SEQUENCE LISTING

<110> Genepod Therapeutics AB

<120> Novel rAAV Vector Construct

<130> P2220PC00

<150> 61/259,502
<151> 2009-11-09

<160> 22

<170> PatentIn version 3.5

<210> 1
<211> 250
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(250)
<223> GTP cyclohydrolase 1

<400> 1

Met Glu Lys Gly Pro Val Arg Ala Pro Ala Glu Lys Pro Arg Gly Ala
1 5 10 15

Arg Cys Ser Asn Gly Phe Pro Glu Arg Asp Pro Pro Arg Pro Gly Pro
20 25 30

Ser Arg Pro Ala Glu Lys Pro Pro Arg Pro Glu Ala Lys Ser Ala Gln
35 40 45

Pro Ala Asp Gly Trp Lys Gly Glu Arg Pro Arg Ser Glu Glu Asp Asn
50 55 60

Glu Leu Asn Leu Pro Asn Leu Ala Ala Ala Tyr Ser Ser Ile Leu Ser
65 70 75 80

Ser Leu Gly Glu Asn Pro Gln Arg Gln Gly Leu Leu Lys Thr Pro Trp
85 90 95

Arg Ala Ala Ser Ala Met Gln Phe Phe Thr Lys Gly Tyr Gln Glu Thr
100 105 110

```
Ile Ser Asp Val Leu Asn Asp Ala Ile Phe Asp Glu Asp His Asp Glu
        115                 120                 125


Met Val Ile Val Lys Asp Ile Asp Met Phe Ser Met Cys Glu His His
    130                 135                 140


Leu Val Pro Phe Val Gly Lys Val His Ile Gly Tyr Leu Pro Asn Lys
145                 150                 155                 160


Gln Val Leu Gly Leu Ser Lys Leu Ala Arg Ile Val Glu Ile Tyr Ser
                165                 170                 175


Arg Arg Leu Gln Val Gln Glu Arg Leu Thr Lys Gln Ile Ala Val Ala
            180                 185                 190


Ile Thr Glu Ala Leu Arg Pro Ala Gly Val Gly Val Val Val Glu Ala
        195                 200                 205


Thr His Met Cys Met Val Met Arg Gly Val Gln Lys Met Asn Ser Lys
    210                 215                 220


Thr Val Thr Ser Thr Met Leu Gly Val Phe Arg Glu Asp Pro Lys Thr
225                 230                 235                 240


Arg Glu Glu Phe Leu Thr Leu Ile Arg Ser
                245                 250


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


<220>
<221>  MISC_FEATURE
<222>  (1)..(213)
<223>  GTP cyclohydrolase 1 Isoform GCH-2

<400>  2

Met Glu Lys Gly Pro Val Arg Ala Pro Ala Glu Lys Pro Arg Gly Ala
1               5                   10                  15
```

```
Arg Cys Ser Asn Gly Phe Pro Glu Arg Asp Pro Pro Arg Pro Gly Pro
            20                  25                  30

Ser Arg Pro Ala Glu Lys Pro Pro Arg Pro Glu Ala Lys Ser Ala Gln
        35                  40                  45

Pro Ala Asp Gly Trp Lys Gly Glu Arg Pro Arg Ser Glu Glu Asp Asn
    50                  55                  60

Glu Leu Asn Leu Pro Asn Leu Ala Ala Ala Tyr Ser Ser Ile Leu Ser
65                  70                  75                  80

Ser Leu Gly Glu Asn Pro Gln Arg Gln Gly Leu Leu Lys Thr Pro Trp
                85                  90                  95

Arg Ala Ala Ser Ala Met Gln Phe Phe Thr Lys Gly Tyr Gln Glu Thr
            100                 105                 110

Ile Ser Asp Val Leu Asn Asp Ala Ile Phe Asp Glu Asp His Asp Glu
        115                 120                 125

Met Val Ile Val Lys Asp Ile Asp Met Phe Ser Met Cys Glu His His
    130                 135                 140

Leu Val Pro Phe Val Gly Lys Val His Ile Gly Tyr Leu Pro Asn Lys
145                 150                 155                 160

Gln Val Leu Gly Leu Ser Lys Leu Ala Arg Ile Val Glu Ile Tyr Ser
                165                 170                 175

Arg Arg Leu Gln Val Gln Glu Arg Leu Thr Lys Gln Ile Ala Val Ala
            180                 185                 190

Ile Thr Glu Ala Leu Arg Pro Ala Gly Val Gly Val Val Val Glu Ala
        195                 200                 205

Thr Ser Ala Glu Pro
    210
```

<210> 3

<211> 209
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(209)
<223> GTP cyclohydrolase 1 Isoform GCH-3

<400> 3

Met Glu Lys Gly Pro Val Arg Ala Pro Ala Glu Lys Pro Arg Gly Ala
1 5 10 15

Arg Cys Ser Asn Gly Phe Pro Glu Arg Asp Pro Pro Arg Pro Gly Pro
20 25 30

Ser Arg Pro Ala Glu Lys Pro Pro Arg Pro Glu Ala Lys Ser Ala Gln
35 40 45

Pro Ala Asp Gly Trp Lys Gly Glu Arg Pro Arg Ser Glu Glu Asp Asn
50 55 60

Glu Leu Asn Leu Pro Asn Leu Ala Ala Ala Tyr Ser Ser Ile Leu Ser
65 70 75 80

Ser Leu Gly Glu Asn Pro Gln Arg Gln Gly Leu Leu Lys Thr Pro Trp
85 90 95

Arg Ala Ala Ser Ala Met Gln Phe Phe Thr Lys Gly Tyr Gln Glu Thr
100 105 110

Ile Ser Asp Val Leu Asn Asp Ala Ile Phe Asp Glu Asp His Asp Glu
115 120 125

Met Val Ile Val Lys Asp Ile Asp Met Phe Ser Met Cys Glu His His
130 135 140

Leu Val Pro Phe Val Gly Lys Val His Ile Gly Tyr Leu Pro Asn Lys
145 150 155 160

Gln Val Leu Gly Leu Ser Lys Leu Ala Arg Ile Val Glu Ile Tyr Ser
165 170 175

Arg Arg Leu Gln Val Gln Glu Arg Leu Thr Lys Gln Ile Ala Val Ala
            180   185   190

Ile Thr Glu Ala Leu Arg Pro Ala Gly Val Gly Val Val Val Glu Ala
        195   200   205

Thr

<210> 4
<211> 233
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(233)
<223> GTP cyclohydrolase 1 Isoform GCH-4

<400> 4

Met Glu Lys Gly Pro Val Arg Ala Pro Ala Glu Lys Pro Arg Gly Ala
1   5   10   15

Arg Cys Ser Asn Gly Phe Pro Glu Arg Asp Pro Pro Arg Pro Gly Pro
            20   25   30

Ser Arg Pro Ala Glu Lys Pro Pro Arg Pro Glu Ala Lys Ser Ala Gln
        35   40   45

Pro Ala Asp Gly Trp Lys Gly Glu Arg Pro Arg Ser Glu Glu Asp Asn
    50   55   60

Glu Leu Asn Leu Pro Asn Leu Ala Ala Ala Tyr Ser Ser Ile Leu Ser
65   70   75   80

Ser Leu Gly Glu Asn Pro Gln Arg Gln Gly Leu Leu Lys Thr Pro Trp
                85   90   95

Arg Ala Ala Ser Ala Met Gln Phe Phe Thr Lys Gly Tyr Gln Glu Thr
            100   105   110

```
Ile Ser Asp Val Leu Asn Asp Ala Ile Phe Asp Glu Asp His Asp Glu
        115                 120                 125


Met Val Ile Val Lys Asp Ile Asp Met Phe Ser Met Cys Glu His His
    130                 135                 140


Leu Val Pro Phe Val Gly Lys Val His Ile Gly Tyr Leu Pro Asn Lys
145                 150                 155                 160


Gln Val Leu Gly Leu Ser Lys Leu Ala Arg Ile Val Glu Ile Tyr Ser
                165                 170                 175


Arg Arg Leu Gln Val Gln Glu Arg Leu Thr Lys Gln Ile Ala Val Ala
            180                 185                 190


Ile Thr Glu Ala Leu Arg Pro Ala Gly Val Gly Val Val Val Glu Ala
        195                 200                 205


Thr Lys Ser Asn Lys Tyr Asn Lys Gly Leu Ser Pro Leu Leu Ser Ser
    210                 215                 220


Cys His Leu Phe Val Ala Ile Leu Lys
225                 230


<210>  5
<211>  241
<212>  PRT
<213>  Rattus norvegicus


<220>
<221>  MISC_FEATURE
<222>  (1)..(241)
<223>  GTP cyclohydrolase 1

<400>  5

Met Glu Lys Pro Arg Gly Val Arg Cys Thr Asn Gly Phe Pro Glu Arg
1               5                   10                  15


Glu Leu Pro Arg Pro Gly Ala Ser Arg Pro Ala Glu Lys Ser Arg Pro
            20                  25                  30
```

```
Pro Glu Ala Lys Gly Ala Gln Pro Ala Asp Ala Trp Lys Ala Gly Arg
        35                  40                  45

Pro Arg Ser Glu Glu Asp Asn Glu Leu Asn Leu Pro Asn Leu Ala Ala
    50                  55                  60

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

Gly Leu Leu Lys Thr Pro Trp Arg Ala Ala Thr Ala Met Gln Phe Phe
                85                  90                  95

Thr Lys Gly Tyr Gln Glu Thr Ile Ser Asp Val Leu Asn Asp Ala Ile
            100                 105                 110

Phe Asp Glu Asp His Asp Glu Met Val Ile Val Lys Asp Ile Asp Met
        115                 120                 125

Phe Ser Met Cys Glu His His Leu Val Pro Phe Val Gly Arg Val His
    130                 135                 140

Ile Gly Tyr Leu Pro Asn Lys Gln Val Leu Gly Leu Ser Lys Leu Ala
145                 150                 155                 160

Arg Ile Val Glu Ile Tyr Ser Arg Arg Leu Gln Val Gln Glu Arg Leu
                165                 170                 175

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

Val Gly Val Val Ile Glu Ala Thr His Met Cys Met Val Met Arg Gly
        195                 200                 205

Val Gln Lys Met Asn Ser Lys Thr Val Thr Ser Thr Met Leu Gly Val
    210                 215                 220

Phe Arg Glu Asp Pro Lys Thr Arg Glu Glu Phe Leu Thr Leu Ile Arg
225                 230                 235                 240

Ser
```

<210> 6
<211> 241
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(241)
<223> GTP cyclohydrolase 1

<400> 6

Met Glu Lys Pro Arg Gly Val Arg Cys Thr Asn Gly Phe Ser Glu Arg
1   5   10   15

Glu Leu Pro Arg Pro Gly Ala Ser Pro Pro Ala Glu Lys Ser Arg Pro
            20   25   30

Pro Glu Ala Lys Gly Ala Gln Pro Ala Asp Ala Trp Lys Ala Gly Arg
        35   40   45

His Arg Ser Glu Glu Glu Asn Gln Val Asn Leu Pro Lys Leu Ala Ala
    50   55   60

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

Gly Leu Leu Lys Thr Pro Trp Arg Ala Ala Thr Ala Met Gln Tyr Phe
                85   90   95

Thr Lys Gly Tyr Gln Glu Thr Ile Ser Asp Val Leu Asn Asp Ala Ile
            100   105   110

Phe Asp Glu Asp His Asp Glu Met Val Ile Val Lys Asp Ile Asp Met
        115   120   125

Phe Ser Met Cys Glu His His Leu Val Pro Phe Val Gly Arg Val His
    130   135   140

Ile Gly Tyr Leu Pro Asn Lys Gln Val Leu Gly Leu Ser Lys Leu Ala
145   150   155   160

```
Arg Ile Val Glu Ile Tyr Ser Arg Arg Leu Gln Val Gln Glu Arg Leu
                165                 170                 175

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

Val Gly Val Val Ile Glu Ala Thr His Met Cys Met Val Met Arg Gly
        195                 200                 205

Val Gln Lys Met Asn Ser Lys Thr Val Thr Ser Thr Met Leu Gly Val
    210                 215                 220

Phe Arg Glu Asp Pro Lys Thr Arg Glu Glu Phe Leu Thr Leu Ile Arg
225                 230                 235                 240

Ser
```

<210> 7
<211> 496
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(496)
<223> Tyrosine 3-hydroxylase

<400> 7

```
Met Pro Thr Pro Asp Ala Thr Thr Pro Gln Ala Lys Gly Phe Arg Arg
1               5                   10                  15

Ala Val Ser Glu Leu Asp Ala Lys Gln Ala Glu Ala Ile Met Ser Pro
            20                  25                  30

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

Arg Glu Ala Ala Val Ala Ala Ala Ala Ala Ala Val Pro Ser Glu Pro
    50                  55                  60
```

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

Val Leu Asn Leu Leu Phe Ser Pro Arg Ala Thr Lys Pro Ser Ala Leu
                85                  90                  95

Ser Arg Ala Val Lys Val Phe Glu Thr Phe Glu Ala Lys Ile His His
            100                 105                 110

Leu Glu Thr Arg Pro Ala Gln Arg Pro Arg Ala Gly Gly Pro His Leu
        115                 120                 125

Glu Tyr Phe Val Arg Leu Glu Val Arg Arg Gly Asp Leu Ala Ala Leu
    130                 135                 140

Leu Ser Gly Val Arg Gln Val Ser Glu Asp Val Arg Ser Pro Ala Gly
145                 150                 155                 160

Pro Lys Val Pro Trp Phe Pro Arg Lys Val Ser Glu Leu Asp Lys Cys
                165                 170                 175

His His Leu Val Thr Lys Phe Asp Pro Asp Leu Asp Leu Asp His Pro
            180                 185                 190

Gly Phe Ser Asp Gln Val Tyr Arg Gln Arg Arg Lys Leu Ile Ala Glu
        195                 200                 205

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

Thr Ala Glu Glu Ile Ala Thr Trp Lys Glu Val Tyr Thr Thr Leu Lys
225                 230                 235                 240

Gly Leu Tyr Ala Thr His Ala Cys Gly Glu His Leu Glu Ala Phe Ala
                245                 250                 255

Leu Leu Glu Arg Phe Ser Gly Tyr Arg Glu Asp Asn Ile Pro Gln Leu
            260                 265                 270

Glu Asp Val Ser Arg Phe Leu Lys Glu Arg Thr Gly Phe Gln Leu Arg
        275                 280                 285
```

```
Pro Val Ala Gly Leu Leu Ser Ala Arg Asp Phe Leu Ala Ser Leu Ala
    290                 295                 300

Phe Arg Val Phe Gln Cys Thr Gln Tyr Ile Arg His Ala Ser Ser Pro
305                 310                 315                 320

Met His Ser Pro Glu Pro Asp Cys Cys His Glu Leu Leu Gly His Val
                325                 330                 335

Pro Met Leu Ala Asp Arg Thr Phe Ala Gln Phe Ser Gln Asp Ile Gly
            340                 345                 350

Leu Ala Ser Leu Gly Ala Ser Asp Glu Glu Ile Glu Lys Leu Ser Thr
        355                 360                 365

Leu Tyr Trp Phe Thr Val Glu Phe Gly Leu Cys Lys Gln Asn Gly Glu
    370                 375                 380

Val Lys Ala Tyr Gly Ala Gly Leu Leu Ser Ser Tyr Gly Glu Leu Leu
385                 390                 395                 400

His Cys Leu Ser Glu Glu Pro Glu Ile Arg Ala Phe Asp Pro Glu Ala
                405                 410                 415

Ala Ala Val Gln Pro Tyr Gln Asp Gln Thr Tyr Gln Ser Val Tyr Phe
            420                 425                 430

Val Ser Glu Ser Phe Ser Asp Ala Lys Asp Lys Leu Arg Ser Tyr Ala
        435                 440                 445

Ser Arg Ile Gln Arg Pro Phe Ser Val Lys Phe Asp Pro Tyr Thr Leu
    450                 455                 460

Ala Ile Asp Val Leu Asp Ser Pro Gln Ala Val Arg Arg Ser Leu Glu
465                 470                 475                 480

Gly Val Gln Asp Glu Leu Asp Thr Leu Ala His Ala Leu Ser Ala Ile
                485                 490                 495
```

<210> 8
<211> 528
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(528)
<223> Tyrosine 3-monooxygenase

<400> 8

Met Pro Thr Pro Asp Ala Thr Thr Pro Gln Ala Lys Gly Phe Arg Arg
1   5   10   15

Ala Val Ser Glu Leu Asp Ala Lys Gln Ala Glu Ala Ile Met Val Arg
            20   25   30

Gly Gln Gly Ala Pro Gly Pro Ser Leu Thr Gly Ser Pro Trp Pro Gly
        35   40   45

Thr Ala Ala Pro Ala Ala Ser Tyr Thr Pro Thr Pro Arg Ser Pro Arg
    50   55   60

Phe Ile Gly Arg Arg Gln Ser Leu Ile Glu Asp Ala Arg Lys Glu Arg
65   70   75   80

Glu Ala Ala Val Ala Ala Ala Ala Ala Ala Val Pro Ser Glu Pro Gly
                85   90   95

Asp Pro Leu Glu Ala Val Ala Phe Glu Glu Lys Glu Gly Lys Ala Val
            100   105   110

Leu Asn Leu Leu Phe Ser Pro Arg Ala Thr Lys Pro Ser Ala Leu Ser
        115   120   125

Arg Ala Val Lys Val Phe Glu Thr Phe Glu Ala Lys Ile His His Leu
    130   135   140

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

Tyr Phe Val Arg Leu Glu Val Arg Arg Gly Asp Leu Ala Ala Leu Leu

```
                165                 170                 175

Ser Gly Val Arg Gln Val Ser Glu Asp Val Arg Ser Pro Ala Gly Pro
            180                 185                 190

Lys Val Pro Trp Phe Pro Arg Lys Val Ser Glu Leu Asp Lys Cys His
        195                 200                 205

His Leu Val Thr Lys Phe Asp Pro Asp Leu Asp Leu Asp His Pro Gly
    210                 215                 220

Phe Ser Asp Gln Val Tyr Arg Gln Arg Arg Lys Leu Ile Ala Glu Ile
225                 230                 235                 240

Ala Phe Gln Tyr Arg His Gly Asp Pro Ile Pro Arg Val Glu Tyr Thr
                245                 250                 255

Ala Glu Glu Ile Ala Thr Trp Lys Glu Val Tyr Thr Thr Leu Lys Gly
            260                 265                 270

Leu Tyr Ala Thr His Ala Cys Gly Glu His Leu Glu Ala Phe Ala Leu
        275                 280                 285

Leu Glu Arg Phe Ser Gly Tyr Arg Glu Asp Asn Ile Pro Gln Leu Glu
    290                 295                 300

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

Val Ala Gly Leu Leu Ser Ala Arg Asp Phe Leu Ala Ser Leu Ala Phe
                325                 330                 335

Arg Val Phe Gln Cys Thr Gln Tyr Ile Arg His Ala Ser Ser Pro Met
            340                 345                 350

His Ser Pro Glu Pro Asp Cys Cys His Glu Leu Leu Gly His Val Pro
        355                 360                 365

Met Leu Ala Asp Arg Thr Phe Ala Gln Phe Ser Gln Asp Ile Gly Leu
    370                 375                 380
```

```
Ala Ser Leu Gly Ala Ser Asp Glu Glu Ile Glu Lys Leu Ser Thr Leu
385                 390                 395                 400


Tyr Trp Phe Thr Val Glu Phe Gly Leu Cys Lys Gln Asn Gly Glu Val
                405                 410                 415


Lys Ala Tyr Gly Ala Gly Leu Leu Ser Ser Tyr Gly Glu Leu Leu His
            420                 425                 430


Cys Leu Ser Glu Glu Pro Glu Ile Arg Ala Phe Asp Pro Glu Ala Ala
        435                 440                 445


Ala Val Gln Pro Tyr Gln Asp Gln Thr Tyr Gln Ser Val Tyr Phe Val
    450                 455                 460


Ser Glu Ser Phe Ser Asp Ala Lys Asp Lys Leu Arg Ser Tyr Ala Ser
465                 470                 475                 480


Arg Ile Gln Arg Pro Phe Ser Val Lys Phe Asp Pro Tyr Thr Leu Ala
                485                 490                 495


Ile Asp Val Leu Asp Ser Pro Gln Ala Val Arg Arg Ser Leu Glu Gly
            500                 505                 510


Val Gln Asp Glu Leu Asp Thr Leu Ala His Ala Leu Ser Ala Ile Gly
        515                 520                 525


<210>  9
<211>  497
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<222>  (1)..(497)
<223>  Tyrosine hydroxylase

<400>  9

Met Pro Thr Pro Asp Ala Thr Thr Pro Gln Ala Lys Gly Phe Arg Arg
1               5                   10                  15
```

```
Ala Val Ser Glu Leu Asp Ala Lys Gln Ala Glu Ala Ile Met Ser Pro
            20                  25                  30

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

Arg Glu Ala Ala Val Ala Ala Ala Ala Ala Ala Val Pro Ser Glu Pro
    50                  55                  60

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

Met Leu Asn Leu Leu Phe Ser Pro Arg Ala Thr Lys Pro Ser Ala Leu
                85                  90                  95

Ser Arg Ala Val Lys Val Phe Glu Thr Phe Glu Ala Lys Ile His His
            100                 105                 110

Leu Glu Thr Arg Pro Ala Gln Arg Pro Arg Ala Gly Gly Pro His Leu
        115                 120                 125

Glu Tyr Phe Val Arg Leu Glu Val Arg Arg Gly Asp Leu Ala Ala Leu
    130                 135                 140

Leu Ser Gly Val Arg Gln Val Ser Glu Asp Val Arg Ser Pro Ala Gly
145                 150                 155                 160

Pro Lys Val Pro Trp Phe Pro Arg Lys Val Ser Glu Leu Asp Lys Cys
                165                 170                 175

His His Leu Val Thr Lys Phe Asp Pro Asp Leu Asp Leu Asp His Pro
            180                 185                 190

Gly Phe Ser Asp Gln Val Tyr Arg Gln Arg Arg Lys Leu Ile Ala Glu
        195                 200                 205

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

Thr Ala Glu Glu Ile Ala Thr Trp Lys Glu Val Tyr Thr Thr Leu Lys
225                 230                 235                 240
```

```
Gly Leu Tyr Ala Thr His Ala Cys Gly Glu His Leu Glu Ala Phe Ala
                245                 250                 255

Leu Leu Glu Arg Phe Ser Gly Tyr Arg Glu Asp Asn Ile Pro Gln Leu
            260                 265                 270

Glu Asp Val Ser Arg Phe Leu Lys Glu Arg Thr Gly Phe Gln Leu Arg
        275                 280                 285

Pro Val Ala Gly Leu Leu Ser Ala Arg Asp Phe Leu Ala Ser Leu Ala
    290                 295                 300

Phe Arg Val Phe Gln Cys Thr Gln Tyr Ile Arg His Ala Ser Ser Pro
305                 310                 315                 320

Met His Ser Pro Glu Pro Asp Cys Cys His Glu Leu Leu Gly His Val
                325                 330                 335

Pro Met Leu Ala Asp Arg Thr Phe Ala Gln Phe Ser Gln Asp Ile Gly
            340                 345                 350

Leu Ala Ser Leu Gly Ala Ser Asp Glu Glu Ile Glu Lys Leu Ser Thr
        355                 360                 365

Leu Tyr Trp Phe Thr Val Glu Phe Gly Leu Cys Lys Gln Asn Gly Glu
    370                 375                 380

Val Lys Ala Tyr Gly Ala Gly Leu Leu Ser Ser Tyr Gly Glu Leu Leu
385                 390                 395                 400

His Cys Leu Ser Glu Glu Pro Glu Ile Arg Ala Phe Asp Pro Glu Ala
                405                 410                 415

Ala Ala Val Gln Pro Tyr Gln Asp Gln Thr Tyr Gln Ser Val Tyr Phe
            420                 425                 430

Val Ser Glu Ser Phe Ser Asp Ala Lys Asp Lys Leu Arg Ser Tyr Ala
        435                 440                 445
```

Ser Arg Ile Gln Arg Pro Phe Ser Val Lys Phe Asp Pro Tyr Thr Leu
    450   455   460

Ala Ile Asp Val Leu Asp Ser Pro Gln Ala Val Arg Arg Ser Leu Glu
465   470   475   480

Gly Val Gln Asp Glu Leu Asp Thr Leu Ala His Ala Leu Ser Ala Ile
                485   490   495

Gly

<210> 10
<211> 501
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(501)
<223> Tyrosine hydroxylase

<400> 10

Met Pro Thr Pro Asp Ala Thr Thr Pro Gln Ala Lys Gly Phe Arg Arg
1   5   10   15

Ala Val Ser Glu Leu Asp Ala Lys Gln Ala Glu Ala Ile Met Val Arg
            20   25   30

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

Ala Arg Lys Glu Arg Glu Ala Ala Val Ala Ala Ala Ala Ala Ala Val
    50   55   60

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

Glu Gly Lys Ala Met Leu Asn Leu Leu Phe Ser Pro Arg Ala Thr Lys
                85   90   95

Pro Ser Ala Leu Ser Arg Ala Val Lys Val Phe Glu Thr Phe Glu Ala

```
            100                 105                 110

Lys Ile His His Leu Glu Thr Arg Pro Ala Gln Arg Pro Arg Ala Gly
        115                 120                 125

Gly Pro His Leu Glu Tyr Phe Val Arg Leu Glu Val Arg Arg Gly Asp
    130                 135                 140

Leu Ala Ala Leu Leu Ser Gly Val Arg Gln Val Ser Glu Asp Val Arg
145                 150                 155                 160

Ser Pro Ala Gly Pro Lys Val Pro Trp Phe Pro Arg Lys Val Ser Glu
                165                 170                 175

Leu Asp Lys Cys His His Leu Val Thr Lys Phe Asp Pro Asp Leu Asp
            180                 185                 190

Leu Asp His Pro Gly Phe Ser Asp Gln Val Tyr Arg Gln Arg Arg Lys
        195                 200                 205

Leu Ile Ala Glu Ile Ala Phe Gln Tyr Arg His Gly Asp Pro Ile Pro
    210                 215                 220

Arg Val Glu Tyr Thr Ala Glu Glu Ile Ala Thr Trp Lys Glu Val Tyr
225                 230                 235                 240

Thr Thr Leu Lys Gly Leu Tyr Ala Thr His Ala Cys Gly Glu His Leu
                245                 250                 255

Glu Ala Phe Ala Leu Leu Glu Arg Phe Ser Gly Tyr Arg Glu Asp Asn
            260                 265                 270

Ile Pro Gln Leu Glu Asp Val Ser Arg Phe Leu Lys Glu Arg Thr Gly
        275                 280                 285

Phe Gln Leu Arg Pro Val Ala Gly Leu Leu Ser Ala Arg Asp Phe Leu
    290                 295                 300

Ala Ser Leu Ala Phe Arg Val Phe Gln Cys Thr Gln Tyr Ile Arg His
305                 310                 315                 320
```

```
Ala Ser Ser Pro Met His Ser Pro Glu Pro Asp Cys Cys His Glu Leu
               325                 330                 335

Leu Gly His Val Pro Met Leu Ala Asp His Thr Phe Ala Gln Phe Ser
            340                 345                 350

Gln Asp Ile Gly Leu Ala Ser Leu Gly Ala Ser Asp Glu Glu Ile Glu
        355                 360                 365

Lys Leu Ser Thr Leu Tyr Trp Phe Thr Val Glu Phe Gly Leu Cys Lys
    370                 375                 380

Gln Asn Gly Glu Val Lys Ala Tyr Gly Ala Gly Leu Leu Ser Ser Tyr
385                 390                 395                 400

Gly Glu Leu Leu His Cys Leu Ser Glu Glu Pro Glu Ile Arg Ala Phe
               405                 410                 415

Asp Pro Glu Ala Ala Ala Val Gln Pro Tyr Gln Asp Gln Thr Tyr Gln
            420                 425                 430

Ser Val Tyr Phe Val Ser Glu Ser Phe Ser Asp Ala Lys Asp Lys Leu
        435                 440                 445

Arg Ser Tyr Ala Ser Arg Ile Gln Arg Pro Phe Ser Val Lys Phe Asp
    450                 455                 460

Pro Tyr Thr Leu Ala Ile Asp Val Leu Asp Ser Pro Gln Ala Val Arg
465                 470                 475                 480

Arg Ser Leu Glu Gly Val Gln Asp Glu Leu Asp Thr Leu Ala His Ala
               485                 490                 495

Leu Ser Ala Ile Gly
            500
```

<210> 11
<211> 528
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(528)
<223> Tyrosine 3-monooxygenase

<400> 11

Met Pro Thr Pro Asp Ala Thr Thr Pro Gln Ala Lys Gly Phe Arg Arg
1   5   10   15

Ala Val Ser Glu Leu Asp Ala Lys Gln Ala Glu Ala Ile Met Val Arg
            20   25   30

Gly Gln Gly Ala Pro Gly Pro Ser Leu Thr Gly Ser Pro Trp Pro Gly
        35   40   45

Thr Ala Ala Pro Ala Ala Ser Tyr Thr Pro Thr Pro Arg Ser Pro Arg
    50   55   60

Phe Ile Gly Arg Arg Gln Ser Leu Ile Glu Asp Ala Arg Lys Glu Arg
65   70   75   80

Glu Ala Ala Val Ala Ala Ala Ala Ala Ala Val Pro Ser Glu Pro Gly
                85   90   95

Asp Pro Leu Glu Ala Val Ala Phe Glu Glu Lys Glu Gly Lys Ala Val
            100   105   110

Leu Asn Leu Leu Phe Ser Pro Arg Ala Thr Lys Pro Ser Ala Leu Ser
        115   120   125

Arg Ala Val Lys Val Phe Glu Thr Phe Glu Ala Lys Ile His His Leu
    130   135   140

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

Tyr Phe Val Arg Leu Glu Val Arg Arg Gly Asp Leu Ala Ala Leu Leu
                165   170   175

Ser Gly Val Arg Gln Val Ser Glu Asp Val Arg Ser Pro Ala Gly Pro
            180   185   190

```
Lys Val Pro Trp Phe Pro Arg Lys Val Ser Glu Leu Asp Lys Cys His
        195                 200                 205

His Leu Val Thr Lys Phe Asp Pro Asp Leu Asp Leu Asp His Pro Gly
    210                 215                 220

Phe Ser Asp Gln Val Tyr Arg Gln Arg Arg Lys Leu Ile Ala Glu Ile
225                 230                 235                 240

Ala Phe Gln Tyr Arg His Gly Asp Pro Ile Pro Arg Val Glu Tyr Thr
                245                 250                 255

Ala Glu Glu Ile Ala Thr Trp Lys Glu Val Tyr Thr Thr Leu Lys Gly
            260                 265                 270

Leu Tyr Ala Thr His Ala Cys Gly Glu His Leu Glu Ala Phe Ala Leu
        275                 280                 285

Leu Glu Arg Phe Ser Gly Tyr Arg Glu Asp Asn Ile Pro Gln Leu Glu
    290                 295                 300

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

Val Ala Gly Leu Leu Ser Ala Arg Asp Phe Leu Ala Ser Leu Ala Phe
                325                 330                 335

Arg Val Phe Gln Cys Thr Gln Tyr Ile Arg His Ala Ser Ser Pro Met
            340                 345                 350

His Ser Pro Glu Pro Asp Cys Cys His Glu Leu Leu Gly His Val Pro
        355                 360                 365

Met Leu Ala Asp Arg Thr Phe Ala Gln Phe Ser Gln Asp Ile Gly Leu
    370                 375                 380

Ala Ser Leu Gly Ala Ser Asp Glu Glu Ile Glu Lys Leu Ser Thr Leu
385                 390                 395                 400
```

```
Tyr Trp Phe Thr Val Glu Phe Gly Leu Cys Lys Gln Asn Gly Glu Val
                405                 410                 415


Lys Ala Tyr Gly Ala Gly Leu Leu Ser Ser Tyr Gly Glu Leu Leu His
            420                 425                 430


Cys Leu Ser Glu Glu Pro Glu Ile Arg Ala Phe Asp Pro Glu Ala Ala
        435                 440                 445


Ala Val Gln Pro Tyr Gln Asp Gln Thr Tyr Gln Ser Val Tyr Phe Val
    450                 455                 460


Ser Glu Ser Phe Ser Asp Ala Lys Asp Lys Leu Arg Ser Tyr Ala Ser
465                 470                 475                 480


Arg Ile Gln Arg Pro Phe Ser Val Lys Phe Asp Pro Tyr Thr Leu Ala
                485                 490                 495


Ile Asp Val Leu Asp Ser Pro Gln Ala Val Arg Arg Ser Leu Glu Gly
            500                 505                 510


Val Gln Asp Glu Leu Asp Thr Leu Ala His Ala Leu Ser Ala Ile Gly
        515                 520                 525


<210>  12
<211>  528
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<222>  (1)..(528)
<223>  Tyrosine 3-monooxygenase

<400>  12

Met Pro Thr Pro Asp Ala Thr Thr Pro Gln Ala Lys Gly Phe Arg Arg
1               5                   10                  15


Ala Val Ser Glu Leu Asp Ala Lys Gln Ala Glu Ala Ile Met Val Arg
            20                  25                  30


Gly Gln Gly Ala Pro Gly Pro Ser Leu Thr Gly Ser Pro Trp Pro Gly
```

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        35                  40                  45

Thr Ala Ala Pro Ala Ala Ser Tyr Thr Pro Thr Pro Arg Ser Pro Arg
    50                  55                  60

Phe Ile Gly Arg Arg Gln Ser Leu Ile Glu Asp Ala Arg Lys Glu Arg
65                  70                  75                  80

Glu Ala Ala Val Ala Ala Ala Ala Ala Ala Val Pro Ser Glu Pro Gly
                85                  90                  95

Asp Pro Leu Glu Ala Val Ala Phe Glu Glu Lys Glu Gly Lys Ala Val
            100                 105                 110

Leu Asn Leu Leu Phe Ser Pro Arg Ala Thr Lys Pro Ser Ala Leu Ser
        115                 120                 125

Arg Ala Val Lys Val Phe Glu Thr Phe Glu Ala Lys Ile His His Leu
    130                 135                 140

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

Tyr Phe Val Arg Leu Glu Val Arg Arg Gly Asp Leu Ala Ala Leu Leu
                165                 170                 175

Ser Gly Val Arg Gln Val Ser Glu Asp Val Arg Ser Pro Ala Gly Pro
            180                 185                 190

Lys Val Pro Trp Phe Pro Arg Lys Val Ser Glu Leu Asp Lys Cys His
        195                 200                 205

His Leu Val Thr Lys Phe Asp Pro Asp Leu Asp Leu Asp His Pro Gly
    210                 215                 220

Phe Ser Asp Gln Val Tyr Arg Gln Arg Arg Lys Leu Ile Ala Glu Ile
225                 230                 235                 240

Ala Phe Gln Tyr Arg His Gly Asp Pro Ile Pro Arg Val Glu Tyr Thr
                245                 250                 255
```

```
Ala Glu Glu Ile Ala Thr Trp Lys Glu Val Tyr Thr Thr Leu Lys Gly
            260                 265                 270

Leu Tyr Ala Thr His Ala Cys Gly Glu His Leu Glu Ala Phe Ala Leu
        275                 280                 285

Leu Glu Arg Phe Ser Gly Tyr Arg Glu Asp Asn Ile Pro Gln Leu Glu
    290                 295                 300

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

Val Ala Gly Leu Leu Ser Ala Arg Asp Phe Leu Ala Ser Leu Ala Phe
                325                 330                 335

Arg Val Phe Gln Cys Thr Gln Tyr Ile Arg His Ala Ser Ser Pro Met
            340                 345                 350

His Ser Pro Glu Pro Asp Cys Cys His Glu Leu Leu Gly His Val Pro
        355                 360                 365

Met Leu Ala Asp Arg Thr Phe Ala Gln Phe Ser Gln Asp Ile Gly Leu
    370                 375                 380

Ala Ser Leu Gly Ala Ser Asp Glu Glu Ile Glu Lys Leu Ser Thr Leu
385                 390                 395                 400

Tyr Trp Phe Thr Val Glu Phe Gly Leu Cys Lys Gln Asn Gly Glu Val
                405                 410                 415

Lys Ala Tyr Gly Ala Gly Leu Leu Ser Ser Tyr Gly Glu Leu Leu His
            420                 425                 430

Cys Leu Ser Glu Glu Pro Glu Ile Arg Ala Phe Asp Pro Glu Ala Ala
        435                 440                 445

Ala Val Gln Pro Tyr Gln Asp Gln Thr Tyr Gln Ser Val Tyr Phe Val
    450                 455                 460

Ser Glu Ser Phe Ser Asp Ala Lys Asp Lys Leu Arg Ser Tyr Ala Ser
```

```
465                 470                 475                 480

Arg Ile Gln Arg Pro Phe Ser Val Lys Phe Asp Pro Tyr Thr Leu Ala
                485                 490                 495

Ile Asp Val Leu Asp Ser Pro Gln Ala Val Arg Arg Ser Leu Glu Gly
            500                 505                 510

Val Gln Asp Glu Leu Asp Thr Leu Ala His Ala Leu Ser Ala Ile Gly
        515                 520                 525


<210>  13
<211>  498
<212>  PRT
<213>  Rattus norvegicus


<220>
<221>  MISC_FEATURE
<222>  (1)..(498)
<223>  Tyrosine 3-hydroxylase

<400>  13

Met Pro Thr Pro Ser Ala Pro Ser Pro Gln Pro Lys Gly Phe Arg Arg
1               5                   10                  15

Ala Val Ser Glu Gln Asp Ala Lys Gln Ala Glu Ala Val Thr Ser Pro
            20                  25                  30

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

Arg Glu Ala Ala Ala Ala Ala Ala Ala Ala Ala Val Ala Ser Ser Glu
    50                  55                  60

Pro Gly Asn Pro Leu Glu Ala Val Val Phe Glu Glu Arg Asp Gly Asn
65                  70                  75                  80

Ala Val Leu Asn Leu Leu Phe Ser Leu Arg Gly Thr Lys Pro Ser Ser
                85                  90                  95

Leu Ser Arg Ala Val Lys Val Phe Glu Thr Phe Glu Ala Lys Ile His
            100                 105                 110
```

```
His Leu Glu Thr Arg Pro Ala Gln Arg Pro Leu Ala Gly Ser Pro His
        115                 120                 125

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

Leu Leu Ser Ser Val Arg Arg Val Ser Asp Asp Val Arg Ser Ala Arg
145                 150                 155                 160

Glu Asp Lys Val Pro Trp Phe Pro Arg Lys Val Ser Glu Leu Asp Lys
                165                 170                 175

Cys His His Leu Val Thr Lys Phe Asp Pro Asp Leu Asp Leu Asp His
            180                 185                 190

Pro Gly Phe Ser Asp Gln Val Tyr Arg Gln Arg Arg Lys Leu Ile Ala
        195                 200                 205

Glu Ile Ala Phe Gln Tyr Lys His Gly Glu Pro Ile Pro His Val Glu
    210                 215                 220

Tyr Thr Ala Glu Glu Ile Ala Thr Trp Lys Glu Val Tyr Val Thr Leu
225                 230                 235                 240

Lys Gly Leu Tyr Ala Thr His Ala Cys Arg Glu His Leu Glu Gly Phe
                245                 250                 255

Gln Leu Leu Glu Arg Tyr Cys Gly Tyr Arg Glu Asp Ser Ile Pro Gln
            260                 265                 270

Leu Glu Asp Val Ser Arg Phe Leu Lys Glu Arg Thr Gly Phe Gln Leu
        275                 280                 285

Arg Pro Val Ala Gly Leu Leu Ser Ala Arg Asp Phe Leu Ala Ser Leu
    290                 295                 300

Ala Phe Arg Val Phe Gln Cys Thr Gln Tyr Ile Arg His Ala Ser Ser
305                 310                 315                 320
```

```
Pro Met His Ser Pro Glu Pro Asp Cys Cys His Glu Leu Leu Gly His
                325                 330                 335

Val Pro Met Leu Ala Asp Arg Thr Phe Ala Gln Phe Ser Gln Asp Ile
            340                 345                 350

Gly Leu Ala Ser Leu Gly Ala Ser Asp Glu Glu Ile Glu Lys Leu Ser
        355                 360                 365

Thr Val Tyr Trp Phe Thr Val Glu Phe Gly Leu Cys Lys Gln Asn Gly
    370                 375                 380

Glu Leu Lys Ala Tyr Gly Ala Gly Leu Leu Ser Ser Tyr Gly Glu Leu
385                 390                 395                 400

Leu His Ser Leu Ser Glu Glu Pro Glu Val Arg Ala Phe Asp Pro Asp
                405                 410                 415

Thr Ala Ala Val Gln Pro Tyr Gln Asp Gln Thr Tyr Gln Pro Val Tyr
            420                 425                 430

Phe Val Ser Glu Ser Phe Asn Asp Ala Lys Asp Lys Leu Arg Asn Tyr
        435                 440                 445

Ala Ser Arg Ile Gln Arg Pro Phe Ser Val Lys Phe Asp Pro Tyr Thr
    450                 455                 460

Leu Ala Ile Asp Val Leu Asp Ser Pro His Thr Ile Gln Arg Ser Leu
465                 470                 475                 480

Glu Gly Val Gln Asp Glu Leu His Thr Leu Ala His Ala Leu Ser Ala
                485                 490                 495

Ile Ser
```

<210> 14
<211> 498
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(498)
<223> Tyrosine 3-hydroxylase

<400> 14

Met Pro Thr Pro Ser Ala Ser Ser Pro Gln Pro Lys Gly Phe Arg Arg
1 5 10 15

Ala Val Ser Glu Gln Asp Thr Lys Gln Ala Glu Ala Val Thr Ser Pro
20 25 30

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

Arg Glu Ala Ala Ala Ala Ala Ala Ala Ala Ala Val Ala Ser Ala Glu
50 55 60

Pro Gly Asn Pro Leu Glu Ala Val Val Phe Glu Glu Arg Asp Gly Asn
65 70 75 80

Ala Val Leu Asn Leu Leu Phe Ser Leu Arg Gly Thr Lys Pro Ser Ser
85 90 95

Leu Ser Arg Ala Leu Lys Val Phe Glu Thr Phe Glu Ala Lys Ile His
100 105 110

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

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

Leu Leu Ser Ser Val Arg Arg Val Ser Asp Asp Val Arg Ser Ala Arg
145 150 155 160

Glu Asp Lys Val Pro Trp Phe Pro Arg Lys Val Ser Glu Leu Asp Lys
165 170 175

Cys His His Leu Val Thr Lys Phe Asp Pro Asp Leu Asp Leu Asp His
180 185 190

```
Pro Gly Phe Ser Asp Gln Ala Tyr Arg Gln Arg Arg Lys Leu Ile Ala
        195                 200                 205

Glu Ile Ala Phe Gln Tyr Lys Gln Gly Glu Pro Ile Pro His Val Glu
    210                 215                 220

Tyr Thr Lys Glu Glu Ile Ala Thr Trp Lys Glu Val Tyr Ala Thr Leu
225                 230                 235                 240

Lys Gly Leu Tyr Ala Thr His Ala Cys Arg Glu His Leu Glu Ala Phe
                245                 250                 255

Gln Leu Leu Glu Arg Tyr Cys Gly Tyr Arg Glu Asp Ser Ile Pro Gln
            260                 265                 270

Leu Glu Asp Val Ser His Phe Leu Lys Glu Arg Thr Gly Phe Gln Leu
        275                 280                 285

Arg Pro Val Ala Gly Leu Leu Ser Ala Arg Asp Phe Leu Ala Ser Leu
    290                 295                 300

Ala Phe Arg Val Phe Gln Cys Thr Gln Tyr Ile Arg His Ala Ser Ser
305                 310                 315                 320

Pro Met His Ser Pro Glu Pro Asp Cys Cys His Glu Leu Leu Gly His
                325                 330                 335

Val Pro Met Leu Ala Asp Arg Thr Phe Ala Gln Phe Ser Gln Asp Ile
            340                 345                 350

Gly Leu Ala Ser Leu Gly Ala Ser Asp Glu Glu Ile Glu Lys Leu Ser
        355                 360                 365

Thr Val Tyr Trp Phe Thr Val Glu Phe Gly Leu Cys Lys Gln Asn Gly
    370                 375                 380

Glu Leu Lys Ala Tyr Gly Ala Gly Leu Leu Ser Ser Tyr Gly Glu Leu
385                 390                 395                 400

Leu His Ser Leu Ser Glu Glu Pro Glu Val Arg Ala Phe Asp Pro Asp
```

405 410 415

Thr Ala Ala Val Gln Pro Tyr Gln Asp Gln Thr Tyr Gln Pro Val Tyr
420 425 430

Phe Val Ser Glu Ser Phe Ser Asp Ala Lys Asp Lys Leu Arg Asn Tyr
435 440 445

Ala Ser Arg Ile Gln Arg Pro Phe Ser Val Lys Phe Asp Pro Tyr Thr
450 455 460

Leu Ala Ile Asp Val Leu Asp Ser Pro His Thr Ile Arg Arg Ser Leu
465 470 475 480

Glu Gly Val Gln Asp Glu Leu His Thr Leu Thr Gln Ala Leu Ser Ala
485 490 495

Ile Ser

<210> 15
<211> 145
<212> DNA
<213> adeno-associated virus 2

<220>
<221> misc_feature
<222> (1)..(145)
<223> left terminal sequence

<400> 15
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc
60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg
120

gccaactcca tcactagggg ttcct
145

<210> 16
<211> 145
<212> DNA
<213> adeno-associated virus 2

<220>
<221> misc_feature
<222> (1)..(145)
<223> right terminal sequence

<400> 16
aggaacccct agtgatggag ttggccactc cctctctgcg cgctcgctcg ctcactgagg
60

ccgcccgggc aaagcccggg cgtcgggcga cctttggtcg cccggcctca gtgagcgagc
120

gagcgcgcag agagggagtg gccaa
145

<210> 17
<211> 484
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(484)
<223> Synapsin 1 (SYN1) promoter sequence

<400> 17
ctagactcta gctgcagagg gacctgcgta tgagtgcaag tgggttttag gaccaggatg
60

aggcggggtg ggggtgccta cctgacgacc gaccccgacc cactggacaa gcacccaacc
120

cccattcccc aaattgcgca tcccctatca gagaggggga ggggaaacag gatgcggcga
180

ggcgcgtgcg cactgccagc ttcagcaccg cggacagtgc cttcgccccc gcctggcggc
240

gcgcgccacc gccgcctcag cactgaaggc gcgctgacgt cactcgccgg tcccccgcaa
300

actccccttc ccggccacct tggtcgcgtc cgcgccgccg ccggcccagc cggaccgcac
360

cacgcgaggc gcgagatagg ggggcacggg cgcgaccatc tgcgctgcgg cgccggcgac
420

tcagcgctgc ctcagtctgc ggtgggcagc ggaggagtcg tgtcgtgcct gagagcgcag
480

tcga

484

<210> 18
<211> 748
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(748)
<223> GTP cyclohydrolase 1 (GCH1), transcript variant 1

<400> 18
atggagaagg gccctgtgcg ggcaccggcg gagaagccgc ggggcgccag gtgcagcaat
60

gggttccccg agcgggatcc gccgcggccc gggcccagca ggccggcgga gaagcccccg
120

cggcccgagg ccaagagcgc gcagcccgcg gacggctgga agggcgagcg gccccgcagc
180

gaggaggata acgagctgaa cctccctaac ctggcagccg cctactcgtc catcctgagc
240

tcgctgggcg agaaccccca gcggcaaggg ctgctcaaga cgccctggag ggcggcctcg
300

gccatgcagt tcttcaccaa gggctaccag gagaccatct cagatgtcct aaacgatgct
360

atatttgatg aagatcatga tgagatggtg attgtgaagg acatagacat gttttccatg
420

tgtgagcatc acttggttcc atttgttgga aaggtccata ttggttatct tcctaacaag
480

caagtccttg gcctcagcaa acttgcgagg attgtagaaa tctatagtag aagactacaa
540

gttcaggagc gccttacaaa acaaattgct gtagcaatca cggaagcctt gcggcctgct
600

ggagtcgggg tagtggttga agcaacacac atgtgtatgg taatgcgagg tgtacagaaa
660

atgaacagca aaactgtgac cagcacaatg ttgggtgtgt tccgggagga tccaaagact
720

cgggaagagt tcctgactct cattagga
748

<210> 19
<211> 155
<212> DNA
<213> Simian virus 40

<220>
<221> misc_feature
<222> (1)..(155)
<223> early poly-adenylation sequence

<400> 19
ttcgagcaac ttgtttattg cagcttataa tggttacaaa taaagcaata gcatcacaaa
60

tttcacaaat aaagcatttt tttcactgca ttctagttgt ggtttgtcca aactcatcaa
120

tgtatcttat catgtctgga tcgtctagca tcgaa
155

<210> 20
<211> 192
<212> DNA
<213> Simian virus 40

<220>
<221> misc_feature
<222> (1)..(192)
<223> late poly-adenylation sequence

<400> 20
cagacatgat aagatacatt gatgagtttg gacaaaccac aactagaatg cagtgaaaaa
60

aatgctttat ttgtgaaatt tgtgatgcta ttgctttatt tgtaaccatt ataagctgca
120

ataaacaagt taacaacaac aattgcattc attttatgtt tcaggttcag ggggaggtgt
180

gggaggtttt tt
192

<210> 21
<211> 1490
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1490)
<223> Tyrosine hydroxylase (TH), transcript variant 2

<400> 21
atgcccaccc ccgacgccac cacgccacag gccaagggct tccgcagggc cgtgtctgag
60

ctggacgcca agcaggcaga ggccatcatg tccccgcggt tcattgggcg caggcagagc
120

ctcatcgagg acgcccgcaa ggagcgggag gcggcggtgg cagcagcggc cgctgcagtc
180

ccctcggagc ccggggaccc cctggaggct gtggcctttg aggagaagga ggggaaggcc
240

gtgctaaacc tgctcttctc cccgagggcc accaagccct cggcgctgtc ccgagctgtg
300

aaggtgtttg agacgtttga agccaaaatc caccatctag agacccggcc cgcccagagg
360

ccgcgagctg ggggccccca cctggagtac ttcgtgcgcc tcgaggtgcg ccgaggggac
420

ctggccgccc tgctcagtgg tgtgcgccag gtgtcagagg acgtgcgcag ccccgcgggg
480

cccaaggtcc cctggttccc aagaaaagtg tcagagctgg acaagtgtca tcacctggtc
540

accaagttcg accctgacct ggacttggac cacccgggct tctcggacca ggtgtaccgc
600

cagcgcagga agctgattgc tgagatcgcc ttccagtaca ggcacggcga cccgattccc
660

cgtgtggagt acaccgccga ggagattgcc acctggaagg aggtctacac cacgctgaag
720

ggcctctacg ccacgcacgc ctgcggggag cacctggagg cctttgcttt gctggagcgc
780

ttcagcggct accgggaaga caatatcccc cagctggagg acgtctcccg cttcctgaag
840

gagcgcacgg gcttccagct gcggcctgtg gccggcctgc tgtccgcccg ggacttcctg
900

gccagcctgg ccttccgcgt gttccagtgc acccagtata tccgccacgc gtcctcgccc
960

atgcactccc ctgagccgga ctgctgccac gagctgctgg ggcacgtgcc catgctggcc
1020

gaccgcacct tcgcgcagtt ctcgcaggac attggcctgg cgtccctggg ggcctcggat
1080

gaggaaattg agaagctgtc cacgctgtac tggttcacgg tggagttcgg gctgtgtaag
1140

cagaacgggg aggtgaaggc ctatggtgcc gggctgctgt cctcctacgg ggagctcctg
1200

cactgcctgt ctgaggagcc tgagattcgg gccttcgacc ctgaggctgc ggccgtgcag
1260

ccctaccaag accagacgta ccagtcagtc tacttcgtgt ctgagagctt cagtgacgcc
1320

aaggacaagc tcaggagcta tgcctcacgc atccagcgcc ccttctccgt gaagttcgac
1380

ccgtacacgc tggccatcga cgtgctggac agcccccagg ccgtgcggcg ctccctggag
1440

ggtgtccagg atgagctgga cacccttgcc catgcgctga gtgccattgg
1490

<210> 22
<211> 610
<212> DNA
<213> Woodchuck hepatitis B virus

<220>
<221> misc_feature
<222> (1)..(610)
<223> Woodchuck hepatitis B virus (WHV8) post-transcriptional
       regulatory element sequence

<400> 22
cgtcgacaat caacctctgg attacaaaat ttgtgaaaga ttgactggta ttcttaacta
60

tgttgctcct tttacgctat gtggatacgc tgctttaatg cctttgtatc atgctattgc
120

ttcccgtatg gctttcattt tctcctcctt gtataaatcc tggttgctgt ctctttatga
180

ggagttgtgg cccgttgtca ggcaacgtgg cgtggtgtgc actgtgtttg ctgacgcaac
240

ccccactggt tggggcattg ccaccacctg tcagctcctt tccgggactt tcgctttccc

300

cctccctatt gccacggcgg aactcatcgc cgcctgcctt gcccgctgct ggacaggggc
360

tcggctgttg ggcactgaca attccgtggt gttgtcgggg aagctgacgt cctttccatg
420

gctgctcgcc tgtgttgcca cctggattct gcgcgggacg tccttctgct acgtcccttc
480

ggccctcaat ccagcggacc ttccttcccg cggcctgctg ccggctctgc ggcctcttcc
540

gcgtcttcgc cttcgccctc agacgagtcg gatctccctt tgggccgcct ccccgcctgg
600

aattcgagct
610