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<110> SANOFI-AVENTIS

<120> NOVEL ANTI-CD38 ANTIBODIES FOR THE TREATMENT OF CANCER

<130> FR2006-043

<160> 80

<170> PatentIn version 3.3

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Asp Tyr Trp Met Gln
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Gly Asp Tyr Tyr Gly Ser Asn Ser Leu Asp Tyr
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Lys Ala Ser Gln Asp Val Ser Thr Val Val Ala
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Ser Ala Ser Tyr Arg Tyr Ile
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Gln Gln His Tyr Ser Pro Pro Tyr Thr
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Gly Ser Trp Met Asn
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Asp

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Trp Gly Thr Phe Thr Pro Ser Phe Asp Tyr
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Lys Ala Ser Gln Asp Val Val Thr Ala Val Ala
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Ser Ala Ser His Arg Tyr Thr
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Lys Ala Ser Gln Val Val Gly Ser Ala Val Ala
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Trp Ala Ser Thr Arg His Thr
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Gln Gln Tyr Asn Ser Tyr Pro Tyr Thr
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Asn Phe Gly Met His
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Tyr Ile Arg Ser Gly Ser Gly Thr Ile Tyr Tyr Ser Asp Thr Val Lys
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Gly

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Ser Tyr Tyr Asp Phe Gly Ala Trp Phe Ala Tyr
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Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala
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Gln Gln Tyr Asn Ser Tyr Pro Leu Thr
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1               5                   10                  15

cag agg gcc acc ata tcc tgc aga gcc agt gaa agt gtt gag att tat       96
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Ile Tyr
            20                  25                  30

ggc aat ggt ttt atg aac tgg ttc cag cag aaa cca gga cag cca ccc      144
Gly Asn Gly Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

aaa ctc ctc atc tat cgt gca tcc aac cta gaa tct ggg atc cct gcc      192
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Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
    50                  55                  60

agg ttc agt ggc agt ggg tct agg aca gag ttc acc ctc acc att gat      240
Arg Phe Ser Gly Ser Gly Ser Arg Thr Glu Phe Thr Leu Thr Ile Asp
65                  70                  75                  80

cct gtg gag gct gat gat gtt gca acc tat tac tgt caa caa att aat      288
Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ile Asn
                85                  90                  95

gag gat cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aaa cgg      336
Glu Asp Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105                 110


<210>  38
<211>  112
<212>  PRT
<213>  Mus sp.

<400>  38

Asn Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
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Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Ile Tyr
            20                  25                  30


Gly Asn Gly Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


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


Arg Phe Ser Gly Ser Gly Ser Arg Thr Glu Phe Thr Leu Thr Ile Asp
65                  70                  75                  80


Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ile Asn
                85                  90                  95


Glu Asp Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105                 110


<210>  39
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gac att gta ctg acc caa tct cca gct tct ttg gct gtg tct cta ggg       48
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

cag agg gcc acc ata tcc tgc aga gcc agt gag agt gtt gct att tat       96
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Ala Ile Tyr
            20                  25                  30

ggc aat agt ttt ctg aaa tgg ttc cag cag aaa ccg gga cag cca ccc      144
Gly Asn Ser Phe Leu Lys Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

aaa ctc ctc atc tat cgt gca tcc aac cta gaa tct ggg atc cct gcc      192
Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
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    50                  55                  60

agg ttc agt ggc agt ggg tct ggg aca gac ttc acc ctc acc att aat      240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65                  70                  75                  80

cct gtg gag gct gat gat gtt gca acc tat tac tgt cag caa att aat      288
Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ile Asn
                85                  90                  95

gag gat ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa cgg      336
Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105                 110


<210>  40
<211>  112
<212>  PRT
<213>  Mus sp.

<400>  40

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Ala Ile Tyr
            20                  25                  30

Gly Asn Ser Phe Leu Lys Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65                  70                  75                  80

Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ile Asn
                85                  90                  95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105                 110


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<213>  Mus sp.


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Asp Ile Val Met Ala Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1               5                   10                  15

gac agg gtc agc atc acc tgc aag gcc agt cag gat gtg agt act gtt       96
Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Val
            20                  25                  30

gtg gcc tgg tat caa cag aaa cca gga caa tct cct aaa cga ctg att      144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Arg Leu Ile
        35                  40                  45

tac tcg gca tcc tat cgg tat att gga gtc cct gat cgc ttc act ggc      192
Tyr Ser Ala Ser Tyr Arg Tyr Ile Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60
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agt gga tct ggg acg gat ttc act ttc acc atc agc agt gtg cag gct      240
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Ala
65                  70                  75                  80

gaa gac ctg gca gtt tat tac tgt cag caa cat tat agt cct ccg tac      288
Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser Pro Pro Tyr
                85                  90                  95

acg ttc gga ggg ggg acc aag ctg gaa ata aaa cgg                      324
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105


<210>  42
<211>  108
<212>  PRT
<213>  Mus sp.

<400>  42

Asp Ile Val Met Ala Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1               5                   10                  15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Val
            20                  25                  30

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

Tyr Ser Ala Ser Tyr Arg Tyr Ile Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Ala
65                  70                  75                  80

Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser Pro Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105


<210>  43
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<213>  Mus sp.


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<222>  (1)..(324)

<400>  43
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Asp Ile Val Met Thr Gln Ser His Lys Phe Leu Ser Thr Ser Val Gly
1               5                   10                  15

gac agg gtc agt atc acc tgc aag gcc agt cag gat gtg gtt act gct       96
Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Val Thr Ala
            20                  25                  30

gtt gcc tgg ttt caa cag aaa cca gga caa tct cca aaa cta ctg att      144
Val Ala Trp Phe Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

tat tcg gca tcc cac cgg tac act gga gtc cct gat cgc ttc act ggc      192
Tyr Ser Ala Ser His Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60
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agt gga tct ggg aca gat ttc act ttc acc atc atc agt gtg cag gct      240
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ile Ser Val Gln Ala
65                  70                  75                  80

gaa gac ctg gca gtt tat tac tgt caa caa cat tat act act ccc acg      288
Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Thr
                85                  90                  95

acg ttc ggt gga ggc acc aag ctg gac ttc aga cgg                      324
Thr Phe Gly Gly Gly Thr Lys Leu Asp Phe Arg Arg
            100                 105
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<210> 44
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<212> PRT
<213> Mus sp.

<400> 44

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Asp Ile Val Met Thr Gln Ser His Lys Phe Leu Ser Thr Ser Val Gly
1               5                   10                  15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Val Thr Ala
            20                  25                  30

Val Ala Trp Phe Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ser Ala Ser His Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ile Ser Val Gln Ala
65                  70                  75                  80

Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Thr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Asp Phe Arg Arg
            100                 105
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<210> 45
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<212> DNA
<213> Mus sp.

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<221> CDS
<222> (1)..(324)

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Asp Thr Val Met Thr Gln Ser His Lys Phe Ile Ser Thr Ser Val Gly
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gac agg gtc agc atc acc tgc aag gcc agt cag gtt gtg ggt agt gct       96
Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Val Val Gly Ser Ala
            20                  25                  30

gta gcc tgg tat caa cag aaa cca ggg caa tct cct aaa cta ctg att      144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

tac tgg gca tcc acc cgg cac act gga gtc cct gat cgc ttc aca ggc      192
Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

agt gga tct ggg aca gat ttc act ctc acc att agc aat gtg cag tct      240
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```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
65                  70                  75                  80

gaa gac ttg gca gat tat ttc tgt cag caa tat aac agc tat ccg tac      288
Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr
                85                  90                  95

acg ttc gga ggg ggg acc aag ctg gaa ata aaa cgg                      324
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105


<210>  46
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<212>  PRT
<213>  Mus sp.

<400>  46

Asp Thr Val Met Thr Gln Ser His Lys Phe Ile Ser Thr Ser Val Gly
1               5                   10                  15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Val Val Gly Ser Ala
            20                  25                  30

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

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105


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<212>  DNA
<213>  Mus sp.


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<221>  CDS
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Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1               5                   10                  15

gac agg gtc agc gtc acc tgc aag gcc agt cag aat gtg ggt act aat       96
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
            20                  25                  30

gtt gcc tgg tat caa cac aaa cca gga caa tcc cct aaa ata atg att      144
Val Ala Trp Tyr Gln His Lys Pro Gly Gln Ser Pro Lys Ile Met Ile
        35                  40                  45

tat tcg gcg tcc tcc cgg tac agt gga gtc cct gat cgc ttc aca ggc      192
Tyr Ser Ala Ser Ser Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

agt gga tct ggg aca ctt ttc act ctc acc atc aac aat gtg cag tct      240
Ser Gly Ser Gly Thr Leu Phe Thr Leu Thr Ile Asn Asn Val Gln Ser
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65 70 75 80

gaa gac ttg gca gag tat ttc tgt cag caa tat aac agc tat cct ctc 288
Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

acg ttc ggc tcg ggg aca aag ttg gaa ata aaa cgg 324
Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
100 105

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<212> PRT
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Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

Val Ala Trp Tyr Gln His Lys Pro Gly Gln Ser Pro Lys Ile Met Ile
35 40 45

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

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

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

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
100 105

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<213> Mus sp.

<220>
<221> CDS
<222> (1)..(342)

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

aca gtc aag atc tcc tgc aag gct tct ggg tat acc ctc aca agc tac 96
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Leu Thr Ser Tyr
20 25 30

gga atg aac tgg gtg aag cag gct cca gga aag ggt tta aag tgg atg 144
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

ggc tgg ata aac acc tac act gga gaa cca aca tat gct gat gac ttt 192
Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
50 55 60

aag gga cgt ttt gcc ttc tct ttg gaa acc tct gcc agc act gcc ttt 240
Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe
65 70 75 80

```
ttg cag atc aac aac ctc aaa aat gag gac acg gct aca tat ttc tgt      288
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
                85                  90                  95

gta aga cgc ggg ttt gct tac tgg ggc caa ggg act ctg gtc act gtc      336
Val Arg Arg Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

tct gca                                                              342
Ser Ala
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<210> 50
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<213> Mus sp.

<400> 50

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Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Leu Thr Ser Tyr
            20                  25                  30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
        35                  40                  45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
    50                  55                  60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe
65                  70                  75                  80

Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
                85                  90                  95

Val Arg Arg Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ala
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<212> DNA
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<220>
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<222> (1)..(342)

<400> 51

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cag atc cag ttg gtg cag tct gga cct gag ctg aag aag cct gga gag       48
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1               5                   10                  15

aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc aca aac tct       96
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Ser
            20                  25                  30

gga atg aac tgg gtg aag cag gct cca gga aag ggt tta aag tgg atg      144
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
        35                  40                  45
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ggc tgg ata aac acc tac act gga gag ccg aca tat gct gat gac ttc      192
Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
    50                  55                  60

aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc tct gcc tat      240
Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Ser Ala Tyr
65                  70                  75                  80

ttg cag atc agt aac ctc aaa aat gag gac acg gct aca tat ttc tgt      288
Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
                85                  90                  95

gca aga agg ggt ttt gtt tac tgg ggc caa ggg act ctg gta act gtc      336
Ala Arg Arg Gly Phe Val Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

tct gca                                                             342
Ser Ala
```

<210> 52
<211> 114
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<400> 52

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

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Ser
            20                  25                  30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
        35                  40                  45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
    50                  55                  60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Ser Ala Tyr
65                  70                  75                  80

Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
                85                  90                  95

Ala Arg Arg Gly Phe Val Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ala
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<210> 53
<211> 360
<212> DNA
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<221> CDS
<222> (1)..(360)

<400> 53

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cag gtt cag ctc cag cag tct ggg gct gag ctg gca aga cct ggg act       48
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Thr
1               5                   10                  15

tca gtg aag ttg tcc tgt aag gct tct ggc tac acc ttt act gac tac       96
```

```
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

tgg atg cag tgg gta aaa cag agg cct gga cag ggt ctg gag tgg att      144
Trp Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

ggg act att tat cct gga gat ggt gat act ggg tac gct cag aag ttc      192
Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60

aag ggc aag gcc aca ttg act gcg gat aaa tcc tcc aaa aca gtc tac      240
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Lys Thr Val Tyr
65                  70                  75                  80

atg cac ctc agc agt ttg gct tct gag gac tct gcg gtc tat tac tgt      288
Met His Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

gca aga ggg gat tac tac ggt agt aat tct ttg gac tat tgg ggt caa      336
Ala Arg Gly Asp Tyr Tyr Gly Ser Asn Ser Leu Asp Tyr Trp Gly Gln
            100                 105                 110

gga acc tca gtc acc gtc tcc tca                                     360
Gly Thr Ser Val Thr Val Ser Ser
        115                 120
```

<210> 54
<211> 120
<212> PRT
<213> Mus sp.

<400> 54

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

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

Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Lys Thr Val Tyr
65                  70                  75                  80

Met His Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Asp Tyr Tyr Gly Ser Asn Ser Leu Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Ser Val Thr Val Ser Ser
        115                 120
```

<210> 55
<211> 357
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(357)

<400> 55

```
cag gtc cag tta cag caa tct gga cct gaa ctg gtg agg cct ggg gcc       48
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Ala
1               5                   10                  15

tca gtg aag att tcc tgc aaa act tct ggc tac gca ttc agt ggc tcc       96
Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Ala Phe Ser Gly Ser
            20                  25                  30

tgg atg aac tgg gtg aag cag agg cct gga cag ggt cta gag tgg att      144
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

gga cgg att tat ccg gga gat gga gat atc att tac aat ggg aat ttc      192
Gly Arg Ile Tyr Pro Gly Asp Gly Asp Ile Ile Tyr Asn Gly Asn Phe
    50                  55                  60

agg gac aag gtc aca ctg tct gca gac aaa tcc tcc aac aca gcc tac      240
Arg Asp Lys Val Thr Leu Ser Ala Asp Lys Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80

atg cag ctc agc agc ctg acc tct gtg gac tct gcg gtc tat ttt tgt      288
Met Gln Leu Ser Ser Leu Thr Ser Val Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

tcg aga tgg ggg aca ttt acg ccg agt ttt gac tat tgg ggc caa ggc      336
Ser Arg Trp Gly Thr Phe Thr Pro Ser Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

acc act ctc aca gtc tcc tca                                         357
Thr Thr Leu Thr Val Ser Ser
        115
```

<210> 56
<211> 119
<212> PRT
<213> Mus sp.

<400> 56

```
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Ala
1               5                   10                  15

Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Ala Phe Ser Gly Ser
            20                  25                  30

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

Gly Arg Ile Tyr Pro Gly Asp Gly Asp Ile Ile Tyr Asn Gly Asn Phe
    50                  55                  60

Arg Asp Lys Val Thr Leu Ser Ala Asp Lys Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Ser Ser Leu Thr Ser Val Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Ser Arg Trp Gly Thr Phe Thr Pro Ser Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Leu Thr Val Ser Ser
        115
```

<210> 57
<211> 351

<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(351)

<400> 57

```
gac gtg aag ctg gtg gag tct ggg gga ggc tta gtg aag cct gga ggg        48
Asp Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                  10                  15

tcc ctg aaa ctc tcc tgt gaa gcc tct gga ttc act ttc agt agc tat        96
Ser Leu Lys Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

acc ctg tct tgg gtt cgc cag act ccg gag acg agg ctg gag tgg gtc       144
Thr Leu Ser Trp Val Arg Gln Thr Pro Glu Thr Arg Leu Glu Trp Val
        35                  40                  45

gca acc att agt att ggt ggt cgc tac acc tat tat cca gac agt gtg       192
Ala Thr Ile Ser Ile Gly Gly Arg Tyr Thr Tyr Tyr Pro Asp Ser Val
    50                  55                  60

gag ggc cga ttc acc atc tcc aga gac aat gcc aag aac acc ctg tac       240
Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80

ctg caa atg aac agt ctg aag tct gag gac aca gcc atg tat tac tgt       288
Leu Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

aca aga gat ttt aat ggt tac tct gac ttc tgg ggc caa ggc acc act       336
Thr Arg Asp Phe Asn Gly Tyr Ser Asp Phe Trp Gly Gln Gly Thr Thr
            100                 105                 110

ctc aca gtc tcc tca                                                   351
Leu Thr Val Ser Ser
        115
```

<210> 58
<211> 117
<212> PRT
<213> Mus sp.

<400> 58

```
Asp Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                  10                  15

Ser Leu Lys Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Thr Leu Ser Trp Val Arg Gln Thr Pro Glu Thr Arg Leu Glu Trp Val
        35                  40                  45

Ala Thr Ile Ser Ile Gly Gly Arg Tyr Thr Tyr Tyr Pro Asp Ser Val
    50                  55                  60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Thr Arg Asp Phe Asn Gly Tyr Ser Asp Phe Trp Gly Gln Gly Thr Thr
            100                 105                 110
```

```
Leu Thr Val Ser Ser
        115


<210>  59
<211>  360
<212>  DNA
<213>  Mus sp.


<220>
<221>  CDS
<222>  (1)..(360)

<400>  59
aat gta cag ctg gta gag tct ggg gga ggc tta gtg cag cct gga ggg       48
Asn Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

tcc cgg aaa ctc tcc tgt gca gcc tct gga ttc act ttc agt aac ttt       96
Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Phe
            20                  25                  30

gga atg cac tgg gtt cgt cag gct cca gag aag ggt ctg gag tgg gtc      144
Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val
        35                  40                  45

gca tac att cgt agt ggc agt ggt acc atc tac tat tca gac aca gtg      192
Ala Tyr Ile Arg Ser Gly Ser Gly Thr Ile Tyr Tyr Ser Asp Thr Val
    50                  55                  60

aag ggc cga ttc acc atc tcc aga gac aat ccc aag aac acc ctg ttc      240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn Thr Leu Phe
65                  70                  75                  80

ctg caa atg acc agt cta agg tct gag gac acg gcc atg tat tac tgt      288
Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

gca aga tcc tac tat gat ttc ggg gcc tgg ttt gct tac tgg ggc caa      336
Ala Arg Ser Tyr Tyr Asp Phe Gly Ala Trp Phe Ala Tyr Trp Gly Gln
            100                 105                 110

ggg act ctg gtc act gtc tct gca                                     360
Gly Thr Leu Val Thr Val Ser Ala
        115                 120


<210>  60
<211>  120
<212>  PRT
<213>  Mus sp.

<400>  60

Asn Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15


Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Phe
            20                  25                  30


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


Ala Tyr Ile Arg Ser Gly Ser Gly Thr Ile Tyr Tyr Ser Asp Thr Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn Thr Leu Phe
65                  70                  75                  80
```

```
Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Tyr Tyr Asp Phe Gly Ala Trp Phe Ala Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ala
        115                 120
```

<210> 61
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(324)

<400> 61

```
gat atc gta atg acc cag tcc cac ctg agt atg agt acc tcc ctg gga       48
Asp Ile Val Met Thr Gln Ser His Leu Ser Met Ser Thr Ser Leu Gly
1               5                   10                  15

gat cct gtg tca atc act tgc aag gcc tca cag gat gtg agc acc gtc       96
Asp Pro Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Val
            20                  25                  30

gtt gct tgg tat cag cag aag ccc ggg caa tca ccc aga cgt ctc atc      144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Arg Arg Leu Ile
        35                  40                  45

tac tca gca tca tac cgt tac atc ggg gtg cct gac cga ttt act ggc      192
Tyr Ser Ala Ser Tyr Arg Tyr Ile Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

tct ggc gct ggc aca gat ttc acc ttt aca att agt tcc gtc cag gcc      240
Ser Gly Ala Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Ala
65                  70                  75                  80

gaa gac ctg gcc gtg tac tac tgc cag cag cac tac agt ccc cca tac      288
Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser Pro Pro Tyr
                85                  90                  95

act ttc ggg gga ggg act aag ctc gaa atc aaa cgt                      324
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105
```

<210> 62
<211> 108
<212> PRT
<213> Homo sapiens

<400> 62

```
Asp Ile Val Met Thr Gln Ser His Leu Ser Met Ser Thr Ser Leu Gly
1               5                   10                  15

Asp Pro Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Val
            20                  25                  30

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

Tyr Ser Ala Ser Tyr Arg Tyr Ile Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Gly Ala Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Ala
```

65 70 75 80

Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser Pro Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 63
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(324)

<400> 63
gac att gtt atg gct caa agc cat ctg tct atg agc aca tct ctg gga 48
Asp Ile Val Met Ala Gln Ser His Leu Ser Met Ser Thr Ser Leu Gly
1 5 10 15

gat cct gtg tcc atc act tgc aaa gcc agt caa gac gtg tct aca gtt 96
Asp Pro Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Val
20 25 30

gtt gca tgg tat caa cag aag cca ggc cag tca ccc aga cgg ctc att 144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Arg Arg Leu Ile
35 40 45

tac tca gct tct tac cga tac atc ggg gtc cct gac aga ttt aca ggt 192
Tyr Ser Ala Ser Tyr Arg Tyr Ile Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

agt ggg gcc ggt act gac ttc act ttt act atc tca tcc gta caa gcc 240
Ser Gly Ala Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Ala
65 70 75 80

gaa gac ctg gca gta tat tac tgc cag caa cat tat tcc cca ccc tac 288
Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser Pro Pro Tyr
85 90 95

aca ttc ggc ggg ggt act aag ctg gaa att aaa cgt 324
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 64
<211> 108
<212> PRT
<213> Homo sapiens

<400> 64

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

Asp Pro Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Val
20 25 30

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

Tyr Ser Ala Ser Tyr Arg Tyr Ile Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ala Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Ala
65 70 75 80

```
Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser Pro Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105

<210>  65
<211>  360
<212>  DNA
<213>  Homo sapiens

<220>
<221>  CDS
<222>  (1)..(360)

<400>  65
cag gta cag ctc gtt cag tcc ggc gcc gag gta gct aag cct ggt act       48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Ala Lys Pro Gly Thr
1               5                   10                  15

tcc gta aaa ttg tcc tgt aag gct tcc ggg tac aca ttt aca gac tac       96
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

tgg atg cag tgg gta aaa cag cgg cca ggt cag ggc ctg gag tgg att      144
Trp Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

gga aca ata tat ccc ggc gac ggc gac aca ggc tat gcc cag aag ttt      192
Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60

caa ggc aag gca acc ctt act gct gat aaa tct tcc aag act gtc tac      240
Gln Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Lys Thr Val Tyr
65                  70                  75                  80

atg cat ctg tct tcc ttg gca tct gag gat agc gct gtc tat tac tgt      288
Met His Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

gct agg ggg gac tac tat ggg tca aat tcc ctg gat tac tgg ggc cag      336
Ala Arg Gly Asp Tyr Tyr Gly Ser Asn Ser Leu Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc agt gtc acc gtg agc agc                                     360
Gly Thr Ser Val Thr Val Ser Ser
        115                 120

<210>  66
<211>  120
<212>  PRT
<213>  Homo sapiens

<400>  66

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

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

Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60
```

```
Gln Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Lys Thr Val Tyr
65                  70                  75                  80

Met His Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Asp Tyr Tyr Gly Ser Asn Ser Leu Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Ser Val Thr Val Ser Ser
        115                 120
```

<210> 67
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(324)

<400> 67

```
gac acc gtg atg acc cag tcc ccc tcc acc atc tcc acc tct gtg ggc       48
Asp Thr Val Met Thr Gln Ser Pro Ser Thr Ile Ser Thr Ser Val Gly
1               5                   10                  15

gac cgg gtg tcc atc acc tgt aag gcc tcc cag gtg gtg ggc tcc gcc       96
Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Val Val Gly Ser Ala
            20                  25                  30

gtg gcc tgg tat cag cag aag cct ggc cag tcc cct aag ctg ctg atc      144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

tac tgg gcc tcc acc cgg cat acc ggc gtg cct gac cgg ttc acc ggc      192
Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

tcc ggc agc ggc acc gac ttc acc ctg acc atc tcc aac gtg cag tcc      240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
65                  70                  75                  80

gac gac ctg gcc gac tac ttc tgc cag cag tac aac tcc tac cct tac      288
Asp Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr
                85                  90                  95

acc ttt ggc ggc gga aca aag ctg gag atc aag cgt                      324
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105
```

<210> 68
<211> 108
<212> PRT
<213> Homo sapiens

<400> 68

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

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Val Val Gly Ser Ala
            20                  25                  30

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

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

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

Asp Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 69
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(324)

<400> 69

```
gac acc gtg atg acc cag tcc ccc tcc tcc atc tcc acc tcc atc ggc        48
Asp Thr Val Met Thr Gln Ser Pro Ser Ser Ile Ser Thr Ser Ile Gly
1               5                   10                  15

gac cgg gtg tcc atc acc tgt aag gcc tcc cag gtg gtg ggc tcc gcc        96
Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Val Val Gly Ser Ala
            20                  25                  30

gtg gcc tgg tat cag cag aag cct ggc cag tcc cct aag ctg ctg atc       144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

tac tgg gcc tcc acc cgg cat acc ggc gtg cct gcc cgg ttc acc ggc       192
Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ala Arg Phe Thr Gly
    50                  55                  60

tcc ggc agc ggc acc gac ttc acc ctg acc atc tcc aac gtg cag tcc       240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
65                  70                  75                  80

gag gac ctg gcc gac tac ttc tgc cag cag tac aac tcc tac cct tac       288
Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr
                85                  90                  95

acc ttt ggc ggc gga aca aag ctg gag atc aag cgt                       324
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105
```

<210> 70
<211> 108
<212> PRT
<213> Homo sapiens

<400> 70

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

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Val Val Gly Ser Ala
20 25 30

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

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ala Arg Phe Thr Gly

50 55 60

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 71
<211> 351
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(351)

<400> 71
gag gtg cag ctg gtg gag tct ggc ggc gga ctg gtg aag cct ggc ggc 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

tcc ctg agg ctg tcc tgt gag gcc tcc ggc ttc acc ttc tcc tcc tac 96
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

acc ctg tcc tgg gtg agg cag acc cct ggc aag ggc ctg gag tgg gtg 144
Thr Leu Ser Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gcc acc atc tcc atc ggc ggc agg tac acc tac tac cct gac tcc gtg 192
Ala Thr Ile Ser Ile Gly Gly Arg Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

aag ggc cgg ttc acc atc tcc cgg gac aac gcc aag aac acc ctg tac 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

ctg cag atg aac tcc ctg aag tcc gag gac acc gcc atg tac tac tgt 288
Leu Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

acc cgg gac ttc aac ggc tac tcc gac ttc tgg ggc cag ggc acc aca 336
Thr Arg Asp Phe Asn Gly Tyr Ser Asp Phe Trp Gly Gln Gly Thr Thr
100 105 110

ctg acc gtg tcc tcc 351
Leu Thr Val Ser Ser
115

<210> 72
<211> 117
<212> PRT
<213> Homo sapiens

<400> 72

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

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Thr Leu Ser Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Ile Gly Gly Arg Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Thr Arg Asp Phe Asn Gly Tyr Ser Asp Phe Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 73
<211> 36
<212> DNA
<213> Mus sp.

<400> 73
ggaggatcca tagacagatg ggggtgtcgt tttggc 36

<210> 74
<211> 32
<212> DNA
<213> Mus sp.

<400> 74
ggaggatccc ttgaccaggc atcctagagt ca 32

<210> 75
<211> 32
<212> DNA
<213> Mus sp.

<220>
<221> misc_feature
<222> (1)..(32)
<223> mixed bases are defined as follows: H=A+T+C, S=G+C, Y=C+T, K=
G+T, M=A+C, R=A+G, W=A+T, V = A+C+G, N = A+C+G+T

<400> 75
cttccggaat tcsargtnma gctgsagsag tc 32

<210> 76
<211> 35
<212> DNA
<213> Mus sp.

<220>
<221> misc_feature
<222> (1)..(35)
<223> mixed bases are defined as follows: H=A+T+C, S=G+C, Y=C+T, K=
G+T, M=A+C, R=A+G, W=A+T, V = A+C+G, N = A+C+G+T

<400> 76
cttccggaat tcsargtnma gctgsagsag tcwgg 35

<210> 77
<211> 31
<212> DNA
<213> Mus sp.

<220>
<221> misc_feature
<222> (1)..(31)
<223> mixed bases are defined as follows: H=A+T+C, S=G+C, Y=C+T, K=
G+T, M=A+C, R=A+G, W=A+T, V = A+C+G, N = A+C+G+T

<400> 77
ggagctcgay attgtgmtsa cmcarwctmc a 31

<210> 78
<211> 46
<212> DNA
<213> Mus sp.

<400> 78
tatagagctc aagcttggat ggtgggaaga tggatacagt tggtgc 46

<210> 79
<211> 21
<212> DNA
<213> Mus sp.

<400> 79
atggagtcac agattcaggt c 21

<210> 80
<211> 32
<212> DNA
<213> Mus sp.

<400> 80
ttttgaattc cagtaacttc aggtgtccac tc 32