Thr Leu Ile Ile Ile Gly Ser Phe Phe Val Leu Asn Leu Val  
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Leu Gly Val Leu Ser Gly Glu Phe Ser Lys Glu Arg Glu Lys Ala Lys  
405 410 415

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

Gly Gly Asp Ile Glu Gly Glu Asn Cys Gly Ala Arg Leu Ala His Arg  
485 490 495

Ile Ser Lys Ser Lys Phe Ser Arg Tyr Trp Arg Arg Trp Asn Arg Phe  
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Cys Arg Arg Lys Cys Arg Ala Ala Val Lys Ser Asn Val Phe Tyr Trp  
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Leu Val Ile Phe Leu Val Phe Leu Asn Thr Leu Thr Ile Ala Ser Glu  
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His Tyr Asn Gln Pro Asn Trp Leu Thr Glu Val Gln Asp Thr Ala Asn  
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Lys Ala Leu Leu Ala Leu Phe Thr Ala Glu Met Leu Leu Lys Met Tyr  
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Ser Leu Gly Leu Gln Ala Tyr Phe Val Ser Leu Phe Asn Arg Phe Asp  
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Cys Phe Val Val Cys Gly Gly Ile Leu Glu Thr Ile Leu Val Glu Thr  
595 600 605

Lys Ile Met Ser Pro Leu Gly Ile Ser Val Leu Arg Cys Val Arg Leu  
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Leu Arg Ile Phe Lys Ile Thr Arg Tyr Trp Asn Ser Leu Ser Asn Leu  
625 630 635 640

Val Ala Ser Leu Leu Asn Ser Val Arg Ser Ile Ala Ser Leu Leu Leu  
645 650 655

Leu Leu Phe Leu Phe Ile Ile Ile Phe Ser Leu Leu Gly Met Gln Leu  
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Phe Gly Gly Lys Phe Asn Phe Asp Glu Met Gln Thr Arg Arg Ser Thr  
675 680 685

Phe Asp Asn Phe Pro Gln Ser Leu Leu Thr Val Phe Gln Ile Leu Thr  
690 695 700

Gly Glu Asp Trp Asn Ser Val Met Tyr Asp Gly Ile Met Ala Tyr Gly  
705 710 715 720

Gly Pro Ser Phe Pro Gly Met Leu Val Cys Ile Tyr Phe Ile Ile Leu  
725 730 735

Phe Ile Cys Gly Asn Tyr Ile Leu Leu Asn Val Phe Leu Ala Ile Ala  
740 745 750

Val Asp Asn Leu Ala Asp Ala Glu Ser Leu Thr Ser Ala Gln Lys Glu  
755 760 765

Glu Glu Glu Glu Lys Glu Arg Lys Lys Leu Ala Arg Thr Ala Ser Pro  
770 775 780

Glu Lys Lys Gln Glu Leu Val Glu Lys Pro Ala Val Gly Glu Ser Lys  
785 790 795 800

Glu Glu Lys Ile Glu Leu Lys Ser Ile Thr Ala Asp Gly Glu Ser Pro  
805 810 815

Pro Ala Thr Lys Ile Asn Met Asp Asp Leu Gln Pro Asn Glu Asn Glu  
820 825 830

Asp Lys Ser Pro Tyr Pro Asn Pro Glu Thr Thr Gly Glu Glu Asp Glu  
835 840 845

Glu Glu Pro Glu Met Pro Val Gly Pro Arg Pro Arg Pro Leu Ser Glu  
850 855 860

Leu His Leu Lys Glu Lys Ala Val Pro Met Pro Glu Ala Ser Ala Phe  
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Phe Ile Phe Ser Ser Asn Asn Arg Phe Arg Leu Gln Cys His Arg Ile  
885 890 895

Val Asn Asp Thr Ile Phe Thr Asn Leu Ile Leu Phe Phe Ile Leu Leu  
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Ser Ser Ile Ser Leu Ala Ala Glu Asp Pro Val Gln His Thr Ser Phe  
915 920 925

Arg Asn His Ile Leu Phe Tyr Phe Asp Ile Val Phe Thr Thr Ile Phe  
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Thr Ile Glu Ile Ala Leu Lys Ile Leu Gly Asn Ala Asp Tyr Val Phe  
945 950 955 960

Thr Ser Ile Phe Thr Leu Glu Ile Ile Leu Lys Met Thr Ala Tyr Gly  
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Ala Phe Leu His Lys Gly Ser Phe Cys Arg Asn Tyr Phe Asn Ile Leu  
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Asp Leu Leu Val Val Ser Val Ser Leu Ile Ser Phe Gly Ile Gln Ser  
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Ser Ala Ile Asn Val Val Lys Ile Leu Arg Val Leu Arg Val Leu  
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Arg Pro Leu Arg Ala Ile Asn Arg Ala Lys Gly Leu Lys His Val  
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Val Gln Cys Val Phe Val Ala Ile Arg Thr Ile Gly Asn Ile Val  
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Gln Leu Phe Lys Gly Lys Leu Tyr Thr Cys Ser Asp Ser Ser Lys  
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Gln Thr Glu Ala Glu Cys Lys Gly Asn Tyr Ile Thr Tyr Lys Asp  
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Ser Lys Phe Asp Phe Asp Asn Val Leu Ala Ala Met Met Ala Leu  
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Phe Thr Val Ser Thr Phe Glu Gly Trp Pro Glu Leu Leu Tyr Arg  
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Ser Ile Asp Ser His Thr Glu Asp Lys Gly Pro Ile Tyr Asn Tyr  
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Arg Val Glu Ile Ser Ile Phe Phe Ile Ile Tyr Ile Ile Ile Ile  
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Ala Phe Phe Met Met Asn Ile Phe Val Gly Phe Val Ile Val Thr  
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Phe Gln Glu Gln Gly Glu Gln Glu Tyr Lys Asn Cys Glu Leu Asp  
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Lys Asn Gln Arg Gln Cys Val Glu Tyr Ala Leu Lys Ala Arg Pro  
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Leu Arg Arg Tyr Ile Pro Lys Asn Gln His Gln Tyr Lys Val Trp  
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Tyr Val Val Asn Ser Thr Tyr Phe Glu Tyr Leu Met Phe Val Leu  
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Ile Leu Leu Asn Thr Ile Cys Leu Ala Met Gln His Tyr Gly Gln  
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Ser Cys Leu Phe Lys Ile Ala Met Asn Ile Leu Asn Met Leu Phe  
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Thr Gly Leu Phe Thr Val Glu Met Ile Leu Lys Leu Ile Ala Phe  
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Lys Pro Lys Gly Tyr Phe Ser Asp Pro Trp Asn Val Phe Asp Phe  
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Leu Ile Val Ile Gly Ser Ile Ile Asp Val Ile Leu Ser Glu Thr  
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Asn His Tyr Phe Cys Asp Ala Trp Asn Thr Phe Asp Ala Leu Ile  
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Val Val Gly Ser Ile Val Asp Ile Ala Ile Thr Glu Val Asn Pro  
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Ala Glu His Thr Gln Cys Ser Pro Ser Met Asn Ala Glu Glu Asn  
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Ser Arg Ile Ser Ile Thr Phe Phe Arg Leu Phe Arg Val Met Arg  
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Leu Val Lys Leu Leu Ser Arg Gly Glu Gly Ile Arg Thr Leu Leu  
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Trp Thr Phe Ile Lys Ser Phe Gln Ala Leu Pro Tyr Val Ala Leu  
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Leu Ile Val Met Leu Phe Phe Ile Tyr Ala Val Ile Gly Met Gln  
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Val Phe Gly Lys Ile Ala Leu Asn Asp Thr Thr Glu Ile Asn Arg  
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Asn Asn Asn Phe Gln Thr Phe Pro Gln Ala Val Leu Leu Leu Phe  
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Arg Cys Ala Thr Gly Glu Ala Trp Gln Asp Ile Met Leu Ala Cys  
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Met Pro Gly Lys Lys Cys Ala Pro Glu Ser Glu Pro Ser Asn Ser  
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Thr Glu Gly Glu Thr Pro Cys Gly Ser Ser Phe Ala Val Phe Tyr  
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Phe Ile Ser Phe Tyr Met Leu Cys Ala Phe Leu Ile Ile Asn Leu  
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Trp Ser Ile Leu Gly Pro His His Leu Asp Glu Phe Lys Arg Ile  
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Trp Ala Glu Tyr Asp Pro Glu Ala Lys Gly Arg Ile Lys His Leu  
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Gly Lys Leu Cys Pro His Arg Val Ala Cys Lys Arg Leu Val Ser  
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Gly Asn Leu Glu Gln Ala Asn Glu Glu Leu Arg Ala Ile Ile Lys  
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Lys Ile Trp Lys Arg Thr Ser Met Lys Leu Leu Asp Gln Val Val  
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Pro Pro Ala Gly Asp Asp Glu Val Thr Val Gly Lys Phe Tyr Ala  
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Thr Phe Leu Ile Gln Glu Tyr Phe Arg Lys Phe Lys Lys Arg Lys  
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Glu Gln Gly Leu Val Gly Lys Pro Ser Gln Arg Asn Ala Leu Ser  
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Leu Gln Ala Gly Leu Arg Thr Leu His Asp Ile Gly Pro Glu Ile  
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Lys Ala Met Lys Glu Ala Val Ser Ala Ala Ser Glu Asp Asp Ile  
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Phe Arg Arg Ala Gly Gly Leu Phe Gly Asn His Val Ser Tyr Tyr  
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Gln Ser Asp Gly Arg Ser Ala Phe Pro Gln Thr Phe Thr Thr Gln  
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Arg Pro Leu His Ile Asn Lys Ala Gly Ser Ser Gln Gly Asp Thr  
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Glu Ser Pro Ser His Glu Lys Leu Val Asp Ser Thr Phe Thr Pro  
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Ser Ser Tyr Ser Ser Thr Gly Ser Asn Ala Asn Ile Asn Asn Ala  
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Asn Asn Thr Ala Leu Gly Arg Leu Pro Arg Pro Ala Gly Tyr Pro  
1820 1825 1830

Ser Thr Val Ser Thr Val Glu Gly His Gly Pro Pro Leu Ser Pro  
1835 1840 1845

Ala Ile Arg Val Gln Glu Val Ala Trp Lys Leu Ser Ser Asn Arg  
1850 1855 1860

Glu Arg His Val Pro Met Cys Glu Asp Leu Glu Leu Arg Arg Asp  
1865 1870 1875

Ser Gly Ser Ala Gly Thr Gln Ala His Cys Leu Leu Leu Arg Arg  
1880 1885 1890

Ala Asn Pro Ser Arg Cys His Ser Arg Glu Ser Gln Ala Ala Met  
1895 1900 1905

Ala Gly Gln Glu Glu Thr Ser Gln Asp Glu Thr Tyr Glu Val Lys  
1910 1915 1920

Met Asn His Asp Thr Glu Ala Cys Ser Glu Pro Ser Leu Leu Ser  
1925 1930 1935

Thr Glu Met Leu Ser Tyr Gln Asp Asp Glu Asn Arg Gln Leu Thr  
1940 1945 1950

Leu Pro Glu Glu Asp Lys Arg Asp Ile Arg Gln Ser Pro Lys Arg  
1955 1960 1965

Gly Phe Leu Arg Ser Ala Ser Leu Gly Arg Arg Ala Ser Phe His  
1970 1975 1980

Leu Glu Cys Leu Lys Arg Gln Lys Asp Arg Gly Gly Asp Ile Ser  
1985 1990 1995

Gln Lys Thr Val Leu Pro Leu His Leu Val His His Gln Ala Leu  
2000 2005 2010

Ala Val Ala Gly Leu Ser Pro Leu Leu Gln Arg Ser His Ser Pro  
2015 2020 2025

Ala Ser Phe Pro Arg Pro Phe Ala Thr Pro Pro Ala Thr Pro Gly  
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Ser Arg Gly Trp Pro Pro Gln Pro Val Pro Thr Leu Arg Leu Glu  
2045 2050 2055

Gly Val Glu Ser Ser Glu Lys Leu Asn Ser Ser Phe Pro Ser Ile  
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His Cys Gly Ser Trp Ala Glu Thr Thr Pro Gly Gly Gly Gly Ser  
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Ser Ala Ala Arg Arg Val Arg Pro Val Ser Leu Met Val Pro Ser  
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Gln Ala Gly Ala Pro Gly Arg Gln Phe His Gly Ser Ala Ser Ser  
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Gln Asp Pro Lys Phe Ile Glu Val Thr Thr Gln Glu Leu Ala Asp  
2135 2140 2145

Ala Cys Asp Met Thr Ile Glu Glu Met Glu Ser Ala Ala Asp Asn  
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Ile Leu Ser Gly Gly Ala Pro Gln Ser Pro Asn Gly Ala Leu Leu  
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Pro Phe Val Asn Cys Arg Asp Ala Gly Gln Asp Arg Ala Gly Gly  
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gcatgtgatg ccttggacca gcacaacctc aagcaaaatg accagcccat ggatatcctg 240  
cagattatta attgtttgac cactatttat gaccgcctgg agcaagagca caacaatttg 300  
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|                                                                     |      |
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| cctcctgaaa tgatgcccac ctctccccag agtccccggg atgctgagct cattgctgag   | 1440 |
| gccaagctac tgcgtcaaca caaaggccgc ctggaagcca ggatgcaaact cctggaagac  | 1500 |
| cacaataaac agctggagtc acagttacac aggctaaggc agctgctgga gcaaccccag   | 1560 |
| gcagaggcca aagtgaatgg cacaacgggtg tcctctcctt ctacctctct acagagggtcc | 1620 |
| gacagcagtc agcctatgct gctccgagtg gttggcagtc aaacttcgga ctccatgggt   | 1680 |
| gaggaagatc ttctcagtcc tccccaggac acaagcacag ggtagagga ggtgatggag    | 1740 |
| caactcaaca actccttccc tagttcaaga ggacacaatg taggaagtct tttccacatg   | 1800 |
| gcagatgatt tgggcagagc gatggagtcc ttagtatcag tcatgacaga tgaagaagga   | 1860 |
| gcagaataa                                                           | 1869 |

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 <213> Homo sapiens

<400> 118

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| Met | Arg | Glu | Gln | Leu | Lys | Gly | His | Glu | Thr | Gln | Thr | Thr | Cys | Trp | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Lys | Met | Thr | Glu | Leu | Tyr | Gln | Ser | Leu | Ala | Asp | Leu | Asn | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Phe | Ser | Ala | Tyr | Arg | Thr | Ala | Met | Lys | Leu | Arg | Arg | Leu | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Leu | Cys | Leu | Asp | Leu | Leu | Ser | Leu | Ser | Ala | Ala | Cys | Asp | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Gln | His | Asn | Leu | Lys | Gln | Asn | Asp | Gln | Pro | Met | Asp | Ile | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ile | Ile | Asn | Cys | Leu | Thr | Thr | Ile | Tyr | Asp | Arg | Leu | Glu | Gln | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

His Asn Asn Leu Val Asn Val Pro Leu Cys Val Asp Met Cys Leu Asn  
100 105 110

Trp Leu Leu Asn Val Tyr Asp Thr Gly Arg Thr Gly Arg Ile Arg Val  
115 120 125

Leu Ser Phe Lys Thr Gly Ile Ile Ser Leu Cys Lys Ala His Leu Glu  
130 135 140

Asp Lys Tyr Arg Tyr Leu Phe Lys Gln Val Ala Ser Ser Thr Gly Phe  
145 150 155 160

Cys Asp Gln Arg Arg Leu Gly Leu Leu Leu His Asp Ser Ile Gln Ile  
165 170 175

Pro Arg Gln Leu Gly Glu Val Ala Ser Phe Gly Gly Ser Asn Ile Glu  
180 185 190

Pro Ser Val Arg Ser Cys Phe Gln Phe Ala Asn Asn Lys Pro Glu Ile  
195 200 205

Glu Ala Ala Leu Phe Leu Asp Trp Met Arg Leu Glu Pro Gln Ser Met  
210 215 220

Val Trp Leu Pro Val Leu His Arg Val Ala Ala Ala Glu Thr Ala Lys  
225 230 235 240

His Gln Ala Lys Cys Asn Ile Cys Lys Glu Cys Pro Ile Ile Gly Phe  
245 250 255

Arg Tyr Arg Ser Leu Lys His Phe Asn Tyr Asp Ile Cys Gln Ser Cys  
260 265 270

Phe Phe Ser Gly Arg Val Ala Lys Gly His Lys Met His Tyr Pro Met  
275 280 285



Val Glu Tyr Cys Thr Pro Thr Thr Ser Gly Glu Asp Val Arg Asp Phe  
290 295 300

Ala Lys Val Leu Lys Asn Lys Phe Arg Thr Lys Arg Tyr Phe Ala Lys  
305 310 315 320

His Pro Arg Met Gly Tyr Leu Pro Val Gln Thr Val Leu Glu Gly Asp  
325 330 335

Asn Met Glu Thr Pro Ala Ser Ser Pro Gln Leu Ser His Asp Asp Thr  
340 345 350

His Ser Arg Ile Glu His Tyr Ala Ser Arg Leu Ala Glu Met Glu Asn  
355 360 365

Ser Asn Gly Ser Tyr Leu Asn Asp Ser Ile Ser Pro Asn Glu Ser Ile  
370 375 380

Asp Asp Glu His Leu Leu Ile Gln His Tyr Cys Gln Ser Leu Asn Gln  
385 390 395 400

Asp Ser Pro Leu Ser Gln Pro Arg Ser Pro Ala Gln Ile Leu Ile Ser  
405 410 415

Leu Glu Ser Glu Glu Arg Gly Glu Leu Glu Arg Ile Leu Ala Asp Leu  
420 425 430

Glu Glu Glu Asn Arg Asn Leu Gln Ala Glu Tyr Asp Arg Leu Lys Gln  
435 440 445

Gln His Glu His Lys Gly Leu Ser Pro Leu Pro Ser Pro Pro Glu Met  
450 455 460

Met Pro Thr Ser Pro Gln Ser Pro Arg Asp Ala Glu Leu Ile Ala Glu  
465 470 475 480

Ala Lys Leu Leu Arg Gln His Lys Gly Arg Leu Glu Ala Arg Met Gln  
485 490 495

Ile Leu Glu Asp His Asn Lys Gln Leu Glu Ser Gln Leu His Arg Leu  
500 505 510

Arg Gln Leu Leu Glu Gln Pro Gln Ala Glu Ala Lys Val Asn Gly Thr  
515 520 525

Thr Val Ser Ser Pro Ser Thr Ser Leu Gln Arg Ser Asp Ser Ser Gln  
530 535 540

Pro Met Leu Leu Arg Val Val Gly Ser Gln Thr Ser Asp Ser Met Gly  
545 550 555 560

Glu Glu Asp Leu Leu Ser Pro Pro Gln Asp Thr Ser Thr Gly Leu Glu  
565 570 575

Glu Val Met Glu Gln Leu Asn Asn Ser Phe Pro Ser Ser Arg Gly His  
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595 600 605

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| atcacgcagc tgcacttcgc cttccaggat gagaactacc tgtacctggt catggagtat   | 480  |
| tacgtgggcg gggacctgct gacactgctg agcaagtttg gggagcggat tccggccgag   | 540  |
| atggcgcgct tctacctggc ggagattgtc atggccatag actcggtgca ccggcttggc   | 600  |
| tacgtgcaca gggacatcaa acccgacaac atcctgctgg accgctgtgg ccacatccgc   | 660  |
| ctggccgact tcggctcttg cctcaagctg cgggcagatg gaacgggtgcg gtcgctgggtg | 720  |
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| gggacaggca gctacgggcc cgagtgtgac tgggtgggcgc tgggtgtatt cgccatgaa   | 840  |
| atgttctatg ggcagacgcc cttctacgcg gattccacgg cggagaccta tggcaagatc   | 900  |
| gtccactaca aggagcacct ctctctgccg ctgggtggacg aaggggtccc tgaggaggct  | 960  |
| cgagacttca ttcagcgggt gctgtgtccc ccggagacac ggctgggccc ggggtggagca  | 1020 |
| ggcgacttcc ggacacatcc cttcttcttt ggcctcgact gggatgggtct ccgggacagc  | 1080 |
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| gaggacgggc tactgccat ggtgagcggg ggcggggaga cactgtcggga cattcgggaa   | 1200 |
| ggtgcgccgc taggggtcca cctgcctttt gtgggtact cctactcctg catggccctc    | 1260 |
| agggacagtg aggtcccagg cccacacccc atggaactgg aggccgagca gctgcttgag   | 1320 |
| ccacacgtgc aagcggccag cctggagccc tcgggtgtccc cacaggatga aacagctgaa  | 1380 |
| gtggcagttc cagcggctgt ccctgcggca gaggctgagg ccgaggtgac gctgcgggag   | 1440 |
| ctccaggaag ccctggagga ggaggtgctc acccggcaga gcctgagccg ggagatggag   | 1500 |
| gccatccgca cggacaacca gaacttcgcc agtcaactac gcgaggcaga ggctcggaac   | 1560 |
| cgggacctag aggcacacgt ccggcagttg caggagcggga tggagttgct gcaggcagag  | 1620 |
| ggagccacag ctgtcacggg ggtccccagt ccccgggcca cggatccacc ttcccatcta   | 1680 |
| gatggcccc cggccgtggc tgtgggccag tgcccgtgg tggggccagg ccccatgcac     | 1740 |
| cgccgccacc tgctgtctcc tgccagggtc ctaggcctg gcctatcgga ggcgctttcc    | 1800 |

ctgctcctgt tcgccgttgt tctgtctcgt gccgccgccc tgggctgcat tgggttggtg 1860

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<211> 639

<212> PRT

<213> Homo sapiens

<400> 120

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

Ala Leu Ser Gly Asp Pro Arg Phe Phe Ser Pro Thr Thr Pro Pro Ala  
50 55 60

Glu Pro Ile Val Val Arg Leu Lys Glu Val Arg Leu Gln Arg Asp Asp  
65 70 75 80

Phe Glu Ile Leu Lys Val Ile Gly Arg Gly Ala Phe Ser Glu Val Ala  
85 90 95

Val Val Lys Met Lys Gln Thr Gly Gln Val Tyr Ala Met Lys Ile Met  
100 105 110

Asn Lys Trp Asp Met Leu Lys Arg Gly Glu Val Ser Cys Phe Arg Glu  
115 120 125

Glu Arg Asp Val Leu Val Asn Gly Asp Arg Arg Trp Ile Thr Gln Leu  
130 135 140

His Phe Ala Phe Gln Asp Glu Asn Tyr Leu Tyr Leu Val Met Glu Tyr  
145 150 155 160

Tyr Val Gly Gly Asp Leu Leu Thr Leu Leu Ser Lys Phe Gly Glu Arg  
165 170 175

Ile Pro Ala Glu Met Ala Arg Phe Tyr Leu Ala Glu Ile Val Met Ala  
180 185 190

Ile Asp Ser Val His Arg Leu Gly Tyr Val His Arg Asp Ile Lys Pro  
195 200 205

Asp Asn Ile Leu Leu Asp Arg Cys Gly His Ile Arg Leu Ala Asp Phe  
210 215 220

Gly Ser Cys Leu Lys Leu Arg Ala Asp Gly Thr Val Arg Ser Leu Val  
225 230 235 240

Ala Val Gly Thr Pro Asp Tyr Leu Ser Pro Glu Ile Leu Gln Ala Val  
245 250 255

Gly Gly Gly Pro Gly Thr Gly Ser Tyr Gly Pro Glu Cys Asp Trp Trp  
260 265 270

Ala Leu Gly Val Phe Ala Tyr Glu Met Phe Tyr Gly Gln Thr Pro Phe  
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Tyr Ala Asp Ser Thr Ala Glu Thr Tyr Gly Lys Ile Val His Tyr Lys  
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Glu His Leu Ser Leu Pro Leu Val Asp Glu Gly Val Pro Glu Glu Ala  
305 310 315 320

Arg Asp Phe Ile Gln Arg Leu Leu Cys Pro Pro Glu Thr Arg Leu Gly  
325 330 335

Arg Gly Gly Ala Gly Asp Phe Arg Thr His Pro Phe Phe Phe Gly Leu  
340 345 350

Asp Trp Asp Gly Leu Arg Asp Ser Val Pro Pro Phe Thr Pro Asp Phe  
355 360 365

Glu Gly Ala Thr Asp Thr Cys Asn Phe Asp Leu Val Glu Asp Gly Leu  
370 375 380

Thr Ala Met Val Ser Gly Gly Gly Glu Thr Leu Ser Asp Ile Arg Glu  
385 390 395 400

Gly Ala Pro Leu Gly Val His Leu Pro Phe Val Gly Tyr Ser Tyr Ser  
405 410 415

Cys Met Ala Leu Arg Asp Ser Glu Val Pro Gly Pro Thr Pro Met Glu  
420 425 430

Leu Glu Ala Glu Gln Leu Leu Glu Pro His Val Gln Ala Pro Ser Leu  
435 440 445

Glu Pro Ser Val Ser Pro Gln Asp Glu Thr Ala Glu Val Ala Val Pro  
450 455 460

Ala Ala Val Pro Ala Ala Glu Ala Glu Ala Glu Val Thr Leu Arg Glu  
465 470 475 480

Leu Gln Glu Ala Leu Glu Glu Glu Val Leu Thr Arg Gln Ser Leu Ser  
485 490 495

Arg Glu Met Glu Ala Ile Arg Thr Asp Asn Gln Asn Phe Ala Ser Gln  
500 505 510

Leu Arg Glu Ala Glu Ala Arg Asn Arg Asp Leu Glu Ala His Val Arg  
515 520 525

Gln Leu Gln Glu Arg Met Glu Leu Leu Gln Ala Glu Gly Ala Thr Ala  
530 535 540

Val Thr Gly Val Pro Ser Pro Arg Ala Thr Asp Pro Pro Ser His Leu  
545 550 555 560

Asp Gly Pro Pro Ala Val Ala Val Gly Gln Cys Pro Leu Val Gly Pro  
565 570 575

Gly Pro Met His Arg Arg His Leu Leu Leu Pro Ala Arg Val Pro Arg  
580 585 590

Pro Gly Leu Ser Glu Ala Leu Ser Leu Leu Leu Phe Ala Val Val Leu  
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Gln Leu Thr Ala Val Trp Arg Arg Pro Gly Ala Ala Arg Ala Pro  
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aaggtggtaa ctgattccca gctccaggat gatgccagtg gacaaaatga gagtgaatg 240  
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aaggtccacc ctggagacaa tggttgaact aaagtagaaa cccccaagaa cttcacagag 420  
gtagaggaaa atatgtcggg acaagggtgga ctttcagaaa gtgcaccca atctaatttt 480  
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gacaaacaag gcctggtttg ttcttcagag gtgccacaga atgttggctt gcagagttct 600  
tgcccagcca aacatggttt tcagacacct agagtgaaga aactgtatcc ccagttgcca 660

|                                                                    |      |
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| cgactctacc cagaactccc gtctcaactg gaactagtag catttactaa agaacagcta  | 780  |
| aaaatcttgg agcctgggtc atggctggaa aatgttgagt catatttaga agaatttgac  | 840  |
| agcatggctc atcaagacag gcatgaattt tatgagttgc ttttgaacta ctcacgatgt  | 900  |
| aggaagcaac tgctgctggc tgaagctgag ctgcttactc tgacatctga ttgccaaaat  | 960  |
| gctaaaagtc ggctgtggca gtttaaggag gaacaaatgt ctgtacaggg tatctgtgca  | 1020 |
| gatcaagtga aagttttcag ctatcatcgc taccaaagag tagaaatgaa tgaaaatgca  | 1080 |
| ctgggtggagc taaagaagct attcgatgcc aaatctgagc acctccacca gaccctggcc | 1140 |
| cttcattctt atacttctgt gctctcaaga ttgcaagtgg agtcttacat ctatgcattg  | 1200 |
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| cagaaaattgg tatccgtgct acaaagagtt ggctgtcctg gagatcacct cttccttcta | 1440 |
| aaccatattc ttcgatgccc cgctgggtgtt agtaaatggg ctgttccttt tatccagatc | 1500 |
| aaagtgttgc ataaccatc aggggtcttt cattttatgc aatcccttgc cctgctgatg   | 1560 |
| tctcctgtca aaaatcgagc tgagtttatg tgccacatga agcccagcga gcggaagcca  | 1620 |
| tcctcctcag ggcttgggtc tgggacttgg acgctagtag acgaaggagg agaagaggat  | 1680 |
| gaagaccctg agaccagttg gattctcctt aatgaagatg atttggttac cattttagca  | 1740 |
| cagttccccct ttcatgaact ctttcagcat cttcttgggt ttaaagcaaa aggtgattat | 1800 |
| ttacctgaaa caacaagacc tcaagagatg atgaaaattt ttgcctttgc caactcacta  | 1860 |
| gtggaacttc tggctgtggg gttagaaacc tttaatagag cacgctatag gcagtttgtg  | 1920 |
| aagcgaattg gttatatgat caggatgact cttggttatg taagtacca ttgggcacag   | 1980 |
| tatgtgagcc ataaccaagg ctcaggattg gcccacagc cctactctat ggagaaaacta  | 2040 |
| caggttgaat ttgatgaact gtttttgagg gctgtcctac atgtgctgaa ggccaaaaga  | 2100 |
| cttggcattt ggctgtttat gtccgagatg ccctttggga ctctgtctgt gcaaatgctg  | 2160 |



|                                                                    |      |
|--------------------------------------------------------------------|------|
| tggaagctct tctacctcat gcaccaggtg gagagcgaga acctgcagca gctctcctcc  | 2220 |
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| gagaagtgtc tttcttctat gaatagctca gaagagattt gccttctgac tacctttgct  | 2340 |
| cagatggctc aggccagaag aaccaatgtg gacgaagact tcataaaaaat tattgttctg | 2400 |
| gagatatatg aggtatctta tgtcaccttg tctaccagag agactttttc aaaggttggt  | 2460 |
| cgagagcttt tagggactat cacagctgtt caccctgaga taatttccgt ccttctggat  | 2520 |
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| aattacaacc tgacagtggg gaagaataaa ctggcctgtg ttattcttga aggactgaat  | 2700 |
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| tctgaaagta tgaagcaggt ttcatatattg gccagtattg ttcgatatgg agagacaccc | 2880 |
| gagacctcat ttaaccaatg ggcctggaat ttaatcttga ggctaaaaact gcacaaaaac | 2940 |
| gattatggaa tacagccgaa ttgtccagct gttcccttct ccgtcactgt gcctgacatg  | 3000 |
| acagagtcac ccacgtttca tcctctcttg aaggctgtga aagcgggcat gccattggc   | 3060 |
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| ggcatccac tattgggaat tctggtccag tcaagacatt tgagaacagt ggttcatgtc   | 3180 |
| ctggataaga ttctgccttt attttaccct tgccagtatt accttctgaa gaatgagcag  | 3240 |
| tttttatcgc atctcctctt gttcctacac ttggacagcg gtgtccctca ggggtgcaca  | 3300 |
| caacaggtca cccacaaggt ggcacagcac ctgacaggag ccagccatgg ggacaacgtg  | 3360 |
| aagcttctca acagcatgat ccaggcacac atatctgtaa gcactcagcc caatgaagtg  | 3420 |
| ggccccgttg ctgtgttgga gttctgggtt caggctctca taagccagca tctctggtag  | 3480 |
| cgagaacaac ctatcctctt cctcatggac cacttggtga aagcagcttt tcagctgatg  | 3540 |
| caggaagact gcatacagaa attactctac caacaacata agaatgcctt gggttaccac  | 3600 |
| tgtgaccgga gtctgtctc atctttggta agctggattg tggcaggcaa catcactcct   | 3660 |

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| ataaactctg ctttcacccc tgaccaagct ctgaagaaag cccagaccca gctgaagctc  | 3840 |
| cccatcgtgc catccctcca gaggctgctg atttatcgct gggcccacca ggctctggtc  | 3900 |
| acaccttctg atcacccctt cctgccactc atttggcaga agttcttcct tctgtatctt  | 3960 |
| caccgtccgg gaccacagta tgggttaccc atagatgggt gtattggaag aagggttttt  | 4020 |
| caaagtcctg ctcatatcaa tttgttgaaa gaaatgaaga gacgtttgac cgagggtggct | 4080 |
| gacttccacc atgtgcaag caaggccctc cgtgttccag cagagggcag tgaagggtg    | 4140 |
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| gagactgttg gtctgtggac acaggccaag cttgagtccc attccacacc ctgcagtttg  | 4440 |
| tccgtgcagc tggacttcac tgatcctttg ctggctaaag aaagggtttt aagtaacttg  | 4500 |
| cggaagcatg aggctcccca gcctcccctt gctctgcacc cgacgaagcc tcctgtgcca  | 4560 |
| gttatttcct ctgctgtgct attgagtcag aaggacgcca cccagctggt gtgcacagac  | 4620 |
| ctgaatctgt tgcaacagca ggccagaacc gcagctcttc gggaatctca gcaggttgct  | 4680 |
| ctggatgggtg agctgttaga cacaatgcca aagcagtatg tgaatcgtga agaacagacc | 4740 |
| acactacatt tggagtgcag aggcagcagc ggtaagaaat gccaaggagc cgcagttgtc  | 4800 |
| acggttcagt ttgaaggcat gcataagaat gaagccataa gccaacagct tcatgtttta  | 4860 |
| cggaaggaag tgaagcagtt gcaagcagaa gctgctaaac caccatcact taatattgtg  | 4920 |
| gaagctgctg tacatgcaga aaacttgatc acggccttag tgaatgccta caagttgcag  | 4980 |
| cctacacctg ggattcagaa agttggcatt agccttttct ttactattgt ggattacgtc  | 5040 |
| agcgatgaga cgcagcgtca tcccccaaca aggcagttct ttacttcatg tattgagatc  | 5100 |
| ttgggacagg tattttatcag tggcattaaa tcagagtgc gaaaagtact tgaaaccatt  | 5160 |

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| atgattttca tgctgctaac caagttcgat cttaaacaat ggtaaagcgc cactaaacct  | 5340 |
| cctctgtctg atcgtaccag gcttctggag tccattcact tggcacttac tgctgggggc  | 5400 |
| cttgaaccag atgaggatat tttgatgcca tttaatcttt tctgtaagca ctggacttat  | 5460 |
| cttcttctct accagtttcc tgaccagtac agtgacattc tcaggctgct tatgcaaagc  | 5520 |
| tccgcggagc agcttctgag ccccgagtgt tggaaggcca ctctgagagc cctgggctgc  | 5580 |
| tgcgcccca gctgccagca gggggcagcg tccaccgagg gcgccgtgct tcccagctct   | 5640 |
| tctgatgctc tcttgtcaga caagcaggta atggagacta tacagtggct ttcagacttt  | 5700 |
| ttttataagc ttcggttatc caagatggac tttaaaagct ttggtttatt ctcaaaatgg  | 5760 |
| agtccttata tggctgatgt gaagacattc ttgggctacc ttgtgaaaag gctgattgac  | 5820 |
| ttagaaatga cctgtttggc ccaagacca actgccagca ggaaaacagt gctgaaatcc   | 5880 |
| ctacattcag taatcattca gctctttaag ccatggatcc tggttttaga ggacaacgaa  | 5940 |
| agcagccaac agcggcatta cccctggcta gagagtgata ctgtggtggc ctcaagcatt  | 6000 |
| gtgcagctgt tctactgactg tattgactca ctgcatgaga gttttaaaga taagctgttg | 6060 |
| ccaggtgatg caggagccct ttggttgac ctgatgcatt attgtgaagc atgtacagca   | 6120 |
| cccaaaatgc cagagttcat tctgtacgct ttccatagca cgtaccggaa actgccatgg  | 6180 |
| aaggacctgc accctgacca gatgctcatg gaggccttct tcaaagtgga acgaggaagc  | 6240 |
| ccaagagct gtttcttatt tttgggtct gtactctgtg aagtcaactg ggtagtgtg     | 6300 |
| ctctctgatg cctggaattc cagtccccac ccagaaaccc gcagcatgat tgtctgcctc  | 6360 |
| cttttcatga tgattttatt ggcaaaggaa gttcaactgg tagaccaaac agattcacct  | 6420 |
| ttacttagtc tccttgga gacaagctca ctttcatggc atcttgtgga tattgtgtcg    | 6480 |
| taccagagtg tgctaagtta tttcagcagc cattaccgcg cgtccatcat cctggcaaaa  | 6540 |
| gaatcttatg ctgaattaat catgaagctc ctaaaagtgt ctgcgggcct ttctattcct  | 6600 |
| actgacagcc agaagcatct tgatgcagtt ccaaaatgcc aagcttttac tcatcagatg  | 6660 |

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|----------------------------------------------------------------------|------|
| gttcaattcc tcagcacccct ggaacaaaaat ggaaaaaatca ccttagcagt cctagaacag | 6720 |
| gaaatgtcta agctcttaga cgatatcatt gtctttaacc cgcccacat ggacagccag     | 6780 |
| acccgccaca tggccctcag cagcctcttt atggaagtcc tgatgatgat gaacaacgcg    | 6840 |
| actattccaa cagcagagtt ccttcggggc agtatccgga cctggattgg ccaaaaaatg    | 6900 |
| catgggctgg tggtgctgcc ccttttaaca gcagcctgcc agagcctggc gtccgtccgc    | 6960 |
| cacatggctg agactacaga agcctgcac actgcctact tcaaagaaaag ccctctcaat    | 7020 |
| cagaattcag gatggggacc cattctggta tcccttcagg ttcccagagct caccatggaa   | 7080 |
| gagttcctgc aggagtgcct caccttgggc agttacttga ctctttacgt ctacttgctt    | 7140 |
| cagtgtttaa acagcgaaca gactttaagg aatgaaatga aagtgctgct catcttaagc    | 7200 |
| aagtggctgg aacaggtgta cccaagctcc gtggaggaag aggcaaagct gtttttgtgg    | 7260 |
| tggcaccaag tccttcagct ctccctcatt cagacagagc agaatgactc cgtcctgaca    | 7320 |
| gaatctgtca ttcgaattct gctcttggtt cagagcaggc agaacctcgt ggctgaggag    | 7380 |
| agactcagct ctgggatcct gggggcaatt gggtttggcc ggaagtcgcc tttgtctaac    | 7440 |
| aggttccgag tggttgccccg aagcatggct gccttccttt cagttcagggt tcctatggaa  | 7500 |
| gatcagatcc gtttgaggcc tggctctgaa ttacatctga ccccaaagc tcagcaggct     | 7560 |
| ctgaatgctc ttgaatccat ggcatcaagt aagcagtatg ttgaatacca ggatcaaata    | 7620 |
| ttgcaagcca cccaatttat aaggcatcct ggccattgcc ttcaagatgg gaaaagcttc    | 7680 |
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 <213> Homo sapiens

<400> 122

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| Met | Ala | Glu | Ala | Val | Lys | Pro | Gln | Arg | Arg | Ala | Lys | Ala | Lys | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Lys | Thr | Lys | Glu | Lys | Lys | Lys | Tyr | Glu | Thr | Pro | Gln | Arg | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Glu Ser Ser Glu Val Ser Leu Pro Lys Thr Ser Arg Glu Gln Glu Ile  
35 40 45

Pro Ser Leu Ala Cys Glu Phe Lys Gly Asp His Leu Lys Val Val Thr  
50 55 60

Asp Ser Gln Leu Gln Asp Asp Ala Ser Gly Gln Asn Glu Ser Glu Met  
65 70 75 80

Phe Asp Val Pro Leu Thr Ser Leu Thr Ile Ser Asn Glu Glu Ser Leu  
85 90 95

Thr Cys Asn Thr Glu Pro Pro Lys Glu Gly Gly Glu Ala Arg Pro Cys  
100 105 110

Val Gly Asp Ser Ala Val Thr Pro Lys Val His Pro Gly Asp Asn Val  
115 120 125

Gly Thr Lys Val Glu Thr Pro Lys Asn Phe Thr Glu Val Glu Glu Asn  
130 135 140

Met Ser Val Gln Gly Gly Leu Ser Glu Ser Ala Pro Gln Ser Asn Phe  
145 150 155 160

Ser Tyr Thr Gln Pro Ala Met Glu Asn Ile Gln Val Arg Glu Thr Gln  
165 170 175

Asn Ser Lys Glu Asp Lys Gln Gly Leu Val Cys Ser Ser Glu Val Pro  
180 185 190

Gln Asn Val Gly Leu Gln Ser Ser Cys Pro Ala Lys His Gly Phe Gln  
195 200 205

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

Gly Glu Ala Pro Ala Leu Val Ala Val Lys Pro Leu Leu Arg Ser Glu  
225 230 235 240

Arg Leu Tyr Pro Glu Leu Pro Ser Gln Leu Glu Leu Val Pro Phe Thr  
245 250 255

Lys Glu Gln Leu Lys Ile Leu Glu Pro Gly Ser Trp Leu Glu Asn Val  
260 265 270

Glu Ser Tyr Leu Glu Glu Phe Asp Ser Met Ala His Gln Asp Arg His  
275 280 285

Glu Phe Tyr Glu Leu Leu Leu Asn Tyr Ser Arg Cys Arg Lys Gln Leu  
290 295 300

Leu Leu Ala Glu Ala Glu Leu Leu Thr Leu Thr Ser Asp Cys Gln Asn  
305 310 315 320

Ala Lys Ser Arg Leu Trp Gln Phe Lys Glu Glu Gln Met Ser Val Gln  
325 330 335

Gly Ile Cys Ala Asp Gln Val Lys Val Phe Ser Tyr His Arg Tyr Gln  
340 345 350

Arg Val Glu Met Asn Glu Asn Ala Leu Val Glu Leu Lys Lys Leu Phe  
355 360 365

Asp Ala Lys Ser Glu His Leu His Gln Thr Leu Ala Leu His Ser Tyr  
370 375 380

Thr Ser Val Leu Ser Arg Leu Gln Val Glu Ser Tyr Ile Tyr Ala Leu  
385 390 395 400

Leu Ser Ser Ser Ala Val Leu Arg Ser Ser Ala Ile His Gln Gln Gly  
405 410 415

Arg Ala Ser Lys Gln Thr Glu Ser Ile Pro Ser Asp Leu Cys Gln Leu  
420 425 430

Lys Glu Cys Ile Ser Val Leu Phe Met Phe Thr Arg Arg Val Asn Glu  
435 440 445

Asp Thr Gln Phe His Asp Asp Ile Leu Leu Trp Leu Gln Lys Leu Val  
450 455 460

Ser Val Leu Gln Arg Val Gly Cys Pro Gly Asp His Leu Phe Leu Leu  
465 470 475 480

Asn His Ile Leu Arg Cys Pro Ala Gly Val Ser Lys Trp Ala Val Pro  
485 490 495

Phe Ile Gln Ile Lys Val Leu His Asn Pro Ser Gly Val Phe His Phe  
500 505 510

Met Gln Ser Leu Ala Leu Leu Met Ser Pro Val Lys Asn Arg Ala Glu  
515 520 525

Phe Met Cys His Met Lys Pro Ser Glu Arg Lys Pro Ser Ser Ser Gly  
530 535 540

Pro Gly Ser Gly Thr Trp Thr Leu Val Asp Glu Gly Gly Glu Glu Asp  
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Glu Asp Pro Glu Thr Ser Trp Ile Leu Leu Asn Glu Asp Asp Leu Val  
565 570 575

Thr Ile Leu Ala Gln Phe Pro Phe His Glu Leu Phe Gln His Leu Leu  
580 585 590

Gly Phe Lys Ala Lys Gly Asp Tyr Leu Pro Glu Thr Thr Arg Pro Gln  
595 600 605

Glu Met Met Lys Ile Phe Ala Phe Ala Asn Ser Leu Val Glu Leu Leu  
610 615 620

Ala Val Gly Leu Glu Thr Phe Asn Arg Ala Arg Tyr Arg Gln Phe Val  
625 630 635 640

Lys Arg Ile Gly Tyr Met Ile Arg Met Thr Leu Gly Tyr Val Ser Asp  
645 650 655

His Trp Ala Gln Tyr Val Ser His Asn Gln Gly Ser Gly Leu Ala Gln  
660 665 670

Gln Pro Tyr Ser Met Glu Lys Leu Gln Val Glu Phe Asp Glu Leu Phe  
675 680 685

Leu Arg Ala Val Leu His Val Leu Lys Ala Lys Arg Leu Gly Ile Trp  
690 695 700

Leu Phe Met Ser Glu Met Pro Phe Gly Thr Leu Ser Val Gln Met Leu  
705 710 715 720

Trp Lys Leu Phe Tyr Leu Met His Gln Val Glu Ser Glu Asn Leu Gln  
725 730 735

Gln Leu Ser Ser Ser Leu Gln Pro Ala Gln Cys Lys Gln Gln Leu Gln  
740 745 750

Asp Pro Glu His Phe Thr Asn Phe Glu Lys Cys Leu Ser Ser Met Asn  
755 760 765

Ser Ser Glu Glu Ile Cys Leu Leu Thr Thr Phe Ala Gln Met Ala Gln  
770 775 780

Ala Arg Arg Thr Asn Val Asp Glu Asp Phe Ile Lys Ile Ile Val Leu  
785 790 795 800

Glu Ile Tyr Glu Val Ser Tyr Val Thr Leu Ser Thr Arg Glu Thr Phe  
805 810 815

Ser Lys Val Gly Arg Glu Leu Leu Gly Thr Ile Thr Ala Val His Pro  
820 825 830



Glu Ile Ile Ser Val Leu Leu Asp Arg Val Gln Glu Thr Ile Asp Gln  
835 840 845

Val Gly Met Val Ser Leu Tyr Leu Phe Lys Glu Leu Pro Leu Tyr Leu  
850 855 860

Trp Gln Pro Ser Ala Ser Glu Ile Ala Val Ile Arg Asp Trp Leu Leu  
865 870 875 880

Asn Tyr Asn Leu Thr Val Val Lys Asn Lys Leu Ala Cys Val Ile Leu  
885 890 895

Glu Gly Leu Asn Trp Gly Phe Ala Lys Gln Ala Thr Leu His Leu Asp  
900 905 910

Gln Ala Val His Ala Glu Val Ala Leu Met Val Leu Glu Ala Tyr Gln  
915 920 925

Lys Tyr Leu Ala Gln Lys Pro Tyr Ala Gly Ile Leu Ser Glu Ser Met  
930 935 940

Lys Gln Val Ser Tyr Leu Ala Ser Ile Val Arg Tyr Gly Glu Thr Pro  
945 950 955 960

Glu Thr Ser Phe Asn Gln Trp Ala Trp Asn Leu Ile Leu Arg Leu Lys  
965 970 975

Leu His Lys Asn Asp Tyr Gly Ile Gln Pro Asn Cys Pro Ala Val Pro  
980 985 990

Phe Ser Val Thr Val Pro Asp Met Thr Glu Ser Pro Thr Phe His Pro  
995 1000 1005

Leu Leu Lys Ala Val Lys Ala Gly Met Pro Ile Gly Cys Tyr Leu  
1010 1015 1020

Ala Leu Ser Met Thr Ala Val Gly His Ser Ile Glu Lys Phe Cys  
1025 1030 1035

Ala Glu Gly Ile Pro Leu Leu Gly Ile Leu Val Gln Ser Arg His  
1040 1045 1050

Leu Arg Thr Val Val His Val Leu Asp Lys Ile Leu Pro Leu Phe  
1055 1060 1065

Tyr Pro Cys Gln Tyr Tyr Leu Leu Lys Asn Glu Gln Phe Leu Ser  
1070 1075 1080

His Leu Leu Leu Phe Leu His Leu Asp Ser Gly Val Pro Gln Gly  
1085 1090 1095

Val Thr Gln Gln Val Thr His Lys Val Ala Gln His Leu Thr Gly  
1100 1105 1110

Ala Ser His Gly Asp Asn Val Lys Leu Leu Asn Ser Met Ile Gln  
1115 1120 1125

Ala His Ile Ser Val Ser Thr Gln Pro Asn Glu Val Gly Pro Val  
1130 1135 1140

Ala Val Leu Glu Phe Trp Val Gln Ala Leu Ile Ser Gln His Leu  
1145 1150 1155

Trp Tyr Arg Glu Gln Pro Ile Leu Phe Leu Met Asp His Leu Cys  
1160 1165 1170

Lys Ala Ala Phe Gln Leu Met Gln Glu Asp Cys Ile Gln Lys Leu  
1175 1180 1185

Leu Tyr Gln Gln His Lys Asn Ala Leu Gly Tyr His Cys Asp Arg  
1190 1195 1200

Ser Leu Leu Ser Ser Leu Val Ser Trp Ile Val Ala Gly Asn Ile  
1205 1210 1215

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr  | Pro | Ser | Phe | Val | Glu | Gly  | Leu | Ala | Thr | Pro | Thr  | Gln | Val | Trp |
| 1220 |     |     |     |     |     | 1225 |     |     |     |     | 1230 |     |     |     |
| Phe  | Ala | Trp | Thr | Val | Leu | Asn  | Met | Glu | Ser | Ile | Phe  | Glu | Glu | Asp |
| 1235 |     |     |     |     |     | 1240 |     |     |     |     | 1245 |     |     |     |
| Ser  | Gln | Leu | Arg | Arg | Val | Ile  | Glu | Gly | Glu | Leu | Val  | Ile | Asn | Ser |
| 1250 |     |     |     |     |     | 1255 |     |     |     |     | 1260 |     |     |     |
| Ala  | Phe | Thr | Pro | Asp | Gln | Ala  | Leu | Lys | Lys | Ala | Gln  | Thr | Gln | Leu |
| 1265 |     |     |     |     |     | 1270 |     |     |     |     | 1275 |     |     |     |
| Lys  | Leu | Pro | Ile | Val | Pro | Ser  | Leu | Gln | Arg | Leu | Leu  | Ile | Tyr | Arg |
| 1280 |     |     |     |     |     | 1285 |     |     |     |     | 1290 |     |     |     |
| Trp  | Ala | His | Gln | Ala | Leu | Val  | Thr | Pro | Ser | Asp | His  | Pro | Leu | Leu |
| 1295 |     |     |     |     |     | 1300 |     |     |     |     | 1305 |     |     |     |
| Pro  | Leu | Ile | Trp | Gln | Lys | Phe  | Phe | Leu | Leu | Tyr | Leu  | His | Arg | Pro |
| 1310 |     |     |     |     |     | 1315 |     |     |     |     | 1320 |     |     |     |
| Gly  | Pro | Gln | Tyr | Gly | Leu | Pro  | Ile | Asp | Gly | Cys | Ile  | Gly | Arg | Arg |
| 1325 |     |     |     |     |     | 1330 |     |     |     |     | 1335 |     |     |     |
| Phe  | Phe | Gln | Ser | Pro | Ala | His  | Ile | Asn | Leu | Leu | Lys  | Glu | Met | Lys |
| 1340 |     |     |     |     |     | 1345 |     |     |     |     | 1350 |     |     |     |
| Arg  | Arg | Leu | Thr | Glu | Val | Ala  | Asp | Phe | His | His | Ala  | Ala | Ser | Lys |
| 1355 |     |     |     |     |     | 1360 |     |     |     |     | 1365 |     |     |     |
| Ala  | Leu | Arg | Val | Pro | Ala | Glu  | Gly | Ser | Glu | Gly | Leu  | Pro | Glu | Ser |
| 1370 |     |     |     |     |     | 1375 |     |     |     |     | 1380 |     |     |     |
| His  | Ser | Gly | Thr | Pro | Gly | Tyr  | Leu | Thr | Ser | Pro | Glu  | Leu | His | Lys |
| 1385 |     |     |     |     |     | 1390 |     |     |     |     | 1395 |     |     |     |

Glu Leu Val Arg Leu Phe Asn Val Tyr Ile Leu Trp Leu Glu Asp  
1400 1405 1410

Glu Asn Phe Gln Lys Gly Asp Thr Tyr Ile Pro Ser Leu Pro Lys  
1415 1420 1425

His Tyr Asp Ile His Arg Leu Ala Lys Val Met Gln Asn Gln Gln  
1430 1435 1440

Asp Leu Trp Met Glu Tyr Leu Asn Met Glu Arg Ile Tyr His Glu  
1445 1450 1455

Phe Gln Glu Thr Val Gly Leu Trp Thr Gln Ala Lys Leu Glu Ser  
1460 1465 1470

His Ser Thr Pro Cys Ser Leu Ser Val Gln Leu Asp Phe Thr Asp  
1475 1480 1485

Pro Leu Leu Ala Lys Glu Arg Val Leu Ser Asn Leu Arg Lys His  
1490 1495 1500

Glu Ala Pro Gln Pro Pro Leu Ala Leu His Pro Thr Lys Pro Pro  
1505 1510 1515

Val Pro Val Ile Ser Ser Ala Val Leu Leu Ser Gln Lys Asp Ala  
1520 1525 1530

Thr Gln Leu Val Cys Thr Asp Leu Asn Leu Leu Gln Gln Gln Ala  
1535 1540 1545

Arg Thr Ala Ala Leu Arg Glu Ser Gln Gln Val Ala Leu Asp Gly  
1550 1555 1560

Glu Leu Leu Asp Thr Met Pro Lys Gln Tyr Val Asn Arg Glu Glu  
1565 1570 1575

Gln Thr Thr Leu His Leu Glu Cys Arg Gly Ser Ser Gly Lys Lys  
1580 1585 1590

Cys Gln Gly Ala Ala Val Val Thr Val Gln Phe Glu Gly Met His  
1595 1600 1605

Lys Asn Glu Ala Ile Ser Gln Gln Leu His Val Leu Arg Lys Glu  
1610 1615 1620

Val Lys Gln Leu Gln Ala Glu Ala Ala Lys Pro Pro Ser Leu Asn  
1625 1630 1635

Ile Val Glu Ala Ala Val His Ala Glu Asn Leu Ile Thr Ala Leu  
1640 1645 1650

Val Asn Ala Tyr Lys Leu Gln Pro Thr Pro Gly Ile Gln Lys Val  
1655 1660 1665

Gly Ile Ser Leu Phe Phe Thr Ile Val Asp Tyr Val Ser Asp Glu  
1670 1675 1680

Thr Gln Arg His Pro Pro Thr Arg Gln Phe Phe Thr Ser Cys Ile  
1685 1690 1695

Glu Ile Leu Gly Gln Val Phe Ile Ser Gly Ile Lys Ser Glu Cys  
1700 1705 1710

Arg Lys Val Leu Glu Thr Ile Leu Lys Asn Ser Arg Leu Cys Ser  
1715 1720 1725

Leu Leu Ser Pro Phe Phe Thr Pro Asn Ala Ala Pro Ala Glu Phe  
1730 1735 1740

Ile Gln Leu Tyr Glu Gln Val Val Lys Phe Leu Ser Glu Asp Asn  
1745 1750 1755

Ser Asp Met Ile Phe Met Leu Leu Thr Lys Phe Asp Leu Lys Gln  
1760 1765 1770

Trp Leu Ser Ala Thr Lys Pro Pro Leu Ser Asp Arg Thr Arg Leu  
1775 1780 1785

Leu Glu Ser Ile His Leu Ala Leu Thr Ala Trp Gly Leu Glu Pro  
1790 1795 1800

Asp Glu Asp Ile Leu Met Pro Phe Asn Leu Phe Cys Lys His Trp  
1805 1810 1815

Thr Tyr Leu Leu Leu Tyr Gln Phe Pro Asp Gln Tyr Ser Asp Ile  
1820 1825 1830

Leu Arg Leu Leu Met Gln Ser Ser Ala Glu Gln Leu Leu Ser Pro  
1835 1840 1845

Glu Cys Trp Lys Ala Thr Leu Arg Ala Leu Gly Cys Cys Ala Pro  
1850 1855 1860

Ser Cys Gln Gln Gly Ala Ala Ser Thr Glu Gly Ala Val Leu Pro  
1865 1870 1875

Ser Ser Ser Asp Ala Leu Leu Ser Asp Lys Gln Val Met Glu Thr  
1880 1885 1890

Ile Gln Trp Leu Ser Asp Phe Phe Tyr Lys Leu Arg Leu Ser Lys  
1895 1900 1905

Met Asp Phe Lys Ser Phe Gly Leu Phe Ser Lys Trp Ser Pro Tyr  
1910 1915 1920

Met Ala Asp Val Lys Thr Phe Leu Gly Tyr Leu Val Lys Arg Leu  
1925 1930 1935

Ile Asp Leu Glu Met Thr Cys Leu Ala Gln Asp Pro Thr Ala Ser  
1940 1945 1950

Arg Lys Thr Val Leu Lys Ser Leu His Ser Val Ile Ile Gln Leu  
1955 1960 1965

Phe Lys Pro Trp Ile Leu Val Leu Glu Asp Asn Glu Ser Ser Gln  
1970 1975 1980

Gln Arg His Tyr Pro Trp Leu Glu Ser Asp Thr Val Val Ala Ser  
1985 1990 1995

Ser Ile Val Gln Leu Phe Thr Asp Cys Ile Asp Ser Leu His Glu  
2000 2005 2010

Ser Phe Lys Asp Lys Leu Leu Pro Gly Asp Ala Gly Ala Leu Trp  
2015 2020 2025

Leu His Leu Met His Tyr Cys Glu Ala Cys Thr Ala Pro Lys Met  
2030 2035 2040

Pro Glu Phe Ile Leu Tyr Ala Phe His Ser Thr Tyr Arg Lys Leu  
2045 2050 2055

Pro Trp Lys Asp Leu His Pro Asp Gln Met Leu Met Glu Ala Phe  
2060 2065 2070

Phe Lys Val Glu Arg Gly Ser Pro Lys Ser Cys Phe Leu Phe Leu  
2075 2080 2085

Gly Ser Val Leu Cys Glu Val Asn Trp Val Ser Val Leu Ser Asp  
2090 2095 2100

Ala Trp Asn Ser Ser Pro His Pro Glu Thr Arg Ser Met Ile Val  
2105 2110 2115

Cys Leu Leu Phe Met Met Ile Leu Leu Ala Lys Glu Val Gln Leu  
2120 2125 2130

Val Asp Gln Thr Asp Ser Pro Leu Leu Ser Leu Leu Gly Gln Thr  
2135 2140 2145

Ser Ser Leu Ser Trp His Leu Val Asp Ile Val Ser Tyr Gln Ser  
2150 2155 2160

Val Leu Ser Tyr Phe Ser Ser His Tyr Pro Pro Ser Ile Ile Leu  
2165 2170 2175

Ala Lys Glu Ser Tyr Ala Glu Leu Ile Met Lys Leu Leu Lys Val  
2180 2185 2190

Ser Ala Gly Leu Ser Ile Pro Thr Asp Ser Gln Lys His Leu Asp  
2195 2200 2205

Ala Val Pro Lys Cys Gln Ala Phe Thr His Gln Met Val Gln Phe  
2210 2215 2220

Leu Ser Thr Leu Glu Gln Asn Gly Lys Ile Thr Leu Ala Val Leu  
2225 2230 2235

Glu Gln Glu Met Ser Lys Leu Leu Asp Asp Ile Ile Val Phe Asn  
2240 2245 2250

Pro Pro Asp Met Asp Ser Gln Thr Arg His Met Ala Leu Ser Ser  
2255 2260 2265

Leu Phe Met Glu Val Leu Met Met Met Asn Asn Ala Thr Ile Pro  
2270 2275 2280

Thr Ala Glu Phe Leu Arg Gly Ser Ile Arg Thr Trp Ile Gly Gln  
2285 2290 2295

Lys Met His Gly Leu Val Val Leu Pro Leu Leu Thr Ala Ala Cys  
2300 2305 2310

Gln Ser Leu Ala Ser Val Arg His Met Ala Glu Thr Thr Glu Ala  
2315 2320 2325

Cys Ile Thr Ala Tyr Phe Lys Glu Ser Pro Leu Asn Gln Asn Ser  
2330 2335 2340



Gly Trp Gly Pro Ile Leu Val Ser Leu Gln Val Pro Glu Leu Thr  
2345 2350 2355

Met Glu Glu Phe Leu Gln Glu Cys Leu Thr Leu Gly Ser Tyr Leu  
2360 2365 2370

Thr Leu Tyr Val Tyr Leu Leu Gln Cys Leu Asn Ser Glu Gln Thr  
2375 2380 2385

Leu Arg Asn Glu Met Lys Val Leu Leu Ile Leu Ser Lys Trp Leu  
2390 2395 2400

Glu Gln Val Tyr Pro Ser Ser Val Glu Glu Glu Ala Lys Leu Phe  
2405 2410 2415

Leu Trp Trp His Gln Val Leu Gln Leu Ser Leu Ile Gln Thr Glu  
2420 2425 2430

Gln Asn Asp Ser Val Leu Thr Glu Ser Val Ile Arg Ile Leu Leu  
2435 2440 2445

Leu Val Gln Ser Arg Gln Asn Leu Val Ala Glu Glu Arg Leu Ser  
2450 2455 2460

Ser Gly Ile Leu Gly Ala Ile Gly Phe Gly Arg Lys Ser Pro Leu  
2465 2470 2475

Ser Asn Arg Phe Arg Val Val Ala Arg Ser Met Ala Ala Phe Leu  
2480 2485 2490

Ser Val Gln Val Pro Met Glu Asp Gln Ile Arg Leu Arg Pro Gly  
2495 2500 2505

Ser Glu Leu His Leu Thr Pro Lys Ala Gln Gln Ala Leu Asn Ala  
2510 2515 2520

Leu Glu Ser Met Ala Ser Ser Lys Gln Tyr Val Glu Tyr Gln Asp  
2525 2530 2535

Gln Ile Leu Gln Ala Thr Gln Phe Ile Arg His Pro Gly His Cys  
2540 2545 2550

Leu Gln Asp Gly Lys Ser Phe Leu Ala Leu Leu Val Asn Cys Leu  
2555 2560 2565

Tyr Pro Glu Val His Tyr Leu Asp His Ile Arg  
2570 2575

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<211> 2979  
<212> DNA  
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ctgcggccgg cgcccgccct gctggccccc gccgtgctgc tgggcgccgc gctcggcctc 120  
ggcctcggcc tttggcttgg ctgccgcgcg ggccgccagc gcacgcgaca ccagaaagac 180  
gacactcaaa atctgctcaa gaatttggag tctaatgcgc agacccccctc ggaaactggc 240  
tccccatcaa ggaggaggaa gagagaagtg cagatgtcga aggacaagga agctgttgat 300  
gaatgtgagc cgcccttcaa cagcaatatc acagcattcg ccctgaaggc caaagtcac 360  
taccatca atcagaagtt ccggcctctg gccgatggct cctccaaccc gtctctgcat 420  
gaaaacttaa agcaggctgt tttgccacac cagccggtag aggcctctcc ttccagcagt 480  
ctggggagcc tgagccaggg tgagaaggac gactgcagct cctcatccag cgtccactcg 540  
gccaccagcg atgacagggt tctcagccgc accttcctcc gggatgaacgc cttccctgaa 600  
gtgctggcct gcgagagtgt agacgttgac ctgtgtatct acagccttca cttaaaagac 660  
ctgctgcatt tggacacggc actgaggcag gaaaagcata tgatgtttat tcagattttt 720  
aaaatgtgcc tccttgacct tcttcctaaa aagaagtcag atgatgaact ataccagaag 780  
atcctttcaa aacaagaaaa agatttggag gaactagaaa agggacttca ggtcaaactg 840

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tcaaacacag aaatgtcggg ggctggtgac tctgagtaca tcaccctggc tgatgtggaa  | 900  |
| aagaaggaga gagaatactc tgaacagcta atcgataata tggaagcttt ctggaaacag  | 960  |
| atggcaaata tccagcactt tcttgtggac cagtttaagt gttccagctc caaagcccga  | 1020 |
| cagctgatga tgactctgac ggaaagaatg attgcagccg aagggtatt gtgcgattct   | 1080 |
| caggagctgc aggctctgga cgccctggag aggacgatgg ggcgggcgca catggcaaaa  | 1140 |
| gtgattgagt ttctgaagct gcaagtccag gaggagacca ggtgccggct ggctgccatc  | 1200 |
| tcccacggcc tggagctgct ggctggtgag gggaagctgt ccgggcggca gaaggaggag  | 1260 |
| ctgctcacgc agcagcaca ggcccttctgg caggaggcag agcgcttcag ccgggagttt  | 1320 |
| gtccagcgag gcaaagacct ggtcacggcg tctctggctc accaggtgga gggaacggca  | 1380 |
| aaactcacgc tggcccaaga ggaggaacag agaagcttcc tggctgaggc ccagccgact  | 1440 |
| gctgaccggg aaaagtttct cgaggctttt catgaggctc tggagaggca gaggctgatg  | 1500 |
| cagtgtgacc tggaggaaga ggagaatgtc agagccaccg aggctgtggt tgcactctgc  | 1560 |
| caggagctgt acttcagcac cgtggacact ttccagaagt tcgtggatgc cctgttcctt  | 1620 |
| cagacgctcc ctggcatgac tggcctcccc ccggaagagt gtgactactt gaggcaggaa  | 1680 |
| gtccaggaga acgctgcctg gcagctgggg aagtcaaadc gcttccggag gcagcagtgg  | 1740 |
| aaactcttcc aggagctcct agagcaagac cagcagggtg ggatggagga gtgtgcgctg  | 1800 |
| tccagcgtgc tgcagacaca cctgcgggag gaccacgagg gcaccatccg cggcgtcttg  | 1860 |
| ggccgactgg gcggcctcac tgaagagtcc acgcggtgtg tcctgcaggg gcatgacctg  | 1920 |
| ctgttgcgct cagccctccg gaggctggca ctccgcggca acgcccctggc caccctgacg | 1980 |
| cagatgcggc tatcggggaa gaagcacctc ctgcaggagc tgcgggaaca gcgtgcactg  | 2040 |
| gagcaggggt cctcccagtg cctggacgag catcagtggc agctgctcag ggccctggag  | 2100 |
| gcgcgtgtgc tggaggaggc cagccggcta gaggaggaag cacagcagac acggctgcag  | 2160 |
| ctccagcagc ggctcctggc cgaggcccag gaggtagggc agcttctgca gcagcacatg  | 2220 |
| gagtgcgcca ttgggcaggc gctgctggtg catgcacgga atgcagccac caagagccgg  | 2280 |
| gccaaggaca gggatgactt caagaggaca ctgatggagg cggcagtgga gagcgtctac  | 2340 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gtgaccagcg ctggtgtcag ccgcctgggtg caggcgtatt accagcaaat cggaaggatc | 2400 |
| atggaggacc acgaggagag aaaactgcag cacctgaaga ccctgcaggg tgagaggatg  | 2460 |
| gaaaattaca aactgcggaa aaagcaagaa ctcagcaacc cttcgtcggg cagcaggacg  | 2520 |
| gcaggtggcg ctcatgagac ctcccaggcg gtccaccaga ggatgctgtc ccagcagaag  | 2580 |
| aggttcctgg cccagttccc agtgcaccag cagatgcgtc tgcacgcca gcagcagcag   | 2640 |
| gcaggagtca tggaccttct ggaagcccag ctggagaccc agctacagga agctgaacag  | 2700 |
| aacttcatct ccgagctggc agccttggcc cgagtgcccc ttgctgaaag caaactgttg  | 2760 |
| cctgctaagc gtgggctgct agagaagccc ctaaggacta aaaggaagaa gcccctgccc  | 2820 |
| caggaaaagag gggacctggg ggtgcccac aatgaggacc ttgcctccgg ggaccagacc  | 2880 |
| tcaggctcac tcagcagcaa aaggctgagt cagcaagaaa gtgaagctgg ggacagtggg  | 2940 |
| aactcaaaga agatgctaaa gagaagaagc aacttgtag                         | 2979 |

<210> 124  
 <211> 992  
 <212> PRT  
 <213> Homo sapiens

<400> 124

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Arg | Gly | Gly | Ala | Ala | Cys | Lys | Ser | Asp | Ala | Arg | Leu | Leu | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Asp | Ala | Leu | Arg | Pro | Ala | Pro | Ala | Leu | Leu | Ala | Pro | Ala | Val |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Gly | Ala | Ala | Leu | Gly | Leu | Gly | Leu | Gly | Leu | Trp | Leu | Gly | Cys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Gly | Arg | Gln | Arg | Thr | Arg | His | Gln | Lys | Asp | Asp | Thr | Gln | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Lys | Asn | Leu | Glu | Ser | Asn | Ala | Gln | Thr | Pro | Ser | Glu | Thr | Gly |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |

Ser Pro Ser Arg Arg Arg Lys Arg Glu Val Gln Met Ser Lys Asp Lys  
85 90 95

Glu Ala Val Asp Glu Cys Glu Pro Pro Ser Asn Ser Asn Ile Thr Ala  
100 105 110

Phe Ala Leu Lys Ala Lys Val Ile Tyr Pro Ile Asn Gln Lys Phe Arg  
115 120 125

Pro Leu Ala Asp Gly Ser Ser Asn Pro Ser Leu His Glu Asn Leu Lys  
130 135 140

Gln Ala Val Leu Pro His Gln Pro Val Glu Ala Ser Pro Ser Ser Ser  
145 150 155 160

Leu Gly Ser Leu Ser Gln Gly Glu Lys Asp Asp Cys Ser Ser Ser Ser  
165 170 175

Ser Val His Ser Ala Thr Ser Asp Asp Arg Phe Leu Ser Arg Thr Phe  
180 185 190

Leu Arg Val Asn Ala Phe Pro Glu Val Leu Ala Cys Glu Ser Val Asp  
195 200 205

Val Asp Leu Cys Ile Tyr Ser Leu His Leu Lys Asp Leu Leu His Leu  
210 215 220

Asp Thr Ala Leu Arg Gln Glu Lys His Met Met Phe Ile Gln Ile Phe  
225 230 235 240

Lys Met Cys Leu Leu Asp Leu Leu Pro Lys Lys Lys Ser Asp Asp Glu  
245 250 255

Leu Tyr Gln Lys Ile Leu Ser Lys Gln Glu Lys Asp Leu Glu Glu Leu  
260 265 270

Glu Lys Gly Leu Gln Val Lys Leu Ser Asn Thr Glu Met Ser Gly Ala  
275 280 285

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

Glu Tyr Ser Glu Gln Leu Ile Asp Asn Met Glu Ala Phe Trp Lys Gln  
305 310 315 320

Met Ala Asn Ile Gln His Phe Leu Val Asp Gln Phe Lys Cys Ser Ser  
325 330 335

Ser Lys Ala Arg Gln Leu Met Met Thr Leu Thr Glu Arg Met Ile Ala  
340 345 350

Ala Glu Gly Leu Leu Cys Asp Ser Gln Glu Leu Gln Ala Leu Asp Ala  
355 360 365

Leu Glu Arg Thr Met Gly Arg Ala His Met Ala Lys Val Ile Glu Phe  
370 375 380

Leu Lys Leu Gln Val Gln Glu Glu Thr Arg Cys Arg Leu Ala Ala Ile  
385 390 395 400

Ser His Gly Leu Glu Leu Leu Ala Gly Glu Gly Lys Leu Ser Gly Arg  
405 410 415

Gln Lys Glu Glu Leu Leu Thr Gln Gln His Lys Ala Phe Trp Gln Glu  
420 425 430

Ala Glu Arg Phe Ser Arg Glu Phe Val Gln Arg Gly Lys Asp Leu Val  
435 440 445

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

Ala Gln Glu Glu Glu Gln Arg Ser Phe Leu Ala Glu Ala Gln Pro Thr  
465 470 475 480

Ala Asp Pro Glu Lys Phe Leu Glu Ala Phe His Glu Val Leu Glu Arg  
485 490 495

Gln Arg Leu Met Gln Cys Asp Leu Glu Glu Glu Asn Val Arg Ala  
500 505 510

Thr Glu Ala Val Val Ala Leu Cys Gln Glu Leu Tyr Phe Ser Thr Val  
515 520 525

Asp Thr Phe Gln Lys Phe Val Asp Ala Leu Phe Leu Gln Thr Leu Pro  
530 535 540

Gly Met Thr Gly Leu Pro Pro Glu Glu Cys Asp Tyr Leu Arg Gln Glu  
545 550 555 560

Val Gln Glu Asn Ala Ala Trp Gln Leu Gly Lys Ser Asn Arg Phe Arg  
565 570 575

Arg Gln Gln Trp Lys Leu Phe Gln Glu Leu Leu Glu Gln Asp Gln Gln  
580 585 590

Val Trp Met Glu Glu Cys Ala Leu Ser Ser Val Leu Gln Thr His Leu  
595 600 605

Arg Glu Asp His Glu Gly Thr Ile Arg Gly Val Leu Gly Arg Leu Gly  
610 615 620

Gly Leu Thr Glu Glu Ser Thr Arg Cys Val Leu Gln Gly His Asp Leu  
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Ala Thr Leu Thr Gln Met Arg Leu Ser Gly Lys Lys His Leu Leu Gln  
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Glu Leu Arg Glu Gln Arg Ala Leu Glu Gln Gly Ser Ser Gln Cys Leu  
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Asp Glu His Gln Trp Gln Leu Leu Arg Ala Leu Glu Ala Arg Val Leu  
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Glu Glu Ala Ser Arg Leu Glu Glu Glu Ala Gln Gln Thr Arg Leu Gln  
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Leu Gln Gln Arg Leu Leu Ala Glu Ala Gln Glu Val Gly Gln Leu Leu  
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Gln Gln His Met Glu Cys Ala Ile Gly Gln Ala Leu Leu Val His Ala  
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Arg Asn Ala Ala Thr Lys Ser Arg Ala Lys Asp Arg Asp Asp Phe Lys  
755 760 765

Arg Thr Leu Met Glu Ala Ala Val Glu Ser Val Tyr Val Thr Ser Ala  
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Gly Val Ser Arg Leu Val Gln Ala Tyr Tyr Gln Gln Ile Gly Arg Ile  
785 790 795 800

Met Glu Asp His Glu Glu Arg Lys Leu Gln His Leu Lys Thr Leu Gln  
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Gly Glu Arg Met Glu Asn Tyr Lys Leu Arg Lys Lys Gln Glu Leu Ser  
820 825 830

Asn Pro Ser Ser Gly Ser Arg Thr Ala Gly Gly Ala His Glu Thr Ser  
835 840 845

Gln Ala Val His Gln Arg Met Leu Ser Gln Gln Lys Arg Phe Leu Ala  
850 855 860

Gln Phe Pro Val His Gln Gln Met Arg Leu His Ala Gln Gln Gln Gln  
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Ala Gly Val Met Asp Leu Leu Glu Ala Gln Leu Glu Thr Gln Leu Gln  
885 890 895

Glu Ala Glu Gln Asn Phe Ile Ser Glu Leu Ala Ala Leu Ala Arg Val  
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Pro Leu Ala Glu Ser Lys Leu Leu Pro Ala Lys Arg Gly Leu Leu Glu  
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Lys Pro Leu Arg Thr Lys Arg Lys Lys Pro Leu Pro Gln Glu Arg Gly  
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Asp Leu Gly Val Pro Asn Asn Glu Asp Leu Ala Ser Gly Asp Gln Thr  
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| Met | Ile | Trp | Pro | Lys | Val | Glu | Cys | Cys | His | Phe | Lys | Thr | Ala | Val | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Leu | Gly | Met | Lys | Leu | Asp | Lys | Lys | Met | Glu | Val | Phe | Ile | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Thr | Ser | Ala | Ala | Ser | Ser | Gly | Pro | Trp | Ala | His | Ser | Leu | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Phe | Ile | Pro | Ser | Trp | Pro | Lys | Lys | Asn | Leu | Phe | Lys | Arg | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ile | Thr | His | Arg | Leu | Tyr | Gly | Asp | Ile | Ser | Arg | Glu | Val | Gln | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Glu | Asn | Gly | Val | Ile | Phe | Gln | Lys | Cys | Ala | Leu | Val | Ser | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Glu | Ala | Gln | Thr | Ala | Arg | Ile | Trp | Leu | Leu | Val | Asn | Asn | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Thr | Ser | Ser | Ala | Asn | Leu | Ser | Glu | Leu | Leu | Leu | Leu | Asp | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ala | Gly | Leu | Thr | Ile | Trp | Asp | Ser | Val | Gly | Asn | Arg | Thr | Ser | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

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Ala Val Ser Tyr Ala Ala Thr Leu Gln Ala Gly Asp Leu Gly Asn Gly  
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Glu Ser Leu Lys Leu Pro Ala Gln Leu Thr Phe Gln Ser Ser Ser Arg  
180 185 190

Asn Arg Thr Gln Leu Lys Val Leu Phe Ser Ile Thr Ala Glu Glu Asn  
195 200 205

Val Thr Val Leu Pro His His Gly Leu His Ala Ala Gly Phe Phe Ile  
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Ala Phe Leu Leu Ser Leu Val Leu Thr Trp Ala Ala Leu Phe Leu Met  
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Val Arg Tyr Gln Cys Leu Lys Gly Asn Met Leu Thr Arg His Arg Val  
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Trp Gln Tyr Glu Ser Lys Leu Glu Pro Leu Pro Phe Thr Ser Ala Asp  
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Gly Val Asn Glu Asp Leu Ser Leu Asn Asp Gln Met Ile Asp Ile Leu  
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Ser Ser Glu Asp Pro Gly Ser Met Leu Gln Ala Leu Glu Glu Leu Glu  
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Ile Ala Thr Leu Asn Arg Ala Asp Ala Asp Leu Glu Ala Cys Arg Thr  
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Gln Ile Ser Lys Asp Ile Ile Ala Leu Leu Leu Lys Asn Leu Thr Ser  
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Ser Gly His Leu Ser Pro Gln Val Glu Arg Lys Met Ser Ala Val Phe  
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Lys Lys Gln Phe Leu Leu Leu Glu Asn Glu Ile Gln Glu Glu Tyr Asp  
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Arg Lys Met Val Ala Leu Thr Ala Glu Cys Asp Leu Glu Thr Arg Lys  
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Lys Met Glu Asn Gln Tyr Gln Arg Glu Met Met Ala Met Glu Glu Ala  
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Glu Glu Leu Leu Lys Arg Ala Gly Glu Arg Ser Ala Val Glu Cys Ser  
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Asn Leu Leu Arg Thr Leu His Gly Leu Glu Gln Glu His Leu Arg Lys  
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Ser Leu Ala Leu Gln Gln Glu Glu Asp Phe Ala Lys Ala His Arg Gln  
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Leu Ala Val Phe Gln Arg Asn Glu Leu His Ser Ile Phe Phe Thr Gln  
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Ile Lys Ser Ala Ile Phe Lys Gly Glu Leu Lys Pro Glu Ala Ala Lys  
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Met Asp Phe Phe Gln Ala Ser Lys Arg Tyr His Leu Ser Lys Arg Phe  
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Gly His Arg Glu Tyr Leu Val Gln Asn Leu Gln Ser Ser Glu Thr Arg  
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Val Gln Gly Leu Leu Ser Thr Ala Ala Ala Gln Leu Thr His Leu Ile  
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Gln Lys His Glu Arg Ala Gly Tyr Leu Asp Glu Asp Gln Met Glu Met  
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Leu Leu Glu Arg Ala Gln Thr Glu Val Phe Ser Ile Lys Gln Lys Leu  
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Asp Asn Asp Leu Lys Gln Glu Lys Lys Lys Leu His Gln Lys Leu Ile  
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Thr Lys Arg Arg Arg Glu Leu Leu Gln Lys His Arg Glu Gln Arg Arg  
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Glu Gln Ala Ser Val Gly Glu Ala Phe Arg Thr Val Glu Asp Ala Gly  
610 615 620

Gln Tyr Leu His Gln Lys Arg Ser Leu Met Glu Glu His Gly Ala Thr  
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Leu Glu Glu Leu Gln Glu Arg Leu Asp Gln Ala Ala Leu Asp Asp Leu  
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Arg Thr Leu Thr Leu Ser Leu Phe Glu Lys Ala Thr Asp Glu Leu Arg  
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Pro Trp Leu Phe Leu Gln Gln Ile Leu Glu Glu His Gly Lys Glu Met  
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Ala Ala Arg Ala Glu Gln Leu Glu Gly Glu Glu Arg Asp Arg Asp Gln  
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Glu Gly Val Gln Ser Val Arg Gln Arg Leu Lys Asp Asp Ala Pro Glu  
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Ala Val Thr Glu Glu Gln Ala Glu Leu Arg Arg Trp Glu His Leu Ile  
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Phe Met Lys Leu Cys Ser Ser Val Phe Ser Leu Ser Glu Glu Glu Leu  
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Leu Arg Met Arg Gln Glu Val His Gly Cys Phe Ala Gln Met Asp Arg  
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Ser Leu Ala Leu Pro Lys Ile Arg Ala Arg Val Leu Leu Gln Gln Phe  
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Gln Thr Ala Trp Arg Glu Ala Glu Phe Val Lys Leu Asp Gln Ala Val  
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Ala Ala Pro Glu Leu Gln Gln Gln Ser Lys Val Arg Lys Ser Arg Ser  
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Lys Ser Lys Ser Lys Gly Glu Leu Leu Lys Lys Cys Ile Glu Asp Lys  
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Ile His Leu Cys Glu Glu Gln Ala Ser Glu Asp Leu Val Glu Lys Val  
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Gly Gly Phe Ala Gln Ser Leu Val Ala Leu Gln Phe Gln Lys Ala Ser  
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Arg Val Thr Glu Thr Leu Ser Ala Tyr Thr Ala Leu Leu Ser Ile Gln  
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Asp Leu Leu Leu Glu Glu Leu Ser Ala Ser Glu Met Leu Thr Lys Ser  
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Ala Cys Thr Gln Ile Leu Glu Ser His Ser Arg Glu Leu Gln Glu Leu  
930 935 940



Glu Arg Lys Leu Glu Asp Gln Leu Val Gln Gln Glu Ala Ala Gln Gln  
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Gln Gln Ala Leu Ala Ser Trp Gln Gln Trp Val Ala Asp Gly Pro Gly  
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Ser Gln Glu Leu Arg Leu Ala Ser Tyr Leu Ala Arg Met Ala Met  
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Thr Ala Ser Gln Pro Gln Leu Leu Ala Leu Leu Asp Ser Ala Thr  
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Glu Arg His Val Asp His Ala Ala Glu Ser Asp Gly Gly Ala Glu  
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Gln Ala Asp Val Gly Arg Arg Arg Lys His Gln Ser Trp Trp Gln  
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Gly Glu Lys Leu Phe Ile Phe Arg Asn Pro Lys Glu Pro Glu Ile  
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| gtcaatgagt gtgacctgaa tccaaatatc tgcctaagtg ggacctgtga aaacacgaaa  | 3900 |
| ggctcattta tctgccactg tgatatgggc tactccggca aaaaaggaaa aactggctgt  | 3960 |
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| atcgaggatc agtctgagac agaagccaat gtgagtcttg caagttggga tgttgagaag   | 8280 |
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| aagccagtgg ctggaacctt ttattacaa atcagtagta ctccacttta taaaaagaaa    | 8520 |
| gaacttaacc aactagaaga caaatatgac aaagactacc tcagtgggtga actgggtgat  | 8580 |
| aatctgaaga tgaaaatcca ggttttgctt cattaa                             | 8616 |

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 <211> 2871  
 <212> PRT  
 <213> Homo sapiens

<400> 128

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Arg | Gly | Arg | Leu | Leu | Glu | Ile | Ala | Leu | Gly | Phe | Thr | Val | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Ser | Tyr | Thr | Ser | His | Gly | Ala | Asp | Ala | Asn | Leu | Glu | Ala | Gly |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Lys | Glu | Thr | Arg | Ala | Ser | Arg | Ala | Lys | Arg | Arg | Gly | Gly | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | His | Asp | Ala | Leu | Lys | Gly | Pro | Asn | Val | Cys | Gly | Ser | Arg | Tyr | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Tyr | Cys | Cys | Pro | Gly | Trp | Lys | Thr | Leu | Pro | Gly | Gly | Asn | Gln | Cys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |



Ile Val Pro Ile Cys Arg His Ser Cys Gly Asp Gly Phe Cys Ser Arg  
85 90 95

Pro Asn Met Cys Thr Cys Pro Ser Gly Gln Ile Ala Pro Ser Cys Gly  
100 105 110

Ser Arg Ser Ile Gln His Cys Asn Ile Arg Cys Met Asn Gly Gly Ser  
115 120 125

Cys Ser Asp Asp His Cys Leu Cys Gln Lys Gly Tyr Ile Gly Thr His  
130 135 140

Cys Gly Gln Pro Val Cys Glu Ser Gly Cys Leu Asn Gly Gly Arg Cys  
145 150 155 160

Val Ala Pro Asn Arg Cys Ala Cys Thr Tyr Gly Phe Thr Gly Pro Gln  
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Cys Glu Arg Asp Tyr Arg Thr Gly Pro Cys Phe Thr Val Ile Ser Asn  
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Gln Met Cys Gln Gly Gln Leu Ser Gly Ile Val Cys Thr Lys Thr Leu  
195 200 205

Cys Cys Ala Thr Val Gly Arg Ala Trp Gly His Pro Cys Glu Met Cys  
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Pro Ala Gln Pro His Pro Cys Arg Arg Gly Phe Ile Pro Asn Ile Arg  
225 230 235 240

Thr Gly Ala Cys Gln Asp Val Asp Glu Cys Gln Ala Ile Pro Gly Leu  
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Cys Gln Gly Gly Asn Cys Ile Asn Thr Val Gly Ser Phe Glu Cys Lys  
260 265 270

Cys Pro Ala Gly His Lys Leu Asn Glu Val Ser Gln Lys Cys Glu Asp  
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Ile Asp Glu Cys Ser Thr Ile Pro Gly Ile Cys Glu Gly Gly Glu Cys  
290 295 300

Thr Asn Thr Val Ser Ser Tyr Phe Cys Lys Cys Pro Pro Gly Phe Tyr  
305 310 315 320

Thr Ser Pro Asp Gly Thr Arg Cys Ile Asp Val Arg Pro Gly Tyr Cys  
325 330 335

Tyr Thr Ala Leu Thr Asn Gly Arg Cys Ser Asn Gln Leu Pro Gln Ser  
340 345 350

Ile Thr Lys Met Gln Cys Cys Cys Asp Ala Gly Arg Cys Trp Ser Pro  
355 360 365

Gly Val Thr Val Ala Pro Glu Met Cys Pro Ile Arg Ala Thr Glu Asp  
370 375 380

Phe Asn Lys Leu Cys Ser Val Pro Met Val Ile Pro Gly Arg Pro Glu  
385 390 395 400

Tyr Pro Pro Pro Pro Leu Gly Pro Ile Pro Pro Val Leu Pro Val Pro  
405 410 415

Pro Gly Phe Pro Pro Gly Pro Gln Ile Pro Val Pro Arg Pro Pro Val  
420 425 430

Glu Tyr Leu Tyr Pro Ser Arg Glu Pro Pro Arg Val Leu Pro Val Asn  
435 440 445

Val Thr Asp Tyr Cys Gln Leu Val Arg Tyr Leu Cys Gln Asn Gly Arg  
450 455 460

Cys Ile Pro Thr Pro Gly Ser Tyr Arg Cys Glu Cys Asn Lys Gly Phe  
465 470 475 480

Gln Leu Asp Leu Arg Gly Glu Cys Ile Asp Val Asp Glu Cys Glu Lys  
485 490 495

Asn Pro Cys Ala Gly Gly Glu Cys Ile Asn Asn Gln Gly Ser Tyr Thr  
500 505 510

Cys Gln Cys Arg Ala Gly Tyr Gln Ser Thr Leu Thr Arg Thr Glu Cys  
515 520 525

Arg Asp Ile Asp Glu Cys Leu Gln Asn Gly Arg Ile Cys Asn Asn Gly  
530 535 540

Arg Cys Ile Asn Thr Asp Gly Ser Phe His Cys Val Cys Asn Ala Gly  
545 550 555 560

Phe His Val Thr Arg Asp Gly Lys Asn Cys Glu Asp Met Asp Glu Cys  
565 570 575

Ser Ile Arg Asn Met Cys Leu Asn Gly Met Cys Ile Asn Glu Asp Gly  
580 585 590

Ser Phe Lys Cys Ile Cys Lys Pro Gly Phe Gln Leu Ala Ser Asp Gly  
595 600 605

Arg Tyr Cys Lys Asp Ile Asn Glu Cys Glu Thr Pro Gly Ile Cys Met  
610 615 620

Asn Gly Arg Cys Val Asn Thr Asp Gly Ser Tyr Arg Cys Glu Cys Phe  
625 630 635 640

Pro Gly Leu Ala Val Gly Leu Asp Gly Arg Val Cys Val Asp Thr His  
645 650 655

Met Arg Ser Thr Cys Tyr Gly Gly Tyr Lys Arg Gly Gln Cys Ile Lys  
660 665 670

Pro Leu Phe Gly Ala Val Thr Lys Ser Glu Cys Cys Cys Ala Ser Thr  
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Glu Tyr Ala Phe Gly Glu Pro Cys Gln Pro Cys Pro Ala Gln Asn Ser  
690 695 700

Ala Glu Tyr Gln Ala Leu Cys Ser Ser Gly Pro Gly Met Thr Ser Ala  
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Gly Ser Asp Ile Asn Glu Cys Ala Leu Asp Pro Asp Ile Cys Pro Asn  
725 730 735

Gly Ile Cys Glu Asn Leu Arg Gly Thr Tyr Lys Cys Ile Cys Asn Ser  
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Gly Tyr Glu Val Asp Ser Thr Gly Lys Asn Cys Val Asp Ile Asn Glu  
755 760 765

Cys Val Leu Asn Ser Leu Leu Cys Asp Asn Gly Gln Cys Arg Asn Thr  
770 775 780

Pro Gly Ser Phe Val Cys Thr Cys Pro Lys Gly Phe Ile Tyr Lys Pro  
785 790 795 800

Asp Leu Lys Thr Cys Glu Asp Ile Asp Glu Cys Glu Ser Ser Pro Cys  
805 810 815

Ile Asn Gly Val Cys Lys Asn Ser Pro Gly Ser Phe Ile Cys Glu Cys  
820 825 830

Ser Ser Glu Ser Thr Leu Asp Pro Thr Lys Thr Ile Cys Ile Glu Thr  
835 840 845

Ile Lys Gly Thr Cys Trp Gln Thr Val Ile Asp Gly Arg Cys Glu Ile  
850 855 860

Asn Ile Asn Gly Ala Thr Leu Lys Ser Gln Cys Cys Ser Ser Leu Gly  
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Thr Arg Gly Ser Phe Lys Cys Gln Cys Pro Ser Gly Met Thr Leu Asp  
930 935 940

Ala Thr Gly Arg Ile Cys Leu Asp Ile Arg Leu Glu Thr Cys Phe Leu  
945 950 955 960

Arg Tyr Glu Asp Glu Glu Cys Thr Leu Pro Ile Ala Gly Arg His Arg  
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Met Asp Ala Cys Cys Cys Ser Val Gly Ala Ala Trp Gly Thr Glu Glu  
980 985 990

Cys Glu Glu Cys Pro Met Arg Asn Thr Pro Glu Tyr Glu Glu Leu Cys  
995 1000 1005

Pro Arg Gly Pro Gly Phe Ala Thr Lys Glu Ile Thr Asn Gly Lys  
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Pro Phe Phe Lys Asp Ile Asn Glu Cys Lys Met Ile Pro Ser Leu  
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Cys Thr His Gly Lys Cys Arg Asn Thr Ile Gly Ser Phe Lys Cys  
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Arg Cys Asp Ser Gly Phe Ala Leu Asp Ser Glu Glu Arg Asn Cys  
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Thr Asp Ile Asp Glu Cys Arg Ile Ser Pro Asp Leu Cys Gly Arg  
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Gly Gln Cys Val Asn Thr Pro Gly Asp Phe Glu Cys Lys Cys Asp  
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1100 1105 1110

Ile Asp Glu Cys Gln Arg Asp Pro Leu Leu Cys Arg Gly Gly Val  
1115 1120 1125

Cys His Asn Thr Glu Gly Ser Tyr Arg Cys Glu Cys Pro Pro Gly  
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His Gln Leu Ser Pro Asn Ile Ser Ala Cys Ile Asp Ile Asn Glu  
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Cys Glu Leu Ser Ala His Leu Cys Pro Asn Gly Arg Cys Val Asn  
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Leu Ile Gly Lys Tyr Gln Cys Ala Cys Asn Pro Gly Tyr His Ser  
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Met Asn Gly Gly Cys Glu Thr Phe Cys Thr Asn Ser Glu Gly Ser  
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Cys Thr Asn Thr Ala Gly Ser Phe Lys Cys Ser Cys Ser Pro Gly  
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Glu Cys Gln Glu Leu Pro Gly Leu Cys Gln Gly Gly Lys Cys Ile  
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| Met | Ala | Ala | His | Arg | Pro | Val | Glu | Trp | Val | Gln | Ala | Val | Val | Ser | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Asp | Glu | Gln | Leu | Pro | Ile | Lys | Thr | Gly | Gln | Gln | Asn | Thr | His | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Ser | Thr | Glu | His | Asn | Lys | Glu | Cys | Leu | Ile | Asn | Ile | Ser | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Lys | Phe | Ser | Leu | Val | Ile | Ser | Gly | Leu | Thr | Thr | Ile | Leu | Lys | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Asn | Met | Arg | Ile | Phe | Gly | Glu | Ala | Ala | Glu | Lys | Asn | Leu | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

Leu Ser Gln Leu Ile Ile Leu Asp Thr Leu Glu Lys Cys Leu Ala Gly  
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Gln Pro Lys Asp Thr Met Arg Leu Asp Glu Thr Met Leu Val Lys Gln  
100 105 110

Leu Leu Pro Glu Ile Cys His Phe Leu His Thr Cys Arg Glu Gly Asn  
115 120 125

Gln His Ala Ala Glu Leu Arg Asn Ser Ala Ser Gly Val Leu Phe Ser  
130 135 140

Leu Ser Cys Asn Asn Phe Asn Ala Val Phe Ser Arg Ile Ser Thr Arg  
145 150 155 160

Leu Gln Glu Leu Thr Val Cys Ser Glu Asp Asn Val Asp Val His Asp  
165 170 175

Ile Glu Leu Leu Gln Tyr Ile Asn Val Asp Cys Ala Lys Leu Lys Arg  
180 185 190

Leu Leu Lys Glu Thr Ala Phe Lys Phe Lys Ala Leu Lys Lys Val Ala  
195 200 205

Gln Leu Ala Val Ile Asn Ser Leu Glu Lys Ala Phe Trp Asn Trp Val  
210 215 220

Glu Asn Tyr Pro Asp Glu Phe Thr Lys Leu Tyr Gln Ile Pro Gln Thr  
225 230 235 240

Asp Met Ala Glu Cys Ala Glu Lys Leu Phe Asp Leu Val Asp Gly Phe  
245 250 255

Ala Glu Ser Thr Lys Arg Lys Ala Ala Val Trp Pro Leu Gln Ile Ile  
260 265 270

Leu Leu Ile Leu Cys Pro Glu Ile Ile Gln Asp Ile Ser Lys Asp Val  
275 280 285

Val Asp Glu Asn Asn Met Asn Lys Lys Leu Phe Leu Asp Ser Leu Arg  
290 295 300

Lys Ala Leu Ala Gly His Gly Gly Ser Arg Gln Leu Thr Glu Ser Ala  
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Ala Ile Ala Cys Val Lys Leu Cys Lys Ala Ser Thr Tyr Ile Asn Trp  
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Glu Asp Asn Ser Val Ile Phe Leu Leu Val Gln Ser Met Val Val Asp  
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Leu Lys Asn Leu Leu Phe Asn Pro Ser Lys Pro Phe Ser Arg Gly Ser  
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Gln Pro Ala Asp Val Asp Leu Met Ile Asp Cys Leu Val Ser Cys Phe  
370 375 380

Arg Ile Ser Pro His Asn Asn Gln His Phe Lys Ile Cys Leu Ala Gln  
385 390 395 400

Asn Ser Pro Ser Thr Phe His Tyr Val Leu Val Asn Ser Leu His Arg  
405 410 415

Ile Ile Thr Asn Ser Ala Leu Asp Trp Trp Pro Lys Ile Asp Ala Val  
420 425 430

Tyr Cys His Ser Val Glu Leu Arg Asn Met Phe Gly Glu Thr Leu His  
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Lys Ala Val Gln Gly Cys Gly Ala His Pro Ala Ile Arg Met Ala Pro  
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Ser Leu Thr Phe Lys Glu Lys Val Thr Ser Leu Lys Phe Lys Glu Lys  
465 470 475 480

Pro Thr Asp Leu Glu Thr Arg Ser Tyr Lys Tyr Leu Leu Leu Ser Met  
485 490 495

Val Lys Leu Ile His Ala Asp Pro Lys Leu Leu Leu Cys Asn Pro Arg  
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Lys Gln Gly Pro Glu Thr Gln Gly Ser Thr Ala Glu Leu Ile Thr Gly  
515 520 525

Leu Val Gln Leu Val Pro Gln Ser His Met Pro Glu Ile Ala Gln Glu  
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Ala Met Glu Ala Leu Leu Val Leu His Gln Leu Asp Ser Ile Asp Leu  
545 550 555 560

Trp Asn Pro Asp Ala Pro Val Glu Thr Phe Trp Glu Ile Ser Ser Gln  
565 570 575

Met Leu Phe Tyr Ile Cys Lys Lys Leu Thr Ser His Gln Met Leu Ser  
580 585 590

Ser Thr Glu Ile Leu Lys Trp Leu Arg Glu Ile Leu Ile Cys Arg Asn  
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Lys Phe Leu Leu Lys Asn Lys Gln Ala Asp Arg Ser Ser Cys His Phe  
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Leu Leu Phe Tyr Gly Val Gly Cys Asp Ile Pro Ser Ser Gly Asn Thr  
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Ser Gln Met Ser Met Asp His Glu Glu Leu Leu Arg Thr Pro Gly Ala  
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Ser Leu Arg Lys Gly Lys Gly Asn Ser Ser Met Asp Ser Ala Ala Gly  
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Cys Ser Gly Thr Pro Pro Ile Cys Arg Gln Ala Gln Thr Lys Leu Glu  
675 680 685



Val Ala Leu Tyr Met Phe Leu Trp Asn Pro Asp Thr Glu Ala Val Leu  
690 695 700

Val Ala Met Ser Cys Phe Arg His Leu Cys Glu Glu Ala Asp Ile Arg  
705 710 715 720

Cys Gly Val Asp Glu Val Ser Val His Asn Leu Leu Pro Asn Tyr Asn  
725 730 735

Thr Phe Met Glu Phe Ala Ser Val Ser Asn Met Met Ser Thr Gly Arg  
740 745 750

Ala Ala Leu Gln Lys Arg Val Met Ala Leu Leu Arg Arg Ile Glu His  
755 760 765

Pro Thr Ala Gly Asn Thr Glu Ala Trp Glu Asp Thr His Ala Lys Trp  
770 775 780

Glu Gln Ala Thr Lys Leu Ile Leu Asn Tyr Pro Lys Ala Lys Met Glu  
785 790 795 800

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

Met Ser His Val Ser Gly Gly Gly Ser Ile Asp Leu Ser Asp Thr Asp  
820 825 830

Ser Leu Gln Glu Trp Ile Asn Met Thr Gly Phe Leu Cys Ala Leu Gly  
835 840 845

Gly Val Cys Leu Gln Gln Arg Ser Asn Ser Gly Leu Ala Thr Tyr Ser  
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Pro Pro Met Gly Pro Val Ser Glu Arg Lys Gly Ser Met Ile Ser Val  
865 870 875 880

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

Arg Leu Leu Ser Leu Met Val Cys Asn His Glu Lys Val Gly Leu Gln  
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Ile Arg Thr Asn Val Lys Asp Leu Val Gly Leu Glu Leu Ser Pro Ala  
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Leu Tyr Pro Met Leu Phe Asn Lys Leu Lys Asn Thr Ile Ser Lys Phe  
930 935 940

Phe Asp Ser Gln Gly Gln Val Leu Leu Thr Asp Thr Asn Thr Gln Phe  
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Val Glu Gln Thr Ile Ala Ile Met Lys Asn Leu Leu Asp Asn His Thr  
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Glu Gly Ser Ser Glu His Leu Gly Gln Ala Ser Ile Glu Thr Met Met  
980 985 990

Leu Asn Leu Val Arg Tyr Val Arg Val Leu Gly Asn Met Val His Ala  
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Ile Gln Ile Lys Thr Lys Leu Cys Gln Leu Val Glu Val Met Met  
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Ala Arg Arg Asp Asp Leu Ser Phe Cys Gln Glu Met Lys Phe Arg  
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Asn Lys Met Val Glu Tyr Leu Thr Asp Trp Val Met Gly Thr Ser  
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Pro Leu Gln Pro Glu Glu Gly Asp Gly Val Glu Leu Met Glu Ala  
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Lys Ser Gln Leu Phe Leu Lys Tyr Phe Thr Leu Phe Met Asn Leu  
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Leu Asn Asp Cys Ser Glu Val Glu Asp Glu Ser Ala Gln Thr Gly  
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Gly Arg Lys Arg Gly Met Ser Arg Arg Leu Ala Ser Leu Arg His  
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Cys Thr Val Leu Ala Met Ser Asn Leu Leu Asn Ala Asn Val Asp  
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Ser Gly Leu Met His Ser Ile Gly Leu Gly Tyr His Lys Asp Leu  
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Gln Thr Arg Ala Thr Phe Met Glu Val Leu Thr Lys Ile Leu Gln  
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Gln Gly Thr Glu Phe Asp Thr Leu Ala Glu Thr Val Leu Ala Asp  
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Arg Phe Glu Arg Leu Val Glu Leu Val Thr Met Met Gly Asp Gln  
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Gly Glu Leu Pro Ile Ala Met Ala Leu Ala Asn Val Val Pro Cys  
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Ser Gln Trp Asp Glu Leu Ala Arg Val Leu Val Thr Leu Phe Asp  
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Ser Arg His Leu Leu Tyr Gln Leu Leu Trp Asn Met Phe Ser Lys  
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Glu Val Glu Leu Ala Asp Ser Met Gln Thr Leu Phe Arg Gly Asn  
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Ser Leu Ala Ser Lys Ile Met Thr Phe Cys Phe Lys Val Tyr Gly  
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Ala Thr Tyr Leu Gln Lys Leu Leu Asp Pro Leu Leu Arg Ile Val  
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Thr Arg Leu Glu Pro Ser Glu Ser Leu Glu Glu Asn Gln Arg Asn  
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Leu Leu Gln Met Thr Glu Lys Phe Phe His Ala Ile Ile Ser Ser  
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Ser Ser Glu Phe Pro Pro Gln Leu Arg Ser Val Cys His Cys Leu  
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Tyr Gln Ala Thr Cys His Ser Leu Leu Asn Lys Ala Thr Val Lys  
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Glu Lys Lys Glu Asn Lys Lys Ser Val Val Ser Gln Arg Phe Pro  
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Gln Asn Ser Ile Gly Ala Val Gly Ser Ala Met Phe Leu Arg Phe  
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Ile Asn Pro Ala Ile Val Ser Pro Tyr Glu Ala Gly Ile Leu Asp  
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Lys Lys Pro Pro Pro Arg Ile Glu Arg Gly Leu Lys Leu Met Ser  
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Lys Ile Leu Gln Ser Ile Ala Asn His Val Leu Phe Thr Lys Glu  
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Glu His Met Arg Pro Phe Asn Asp Phe Val Lys Ser Asn Phe Asp  
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Ala Ala Arg Arg Phe Phe Leu Asp Ile Ala Ser Asp Cys Pro Thr  
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Ser Asp Ala Val Asn His Ser Leu Ser Phe Ile Ser Asp Gly Asn  
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Val Leu Ala Leu His Arg Leu Leu Trp Asn Asn Gln Glu Lys Ile  
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Gly Gln Tyr Leu Ser Ser Asn Arg Asp His Lys Ala Val Gly Arg  
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Arg Pro Phe Asp Lys Met Ala Thr Leu Leu Ala Tyr Leu Gly Pro  
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Pro Glu His Lys Pro Val Ala Asp Thr His Trp Ser Ser Leu Asn  
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Leu Thr Ser Ser Lys Phe Glu Glu Phe Met Thr Arg His Gln Val  
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His Glu Lys Glu Glu Phe Lys Ala Leu Lys Thr Leu Ser Ile Phe  
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Tyr Gln Ala Gly Thr Ser Lys Ala Gly Asn Pro Ile Phe Tyr Tyr  
1595 1600 1605

Val Ala Arg Arg Phe Lys Thr Gly Gln Ile Asn Gly Asp Leu Leu  
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Ile Tyr His Val Leu Leu Thr Leu Lys Pro Tyr Tyr Ala Lys Pro  
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Tyr Glu Ile Val Val Asp Leu Thr His Thr Gly Pro Ser Asn Arg  
1640 1645 1650

Phe Lys Thr Asp Phe Leu Ser Lys Trp Phe Val Val Phe Pro Gly  
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Phe Ala Tyr Asp Asn Val Ser Ala Val Tyr Ile Tyr Asn Cys Asn  
1670 1675 1680

Ser Trp Val Arg Glu Tyr Thr Lys Tyr His Glu Arg Leu Leu Thr  
1685 1690 1695

Gly Leu Lys Gly Ser Lys Arg Leu Val Phe Ile Asp Cys Pro Gly  
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Lys Leu Ala Glu His Ile Glu His Glu Gln Gln Lys Leu Pro Ala  
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Ala Thr Leu Ala Leu Glu Glu Asp Leu Lys Val Phe His Asn Ala  
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Leu Lys Leu Ala His Lys Asp Thr Lys Val Ser Ile Lys Val Gly  
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Ser Thr Ala Val Gln Val Thr Ser Ala Glu Arg Thr Lys Val Leu  
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Gly Gln Ser Val Phe Leu Asn Asp Ile Tyr Tyr Ala Ser Glu Ile  
1775 1780 1785

Glu Glu Ile Cys Leu Val Asp Glu Asn Gln Phe Thr Leu Thr Ile  
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Ala Asn Gln Gly Thr Pro Leu Thr Phe Met His Gln Glu Cys Glu  
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Ala Ile Val Gln Ser Ile Ile His Ile Arg Thr Arg Trp Glu Leu  
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Ser Gln Pro Asp Ser Ile Pro Gln His Thr Lys Ile Arg Pro Lys  
1835 1840 1845

Asp Val Pro Gly Thr Leu Leu Asn Ile Ala Leu Leu Asn Leu Gly  
1850 1855 1860

Ser Ser Asp Pro Ser Leu Arg Ser Ala Ala Tyr Asn Leu Leu Cys  
1865 1870 1875

Ala Leu Thr Cys Thr Phe Asn Leu Lys Ile Glu Gly Gln Leu Leu  
1880 1885 1890

Glu Thr Ser Gly Leu Cys Ile Pro Ala Asn Asn Thr Leu Phe Ile  
1895 1900 1905

Val Ser Ile Ser Lys Thr Leu Ala Ala Asn Glu Pro His Leu Thr  
1910 1915 1920

Leu Glu Phe Leu Glu Glu Cys Ile Ser Gly Phe Ser Lys Ser Ser  
1925 1930 1935

Ile Glu Leu Lys His Leu Cys Leu Glu Tyr Met Thr Pro Trp Leu  
1940 1945 1950

Ser Asn Leu Val Arg Phe Cys Lys His Asn Asp Asp Ala Lys Arg  
1955 1960 1965

Gln Arg Val Thr Ala Ile Leu Asp Lys Leu Ile Thr Met Thr Ile  
1970 1975 1980

Asn Glu Lys Gln Met Tyr Pro Ser Ile Gln Ala Lys Ile Trp Gly  
1985 1990 1995

Ser Leu Gly Gln Ile Thr Asp Leu Leu Asp Val Val Leu Asp Ser  
2000 2005 2010

Phe Ile Lys Thr Ser Ala Thr Gly Gly Leu Gly Ser Ile Lys Ala  
2015 2020 2025

Glu Val Met Ala Asp Thr Ala Val Ala Leu Ala Ser Gly Asn Val  
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Lys Leu Val Ser Ser Lys Val Ile Gly Arg Met Cys Lys Ile Ile  
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Asp Lys Thr Cys Leu Ser Pro Thr Pro Thr Leu Glu Gln His Leu  
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Met Trp Asp Asp Ile Ala Ile Leu Ala Arg Tyr Met Leu Met Leu  
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Ser Phe Asn Asn Ser Leu Asp Val Ala Ala His Leu Pro Tyr Leu  
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Phe His Val Val Thr Phe Leu Val Ala Thr Gly Pro Leu Ser Leu  
2105 2110 2115

Arg Ala Ser Thr His Gly Leu Val Ile Asn Ile Ile His Ser Leu  
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Cys Thr Cys Ser Gln Leu His Phe Ser Glu Glu Thr Lys Gln Val  
2135 2140 2145

Leu Arg Leu Ser Leu Thr Glu Phe Ser Leu Pro Lys Phe Tyr Leu  
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Leu Phe Gly Ile Ser Lys Val Lys Ser Ala Ala Val Ile Ala Phe  
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Arg Ser Ser Tyr Arg Asp Arg Ser Phe Ser Pro Gly Ser Tyr Glu  
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Lys Trp Leu Asp Gln Trp Thr Glu Leu Ala Gln Arg Phe Ala Phe  
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Gln Tyr Asn Pro Ser Leu Gln Pro Arg Ala Leu Val Val Phe Gly  
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Cys Ile Ser Lys Arg Val Ser His Gly Gln Ile Lys Gln Ile Ile  
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Arg Ile Leu Ser Lys Ala Leu Glu Ser Cys Leu Lys Gly Pro Asp  
2270 2275 2280

Thr Tyr Asn Ser Gln Val Leu Ile Glu Ala Thr Val Ile Ala Leu  
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Thr Lys Leu Gln Pro Leu Leu Asn Lys Asp Ser Pro Leu His Lys  
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Ala Leu Phe Trp Val Ala Val Ala Val Leu Gln Leu Asp Glu Val  
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Asn Leu Tyr Ser Ala Gly Thr Ala Leu Leu Glu Gln Asn Leu His  
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Thr Leu Asp Ser Leu Arg Ile Phe Asn Asp Lys Ser Pro Glu Glu  
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Val Phe Met Ala Ile Arg Asn Pro Leu Glu Trp His Cys Lys Gln  
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Met Asp His Phe Val Gly Leu Asn Phe Asn Ser Asn Phe Asn Phe  
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Ala Leu Val Gly His Leu Leu Lys Gly Tyr Arg His Pro Ser Pro  
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Ala Ile Val Ala Arg Thr Val Arg Ile Leu His Thr Leu Leu Thr  
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Leu Val Asn Lys His Arg Asn Cys Asp Lys Phe Glu Val Asn Thr  
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Gln Ser Val Ala Tyr Leu Ala Ala Leu Leu Thr Val Ser Glu Glu  
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Val Arg Ser Arg Cys Ser Leu Lys His Arg Lys Ser Leu Leu Leu  
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Thr Asp Ile Ser Met Glu Asn Val Pro Met Asp Thr Tyr Pro Ile  
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His His Gly Asp Pro Ser Tyr Arg Thr Leu Lys Glu Thr Gln Pro  
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Trp Ser Ser Pro Lys Gly Ser Glu Gly Tyr Leu Ala Ala Thr Tyr  
2495 2500 2505

Pro Thr Val Gly Gln Thr Ser Pro Arg Ala Arg Lys Ser Met Ser  
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Leu Asp Met Gly Gln Pro Ser Gln Ala Asn Thr Lys Lys Leu Leu  
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Gly Thr Arg Lys Ser Phe Asp His Leu Ile Ser Asp Thr Lys Ala  
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Pro Lys Arg Gln Glu Met Glu Ser Gly Ile Thr Thr Pro Pro Lys  
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Met Arg Arg Val Ala Glu Thr Asp Tyr Glu Met Glu Thr Gln Arg  
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Ile Ser Ser Ser Gln Gln His Pro His Leu Arg Lys Val Ser Val  
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Ser Glu Ser Asn Val Leu Leu Asp Glu Glu Val Leu Thr Asp Pro  
2600 2605 2610

Lys Ile Gln Ala Leu Leu Leu Thr Val Leu Ala Thr Leu Val Lys  
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Tyr Thr Thr Asp Glu Phe Asp Gln Arg Ile Leu Tyr Glu Tyr Leu  
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Ala Glu Ala Ser Val Val Phe Pro Lys Val Phe Pro Val Val His  
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Asn Leu Leu Asp Ser Lys Ile Asn Thr Leu Leu Ser Leu Cys Gln  
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Asp Pro Asn Leu Leu Asn Pro Ile His Gly Ile Val Gln Ser Val  
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Val Tyr His Glu Glu Ser Pro Pro Gln Tyr Gln Thr Ser Tyr Leu  
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Gln Ser Phe Gly Phe Asn Gly Leu Trp Arg Phe Ala Gly Pro Phe  
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Ser Lys Gln Thr Gln Ile Pro Asp Tyr Ala Glu Leu Ile Val Lys  
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Phe Leu Asp Ala Leu Ile Asp Thr Tyr Leu Pro Gly Ile Asp Glu  
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Glu Thr Ser Glu Glu Ser Leu Leu Thr Pro Thr Ser Pro Tyr Pro  
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Pro Ala Leu Gln Ser Gln Leu Ser Ile Thr Ala Asn Leu Asn Leu  
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Ser Asn Ser Met Thr Ser Leu Ala Thr Ser Gln His Ser Pro Gly  
 2780 2785 2790

Ile Asp Lys Glu Asn Val Glu Leu Ser Pro Thr Thr Gly His Cys  
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Asn Ser Gly Arg Thr Arg His Gly Ser Ala Ser Gln Val Gln Lys  
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Val

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| cagatgctga cctcccaggc tccgtgtgta gatggcttcg aggagccagg agcacggcag  | 1980 |
| cgggccctca gcgcagtcag cgtcctcacc agcgcactgg aagagttaga ggagtctcgc  | 2040 |
| cacaagtgtc caccatgctg gaaccgtctc gcccagcgct acctgatctg ggagtgtctg  | 2100 |

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| ctcaccatca ctatgtgcat cgtactcaac acactcttca tggcgctgga gcactacaac   | 2220 |
| atgacaagtg aattcgagga gatgctgcag gtcggaaacc tggctcttcac agggattttc  | 2280 |
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| tggaacatct tcgacagcat catcgtcatc cttagcctca tggagctggg cctgtcccg    | 2400 |
| atgagcaact tgtcgggtgct gcgctccttc cgcctgctgc gggctcttcaa gctggccaaa | 2460 |
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| acagcagaca tgaccaacac cgctgagctc ctggagcaga tccctgacct cggccaggat   | 3480 |
| gtcaaggacc cagaggactg cttcactgaa ggctgtgtcc ggcgctgtcc ctgctgtg     | 3540 |
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| Met | Ala | Asn | Phe | Leu | Leu | Pro | Arg | Gly | Thr | Ser | Ser | Phe | Arg | Arg | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | Glu | Ser | Leu | Ala | Ala | Ile | Glu | Lys | Arg | Met | Ala | Glu | Lys | Gln |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |



Glu Glu Ala Pro Arg Pro Gln Leu Asp Leu Gln Ala Ser Lys Lys Leu  
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Pro Asp Leu Tyr Gly Asn Pro Pro Gln Glu Leu Ile Gly Glu Pro Leu  
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Glu Asp Leu Asp Pro Phe Tyr Ser Thr Gln Lys Thr Phe Ile Val Leu  
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Asn Lys Gly Lys Thr Ile Phe Arg Phe Ser Ala Thr Asn Ala Leu Tyr  
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Val Leu Ser Pro Phe His Pro Ile Arg Arg Ala Ala Val Lys Ile Leu  
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Val His Ser Leu Phe Asn Met Leu Ile Met Cys Thr Ile Leu Thr Asn  
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Cys Val Phe Met Ala Gln His Asp Pro Pro Pro Trp Thr Lys Tyr Val  
145 150 155 160

Glu Tyr Thr Phe Thr Ala Ile Tyr Thr Phe Glu Ser Leu Val Lys Ile  
165 170 175

Leu Ala Arg Gly Phe Cys Leu His Ala Phe Thr Phe Leu Arg Asp Pro  
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Trp Asn Trp Leu Asp Phe Ser Val Ile Ile Met Ala Tyr Thr Thr Glu  
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Phe Val Asp Leu Gly Asn Val Ser Ala Leu Arg Thr Phe Arg Val Leu  
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Arg Ala Leu Lys Thr Ile Ser Val Ile Ser Gly Leu Lys Thr Ile Val  
225 230 235 240

Gly Ala Leu Ile Gln Ser Val Lys Lys Leu Ala Asp Val Met Val Leu  
245 250 255

Thr Val Phe Cys Leu Ser Val Phe Ala Leu Ile Gly Leu Gln Leu Phe  
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Met Gly Asn Leu Arg His Lys Cys Val Arg Asn Phe Thr Ala Leu Asn  
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Gly Thr Asn Gly Ser Val Glu Ala Asp Gly Leu Val Trp Glu Ser Leu  
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Asp Leu Tyr Leu Ser Asp Pro Glu Asn Tyr Leu Leu Lys Asn Gly Thr  
305 310 315 320

Ser Asp Val Leu Leu Cys Gly Asn Ser Ser Asp Ala Gly Thr Cys Pro  
325 330 335

Glu Gly Tyr Arg Cys Leu Lys Ala Gly Glu Asn Pro Asp His Gly Tyr  
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Thr Ser Phe Asp Ser Phe Ala Trp Ala Phe Leu Ala Leu Phe Arg Leu  
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Met Thr Gln Asp Cys Trp Glu Arg Leu Tyr Gln Gln Thr Leu Arg Ser  
370 375 380

Ala Gly Lys Ile Tyr Met Ile Phe Phe Met Leu Val Ile Phe Leu Gly  
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Ser Phe Tyr Leu Val Asn Leu Ile Leu Ala Val Val Ala Met Ala Tyr  
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Glu Glu Gln Asn Gln Ala Thr Ile Ala Glu Thr Glu Glu Lys Glu Lys  
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Arg Phe Gln Glu Ala Met Glu Met Leu Lys Lys Glu His Glu Ala Leu  
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Thr Ile Arg Gly Val Asp Thr Val Ser Arg Ser Ser Leu Glu Met Ser  
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Pro Leu Ala Pro Val Asn Ser His Glu Arg Arg Ser Lys Arg Arg Lys  
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Ile Phe Thr Phe Arg Arg Arg Asp Leu Gly Ser Glu Ala Asp Phe Ala  
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Asp Asp Glu Asn Ser Thr Ala Gly Glu Ser Glu Ser His His Thr Ser  
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Leu Leu Val Pro Trp Pro Leu Arg Arg Thr Ser Ala Gln Gly Gln Pro  
565 570 575

Ser Pro Gly Thr Ser Ala Pro Gly His Ala Leu His Gly Lys Lys Asn  
580 585 590

Ser Thr Val Asp Cys Asn Gly Val Val Ser Leu Leu Gly Ala Gly Asp  
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Pro Glu Ala Thr Ser Pro Gly Ser His Leu Leu Arg Pro Val Met Leu  
610 615 620

Glu His Pro Pro Asp Thr Thr Thr Pro Ser Glu Glu Pro Gly Gly Pro  
625 630 635 640

Gln Met Leu Thr Ser Gln Ala Pro Cys Val Asp Gly Phe Glu Glu Pro  
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Gly Ala Arg Gln Arg Ala Leu Ser Ala Val Ser Val Leu Thr Ser Ala  
660 665 670

Leu Glu Glu Leu Glu Glu Ser Arg His Lys Cys Pro Pro Cys Trp Asn  
675 680 685

Arg Leu Ala Gln Arg Tyr Leu Ile Trp Glu Cys Cys Pro Leu Trp Met  
690 695 700

Ser Ile Lys Gln Gly Val Lys Leu Val Val Met Asp Pro Phe Thr Asp  
705 710 715 720

Leu Thr Ile Thr Met Cys Ile Val Leu Asn Thr Leu Phe Met Ala Leu  
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Glu His Tyr Asn Met Thr Ser Glu Phe Glu Glu Met Leu Gln Val Gly  
740 745 750

Asn Leu Val Phe Thr Gly Ile Phe Thr Ala Glu Met Thr Phe Lys Ile  
755 760 765

Ile Ala Leu Asp Pro Tyr Tyr Tyr Phe Gln Gln Gly Trp Asn Ile Phe  
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Asp Ser Ile Ile Val Ile Leu Ser Leu Met Glu Leu Gly Leu Ser Arg  
785 790 795 800

Met Ser Asn Leu Ser Val Leu Arg Ser Phe Arg Leu Leu Arg Val Phe  
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Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile Ile  
820 825 830

Gly Asn Ser Val Gly Ala Leu Gly Asn Leu Thr Leu Val Leu Ala Ile  
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Ile Val Phe Ile Phe Ala Val Val Gly Met Gln Leu Phe Gly Lys Asn  
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Gln Asp Val Lys Asp Pro Glu Asp Cys Phe Thr Glu Gly Cys Val  
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Lys Val Trp Trp Arg Leu Arg Lys Thr Cys Tyr His Ile Val Glu  
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His Ser Trp Phe Glu Thr Phe Ile Ile Phe Met Ile Leu Leu Ser  
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Ser Gly Ala Leu Ala Phe Glu Asp Ile Tyr Leu Glu Glu Arg Lys  
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Thr Ile Lys Val Leu Leu Glu Tyr Ala Asp Lys Met Phe Thr Tyr  
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Val Phe Val Leu Glu Met Leu Leu Lys Trp Val Ala Tyr Gly Phe  
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Lys Lys Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp Phe Leu Ile  
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Val Asp Val Ser Leu Val Ser Leu Val Ala Asn Thr Leu Gly Phe  
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Ala Glu Met Gly Pro Ile Lys Ser Leu Arg Thr Leu Arg Ala Leu  
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Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu Phe Leu Val Met  
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| ttctatgatt ttgaaagaga tgcatatctt ttgcaacgaa tggaagaatt tattggaaca  | 2160 |
| gtaagaggta aagcaatgaa aaaatgggtt gaatccatca ctaaaataat ccaaaggaaa  | 2220 |
| aaaattgcaa gagacaatgg accaggtcat aatattacat ttcagagttc acctcccaca  | 2280 |
| gttgagtggc atataagcag acctgggcac atagagactt ttgacctgct caccttacac  | 2340 |
| ccaatagaaa ttgctcgaca actcacttta cttgaatcag atctataaccg agctgtacag | 2400 |

|                                                                    |      |
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| ccatcagaat tagttggaag tgtgtggaca aaagaagaca aagaaattaa ctctccta    | 2460 |
| cttctgaaaa tgattcgaca taccaccaac ctactctgt ggtttgagaa atgtattgta   | 2520 |
| gaaactgaaa atttagaaga aagagtagct gtggtgagtc gaattattga gattctacaa  | 2580 |
| gtctttcaag agttgaacaa cttaaagggt gtccttgagg ttgtcagtc tatgaattca   | 2640 |
| tcacctgttt acagactaga ccacacattt gagcaaatac caagtcgcca gaagaaaatt  | 2700 |
| ttagaagaag ctcatgaatt gagtgaagat cactataaga aatatttggc aaaactcagg  | 2760 |
| tctattaatc caccatgtgt gcctttcttt ggaatttattc tcactaatat cttgaaaaca | 2820 |
| gaagaaggca accctgaggt cctaaaaaga catggaaaag agcttataaa ctttagcaaa  | 2880 |
| aggaggaaaag tagcagaaat aacaggagag atccagcagt accaaaatca gccttactgt | 2940 |
| ttacgagtag aatcagatat caaaagggtt tttgaaaact tgaatccgat gggaaaatagc | 3000 |
| atggagaagg aatttacaga ttatcttttc aacaaatccc tagaaataga accacgaaac  | 3060 |
| cctaagcctc tccaagatt tccaaaaaaa tatagctatc ccctaaaatc tcctggtgtt   | 3120 |
| cgtccatcaa acccaagacc aggtaccatg aggcattcca cacctctgca gcaggagcca  | 3180 |
| aggaaaatta gttatagtag gatccctgaa agtgaaacag aaagtacagc atctgcacca  | 3240 |
| aattctcaa gaacaccgtt aacacctccg cctgcttctg gtgcttcag taccacagat    | 3300 |
| gtttgcagtg tatttgattc cgatcattcg agcccttttc actcaagcaa tgataccgtc  | 3360 |
| tttatccaag ttactctgcc ccatggccca agatctgctt ctgtatcatc tataagtta   | 3420 |
| accaaaggca ctgatgaagt gcctgtccct cctcctgttc ctccacgaag acgaccagaa  | 3480 |
| tctgccccag cagaatcttc accatctaag attatgtcta agcatttgga cagtccccca  | 3540 |
| gccattcctc ctaggcaacc cacatcaaaa gcctattcac cacgatattc aatatcagac  | 3600 |
| cggacctcta tctcagacct tcctgaaagc cctcccttat taccaccacg agaacctgtg  | 3660 |
| aggacacctg atgttttctc aagctcacca ctacatctcc aacctcccc tttgggcaaa   | 3720 |
| aaaagtgacc atggcaatgc cttcttccca aacagccctt ccccttttac accacctcct  | 3780 |
| cctcaaacac cttctcctca cggcacaaga aggcattctgc catcaccacc attgacacaa | 3840 |
| gaagtggacc ttcatccat tgctgggccg cctgttcctc cagacaaaag cacttctcaa   | 3900 |

catatcccta aactccctcc aaaaacttac aaaagggagc acacacaccc atccatgcac 3960

agagatggac caccactgtt ggagaatgcc cattcttcct ga 4002

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<211> 1333

<212> PRT

<213> Homo sapiens

<400> 134

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Pro Lys Trp Arg Gly Leu Leu Val Pro Ala Leu Lys Lys Val Gln Gly  
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Gln Val His Pro Thr Leu Glu Ser Asn Asp Asp Ala Leu Gln Tyr Val  
35 40 45

Glu Glu Leu Ile Leu Gln Leu Leu Asn Met Leu Cys Gln Ala Gln Pro  
50 55 60

Arg Ser Ala Ser Asp Val Glu Glu Arg Val Gln Lys Ser Phe Pro His  
65 70 75 80

Pro Ile Asp Lys Trp Ala Ile Ala Asp Ala Gln Ser Ala Ile Glu Lys  
85 90 95

Arg Lys Arg Arg Asn Pro Leu Ser Leu Pro Val Glu Lys Ile His Pro  
100 105 110

Leu Leu Lys Glu Val Leu Gly Tyr Lys Ile Asp His Gln Val Ser Val  
115 120 125

Tyr Ile Val Ala Val Leu Glu Tyr Ile Ser Ala Asp Ile Leu Lys Leu  
130 135 140

Val Gly Asn Tyr Val Arg Asn Ile Arg His Tyr Glu Ile Thr Lys Gln  
145 150 155 160

Asp Ile Lys Val Ala Met Cys Ala Asp Lys Val Leu Met Asp Met Phe  
165 170 175

His Gln Asp Val Glu Asp Ile Asn Ile Leu Ser Leu Thr Asp Glu Glu  
180 185 190

Pro Ser Thr Ser Gly Glu Gln Thr Tyr Tyr Asp Leu Val Lys Ala Phe  
195 200 205

Met Ala Glu Ile Arg Gln Tyr Ile Arg Glu Leu Asn Leu Ile Ile Lys  
210 215 220

Val Phe Arg Glu Pro Phe Val Ser Asn Ser Lys Leu Phe Ser Ala Asn  
225 230 235 240

Asp Val Glu Asn Ile Phe Ser Arg Ile Val Asp Ile His Glu Leu Ser  
245 250 255

Val Lys Leu Leu Gly His Ile Glu Asp Thr Val Glu Met Thr Asp Glu  
260 265 270

Gly Ser Pro His Pro Leu Val Gly Ser Cys Phe Glu Asp Leu Ala Glu  
275 280 285

Glu Leu Ala Phe Asp Pro Tyr Glu Ser Tyr Ala Arg Asp Ile Leu Arg  
290 295 300

Pro Gly Phe His Asp Arg Phe Leu Ser Gln Leu Ser Lys Pro Gly Ala  
305 310 315 320

Ala Leu Tyr Leu Gln Ser Ile Gly Glu Gly Phe Lys Glu Ala Val Gln  
325 330 335

Tyr Val Leu Pro Arg Leu Leu Leu Ala Pro Val Tyr His Cys Leu His  
340 345 350

Tyr Phe Glu Leu Leu Lys Gln Leu Glu Glu Lys Ser Glu Asp Gln Glu  
355 360 365

Asp Lys Glu Cys Leu Lys Gln Ala Ile Thr Ala Leu Leu Asn Val Gln  
370 375 380

Ser Gly Met Glu Lys Ile Cys Ser Lys Ser Leu Ala Lys Arg Arg Leu  
385 390 395 400

Ser Glu Ser Ala Cys Arg Phe Tyr Ser Gln Gln Met Lys Gly Lys Gln  
405 410 415

Leu Ala Ile Lys Lys Met Asn Glu Ile Gln Lys Asn Ile Asp Gly Trp  
420 425 430

Glu Gly Lys Asp Ile Gly Gln Cys Cys Asn Glu Phe Ile Met Glu Gly  
435 440 445

Thr Leu Thr Arg Val Gly Ala Lys His Glu Arg His Ile Phe Leu Phe  
450 455 460

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

Pro Gly Ala Ser Asn Ala Glu Tyr Arg Leu Lys Glu Lys Phe Phe Met  
485 490 495

Arg Lys Val Gln Ile Asn Asp Lys Asp Asp Thr Asn Glu Tyr Lys His  
500 505 510

Ala Phe Glu Ile Ile Leu Lys Asp Glu Asn Ser Val Ile Phe Ser Ala  
515 520 525

Lys Ser Ala Glu Glu Lys Asn Asn Trp Met Ala Ala Leu Ile Ser Leu  
530 535 540

Gln Tyr Arg Ser Thr Leu Glu Arg Met Leu Asp Val Thr Met Leu Gln  
545 550 555 560



Glu Glu Lys Glu Glu Gln Met Arg Leu Pro Ser Ala Asp Val Tyr Arg  
565 570 575

Phe Ala Glu Pro Asp Ser Glu Glu Asn Ile Ile Phe Glu Glu Asn Met  
580 585 590

Gln Pro Lys Ala Gly Ile Pro Ile Ile Lys Ala Gly Thr Val Ile Lys  
595 600 605

Leu Ile Glu Arg Leu Thr Tyr His Met Tyr Ala Asp Pro Asn Phe Val  
610 615 620

Arg Thr Phe Leu Thr Thr Tyr Arg Ser Phe Cys Lys Pro Gln Glu Leu  
625 630 635 640

Leu Ser Leu Ile Ile Glu Arg Phe Glu Ile Pro Glu Pro Glu Pro Thr  
645 650 655

Glu Ala Asp Arg Ile Ala Ile Glu Asn Gly Asp Gln Pro Leu Ser Ala  
660 665 670

Glu Leu Lys Arg Phe Arg Lys Glu Tyr Ile Gln Pro Val Gln Leu Arg  
675 680 685

Val Leu Asn Val Cys Arg His Trp Val Glu His His Phe Tyr Asp Phe  
690 695 700

Glu Arg Asp Ala Tyr Leu Leu Gln Arg Met Glu Glu Phe Ile Gly Thr  
705 710 715 720

Val Arg Gly Lys Ala Met Lys Lys Trp Val Glu Ser Ile Thr Lys Ile  
725 730 735

Ile Gln Arg Lys Lys Ile Ala Arg Asp Asn Gly Pro Gly His Asn Ile  
740 745 750

Thr Phe Gln Ser Ser Pro Pro Thr Val Glu Trp His Ile Ser Arg Pro  
755 760 765

Gly His Ile Glu Thr Phe Asp Leu Leu Thr Leu His Pro Ile Glu Ile  
770 775 780

Ala Arg Gln Leu Thr Leu Leu Glu Ser Asp Leu Tyr Arg Ala Val Gln  
785 790 795 800

Pro Ser Glu Leu Val Gly Ser Val Trp Thr Lys Glu Asp Lys Glu Ile  
805 810 815

Asn Ser Pro Asn Leu Leu Lys Met Ile Arg His Thr Thr Asn Leu Thr  
820 825 830

Leu Trp Phe Glu Lys Cys Ile Val Glu Thr Glu Asn Leu Glu Glu Arg  
835 840 845

Val Ala Val Val Ser Arg Ile Ile Glu Ile Leu Gln Val Phe Gln Glu  
850 855 860

Leu Asn Asn Phe Asn Gly Val Leu Glu Val Val Ser Ala Met Asn Ser  
865 870 875 880

Ser Pro Val Tyr Arg Leu Asp His Thr Phe Glu Gln Ile Pro Ser Arg  
885 890 895

Gln Lys Lys Ile Leu Glu Glu Ala His Glu Leu Ser Glu Asp His Tyr  
900 905 910

Lys Lys Tyr Leu Ala Lys Leu Arg Ser Ile Asn Pro Pro Cys Val Pro  
915 920 925

Phe Phe Gly Ile Tyr Leu Thr Asn Ile Leu Lys Thr Glu Glu Gly Asn  
930 935 940

Pro Glu Val Leu Lys Arg His Gly Lys Glu Leu Ile Asn Phe Ser Lys  
945 950 955 960

Arg Arg Lys Val Ala Glu Ile Thr Gly Glu Ile Gln Gln Tyr Gln Asn  
965 970 975

Gln Pro Tyr Cys Leu Arg Val Glu Ser Asp Ile Lys Arg Phe Phe Glu  
980 985 990

Asn Leu Asn Pro Met Gly Asn Ser Met Glu Lys Glu Phe Thr Asp Tyr  
995 1000 1005

Leu Phe Asn Lys Ser Leu Glu Ile Glu Pro Arg Asn Pro Lys Pro  
1010 1015 1020

Leu Pro Arg Phe Pro Lys Lys Tyr Ser Tyr Pro Leu Lys Ser Pro  
1025 1030 1035

Gly Val Arg Pro Ser Asn Pro Arg Pro Gly Thr Met Arg His Pro  
1040 1045 1050

Thr Pro Leu Gln Gln Glu Pro Arg Lys Ile Ser Tyr Ser Arg Ile  
1055 1060 1065

Pro Glu Ser Glu Thr Glu Ser Thr Ala Ser Ala Pro Asn Ser Pro  
1070 1075 1080

Arg Thr Pro Leu Thr Pro Pro Pro Ala Ser Gly Ala Ser Ser Thr  
1085 1090 1095

Thr Asp Val Cys Ser Val Phe Asp Ser Asp His Ser Ser Pro Phe  
1100 1105 1110

His Ser Ser Asn Asp Thr Val Phe Ile Gln Val Thr Leu Pro His  
1115 1120 1125

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

Thr Asp Glu Val Pro Val Pro Pro Pro Val Pro Pro Arg Arg Arg  
1145 1150 1155

Pro Glu Ser Ala Pro Ala Glu Ser Ser Pro Ser Lys Ile Met Ser  
1160 1165 1170

Lys His Leu Asp Ser Pro Pro Ala Ile Pro Pro Arg Gln Pro Thr  
1175 1180 1185

Ser Lys Ala Tyr Ser Pro Arg Tyr Ser Ile Ser Asp Arg Thr Ser  
1190 1195 1200

Ile Ser Asp Pro Pro Glu Ser Pro Pro Leu Leu Pro Pro Arg Glu  
1205 1210 1215

Pro Val Arg Thr Pro Asp Val Phe Ser Ser Ser Pro Leu His Leu  
1220 1225 1230

Gln Pro Pro Pro Leu Gly Lys Lys Ser Asp His Gly Asn Ala Phe  
1235 1240 1245

Phe Pro Asn Ser Pro Ser Pro Phe Thr Pro Pro Pro Pro Gln Thr  
1250 1255 1260

Pro Ser Pro His Gly Thr Arg Arg His Leu Pro Ser Pro Pro Leu  
1265 1270 1275

Thr Gln Glu Val Asp Leu His Ser Ile Ala Gly Pro Pro Val Pro  
1280 1285 1290

Pro Arg Gln Ser Thr Ser Gln His Ile Pro Lys Leu Pro Pro Lys  
1295 1300 1305

Thr Tyr Lys Arg Glu His Thr His Pro Ser Met His Arg Asp Gly  
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Pro Pro Leu Leu Glu Asn Ala His Ser Ser  
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<212> DNA  
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gccgccgccc cagtggggcg cttcaccgcg cactggcggg tcccgtgct gaccgccggc 420  
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gccgaggacg acctcagcca ctacaccagg ctgtgcgga ccatgccgcg caaaggccga 720  
gttatctaca tctgcagctc ccctgatgcc ttcagaaccc tcatgctcct ggccctggaa 780  
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caagggtggac agggccctgc tccccgcagg ccctgggaga gaggggatgg gcaggatgtc 900  
agtggccgcc aggcctttca ggctgcaaaa atcattacat ataaagaccc agataatccc 960  
gagtacttgg aattcctgaa gcagttaaaa cacctggcct atgagcagtt caacttcacc 1020  
atggaggatg gcctggtgaa caccatccca gcacccctcc acgacgggct cctgctctat 1080  
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agtggcgatc gggaaacaga cttctccctc tgggatatgg atcccgagaa tgggtgccttc 1260

|             |            |             |            |             |             |      |
|-------------|------------|-------------|------------|-------------|-------------|------|
| agggttgtag  | tgaactacaa | tgggacttcc  | caagagctgg | tggctgtgtc  | ggggcgcaaa  | 1320 |
| ctgaactggc  | ccctggggta | ccctcctcct  | gacatcccca | aatgtggctt  | tgacaacgaa  | 1380 |
| gacccagcat  | gcaaccaaga | tcacctttcc  | accctggagg | tgctggcttt  | ggtgggcagc  | 1440 |
| ctctccttgc  | tcggcattct | gattgtctcc  | ttcttcatat | acaggaagat  | gcagctggag  | 1500 |
| aaggaaactgg | cctcggagct | gtggcgggtg  | cgctgggagg | acgttgagcc  | cagtagcctt  | 1560 |
| gagaggcacc  | tgcggagtgc | aggcagccgg  | ctgaccctga | gcgggagagg  | ctccaattac  | 1620 |
| ggctccctgc  | taaccacaga | gggccagttc  | caagtctttg | ccaagacagc  | atattataag  | 1680 |
| ggcaacctcg  | tggctgtgaa | acgtgtgaac  | cgtaaacgca | ttgagctgac  | acgaaaagtc  | 1740 |
| ctgtttgaac  | tgaagcatat | gcgggatgtg  | cagaatgaac | acctgaccag  | gtttgtggga  | 1800 |
| gcctgcaccg  | acccccccaa | tatctgcatc  | ctcacagagt | actgtccccg  | tgggagcctg  | 1860 |
| caggacattc  | tggagaatga | gagcatcacc  | ctggactgga | tgttccggta  | ctcactcacc  | 1920 |
| aatgacatcg  | tcaagggcat | gctgtttcta  | cacaatgggg | ctatctgttc  | ccatgggaac  | 1980 |
| ctcaagtcac  | ccaactgcgt | ggtagatggg  | cgctttgtgc | tcaagatcac  | cgactatggg  | 2040 |
| ctggagagct  | tcagggacct | ggacccagag  | caaggacaca | ccgtttatgc  | caaaaagctg  | 2100 |
| tggacggccc  | ctgagctcct | gcgaatggct  | tcaccccctg | tgcggggctc  | ccaggctggt  | 2160 |
| gacgtataca  | gctttgggat | catccttcag  | gagattgccc | tgaggagtgg  | ggtcttccac  | 2220 |
| gtggaagggt  | tggacctgag | ccccaaagag  | atcatcgagc | gggtgactcg  | gggtgagcag  | 2280 |
| cccccttcc   | ggccctccct | ggccctgcag  | agtcacctgg | aggagtgggg  | gctgctcatg  | 2340 |
| cagcggtgct  | gggctgagga | cccacaggag  | aggccaccat | tccagcagat  | ccgcctgacg  | 2400 |
| ttgcgcaaat  | ttaacaggga | gaacagcagc  | aacatcctgg | acaacctgct  | gtcccgcacg  | 2460 |
| gagcagtacg  | cgaacaatct | ggagggaactg | gtggaggagc | ggacccaggc  | atacctggag  | 2520 |
| gagaagcgca  | aggctgaggc | cctgctctac  | cagatcctgc | ctcactcagt  | ggctgagcag  | 2580 |
| ctgaagcgtg  | gggagacggg | gcaggccgaa  | gcctttgaca | gtgttaccat  | ctacttcagt  | 2640 |
| gacattgtgg  | gtttcacagc | gctgtcggcg  | gagagcacac | ccatgcagggt | ggtgaccctg  | 2700 |
| ctcaatgacc  | tgtacacttg | ctttgatgct  | gtcatagaca | actttgatgt  | gtacaagggtg | 2760 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gagacaattg gcgatgccta catggtggtg tcagggctcc ctgtgcggaa cgggcggcta  | 2820 |
| cacgcctgcg aggtagcccg catggccctg gcactgctgg atgctgtgcg ctccttccga  | 2880 |
| atccgccacc ggccccagga gcagctgcgc ttgcgcattg gcatccacac aggacctgtg  | 2940 |
| tgtgctggag tgggtgggact gaagatgccc cgttactgtc tctttgggga tacagtcaac | 3000 |
| acagcctcaa gaatggagtc taatggggaa gccctgaaga tccactgtc ttctgagacc   | 3060 |
| aaggctgtcc tggaggagtt tgggtggttc gagctggagc ttcgagggga tgtagaaatg  | 3120 |
| aaggggcaaag gcaaggttcg gacctactgg ctccttgggg agagggggag tagcacccga | 3180 |
| ggctga                                                             | 3186 |

<210> 136  
 <211> 1061  
 <212> PRT  
 <213> Homo sapiens

<400> 136

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gly | Pro | Arg | Arg | Pro | Ala | Gly | Ser | Arg | Leu | Arg | Leu | Leu | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Leu | Leu | Pro | Pro | Leu | Leu | Leu | Leu | Leu | Arg | Gly | Ser | His | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Asn | Leu | Thr | Val | Ala | Val | Val | Leu | Pro | Leu | Ala | Asn | Thr | Ser | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Trp | Ser | Trp | Ala | Arg | Val | Gly | Pro | Ala | Val | Glu | Leu | Ala | Leu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Lys | Ala | Arg | Pro | Asp | Leu | Leu | Pro | Gly | Trp | Thr | Val | Arg | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Gly | Ser | Ser | Glu | Asn | Ala | Leu | Gly | Val | Cys | Ser | Asp | Thr | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Leu | Ala | Ala | Val | Asp | Leu | Lys | Trp | Glu | His | Asn | Pro | Ala | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Phe Leu Gly Pro Gly Cys Val Tyr Ala Ala Ala Pro Val Gly Arg Phe  
115 120 125

Thr Ala His Trp Arg Val Pro Leu Leu Thr Ala Gly Ala Pro Ala Leu  
130 135 140

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

Ser Tyr Ala Lys Leu Gly Asp Phe Val Ala Ala Leu His Arg Arg Leu  
165 170 175

Gly Trp Glu Arg Gln Ala Leu Met Leu Tyr Ala Tyr Arg Pro Gly Asp  
180 185 190

Glu Glu His Cys Phe Phe Leu Val Glu Gly Leu Phe Met Arg Val Arg  
195 200 205

Asp Arg Leu Asn Ile Thr Val Asp His Leu Glu Phe Ala Glu Asp Asp  
210 215 220

Leu Ser His Tyr Thr Arg Leu Leu Arg Thr Met Pro Arg Lys Gly Arg  
225 230 235 240

Val Ile Tyr Ile Cys Ser Ser Pro Asp Ala Phe Arg Thr Leu Met Leu  
245 250 255

Leu Ala Leu Glu Ala Gly Leu Cys Gly Glu Asp Tyr Val Phe Phe His  
260 265 270

Leu Asp Ile Phe Gly Gln Ser Leu Gln Gly Gly Gln Gly Pro Ala Pro  
275 280 285

Arg Arg Pro Trp Glu Arg Gly Asp Gly Gln Asp Val Ser Ala Arg Gln  
290 295 300



Ala Phe Gln Ala Ala Lys Ile Ile Thr Tyr Lys Asp Pro Asp Asn Pro  
305 310 315 320

Glu Tyr Leu Glu Phe Leu Lys Gln Leu Lys His Leu Ala Tyr Glu Gln  
325 330 335

Phe Asn Phe Thr Met Glu Asp Gly Leu Val Asn Thr Ile Pro Ala Ser  
340 345 350

Phe His Asp Gly Leu Leu Leu Tyr Ile Gln Ala Val Thr Glu Thr Leu  
355 360 365

Ala His Gly Gly Thr Val Thr Asp Gly Glu Asn Ile Thr Gln Arg Met  
370 375 380

Trp Asn Arg Ser Phe Gln Gly Val Thr Gly Tyr Leu Lys Ile Asp Ser  
385 390 395 400

Ser Gly Asp Arg Glu Thr Asp Phe Ser Leu Trp Asp Met Asp Pro Glu  
405 410 415

Asn Gly Ala Phe Arg Val Val Leu Asn Tyr Asn Gly Thr Ser Gln Glu  
420 425 430

Leu Val Ala Val Ser Gly Arg Lys Leu Asn Trp Pro Leu Gly Tyr Pro  
435 440 445

Pro Pro Asp Ile Pro Lys Cys Gly Phe Asp Asn Glu Asp Pro Ala Cys  
450 455 460

Asn Gln Asp His Leu Ser Thr Leu Glu Val Leu Ala Leu Val Gly Ser  
465 470 475 480

Leu Ser Leu Leu Gly Ile Leu Ile Val Ser Phe Phe Ile Tyr Arg Lys  
485 490 495

Met Gln Leu Glu Lys Glu Leu Ala Ser Glu Leu Trp Arg Val Arg Trp  
500 505 510

Glu Asp Val Glu Pro Ser Ser Leu Glu Arg His Leu Arg Ser Ala Gly  
515 520 525

Ser Arg Leu Thr Leu Ser Gly Arg Gly Ser Asn Tyr Gly Ser Leu Leu  
530 535 540

Thr Thr Glu Gly Gln Phe Gln Val Phe Ala Lys Thr Ala Tyr Tyr Lys  
545 550 555 560

Gly Asn Leu Val Ala Val Lys Arg Val Asn Arg Lys Arg Ile Glu Leu  
565 570 575

Thr Arg Lys Val Leu Phe Glu Leu Lys His Met Arg Asp Val Gln Asn  
580 585 590

Glu His Leu Thr Arg Phe Val Gly Ala Cys Thr Asp Pro Pro Asn Ile  
595 600 605

Cys Ile Leu Thr Glu Tyr Cys Pro Arg Gly Ser Leu Gln Asp Ile Leu  
610 615 620

Glu Asn Glu Ser Ile Thr Leu Asp Trp Met Phe Arg Tyr Ser Leu Thr  
625 630 635 640

Asn Asp Ile Val Lys Gly Met Leu Phe Leu His Asn Gly Ala Ile Cys  
645 650 655

Ser His Gly Asn Leu Lys Ser Ser Asn Cys Val Val Asp Gly Arg Phe  
660 665 670

Val Leu Lys Ile Thr Asp Tyr Gly Leu Glu Ser Phe Arg Asp Leu Asp  
675 680 685

Pro Glu Gln Gly His Thr Val Tyr Ala Lys Lys Leu Trp Thr Ala Pro  
690 695 700

Glu Leu Leu Arg Met Ala Ser Pro Pro Val Arg Gly Ser Gln Ala Gly  
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Asp Val Tyr Ser Phe Gly Ile Ile Leu Gln Glu Ile Ala Leu Arg Ser  
725 730 735

Gly Val Phe His Val Glu Gly Leu Asp Leu Ser Pro Lys Glu Ile Ile  
740 745 750

Glu Arg Val Thr Arg Gly Glu Gln Pro Pro Phe Arg Pro Ser Leu Ala  
755 760 765

Leu Gln Ser His Leu Glu Glu Leu Gly Leu Leu Met Gln Arg Cys Trp  
770 775 780

Ala Glu Asp Pro Gln Glu Arg Pro Pro Phe Gln Gln Ile Arg Leu Thr  
785 790 795 800

Leu Arg Lys Phe Asn Arg Glu Asn Ser Ser Asn Ile Leu Asp Asn Leu  
805 810 815

Leu Ser Arg Met Glu Gln Tyr Ala Asn Asn Leu Glu Glu Leu Val Glu  
820 825 830

Glu Arg Thr Gln Ala Tyr Leu Glu Glu Lys Arg Lys Ala Glu Ala Leu  
835 840 845

Leu Tyr Gln Ile Leu Pro His Ser Val Ala Glu Gln Leu Lys Arg Gly  
850 855 860

Glu Thr Val Gln Ala Glu Ala Phe Asp Ser Val Thr Ile Tyr Phe Ser  
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Asp Ile Val Gly Phe Thr Ala Leu Ser Ala Glu Ser Thr Pro Met Gln  
885 890 895

Val Val Thr Leu Leu Asn Asp Leu Tyr Thr Cys Phe Asp Ala Val Ile  
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Asp Asn Phe Asp Val Tyr Lys Val Glu Thr Ile Gly Asp Ala Tyr Met  
915 920 925

Val Val Ser Gly Leu Pro Val Arg Asn Gly Arg Leu His Ala Cys Glu  
930 935 940

Val Ala Arg Met Ala Leu Ala Leu Leu Asp Ala Val Arg Ser Phe Arg  
945 950 955 960

Ile Arg His Arg Pro Gln Glu Gln Leu Arg Leu Arg Ile Gly Ile His  
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Thr Gly Pro Val Cys Ala Gly Val Val Gly Leu Lys Met Pro Arg Tyr  
980 985 990

Cys Leu Phe Gly Asp Thr Val Asn Thr Ala Ser Arg Met Glu Ser Asn  
995 1000 1005

Gly Glu Ala Leu Lys Ile His Leu Ser Ser Glu Thr Lys Ala Val  
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Leu Glu Glu Phe Gly Gly Phe Glu Leu Glu Leu Arg Gly Asp Val  
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<211> 3927

<212> DNA

<213> Homo sapiens

<400> 137

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| ggcaacctgg agataaccag cattgagcac aaccgggacc tctccttcct gcggtctgtt  | 240  |
| cgagaagtca caggctacgt gttagtggct cttaatcagt ttcgttacct gcctctggag  | 300  |
| aattttacgca ttattcgtgg gacaaaactt tatgaggatc gatatgcctt ggcaatattt | 360  |
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| tccagttcct gtgtgcgtgc ctgccctagt tccaagatgg aagtagaaga aaatgggatt  | 960  |
| aaaatgtgta aaccttgca tgacatttgc caaaaagctt gtgatggcat tggcacagga   | 1020 |
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| aagatcaatg ggaatttgat ctttctagtc actgggtattc atggggaccc ttacaatgca | 1140 |
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| gtgaccattg gtggaagagt actctatagt ggctgtcct tgcttatcct caagcaacag   | 1320 |
| ggcatcacct ctctacagtt ccagtccctg aaggaaatca gcgcaggaaa catctatatt  | 1380 |
| actgacaaca gcaacctgtg ttattatcat accattaact ggacaacact cttcagcaca  | 1440 |
| atcaaccaga gaatagtaat ccgggacaac agaaaagctg aaaattgtac tgctgaagga  | 1500 |
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| tgcacccaag ggtgtaacgg tcccactagt catgactgca ttactaccc atggacgggc   | 1920 |
| cattccactt taccacaaca tgctagaact cccctgattg cagctggagt aattgggtggg | 1980 |
| ctcttcattc tggtcattgt gggcttgaca tttgctgttt atgttagaag gaagagcatc  | 2040 |
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| catcgggatt tggcagcccg taatgtctta gtgaaatctc caaacatgt gaaaatcaca   | 2580 |
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| aagatgccaa ttaaatggat ggctctggag tgtatacatt acaggaaatt cacccatcag  | 2700 |
| agtgcgttt ggagctatgg agttactata tgggaactga tgacctttgg aggaaaaccc   | 2760 |
| tatgatggaa ttccaacgcg agaaatccct gatttattag agaaaggaga acgtttgcct  | 2820 |
| cagcctcca tctgcactat tgacgtttac atggcatgg tcaaatgttg gatgattgat    | 2880 |
| gctgacagta gacctaaatt taaggaactg gctgctgagt tttcaaggat ggctcgagac  | 2940 |
| cctcaaagat acctagttat tcagggtgat gatcgtatga agcttcccag tccaaatgac  | 3000 |
| agcaagttct ttcagaatct cttggatgaa gaggatttgg aagatatgat ggatgctgag  | 3060 |

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| ggaaaccagt ttgtataccg agatggaggt tttgctgctg aacaaggagt gtctgtgccc  | 3240 |
| tacagagccc caactagcac aattccagaa gtcctgtgg cacagggtgc tactgtgag    | 3300 |
| atttttgatg actcctgctg taatggcacc ctacgcaagc cagtggcacc ccatgtccaa  | 3360 |
| gaggacagta gcacccagag gtacagtgtg gacccaccg tgtttgcccc agaacggagc   | 3420 |
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| gaatacctga atccagtga ggagaaccct tttgtttctc ggagaaaaaa tggagacctt   | 3540 |
| caagcattgg ataatcccga atatcacaat gcatccaatg gtccacccaa ggccgaggat  | 3600 |
| gagtatgtga atgagccact gtacctcaac acctttgcca acaccttggg aaaagctgag  | 3660 |
| tacctgaaga acaacatact gtcaatgcca gagaaggcca agaaagcgtt tgacaaccct  | 3720 |
| gactactgga accacagcct gccacctcgg agcacccttc agcaccacaga ctacctgcag | 3780 |
| gagtacagca caaaatattt ttataaacag aatgggcgga tccggcctat tgtggcagag  | 3840 |
| aatcctgaat acctctctga gttctccctg aagccaggca ctgtgctgcc gcctccacct  | 3900 |
| tacagacacc ggaatactgt ggtgtaa                                      | 3927 |

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<400> 138

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| Met | Lys | Pro | Ala | Thr | Gly | Leu | Trp | Val | Trp | Val | Ser | Leu | Leu | Val | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gly | Thr | Val | Gln | Pro | Ser | Asp | Ser | Gln | Ser | Val | Cys | Ala | Gly | Thr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asn | Lys | Leu | Ser | Ser | Leu | Ser | Asp | Leu | Glu | Gln | Gln | Tyr | Arg | Ala |
|     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |

Leu Arg Lys Tyr Tyr Glu Asn Cys Glu Val Val Met Gly Asn Leu Glu  
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Ile Thr Ser Ile Glu His Asn Arg Asp Leu Ser Phe Leu Arg Ser Val  
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Arg Glu Val Thr Gly Tyr Val Leu Val Ala Leu Asn Gln Phe Arg Tyr  
85 90 95

Leu Pro Leu Glu Asn Leu Arg Ile Ile Arg Gly Thr Lys Leu Tyr Glu  
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Asp Arg Tyr Ala Leu Ala Ile Phe Leu Asn Tyr Arg Lys Asp Gly Asn  
115 120 125

Phe Gly Leu Gln Glu Leu Gly Leu Lys Asn Leu Thr Glu Ile Leu Asn  
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Gly Gly Val Tyr Val Asp Gln Asn Lys Phe Leu Cys Tyr Ala Asp Thr  
145 150 155 160

Ile His Trp Gln Asp Ile Val Arg Asn Pro Trp Pro Ser Asn Leu Thr  
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Leu Val Ser Thr Asn Gly Ser Ser Gly Cys Gly Arg Cys His Lys Ser  
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Cys Thr Gly Arg Cys Trp Gly Pro Thr Glu Asn His Cys Gln Thr Leu  
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Thr Arg Thr Val Cys Ala Glu Gln Cys Asp Gly Arg Cys Tyr Gly Pro  
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Tyr Val Ser Asp Cys Cys His Arg Glu Cys Ala Gly Gly Cys Ser Gly  
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Pro Lys Asp Thr Asp Cys Phe Ala Cys Met Asn Phe Asn Asp Ser Gly  
245 250 255



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

Gly Arg Ile Cys Ile Glu Ser Cys Asn Leu Tyr Asp Gly Glu Phe Arg  
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Glu Phe Glu Asn Gly Ser Ile Cys Val Glu Cys Asp Pro Gln Cys Glu  
545 550 555 560

Lys Met Glu Asp Gly Leu Leu Thr Cys His Gly Pro Gly Pro Asp Asn  
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Cys Thr Lys Cys Ser His Phe Lys Asp Gly Pro Asn Cys Val Glu Lys  
580 585 590

Cys Pro Asp Gly Leu Gln Gly Ala Asn Ser Phe Ile Phe Lys Tyr Ala  
595 600 605

Asp Pro Asp Arg Glu Cys His Pro Cys His Pro Asn Cys Thr Gln Gly  
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Cys Asn Gly Pro Thr Ser His Asp Cys Ile Tyr Tyr Pro Trp Thr Gly  
625 630 635 640

His Ser Thr Leu Pro Gln His Ala Arg Thr Pro Leu Ile Ala Ala Gly  
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Val Ile Gly Gly Leu Phe Ile Leu Val Ile Val Gly Leu Thr Phe Ala  
660 665 670

Val Tyr Val Arg Arg Lys Ser Ile Lys Lys Lys Arg Ala Leu Arg Arg  
675 680 685

Phe Leu Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Thr Ala  
690 695 700

Pro Asn Gln Ala Gln Leu Arg Ile Leu Lys Glu Thr Glu Leu Lys Arg  
705 710 715 720

Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Ile  
725 730 735

Trp Val Pro Glu Gly Glu Thr Val Lys Ile Pro Val Ala Ile Lys Ile  
740 745 750

Leu Asn Glu Thr Thr Gly Pro Lys Ala Asn Val Glu Phe Met Asp Glu  
755 760 765

Ala Leu Ile Met Ala Ser Met Asp His Pro His Leu Val Arg Leu Leu  
770 775 780

Gly Val Cys Leu Ser Pro Thr Ile Gln Leu Val Thr Gln Leu Met Pro  
785 790 795 800

His Gly Cys Leu Leu Glu Tyr Val His Glu His Lys Asp Asn Ile Gly  
805 810 815

Ser Gln Leu Leu Leu Asn Trp Cys Val Gln Ile Ala Lys Gly Met Met  
820 825 830

Tyr Leu Glu Glu Arg Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn  
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Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe Gly Leu  
850 855 860

Ala Arg Leu Leu Glu Gly Asp Glu Lys Glu Tyr Asn Ala Asp Gly Gly  
865 870 875 880

Lys Met Pro Ile Lys Trp Met Ala Leu Glu Cys Ile His Tyr Arg Lys  
885 890 895

Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Ile Trp Glu  
900 905 910

Leu Met Thr Phe Gly Gly Lys Pro Tyr Asp Gly Ile Pro Thr Arg Glu  
915 920 925

Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile  
930 935 940

Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys Trp Met Ile Asp  
945 950 955 960

Ala Asp Ser Arg Pro Lys Phe Lys Glu Leu Ala Ala Glu Phe Ser Arg  
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Met Ala Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln Gly Asp Asp Arg  
980 985 990

Met Lys Leu Pro Ser Pro Asn Asp Ser Lys Phe Phe Gln Asn Leu Leu  
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Asp Glu Glu Asp Leu Glu Asp Met Met Asp Ala Glu Glu Tyr Leu  
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Val Pro Gln Ala Phe Asn Ile Pro Pro Pro Ile Tyr Thr Ser Arg  
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Ala Arg Ile Asp Ser Asn Arg Ser Glu Ile Gly His Ser Pro Pro  
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Pro Ala Tyr Thr Pro Met Ser Gly Asn Gln Phe Val Tyr Arg Asp  
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Gly Gly Phe Ala Ala Glu Gln Gly Val Ser Val Pro Tyr Arg Ala  
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Pro Thr Ser Thr Ile Pro Glu Ala Pro Val Ala Gln Gly Ala Thr  
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Ala Glu Ile Phe Asp Asp Ser Cys Cys Asn Gly Thr Leu Arg Lys  
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Pro Val Ala Pro His Val Gln Glu Asp Ser Ser Thr Gln Arg Tyr  
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Ser Ala Asp Pro Thr Val Phe Ala Pro Glu Arg Ser Pro Arg Gly  
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Glu Leu Asp Glu Glu Gly Tyr Met Thr Pro Met Arg Asp Lys Pro  
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Lys Gln Glu Tyr Leu Asn Pro Val Glu Glu Asn Pro Phe Val Ser  
1160 1165 1170

Arg Arg Lys Asn Gly Asp Leu Gln Ala Leu Asp Asn Pro Glu Tyr  
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His Asn Ala Ser Asn Gly Pro Pro Lys Ala Glu Asp Glu Tyr Val  
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Asn Glu Pro Leu Tyr Leu Asn Thr Phe Ala Asn Thr Leu Gly Lys  
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Pro Arg Ser Thr Leu Gln His Pro Asp Tyr Leu Gln Glu Tyr Ser  
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Thr Lys Tyr Phe Tyr Lys Gln Asn Gly Arg Ile Arg Pro Ile Val  
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Ser Ala Leu Arg Leu Gly Asp Arg Ile Pro Phe Glu Gly Ala Asn Glu  
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Pro Asp Gln Val Ser Leu Lys Glu Asp Ile Asp Met Leu Gln Asn Ala  
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Leu Ala Glu Asn Asp Thr Pro Tyr Tyr Asp Val Ser Arg Asn Ala Arg  
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His Ala Asp Gly Val Phe Thr Ser Asp Phe Ser Lys Leu Leu Gly Gln  
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Leu Ser Ala Lys Lys Tyr Leu Glu Ser Leu Met Gly Lys Arg Val Ser  
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Asn Ile Ser Glu Asp Pro Val Pro Val Lys Arg His Ser Asp Ala Val  
115 120 125

Phe Thr Asp Asn Tyr Thr Arg Leu Arg Lys Gln Met Ala Val Lys Lys  
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| gctgacaagt ctgcctacct catggggctg aactcagccg acctgctcaa ggggctgtgc  | 1200 |
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| atatatgcca ctggggcact ggccaaggca gtgtatgaga ggatgttcaa ctggatggtg  | 1320 |
| acgcgcatca atgccaccct ggagaccaag cagccacgcc agtacttcat aggagtctg   | 1380 |
| gacatcgctg gcttcgagat cttcgatttc aacagctttg agcagctctg catcaacttc  | 1440 |



|                                                                    |      |
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| accaacgaga agctgcagca gttcttcaac caccacatgt ttgtgctgga gcaggaggag  | 1500 |
| tacaagaagg agggcatcga gtggacattc attgactttg gcatggacct gcaggcctgc  | 1560 |
| attgacctca tcgagaagcc catgggcatc atgtccatcc tggaagagga gtgcatgttc  | 1620 |
| cccaaggcca ccgacatgac cttcaaggcc aagctgtttg acaaccacct gggcaaattcc | 1680 |
| gccaacttcc agaagccacg aaatatcaag gggaagcctg aagcccactt ctccctgac   | 1740 |
| cactatgccg gcatcgtgga ctacaacatc attggctggc tgcagaagaa caaggatcct  | 1800 |
| ctcaatgaga ctgtcgtggg cttgtatcag aagtcttccc tcaagttgct cagcaccctg  | 1860 |
| tttgccaact atgctggggc tgatgcgctt attgagaagg gcaaaggcaa ggccaagaaa  | 1920 |
| ggctcgtcct ttgagactgt gtcagctctg cacaggggaaa atctgaacaa gctgatgacc | 1980 |
| aacttgcgct ccacccatcc ccactttgta cgttgatatca tccctaata gacaaagtct  | 2040 |
| ccaggcgtga tggacaaccc cctggtcatg caccagctgc gctgcaatgg tgtgctggag  | 2100 |
| ggcatccgca tctgcaggaa aggcttcccc aaccgcatcc tctacgggga cttccggcag  | 2160 |
| aggtatcgca tcctgaaccc agcggccatc cctgaggggac agttcattga tagcaggaag | 2220 |
| ggggcagaga agctgctcag ctccctggac attgatcaca accagtacaa gtttgggccac | 2280 |
| accaagggtgt tcttcaaggc cgggctgctg gggctgctgg aggaaatgag ggacgagagg | 2340 |
| ctgagccgca tcatcacgcg tatccaggcc cagtcccag gtgtgctcgc cagaatggag   | 2400 |
| tacaaaaagc tgctggaacg tagagactcc ctgctggtaa tccagtggaa cattcggggcc | 2460 |
| ttcatggggg tcaagaattg gccctggatg aagctctact tcaagatcaa gccgctgctg  | 2520 |
| aagagtgcag aaagagagaa ggagatggcc tccatgaagg aggagttcac acgcctcaaa  | 2580 |
| gaggcgctag agaagtccga ggctcgccgc aaggagctgg aggagaagat ggtgtccctg  | 2640 |
| ctgcaggaga agaatgacct gcagctccaa gtgcaggcgg aacaagacaa cctggcagat  | 2700 |
| gctgaggagc gctgtgatca gctgatcaaa aacaagattc agctggaggc taaggatgaag | 2760 |
| gagatgaacg agaggctgga ggatgaggag gagatgaatg ctgagctcac tgccaagaag  | 2820 |
| cgcaagttgg aagatgagtg ctgagagctc aaaagggaca tcgatgatct ggagctgaca  | 2880 |
| ctggccaaag tggagaagga gaaacacgca acagagaaca aggtgaaaaa cctgacagag  | 2940 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gagatggctg ggctggatga gatcattgcc aagctgacca aggagaagaa agctctgcaa  | 3000 |
| gaggcccacc aacaggctct ggatgacctt caggccgagg aggacaaggt caacaccctg  | 3060 |
| actaaggcca aagtcaagct ggagcagcaa gtggatgatc tggaaggatc cctggagcaa  | 3120 |
| gagaagaagg tgcgcatgga cctggagcga gcgaagcgga agctggaggg cgacctgaag  | 3180 |
| ctgacccagg agagcatcat ggacctggag aatgacaagc agcagctgga tgagcggctg  | 3240 |
| aaaaaaaaag actttgagct gaatgctctc aacgcaagga ttgaggatga acaggccctc  | 3300 |
| ggcagccagc tgcagaagaa gctcaaggag cttcaggcac gcatcgagga gctggaggag  | 3360 |
| gagctggagt ccgagcgcac cgccagggct aagggtggaga agctgcgctc agacctgtct | 3420 |
| cgggagctgg aggagatcag cgagcggctg gaagaggccg gcggggccac gtccgtgcag  | 3480 |
| atcgagatga acaagaagcg cgaggccgag ttccagaaga tgcggcggga cctggaggag  | 3540 |
| gccacgctgc agcacgaggc cactgccgcg gccctgcgca agaagcacgc cgacagcgtg  | 3600 |
| gccgagctgg gcgagcagat cgacaacctg cagcgggtga agcagaagct ggagaaggag  | 3660 |
| aagagcgagt tcaagctgga gctggatgac gtcacctcca acatggagca gatcatcaag  | 3720 |
| gccaaggcta acctggagaa gatgtgccgg accttggaag accagatgaa tgagcaccgg  | 3780 |
| agcaaggcgg aggagacca gcgttctgtc aacgacctca ccagccagcg ggccaagttg   | 3840 |
| caaaccgaga atggtgagct gtcccggcag ctggatgaga aggaggcact gatctcccag  | 3900 |
| ctgacccgag gcaagctcac ctacaccag cagctggagg acctcaagag gcagctggag   | 3960 |
| gaggaggtta aggcgaagaa cgccctggcc cacgcactgc agtcggcccg gcatgactgc  | 4020 |
| gacctgctgc gggagcagta cgaggaggag acggaggcca aggccgagct gcagcgcgtc  | 4080 |
| ctttccaagg ccaactcgga ggtggcccag tggaggacca agtatgagac ggacgccatt  | 4140 |
| cagcggactg aggagctcga ggaggccaag aagaagctgg ccagcggct gcaggaagct   | 4200 |
| gaggaggccg tggaggctgt taatgccaag tgctcctgc tggagaagac caagcaccgg   | 4260 |
| ctacagaatg agatcgagga cttgatggtg gacgtagagc gctccaatgc tgctgctgca  | 4320 |
| gccctggaca agaagcagag gaacttcgac aagatcctgg ccgagtggaa gcagaagtat  | 4380 |
| gaggagtcgc agtcggagct ggagtcctcg cagaaggagg ctcgctccct cagcacagag  | 4440 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ctcttcaaac tcaagaacgc ctatgaggag tccctggaac atctggagac cttcaagcgg  | 4500 |
| gagaacaaaa acctgcagga ggagatctcc gacttgactg agcagttggg ttccagcgga  | 4560 |
| aagactatcc atgagctgga gaaggtccga aagcagctgg aggccgagaa gatggagctg  | 4620 |
| cagtcagccc tggaggaggc cgaggcctcc ctggagcacg aggagggcaa gatcctccgg  | 4680 |
| gcccagctgg agttcaacca gatcaaggca gagatcgagc ggaagctggc agagaaggac  | 4740 |
| gaggagatgg aacaggccaa gcgcaaccac ctgcgggtgg tggactcgct gcagacctcc  | 4800 |
| ctggacgcag agacacgcag ccgcaacgag gccctgaggg tgaagaagaa gatggaagga  | 4860 |
| gacctcaatg agatggagat ccagctcagc cacgccaacc gcatggccgc cgaggcccag  | 4920 |
| aagcaagtca agagcctcca gagcttggtg aaggacaccc agattcagct ggacgatgca  | 4980 |
| gtccgtgcca acgacgacct gaaggagaac atcgccatcg tggagcggcg caacaacctg  | 5040 |
| ctgcaggctg agctggagga gttgcgtgcc gtgggtggagc agacagagcg gtcccggaag | 5100 |
| ctggcgggagc aggagctgat tgagactagt gagcgggtgc agctgctgca ttcccagaac | 5160 |
| accagcctca tcaaccagaa gaagaagatg gatgctgacc tgtcccagct ccagactgaa  | 5220 |
| gtggaggagg cagtcagga gtgcaggaat gctgaggaga aggccaagaa ggccatcacg   | 5280 |
| gatgccgcca tgatggcaga ggagctgaag aaggagcagg acaccagcgc ccacctggag  | 5340 |
| cgcatgaaga agaacatgga acagaccatt aaggacctgc agcaccggct ggacgaagcc  | 5400 |
| gagcagatcg ccctcaaggg cggcaagaag cagctgcaga agctggaagc gcgggtgcgg  | 5460 |
| gagctggaga atgagctgga ggccgagcag aagcgcaacg cagagtcggt gaagggcatg  | 5520 |
| aggaagagcg agcggcgcat caaggagctc acctaccaga cggaggagga caggaaaaac  | 5580 |
| ctgctgcggc tgcaggacct ggtagacaag ctgcagctaa aggtcaaggc ctacaagcgc  | 5640 |
| caggccgagg aggcggagga gcaagccaac accaacctgt ccaagttccg caaggtgcag  | 5700 |
| cacgagctgg atgaggcaga ggagcgggcg gacatcgccg agtcccaggt caacaagctg  | 5760 |
| cgggccaaga gccgtgacat tggcacgaag ggcttgaatg aggagtag               | 5808 |

<210> 142  
 <211> 1935  
 <212> PRT

<213> Homo sapiens

<400> 142

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

Leu Lys Lys Asp Val Phe Val Pro Asp Asp Lys Gln Glu Phe Val Lys  
35 40 45

Ala Lys Ile Val Ser Arg Glu Gly Gly Lys Val Thr Ala Glu Thr Glu  
50 55 60

Tyr Gly Lys Thr Val Thr Val Lys Glu Asp Gln Val Met Gln Gln Asn  
65 70 75 80

Pro Pro Lys Phe Asp Lys Ile Glu Asp Met Ala Met Leu Thr Phe Leu  
85 90 95

His Glu Pro Ala Val Leu Tyr Asn Leu Lys Asp Arg Tyr Gly Ser Trp  
100 105 110

Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro Tyr  
115 120 125

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

Lys Lys Arg Ser Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp Asn  
145 150 155 160

Ala Tyr Gln Tyr Met Leu Thr Asp Arg Glu Asn Gln Ser Ile Leu Ile  
165 170 175

Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val Ile  
180 185 190

Gln Tyr Phe Ala Val Ile Ala Ala Ile Gly Asp Arg Ser Lys Lys Asp  
195 200 205

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

Pro Ala Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg Asn Asp Asn  
225 230 235 240

Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly Ala Thr Gly  
245 250 255

Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu Lys Ser Arg  
260 265 270

Val Ile Phe Gln Leu Lys Ala Glu Arg Asp Tyr His Ile Phe Tyr Gln  
275 280 285

Ile Leu Ser Asn Lys Lys Pro Glu Leu Leu Asp Met Leu Leu Ile Thr  
290 295 300

Asn Asn Pro Tyr Asp Tyr Ala Phe Ile Ser Gln Gly Glu Thr Thr Val  
305 310 315 320

Ala Ser Ile Asp Asp Ala Glu Glu Leu Met Ala Thr Asp Asn Ala Phe  
325 330 335

Asp Val Leu Gly Phe Thr Ser Glu Glu Lys Asn Ser Met Tyr Lys Leu  
340 345 350

Thr Gly Ala Ile Met His Phe Gly Asn Met Lys Phe Lys Leu Lys Gln  
355 360 365

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

Ala Tyr Leu Met Gly Leu Asn Ser Ala Asp Leu Leu Lys Gly Leu Cys  
385 390 395 400

His Pro Arg Val Lys Val Gly Asn Glu Tyr Val Thr Lys Gly Gln Asn  
405 410 415

Val Gln Gln Val Ile Tyr Ala Thr Gly Ala Leu Ala Lys Ala Val Tyr  
420 425 430

Glu Arg Met Phe Asn Trp Met Val Thr Arg Ile Asn Ala Thr Leu Glu  
435 440 445

Thr Lys Gln Pro Arg Gln Tyr Phe Ile Gly Val Leu Asp Ile Ala Gly  
450 455 460

Phe Glu Ile Phe Asp Phe Asn Ser Phe Glu Gln Leu Cys Ile Asn Phe  
465 470 475 480

Thr Asn Glu Lys Leu Gln Gln Phe Phe Asn His His Met Phe Val Leu  
485 490 495

Glu Gln Glu Glu Tyr Lys Lys Glu Gly Ile Glu Trp Thr Phe Ile Asp  
500 505 510

Phe Gly Met Asp Leu Gln Ala Cys Ile Asp Leu Ile Glu Lys Pro Met  
515 520 525

Gly Ile Met Ser Ile Leu Glu Glu Glu Cys Met Phe Pro Lys Ala Thr  
530 535 540

Asp Met Thr Phe Lys Ala Lys Leu Phe Asp Asn His Leu Gly Lys Ser  
545 550 555 560

Ala Asn Phe Gln Lys Pro Arg Asn Ile Lys Gly Lys Pro Glu Ala His  
565 570 575

Phe Ser Leu Ile His Tyr Ala Gly Ile Val Asp Tyr Asn Ile Ile Gly  
580 585 590

Trp Leu Gln Lys Asn Lys Asp Pro Leu Asn Glu Thr Val Val Gly Leu  
595 600 605

Tyr Gln Lys Ser Ser Leu Lys Leu Leu Ser Thr Leu Phe Ala Asn Tyr  
610 615 620

Ala Gly Ala Asp Ala Pro Ile Glu Lys Gly Lys Gly Lys Ala Lys Lys  
625 630 635 640

Gly Ser Ser Phe Gln Thr Val Ser Ala Leu His Arg Glu Asn Leu Asn  
645 650 655

Lys Leu Met Thr Asn Leu Arg Ser Thr His Pro His Phe Val Arg Cys  
660 665 670

Ile Ile Pro Asn Glu Thr Lys Ser Pro Gly Val Met Asp Asn Pro Leu  
675 680 685

Val Met His Gln Leu Arg Cys Asn Gly Val Leu Glu Gly Ile Arg Ile  
690 695 700

Cys Arg Lys Gly Phe Pro Asn Arg Ile Leu Tyr Gly Asp Phe Arg Gln  
705 710 715 720

Arg Tyr Arg Ile Leu Asn Pro Ala Ala Ile Pro Glu Gly Gln Phe Ile  
725 730 735

Asp Ser Arg Lys Gly Ala Glu Lys Leu Leu Ser Ser Leu Asp Ile Asp  
740 745 750

His Asn Gln Tyr Lys Phe Gly His Thr Lys Val Phe Phe Lys Ala Gly  
755 760 765

Leu Leu Gly Leu Leu Glu Glu Met Arg Asp Glu Arg Leu Ser Arg Ile  
770 775 780

Ile Thr Arg Ile Gln Ala Gln Ser Arg Gly Val Leu Ala Arg Met Glu  
785 790 795 800

Tyr Lys Lys Leu Leu Glu Arg Arg Asp Ser Leu Leu Val Ile Gln Trp  
805 810 815

Asn Ile Arg Ala Phe Met Gly Val Lys Asn Trp Pro Trp Met Lys Leu  
820 825 830

Tyr Phe Lys Ile Lys Pro Leu Leu Lys Ser Ala Glu Arg Glu Lys Glu  
835 840 845

Met Ala Ser Met Lys Glu Glu Phe Thr Arg Leu Lys Glu Ala Leu Glu  
850 855 860

Lys Ser Glu Ala Arg Arg Lys Glu Leu Glu Glu Lys Met Val Ser Leu  
865 870 875 880

Leu Gln Glu Lys Asn Asp Leu Gln Leu Gln Val Gln Ala Glu Gln Asp  
885 890 895

Asn Leu Ala Asp Ala Glu Glu Arg Cys Asp Gln Leu Ile Lys Asn Lys  
900 905 910

Ile Gln Leu Glu Ala Lys Val Lys Glu Met Asn Glu Arg Leu Glu Asp  
915 920 925

Glu Glu Glu Met Asn Ala Glu Leu Thr Ala Lys Lys Arg Lys Leu Glu  
930 935 940

Asp Glu Cys Ser Glu Leu Lys Arg Asp Ile Asp Asp Leu Glu Leu Thr  
945 950 955 960

Leu Ala Lys Val Glu Lys Glu Lys His Ala Thr Glu Asn Lys Val Lys  
965 970 975

Asn Leu Thr Glu Glu Met Ala Gly Leu Asp Glu Ile Ile Ala Lys Leu  
980 985 990



Thr Lys Glu Lys Lys Ala Leu Gln Glu Ala His Gln Gln Ala Leu Asp  
995 1000 1005

Asp Leu Gln Ala Glu Glu Asp Lys Val Asn Thr Leu Thr Lys Ala  
1010 1015 1020

Lys Val Lys Leu Glu Gln Gln Val Asp Asp Leu Glu Gly Ser Leu  
1025 1030 1035

Glu Gln Glu Lys Lys Val Arg Met Asp Leu Glu Arg Ala Lys Arg  
1040 1045 1050

Lys Leu Glu Gly Asp Leu Lys Leu Thr Gln Glu Ser Ile Met Asp  
1055 1060 1065

Leu Glu Asn Asp Lys Gln Gln Leu Asp Glu Arg Leu Lys Lys Lys  
1070 1075 1080

Asp Phe Glu Leu Asn Ala Leu Asn Ala Arg Ile Glu Asp Glu Gln  
1085 1090 1095

Ala Leu Gly Ser Gln Leu Gln Lys Lys Leu Lys Glu Leu Gln Ala  
1100 1105 1110

Arg Ile Glu Glu Leu Glu Glu Glu Leu Glu Ser Glu Arg Thr Ala  
1115 1120 1125

Arg Ala Lys Val Glu Lys Leu Arg Ser Asp Leu Ser Arg Glu Leu  
1130 1135 1140

Glu Glu Ile Ser Glu Arg Leu Glu Glu Ala Gly Gly Ala Thr Ser  
1145 1150 1155

Val Gln Ile Glu Met Asn Lys Lys Arg Glu Ala Glu Phe Gln Lys  
1160 1165 1170

Met Arg Arg Asp Leu Glu Glu Ala Thr Leu Gln His Glu Ala Thr  
1175 1180 1185

Ala Ala Ala Leu Arg Lys Lys His Ala Asp Ser Val Ala Glu Leu  
1190 1195 1200

Gly Glu Gln Ile Asp Asn Leu Gln Arg Val Lys Gln Lys Leu Glu  
1205 1210 1215

Lys Glu Lys Ser Glu Phe Lys Leu Glu Leu Asp Asp Val Thr Ser  
1220 1225 1230

Asn Met Glu Gln Ile Ile Lys Ala Lys Ala Asn Leu Glu Lys Met  
1235 1240 1245

Cys Arg Thr Leu Glu Asp Gln Met Asn Glu His Arg Ser Lys Ala  
1250 1255 1260

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

Lys Leu Gln Thr Glu Asn Gly Glu Leu Ser Arg Gln Leu Asp Glu  
1280 1285 1290

Lys Glu Ala Leu Ile Ser Gln Leu Thr Arg Gly Lys Leu Thr Tyr  
1295 1300 1305

Thr Gln Gln Leu Glu Asp Leu Lys Arg Gln Leu Glu Glu Glu Val  
1310 1315 1320

Lys Ala Lys Asn Ala Leu Ala His Ala Leu Gln Ser Ala Arg His  
1325 1330 1335

Asp Cys Asp Leu Leu Arg Glu Gln Tyr Glu Glu Glu Thr Glu Ala  
1340 1345 1350

Lys Ala Glu Leu Gln Arg Val Leu Ser Lys Ala Asn Ser Glu Val  
1355 1360 1365

Ala Gln Trp Arg Thr Lys Tyr Glu Thr Asp Ala Ile Gln Arg Thr  
1370 1375 1380

Glu Glu Leu Glu Glu Ala Lys Lys Lys Leu Ala Gln Arg Leu Gln  
1385 1390 1395

Glu Ala Glu Glu Ala Val Glu Ala Val Asn Ala Lys Cys Ser Ser  
1400 1405 1410

Leu Glu Lys Thr Lys His Arg Leu Gln Asn Glu Ile Glu Asp Leu  
1415 1420 1425

Met Val Asp Val Glu Arg Ser Asn Ala Ala Ala Ala Ala Leu Asp  
1430 1435 1440

Lys Lys Gln Arg Asn Phe Asp Lys Ile Leu Ala Glu Trp Lys Gln  
1445 1450 1455

Lys Tyr Glu Glu Ser Gln Ser Glu Leu Glu Ser Ser Gln Lys Glu  
1460 1465 1470

Ala Arg Ser Leu Ser Thr Glu Leu Phe Lys Leu Lys Asn Ala Tyr  
1475 1480 1485

Glu Glu Ser Leu Glu His Leu Glu Thr Phe Lys Arg Glu Asn Lys  
1490 1495 1500

Asn Leu Gln Glu Glu Ile Ser Asp Leu Thr Glu Gln Leu Gly Ser  
1505 1510 1515

Ser Gly Lys Thr Ile His Glu Leu Glu Lys Val Arg Lys Gln Leu  
1520 1525 1530

Glu Ala Glu Lys Met Glu Leu Gln Ser Ala Leu Glu Glu Ala Glu  
1535 1540 1545

Ala Ser Leu Glu His Glu Glu Gly Lys Ile Leu Arg Ala Gln Leu  
1550 1555 1560

Glu Phe Asn Gln Ile Lys Ala Glu Ile Glu Arg Lys Leu Ala Glu  
1565 1570 1575

Lys Asp Glu Glu Met Glu Gln Ala Lys Arg Asn His Leu Arg Val  
1580 1585 1590

Val Asp Ser Leu Gln Thr Ser Leu Asp Ala Glu Thr Arg Ser Arg  
1595 1600 1605

Asn Glu Ala Leu Arg Val Lys Lys Lys Met Glu Gly Asp Leu Asn  
1610 1615 1620

Glu Met Glu Ile Gln Leu Ser His Ala Asn Arg Met Ala Ala Glu  
1625 1630 1635

Ala Gln Lys Gln Val Lys Ser Leu Gln Ser Leu Leu Lys Asp Thr  
1640 1645 1650

Gln Ile Gln Leu Asp Asp Ala Val Arg Ala Asn Asp Asp Leu Lys  
1655 1660 1665

Glu Asn Ile Ala Ile Val Glu Arg Arg Asn Asn Leu Leu Gln Ala  
1670 1675 1680

Glu Leu Glu Glu Leu Arg Ala Val Val Glu Gln Thr Glu Arg Ser  
1685 1690 1695

Arg Lys Leu Ala Glu Gln Glu Leu Ile Glu Thr Ser Glu Arg Val  
1700 1705 1710

Gln Leu Leu His Ser Gln Asn Thr Ser Leu Ile Asn Gln Lys Lys  
1715 1720 1725

Lys Met Asp Ala Asp Leu Ser Gln Leu Gln Thr Glu Val Glu Glu  
1730 1735 1740

Ala Val Gln Glu Cys Arg Asn Ala Glu Glu Lys Ala Lys Lys Ala  
1745 1750 1755

Ile Thr Asp Ala Ala Met Met Ala Glu Glu Leu Lys Lys Glu Gln  
1760 1765 1770

Asp Thr Ser Ala His Leu Glu Arg Met Lys Lys Asn Met Glu Gln  
1775 1780 1785

Thr Ile Lys Asp Leu Gln His Arg Leu Asp Glu Ala Glu Gln Ile  
1790 1795 1800

Ala Leu Lys Gly Gly Lys Lys Gln Leu Gln Lys Leu Glu Ala Arg  
1805 1810 1815

Val Arg Glu Leu Glu Asn Glu Leu Glu Ala Glu Gln Lys Arg Asn  
1820 1825 1830

Ala Glu Ser Val Lys Gly Met Arg Lys Ser Glu Arg Arg Ile Lys  
1835 1840 1845

Glu Leu Thr Tyr Gln Thr Glu Glu Asp Arg Lys Asn Leu Leu Arg  
1850 1855 1860

Leu Gln Asp Leu Val Asp Lys Leu Gln Leu Lys Val Lys Ala Tyr  
1865 1870 1875

Lys Arg Gln Ala Glu Glu Ala Glu Glu Gln Ala Asn Thr Asn Leu  
1880 1885 1890

Ser Lys Phe Arg Lys Val Gln His Glu Leu Asp Glu Ala Glu Glu  
1895 1900 1905

Arg Ala Asp Ile Ala Glu Ser Gln Val Asn Lys Leu Arg Ala Lys  
1910 1915 1920

Ser Arg Asp Ile Gly Thr Lys Gly Leu Asn Glu Glu  
1925 1930 1935

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<211> 736

<212> PRT

<213> Dependoparvovirus Adeno-associated virus serotype 9

<400> 143

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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro

355

360

365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
 450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
 465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
 485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
 500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
 530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
 545 550 555 560



Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 144

<211> 724

<212> PRT

<213> Dependoparvovirus Adeno-associated virus serotype 5

<400> 144

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser  
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln  
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr  
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala  
195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp  
210 215 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro  
225 230 235 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp  
245 250 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr  
260 265 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln  
275 280 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val  
290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr  
305 310 315 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp  
325 330 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys  
340 345 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr  
355 360 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser  
370 375 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn  
385 390 395 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser  
405 410 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp  
420 425 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln  
435 440 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp  
450 455 460

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

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu  
485 490 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr  
500 505 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile  
515 520 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu  
530 535 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg  
545 550 555 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser  
565 570 575

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

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp  
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met  
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn  
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser  
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu  
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln  
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp  
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu  
705 710 715 720

Thr Arg Pro Leu

<210> 145

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 145

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Ser Gln Val Asn Gly Arg Pro Arg Asp Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 146  
<211> 736  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 146

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Gly Tyr His Lys Ser Gly Ala Ala Gln Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 147

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 147

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Asn Val Ser Tyr Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 148  
<211> 736  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 148

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Met Val Asn Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 149  
<211> 736  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 149

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ala Asn Tyr Gly Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 150  
<211> 736  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 150

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Asn Val Gly Thr Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 151  
<211> 736  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 151

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Gly Tyr His Lys Ser Gly Ala Ala Gln Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Asn Val Ser Tyr Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 152

<211> 736

<212> PRT

<213> Artificial Sequence

<220>



<223> Recombinant AAV Capsid Protein

<400> 152

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Leu Asn Ser Met Leu Ile Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 153

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 153

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Gln Asp Ala Ser Leu Leu Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 154  
<211> 736  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 154

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Gly Met Ser Phe Thr Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 155

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 155

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Gly Tyr His Lys Ser Gly Ala Ala Gln Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ala Asn Tyr Gly Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 156  
<211> 736  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 156

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Gly Tyr His Lys Ser Gly Ala Ala Gln Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Gln Asp Ala Ser Leu Leu Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 157

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 157

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Gly Tyr His Lys Ser Gly Ala Ala Gln Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Gly Met Ser Phe Thr Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 158

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 158

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Leu Asn Ser Met Leu Ile Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ala Asn Tyr Gly Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 159  
<211> 726  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 159

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser  
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln  
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr  
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala  
195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp  
210 215 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Ala Leu Pro  
225 230 235 240

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly  
245 250 255

Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly  
260 265 270

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

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn  
290 295 300

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly  
305 310 315 320

Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr  
325 330 335

Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Glu Gly  
340 345 350

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly  
355 360 365

Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser Phe  
370 375 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn  
385 390 395 400

Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser Tyr  
405 410 415

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln  
420 425 430

Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln  
435 440 445

Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val Gln  
450 455 460

Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser  
465 470 475 480

Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala  
485 490 495

Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly Pro  
500 505 510

Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser  
515 520 525

Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val Asp  
530 535 540

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

Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser  
565 570 575

Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu  
580 585 590

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
595 600 605

Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu  
610 615 620

Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys  
625 630 635 640

Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys  
645 650 655

Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu  
660 665 670

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu  
675 680 685

Ile Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala  
690 695 700

Pro Asp Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg  
705 710 715 720

Tyr Leu Thr Arg Pro Leu  
725

<210> 160

<211> 725

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 160

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

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

Val Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn  
65 70 75 80

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

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

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

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

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

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser  
165 170 175



Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp  
180 185 190

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

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr  
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu  
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val  
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly  
260 265 270

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

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg  
290 295 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser  
305 310 315 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr  
325 330 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly  
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly  
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser  
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly  
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser  
405 410 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val  
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val  
435 440 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn  
450 455 460

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

Gly Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met  
485 490 495

Glu Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met  
500 505 510

Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met  
515 520 525

Ile Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu  
530 535 540

Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn  
545 550 555 560

Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser  
565 570 575

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

Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile  
595 600 605

Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala  
610 615 620

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys  
625 630 635 640

Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val  
645 650 655

Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met  
660 665 670

Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile  
675 680 685

Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val  
690 695 700

Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr  
705 710 715 720

Leu Thr Arg Asn Leu  
725

<210> 161  
<211> 725  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 161

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser  
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln  
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr  
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala  
195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp  
210 215 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro  
225 230 235 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp  
245 250 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr  
260 265 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln  
275 280 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val  
290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val  
305 310 315 320

Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp  
325 330 335

Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys  
340 345 350

Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr  
355 360 365

Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr  
370 375 380

Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe  
385 390 395 400

Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala  
405 410 415

His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr  
420 425 430

Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln  
435 440 445

Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly  
450 455 460

Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr  
465 470 475 480

Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser  
485 490 495

Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala  
500 505 510

Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly  
515 520 525

Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala  
530 535 540

Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro  
545 550 555 560

Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala  
565 570 575

Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro  
580 585 590

Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp  
595 600 605

Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met  
610 615 620

Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn  
625 630 635 640

Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu  
645 650 655

Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile  
660 665 670

Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile  
675 680 685

Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val  
690 695 700

Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr  
705 710 715 720

Leu Thr Arg Asn Leu  
725

<210> 162  
<211> 727  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 162

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

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

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

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

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

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser  
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp  
180 185 190

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

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr  
210 215 220



Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu  
225 230 235 240

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser  
245 250 255

Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp  
260 265 270

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

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu  
290 295 300

Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn  
305 310 315 320

Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe  
325 330 335

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

Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr  
355 360 365

Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser  
370 375 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn  
385 390 395 400

Asn Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser  
405 410 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp  
420 425 430

Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn  
435 440 445

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val  
450 455 460

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val  
465 470 475 480

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly  
485 490 495

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly  
500 505 510

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu  
515 520 525

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val  
530 535 540

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

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln  
565 570 575

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile  
580 585 590

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro  
595 600 605

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro  
610 615 620

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile  
625 630 635 640

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp  
645 650 655

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val  
660 665 670

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro  
675 680 685

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe  
690 695 700

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr  
705 710 715 720

Arg Tyr Leu Thr Arg Asn Leu  
725

<210> 163

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 163

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

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

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

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

Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu  
705 710 715 720

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

<210> 164  
<211> 726  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 164

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser  
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln  
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr  
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala  
195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp  
210 215 220

Met Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro  
225 230 235 240

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly  
245 250 255

Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly  
260 265 270



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

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn  
290 295 300

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly  
305 310 315 320

Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr  
325 330 335

Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Glu Gly  
340 345 350

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly  
355 360 365

Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser Phe  
370 375 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn  
385 390 395 400

Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser Phe  
405 410 415

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln  
420 425 430

Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln  
435 440 445

Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val Gln  
450 455 460

Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser  
465 470 475 480

Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala  
485 490 495

Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly Pro  
500 505 510

Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser  
515 520 525

Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val Asp  
530 535 540

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

Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser  
565 570 575

Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu  
580 585 590

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
595 600 605

Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu  
610 615 620

Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys  
625 630 635 640

Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys  
645 650 655

Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu  
660 665 670

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu  
675 680 685

Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala  
690 695 700

Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg  
705 710 715 720

Tyr Leu Thr Arg Asn Leu  
725

<210> 165  
<211> 726  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 165

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser  
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln  
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr  
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala  
195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Gln Trp  
210 215 220

Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro  
225 230 235 240

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly  
245 250 255

Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly  
260 265 270

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

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn  
290 295 300

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly  
305 310 315 320

Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr  
325 330 335

Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Glu Gly  
340 345 350

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly  
355 360 365

Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser Phe  
370 375 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn  
385 390 395 400

Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser Tyr  
405 410 415

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln  
420 425 430

Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln  
435 440 445

Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val Gln  
450 455 460

Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser  
465 470 475 480

Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala  
485 490 495

Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly Pro  
500 505 510

Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser  
515 520 525

Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val Asp  
530 535 540

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

Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser  
565 570 575

Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu  
580 585 590

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
595 600 605

Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu  
610 615 620

Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys  
625 630 635 640

Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys  
645 650 655

Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu  
660 665 670

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu  
675 680 685

Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala  
690 695 700

Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg  
705 710 715 720

Tyr Leu Thr Arg Asn Leu  
725

<210> 166  
<211> 726  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 166

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser  
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln  
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr  
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala  
195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Gln Trp  
210 215 220

Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro  
225 230 235 240

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly  
245 250 255

Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly  
260 265 270

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

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn  
290 295 300

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly  
305 310 315 320



Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr  
325 330 335

Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Glu Gly  
340 345 350

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly  
355 360 365

Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser Phe  
370 375 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn  
385 390 395 400

Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser Tyr  
405 410 415

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln  
420 425 430

Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln  
435 440 445

Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val Gln  
450 455 460

Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser  
465 470 475 480

Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala  
485 490 495

Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly Pro  
500 505 510

Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser  
515 520 525

Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val Asp  
530 535 540

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

Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser  
565 570 575

Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu  
580 585 590

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
595 600 605

Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu  
610 615 620

Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys  
625 630 635 640

Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys  
645 650 655

Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu  
660 665 670

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu  
675 680 685

Ile Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala  
690 695 700

Pro Asp Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg  
705 710 715 720

Tyr Leu Thr Arg Pro Leu  
725

<210> 167  
<211> 727  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 167

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg  
130 135 140

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

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser  
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp  
180 185 190

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

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr  
210 215 220

Trp Met Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu  
225 230 235 240

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser  
245 250 255

Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp  
260 265 270

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

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu  
290 295 300

Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn  
305 310 315 320

Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe  
325 330 335

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

Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr  
355 360 365

Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser  
370 375 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn  
385 390 395 400

Asn Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser  
405 410 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp  
420 425 430

Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn  
435 440 445

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val  
450 455 460

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val  
465 470 475 480

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly  
485 490 495

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly  
500 505 510

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu  
515 520 525

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val  
530 535 540

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

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln  
565 570 575

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile  
580 585 590

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro  
595 600 605

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro  
610 615 620

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile  
625 630 635 640

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp  
645 650 655

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val  
660 665 670

Glu Met Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro  
675 680 685

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe  
690 695 700

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr  
705 710 715 720

Arg Tyr Leu Thr Arg Asn Leu  
725

<210> 168

<211> 726

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 168

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

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

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

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

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

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser  
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp  
180 185 190

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

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr  
210 215 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu  
225 230 235 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val  
245 250 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly  
260 265 270

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

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn  
290 295 300

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly  
305 310 315 320

Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr  
325 330 335

Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Glu Gly  
340 345 350

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly  
355 360 365



Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser Phe  
370 375 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn  
385 390 395 400

Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser Tyr  
405 410 415

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln  
420 425 430

Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln  
435 440 445

Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val Gln  
450 455 460

Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser  
465 470 475 480

Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala  
485 490 495

Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly Pro  
500 505 510

Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser  
515 520 525

Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val Asp  
530 535 540

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

Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser  
565 570 575

Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu  
580 585 590

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
595 600 605

Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu  
610 615 620

Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys  
625 630 635 640

Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys  
645 650 655

Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu  
660 665 670

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu  
675 680 685

Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala  
690 695 700

Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg  
705 710 715 720

Tyr Leu Thr Arg Asn Leu  
725

<210> 169

<211> 726

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 169

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser  
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln  
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr  
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala  
195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp  
210 215 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Ala Leu Pro  
225 230 235 240

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly  
245 250 255

Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly  
260 265 270

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

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn  
290 295 300

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly  
305 310 315 320

Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr  
325 330 335

Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Glu Gly  
340 345 350

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly  
355 360 365

Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser Phe  
370 375 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn  
385 390 395 400

Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser Tyr  
405 410 415

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln  
420 425 430

Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln  
435 440 445

Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val Gln  
450 455 460

Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser  
465 470 475 480

Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala  
485 490 495

Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly Pro  
500 505 510

Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser  
515 520 525

Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val Asp  
530 535 540

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

Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser  
565 570 575

Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu  
580 585 590

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
595 600 605

Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu  
610 615 620

Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys  
625 630 635 640

Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys  
645 650 655

Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu  
660 665 670

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu  
675 680 685

Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala  
690 695 700

Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg  
705 710 715 720

Tyr Leu Thr Arg Asn Leu  
725

<210> 170

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 170

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

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

Val Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn  
65 70 75 80

Glu Gln Leu Glu 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 Lys Ala Val Phe Gln Ala Lys Lys Arg Val 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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

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

Ser Gly Asp 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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



Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

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

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

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

Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu  
705 710 715 720

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

<210> 171  
<211> 735  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 171

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

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

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

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

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

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

Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys  
145 150 155 160

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

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala  
180 185 190

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

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

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

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

Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala  
260 265 270

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

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

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

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

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

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala  
355 360 365

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

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

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

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

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

Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val  
450 455 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly  
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn  
485 490 495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly  
500 505 510

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

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys  
530 535 540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr  
545 550 555 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr  
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr  
580 585 590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp  
595 600 605

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

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

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

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln  
660 665 670

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

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

Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr  
705 710 715 720

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

<210> 172  
<211> 735  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 172

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys  
145 150 155 160

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

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala  
180 185 190

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

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

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

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

Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala  
260 265 270

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

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

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

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

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

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala  
355 360 365

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

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

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

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

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

Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val  
450 455 460



Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly  
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn  
485 490 495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly  
500 505 510

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

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys  
530 535 540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr  
545 550 555 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr  
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr  
580 585 590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp  
595 600 605

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

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

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

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln  
660 665 670

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

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

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

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

<210> 173  
<211> 726  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 173

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser  
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln  
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr  
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala  
195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp  
210 215 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Ala Leu Pro  
225 230 235 240

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly  
245 250 255

Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly  
260 265 270

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

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn  
290 295 300

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly  
305 310 315 320

Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr  
325 330 335

Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Glu Gly  
340 345 350

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly  
355 360 365

Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser Phe  
370 375 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn  
385 390 395 400

Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser Tyr  
405 410 415

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln  
420 425 430

Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln  
435 440 445

Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val Gln  
450 455 460

Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser  
465 470 475 480

Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala  
485 490 495

Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly Pro  
500 505 510

Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser  
515 520 525

Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val Asp  
530 535 540

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

Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser  
565 570 575

Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu  
580 585 590

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
595 600 605

Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu  
610 615 620

Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys  
625 630 635 640

Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys  
645 650 655

Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu  
660 665 670

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu  
675 680 685

Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala  
690 695 700

Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg  
705 710 715 720

Tyr Leu Thr Arg Asn Leu  
725

<210> 174  
<211> 726  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 174

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser  
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln  
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr  
180 185 190

Met Ser Ala Gly Gly Gly Ala Pro Val Ala Asp Asn Asn Glu Gly Ala  
195 200 205

Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp  
210 215 220

Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro  
225 230 235 240

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly  
245 250 255

Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly  
260 265 270

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

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn  
290 295 300

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly  
305 310 315 320

Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr  
325 330 335

Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Glu Gly  
340 345 350

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly  
355 360 365

Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser Phe  
370 375 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn  
385 390 395 400

Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser Tyr  
405 410 415

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln  
420 425 430

Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln  
435 440 445

Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val Gln  
450 455 460

Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser  
465 470 475 480

Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala  
485 490 495

Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly Pro  
500 505 510



Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser  
515 520 525

Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val Asp  
530 535 540

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

Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser  
565 570 575

Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu  
580 585 590

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
595 600 605

Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu  
610 615 620

Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys  
625 630 635 640

Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys  
645 650 655

Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu  
660 665 670

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu  
675 680 685

Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala  
690 695 700

Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg  
705 710 715 720

Tyr Leu Thr Arg Asn Leu  
725

<210> 175  
<211> 726  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 175

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

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

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

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

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

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

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

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser  
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln  
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr  
180 185 190

Met Ser Ala Gly Gly Gly Ala Pro Val Ala Asp Asn Asn Glu Gly Ala  
195 200 205

Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp  
210 215 220

Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro  
225 230 235 240

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly  
245 250 255

Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly  
260 265 270

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

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn  
290 295 300

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly  
305 310 315 320

Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr  
325 330 335

Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Glu Gly  
340 345 350

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly  
355 360 365

Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser Phe  
370 375 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn  
385 390 395 400

Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser Tyr  
405 410 415

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln  
420 425 430

Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln  
435 440 445

Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val Gln  
450 455 460

Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser  
465 470 475 480

Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala  
485 490 495

Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly Pro  
500 505 510

Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser  
515 520 525

Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val Asp  
530 535 540

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

Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser  
565 570 575

Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu  
580 585 590

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
595 600 605

Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu  
610 615 620

Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys  
625 630 635 640

Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys  
645 650 655

Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu  
660 665 670

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu  
675 680 685

Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala  
690 695 700

Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg  
705 710 715 720

Tyr Leu Thr Arg Asn Leu  
725

<210> 176  
<211> 727  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 176

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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

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

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

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser  
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp  
180 185 190

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

Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Gln  
210 215 220

Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu  
225 230 235 240

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser  
245 250 255

Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp  
260 265 270

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

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu  
290 295 300

Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn  
305 310 315 320

Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe  
325 330 335

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

Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr  
355 360 365

Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser  
370 375 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn  
385 390 395 400

Asn Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser  
405 410 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp  
420 425 430

Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn  
435 440 445

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val  
450 455 460

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val  
465 470 475 480

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly  
485 490 495

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly  
500 505 510

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu  
515 520 525

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val  
530 535 540

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



Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln  
565 570 575

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile  
580 585 590

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro  
595 600 605

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro  
610 615 620

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile  
625 630 635 640

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp  
645 650 655

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val  
660 665 670

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro  
675 680 685

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe  
690 695 700

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr  
705 710 715 720

Arg Tyr Leu Thr Arg Asn Leu  
725

<210> 177

<211> 727

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 177

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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 Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

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

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

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

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

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser  
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp  
180 185 190

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

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr  
210 215 220

Trp Met Gly Asp Arg Val Val Thr Thr Ser Thr Arg Thr Trp Ala Leu  
225 230 235 240

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser  
245 250 255

Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp  
260 265 270

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

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu  
290 295 300

Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn  
305 310 315 320

Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe  
325 330 335

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

Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr  
355 360 365

Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser  
370 375 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn  
385 390 395 400

Asn Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser  
405 410 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp  
420 425 430

Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn  
435 440 445

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val  
450 455 460

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val  
465 470 475 480

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly  
485 490 495

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly  
500 505 510

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu  
515 520 525

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val  
530 535 540

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

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln  
565 570 575

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile  
580 585 590

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro  
595 600 605

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro  
610 615 620

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile  
625 630 635 640

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp  
645 650 655

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val  
660 665 670

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro  
675 680 685

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe  
690 695 700

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr  
705 710 715 720

Arg Tyr Leu Thr Arg Asn Leu  
725

<210> 178

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 178

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys  
145 150 155 160

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

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala  
180 185 190

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

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

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

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

Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala  
260 265 270

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

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

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

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

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

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala  
355 360 365

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

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

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

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

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

Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val  
450 455 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly  
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn  
485 490 495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly  
500 505 510

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

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys  
530 535 540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr  
545 550 555 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr  
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr  
580 585 590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp  
595 600 605



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

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

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

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln  
660 665 670

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

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

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

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

<210> 179

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 179

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

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

Val Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn  
65 70 75 80

Glu Gln Leu Glu 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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 180

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 180

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

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

Asn Leu Gly Lys 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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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



Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 181  
<211> 736  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 181

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

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

Asn Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val 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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 182

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 182

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

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

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

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

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

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

Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys  
145 150 155 160

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

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala  
180 185 190

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

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

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

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

Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala  
260 265 270

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

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

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

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

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

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala  
355 360 365

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

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

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

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

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

Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val  
450 455 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly  
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn  
485 490 495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly  
500 505 510

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

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys  
530 535 540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr  
545 550 555 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr  
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr  
580 585 590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp  
595 600 605

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

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

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

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln  
660 665 670

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

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



Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr  
705 710 715 720

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

<210> 183

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 183

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

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

Val Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn  
65 70 75 80

Glu Gln Leu Glu 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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Gly Tyr His Lys Ser Gly Ala Ala Gln Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 184  
<211> 736  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 184

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

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

Val Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn  
65 70 75 80

Glu Gln Leu Glu 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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ala Asn Tyr Gly Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 185

<211> 736

<212> PRT

<213> Artificial Sequence



<220>

<223> Recombinant AAV Capsid Protein

<400> 185

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

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

Val Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn  
65 70 75 80

Glu Gln Leu Glu 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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Gly Tyr His Lys Ser Gly Ala Ala Gln Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Asn Val Ser Tyr Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 186

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 186

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

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

Val Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn  
65 70 75 80

Glu Gln Leu Glu 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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Leu Asn Ser Met Leu Ile Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 187  
<211> 736  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 187

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

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

Val Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn  
65 70 75 80

Glu Gln Leu Glu 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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Gly Tyr His Lys Ser Gly Ala Ala Gln Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ala Asn Tyr Gly Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 188  
<211> 736  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 188

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

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

Val Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn  
65 70 75 80

Glu Gln Leu Glu 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 Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

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

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

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

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 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 Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
260 265 270

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

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

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
305 310 315 320

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

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
355 360 365

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

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

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

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
420 425 430

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

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Leu Asn Ser Met Leu Ile Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

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

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ala Asn Tyr Gly Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile 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 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn 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 Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu 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

<210> 189  
<211> 735  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 189

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80



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

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

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

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

Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys  
145 150 155 160

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

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala  
180 185 190

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

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

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

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

Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala  
260 265 270

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

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

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

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

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

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala  
355 360 365

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

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

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

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

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

Thr Ile Gly Tyr His Lys Ser Gly Ala Ala Gln Leu Lys Phe Ser Val  
450 455 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly  
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn  
485 490 495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly  
500 505 510

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

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys  
530 535 540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr  
545 550 555 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr  
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr  
580 585 590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp  
595 600 605

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

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

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

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln  
660 665 670

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

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

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

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

<210> 190

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 190

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys  
145 150 155 160

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

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala  
180 185 190

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

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

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

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

Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala  
260 265 270

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

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

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

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

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

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala  
355 360 365

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

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

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

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

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

Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val  
450 455 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly  
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn  
485 490 495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly  
500 505 510

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

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys  
530 535 540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr  
545 550 555 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr  
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ala Asn Tyr Gly Gln Ala Gln Thr  
580 585 590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp  
595 600 605

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

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

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

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln  
660 665 670

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

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

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

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

<210> 191  
<211> 735  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 191

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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



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

Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys  
145 150 155 160

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

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala  
180 185 190

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

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

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

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

Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala  
260 265 270

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

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

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

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

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

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala  
355 360 365

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

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

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

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

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

Thr Ile Gly Tyr His Lys Ser Gly Ala Ala Gln Leu Lys Phe Ser Val  
450 455 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly  
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn  
485 490 495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly  
500 505 510

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

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys  
530 535 540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr  
545 550 555 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr  
565 570 575

Gly Gln Val Ala Thr Asn His Gln Asn Val Ser Tyr Gln Ala Gln Thr  
580 585 590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp  
595 600 605

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

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

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

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln  
660 665 670

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

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

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

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

<210> 192

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 192

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys  
145 150 155 160

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

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala  
180 185 190

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

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

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

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

Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala  
260 265 270

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

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

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

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

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

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala  
355 360 365

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

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

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

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

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

Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val  
450 455 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly  
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Leu  
485 490 495

Asn Ser Met Leu Ile Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly  
500 505 510

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

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys  
530 535 540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr  
545 550 555 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr  
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr  
580 585 590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp  
595 600 605

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

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

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

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln  
660 665 670

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

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

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

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

<210> 193

<211> 735

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 193

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys  
145 150 155 160

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



Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala  
180 185 190

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

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

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

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

Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala  
260 265 270

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

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

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

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

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

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala  
355 360 365

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

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

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

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

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

Thr Ile Gly Tyr His Lys Ser Gly Ala Ala Gln Leu Lys Phe Ser Val  
450 455 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly  
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn  
485 490 495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly  
500 505 510

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

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys  
530 535 540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr  
545 550 555 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr  
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ala Asn Tyr Gly Gln Ala Gln Thr  
580 585 590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp  
595 600 605

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

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

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

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln  
660 665 670

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

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

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

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

<210> 194

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 194

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
20 25 30

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

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
65 70 75 80

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

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

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

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

Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys  
145 150 155 160

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

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala  
180 185 190

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

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

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

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

Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala  
260 265 270

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

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

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

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

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

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala  
355 360 365

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

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

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

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

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

Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val  
450 455 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly  
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Leu  
485 490 495

Asn Ser Met Leu Ile Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly  
500 505 510

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

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys  
530 535 540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr  
545 550 555 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr  
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ala Asn Tyr Gly Gln Ala Gln Thr  
580 585 590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp  
595 600 605

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

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

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

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln  
660 665 670

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

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

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

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

<210> 195

<211> 727

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 195

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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

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

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

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser  
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp  
180 185 190

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

Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Gln  
210 215 220



Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu  
225 230 235 240

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser  
245 250 255

Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp  
260 265 270

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

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu  
290 295 300

Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn  
305 310 315 320

Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe  
325 330 335

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

Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr  
355 360 365

Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser  
370 375 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn  
385 390 395 400

Asn Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser  
405 410 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp  
420 425 430

Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Gly Tyr His Lys Ser Gly  
435 440 445

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

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val  
465 470 475 480

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly  
485 490 495

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly  
500 505 510

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu  
515 520 525

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val  
530 535 540

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

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln  
565 570 575

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile  
580 585 590

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro  
595 600 605

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro  
610 615 620

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile  
625 630 635 640

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp  
645 650 655

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val  
660 665 670

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro  
675 680 685

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe  
690 695 700

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr  
705 710 715 720

Arg Tyr Leu Thr Arg Asn Leu  
725

<210> 196

<211> 727

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 196

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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

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

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

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser  
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp  
180 185 190

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

Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Gln  
210 215 220

Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu  
225 230 235 240

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser  
245 250 255

Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp  
260 265 270

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

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu  
290 295 300

Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn  
305 310 315 320

Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe  
325 330 335

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

Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr  
355 360 365

Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser  
370 375 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn  
385 390 395 400

Asn Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser  
405 410 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp  
420 425 430

Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn  
435 440 445

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val  
450 455 460

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val  
465 470 475 480

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly  
485 490 495

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly  
500 505 510

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu  
515 520 525

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val  
530 535 540

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

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln  
565 570 575

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile  
580 585 590

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro  
595 600 605

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro  
610 615 620

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile  
625 630 635 640

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp  
645 650 655

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val  
660 665 670

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro  
675 680 685

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe  
690 695 700

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr  
705 710 715 720

Arg Tyr Leu Thr Arg Asn Leu  
725

<210> 197

<211> 727

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 197

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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

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

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

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser  
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp  
180 185 190

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

Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Gln  
210 215 220

Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu  
225 230 235 240

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser  
245 250 255

Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp  
260 265 270



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

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu  
290 295 300

Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn  
305 310 315 320

Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe  
325 330 335

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

Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr  
355 360 365

Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser  
370 375 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn  
385 390 395 400

Asn Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser  
405 410 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp  
420 425 430

Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Gly Tyr His Lys Ser Gly  
435 440 445

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

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val  
465 470 475 480

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly  
485 490 495

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly  
500 505 510

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu  
515 520 525

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val  
530 535 540

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

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln  
565 570 575

Asn Val Ser Tyr Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile  
580 585 590

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro  
595 600 605

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro  
610 615 620

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile  
625 630 635 640

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp  
645 650 655

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val  
660 665 670

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro  
675 680 685

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe  
690 695 700

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr  
705 710 715 720

Arg Tyr Leu Thr Arg Asn Leu  
725

<210> 198

<211> 727

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant AAV Capsid Protein

<400> 198

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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

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

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

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser  
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp  
180 185 190

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

Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Gln  
210 215 220

Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu  
225 230 235 240

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser  
245 250 255

Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp  
260 265 270

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

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu  
290 295 300

Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn  
305 310 315 320

Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe  
325 330 335

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

Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr  
355 360 365

Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser  
370 375 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn  
385 390 395 400

Asn Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser  
405 410 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp  
420 425 430

Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn  
435 440 445

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val  
450 455 460

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val  
465 470 475 480

Ser Thr Thr Val Thr Gln Asn Leu Asn Ser Met Leu Ile Trp Pro Gly  
485 490 495

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly  
500 505 510

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu  
515 520 525

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val  
530 535 540

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

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln  
565 570 575

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile  
580 585 590

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro  
595 600 605

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro  
610 615 620

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile  
625 630 635 640

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp  
645 650 655

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val  
660 665 670

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro  
675 680 685

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe  
690 695 700

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr  
705 710 715 720

Arg Tyr Leu Thr Arg Asn Leu  
725

<210> 199  
<211> 727  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 199

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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

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

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

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser  
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp  
180 185 190

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

Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Gln  
210 215 220

Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu  
225 230 235 240

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser  
245 250 255

Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp  
260 265 270

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

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu  
290 295 300

Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn  
305 310 315 320



Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe  
325 330 335

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

Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr  
355 360 365

Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser  
370 375 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn  
385 390 395 400

Asn Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser  
405 410 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp  
420 425 430

Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Gly Tyr His Lys Ser Gly  
435 440 445

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

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val  
465 470 475 480

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly  
485 490 495

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly  
500 505 510

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu  
515 520 525

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val  
530 535 540

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

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln  
565 570 575

Ala Asn Tyr Gly Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile  
580 585 590

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro  
595 600 605

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro  
610 615 620

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile  
625 630 635 640

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp  
645 650 655

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val  
660 665 670

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro  
675 680 685

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe  
690 695 700

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr  
705 710 715 720

Arg Tyr Leu Thr Arg Asn Leu  
725

<210> 200  
<211> 727  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant AAV Capsid Protein

<400> 200

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln 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  
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

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

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

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser  
165 170 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp  
180 185 190

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

Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Gln  
210 215 220

Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu  
225 230 235 240

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser  
245 250 255

Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp  
260 265 270

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

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu  
290 295 300

Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn  
305 310 315 320

Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe  
325 330 335

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

Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr  
355 360 365

Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser  
370 375 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn  
385 390 395 400

Asn Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser  
405 410 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp  
420 425 430

Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn  
435 440 445

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val  
450 455 460

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val  
465 470 475 480

Ser Thr Thr Val Thr Gln Asn Leu Asn Ser Met Leu Ile Trp Pro Gly  
485 490 495

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly  
500 505 510

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu  
515 520 525

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val  
530 535 540

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

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln  
565 570 575

Ala Asn Tyr Gly Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile  
580 585 590

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro  
595 600 605

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro  
610 615 620

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile  
625 630 635 640

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp  
645 650 655

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val  
660 665 670

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro  
675 680 685

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe  
690 695 700

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr  
705 710 715 720

Arg Tyr Leu Thr Arg Asn Leu  
725

<210> 201  
<211> 5393  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> rAAV vector

<400> 201  
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aggggttcct tgtagttaat gattaacccg ccatgctact tatctacgta gccatgctct 180  
aggaagatcg gaattctcag tccattagga gccagtagcc tggaagatgt ctttaccccc 240  
agcatcagtt caagtggagc agcacataac tcttgccctc tgccttccaa gattctgggtg 300  
ctgagactta tggagtgtct tggaggttgc cttctgcccc ccaaccctgc tcccagctgg 360  
ccctcccagg cctgggttgc tggcctctgc tttatcagga ttctcaagag ggacagctgg 420  
tttatgttgc atgactgttc cctgcatatc tgctctgggt ttaaataagct tatctgagca 480  
gctggaggac cacatgggct tatatggcgt ggggtacatg ttcctgtagc cttgtccctg 540  
gcacctgcca aaatagcagc caacaccccc cccccacc gccatcccc tgccccaccc 600  
gtcccctgtc gcacattcct ccctccgcag ggctgggtca ccaggcccca gcccacatgc 660  
ctgcttaaag ccctctccat cctctgcctc acccagttcc cgctgagact gagcagacgc 720  
ctccaggatc tgtcggcaga agctttattg cggtagttaa tcacagttaa attgctaacg 780  
cagtcagtgc ttctgacaca acagtctcga acttaagctg cagaagttgg tcgtgaggca 840  
ctgggcaggt aagtatcaag gttacaagac aggtttaagg agaccaatag aaactgggct 900  
tgtcgagaca gagaagactc ttgcgtttct gataggcacc tatttgtctt actgacatcc 960  
actttgcctt tctctccaca ggtgtccact ccagttcaa ttacagctct taaggctaga 1020  
gtacttaata cgactcacta taggctagcc tcgagatgga ttacaaggat gacgacgata 1080  
agcctggtgt gactgttctc aagatgccgg agccaggga gaaaccagtg tcagccttca 1140  
acaagaagcc aaggtcagcg gaggtgaccg ctggcagtgc tgccgtgttc gaggctgaga 1200  
cggagcggtc aggcgtgaag gtgcggtggc agcgggatgg cagcgacatc accgccaatg 1260

|                                                                    |      |
|--------------------------------------------------------------------|------|
| acaagtatgg tttggcagca gagggcaagc gacacacact gacagtgcgg gatgcgagcc  | 1320 |
| ctgatgacca gggttcctac gcggtcattg caggctcctc aaaggtaag tttgacctca   | 1380 |
| aggtcacaga gccagcccct ccagagaagg cagaatctga agttgctcca ggagcccca   | 1440 |
| aagaagtccc tgctccagcc actgagttgg aagaaagtgt ctcaagtcct gaagggtcag  | 1500 |
| tctcggtaac ccaggatggc tcagctgcag agcatcaggg agcccctgat gaccctattg  | 1560 |
| gcctctttct gatgcgacca caggatgggtg aggtgaccgt gggcggcagc attgtcttct | 1620 |
| cagcccgagt ggctggggcc agcctcctga aaccgcctgt ggtcaagtgg ttcaaggga   | 1680 |
| agtgggtgga cctgagcagc aaagtgggccc agcacctgca gctgcatgac agctatgaca | 1740 |
| gagccagcaa ggtctacttg tttgagttgc acatcacaga tgctcagacc acttctgctg  | 1800 |
| ggggctaccg ctgtgaggtg tctaccaagg acaaatttga cagctgtaac ttcaacctca  | 1860 |
| ctgtccatga ggccattggt tctggagacc tggacctcag atcagctttc cgacgcacga  | 1920 |
| gcctggcggg agcaggtcgg agaaccagtg acagccatga agatgctggg actctggact  | 1980 |
| ttagttccct gctgaagaag agagacagtt tccggaggga ctcaaagctg gaggcacctg  | 2040 |
| ctgaagaaga cgtgtgggag atcctgagac aggcaccgcc gtcagaatat gagcgcacg   | 2100 |
| ccttccagca cggagtcaca gaccttcgag gcatgctgaa gaggctcaag ggcatgaagc  | 2160 |
| aggatgaaaa gaagagcaca gcctttcaga agaagctgga gcctgcctac caggtaaaca  | 2220 |
| agggccacaa gattcggcctt actgtggaac tggctgatcc ggacgccgaa gtcaagtggc | 2280 |
| ttaagaatgg acaggagatc cagatgagtg gcagcaagta catcttcgag tccgtcgggtg | 2340 |
| ccaagcgac cctgaccatc agccagtgt cactggctga cgacgcagcc taccagtgtg    | 2400 |
| tggtgggggg cgagaagtgc agcacggagc tctttgtcaa agagcccccg gtgctgatca  | 2460 |
| ctcggtcctt ggaagaccag ctggtgatgg tgggtcagcg ggtggagttt gagtgtgagg  | 2520 |
| tctcagaaga aggggcccac gtcaaatggc tgaaggatgg ggttgagctg acacgtgagg  | 2580 |
| agaccttcaa ataccgggtt aagaaagatg ggcggaacac ccacttgatc atcaatgaag  | 2640 |
| caaccctgga ggatgcagga cactatgcag tacgcacaag tggaggccag tcaactggctg | 2700 |
| agctcattgt gcaagagaag aagttggagg tataccaaag catcgcggac ctggcagtgg  | 2760 |



|                                                                     |      |
|---------------------------------------------------------------------|------|
| gagccaagga ccaggctgtg ttttaagtgtg aggtttcaga tgagaatgta cgcggcgtgt  | 2820 |
| ggctgaagaa tgggaaggaa ctgggtgcctg acaaccgcat aaagggtgtcc catataggcc | 2880 |
| gggtccacaa actgaccatt gacgatgtca cacctgctga tgaggctgac tacagctttg   | 2940 |
| tccctgaagg gtttgcctgc aacctgtctg ccaagctcca cttcatggag gtcaagattg   | 3000 |
| actttgtgcc taggcaggaa cctcccaaga tccacttgga ttgtcccggc agcacaccag   | 3060 |
| acaccattgt ggttgttgct gggaacaagt tacgcctgga tgtccctatt tctggagacc   | 3120 |
| ctgctccac tgtggtctgg cagaagactg taacacaggg gaagaaggcc tcaactgggc    | 3180 |
| cacaccctga tgccccagaa gatgctgggtg ctgatgagga gtgggtgttt gataagaagc  | 3240 |
| tgttgtgtga gactgagggc cgggtccggg tggagaccac caaagaccgc agcgtcttta   | 3300 |
| cagtcgaagg ggcagagaag gaagatgaag gtgtctacac agtcacagta aagaaccccg   | 3360 |
| tgggcgagga ccagggtcaac ctcacagtca aggtcatcga tgtcccagat gctcctgcgg  | 3420 |
| cccctaagat cagcaacgtg ggcgaggact cctgcactgt gcagtgggaa ccgcctgcct   | 3480 |
| atgatggcgg gcagccggtc ctgggataca tcctggagcg caagaagaaa aagagctaca   | 3540 |
| ggtggatgag gctcaacttt gatctgctgc gggagctgag ccacgaggcg aggcgcatga   | 3600 |
| tcgagggtgt agcctatgag atgcgagtct acgcagtcaa tgccgtggga atgtccaggc   | 3660 |
| ccagcccctgc ctctcagccc ttcatgccta ttgggcccc tggcgaacca acccacttgg   | 3720 |
| ctgtggagga tgtgtcagac accactgtct cactcaagtg gcggccccca gagcgcgtgg   | 3780 |
| gggccgggtg cctggacgga tacagcgtgg agtactgcca ggagggatgc tccgagtgga   | 3840 |
| cacctgtctt gcaggggctg acagagcgca catcgatgct ggtgaaggac ctaccactg    | 3900 |
| gggcacggct gctgttccga gtacgggcac acaatgtggc aggtcctgga ggccctatcg   | 3960 |
| tcaccaagga gcctgtgaca gtgcaggaga tactgcaacg accacggctc caactgcca    | 4020 |
| gacacctgcg ccagaccatc cagaagaaaag ttggggagcc tgtgaacctc ctcatccctt  | 4080 |
| tccagggcaa accccggcct caggtgacct ggaccaaaga ggggcagccc ctggcaggtg   | 4140 |
| aggaggtgag catccggaac agccccacag acacgatctt gttcatccga gctgcccgcc   | 4200 |
| gcaccactc gggcacctac caggtgacag ttcgattga gaacatggag gacaaggcaa     | 4260 |

|                                                                     |      |
|---------------------------------------------------------------------|------|
| cgctgatcct gcagattgtg gacaagccaa gtcctcccca ggatatccgg atcgttgaga   | 4320 |
| cttgggggttt caatgtggct ctggagtggga agccacccca agatgatggc aatacagaga | 4380 |
| tctgggggtta tactgtacag aaagctgaca agaagaccat ggagtgggttc acggtttttg | 4440 |
| aacactaccg acgcactcac tgtgtgggtat cagagcttat cattggcaat ggctactact  | 4500 |
| tccgggtctt cagccataac atgggtgggtt ccagtgacaa agctgccgcc accaaggagc  | 4560 |
| cagtctttat tccaagacca ggcatcacat atgagccacc caaataacaag gccctggact  | 4620 |
| tctctgaggc cccaagcttc acccagccct tggcaaatcg ctccatcatt gcaggctata   | 4680 |
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| atggcctgga tctgggagaa gatgctcgct tccgcatggt ctgcaagcag ggagtattga   | 4800 |
| ccctggagat caggaaaccc tgcccctatg atgggtgggtgt ctatgtctgc agggccacca | 4860 |
| acttgaggg cgaggcacag tgtgagtgcc gcctggagggt gcgagttcct cagtgaccag   | 4920 |
| ggatccgtcg acgcggccgc ttccctttag tgagggttaa tgcttcgagc agacatgata   | 4980 |
| agatacattg atgagtttgg acaaaccaca actagaatgc agtgaaaaaa atgctttatt   | 5040 |
| tgtgaaatth gtgatgctat tgctttatth gtaaccatta taagctgcaa taaacaagtt   | 5100 |
| aacaacaaca attgcattca ttttatgtth caggttcagg gggagatgtg ggaggththt   | 5160 |
| taaagcaagt aaaacctcta caaatgtgggt aaattcccga ttaggatctt cctagagcat  | 5220 |
| ggctacgtag ataagtagca tggcgggtta atcattaact acaaggaacc cctagtgatg   | 5280 |
| gagttggcca ctccctctct gcgcgctcgc tcgctcactg aggccgggcg accaaaggtc   | 5340 |
| gcccgcgcc cgggctthtc ccgggcggcc tcagtgcgcg agcgagcgcg cag           | 5393 |