<110> HANMI SIENCE CO., LTD.

<120> Blood coagulation factor VII and VIIa derivatives, conjugates and
complexes comprising the same, and use thereof

<130> OPA12118

<150> KR10-2011-0102099
<151> 2011-10-06

<160> 35

<170> KopatentIn 2.0

<210> 1
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<213> Artificial Sequence

<220>
<223> VIIBHISS F

<400> 1
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34

<210> 2
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> VIIXhoIAS R

<400> 2
gggctcgagc tagggaaatg gggctcgcag g
31

<210> 3
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> FactorVII DNA

<400> 3
atggtctccc aggccctcag gctcctctgc cttctgcttg ggcttcaggg ctgcctggct
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gcagtcttcg taacccagga ggaagcccac ggcgtcctgc accggcgccg gcgcgccaac
120

gcgttcctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc
180

tccttcgagg aggcccggga gatcttcaag gacgcggaga ggacgaagct gttctggatt
240

tcttacagtg atggggacca gtgtgcctca agtccatgcc agaatggggg ctcctgcaag
300

gaccagctcc agtcctatat ctgcttctgc ctccctgcct tcgagggccg gaactgtgag
360

acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggctgtga gcagtactgc
420

agtgaccaca cgggcaccaa gcgctcctgt cggtgccacg aggggtactc tctgctggca
480

gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa
540

aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaaggtgtg ccccaaaggg
600

gagtgtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg
660

atcaacacca tctgggtggt ctccgcggcc cactgtttcg acaaaatcaa gaactggagg
720

aacctgatcg cggtgctggg cgagcacgac ctcagcgagc acgacgggga tgagcagagc
780

cggcgggtgg cgcaggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac
840

atcgcgctgc tccgcctgca ccagcccgtg gtcctcactg accatgtggt gcccctctgc
900

ctgcccgaac ggacgttctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc
960

ggctggggcc agctgctgga ccgtggcgcc acggccctgg agctcatggt cctcaacgtg
1020

ccccggctga tgacccagga ctgcctgcag cagtcacgga aggtgggaga ctccccaaat
1080

atcacggagt acatgttctg tgccggctac tcggatggca gcaaggactc ctgcaagggg
1140

gacagtggag gcccacatgc cacccactac cggggcacgt ggtacctgac gggcatcgtc
1200

agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctcccag
1260

tacatcgagt ggctgcaaaa gctcatgcgc tcagagccac gcccaggagt cctcctgcga
1320

gccccatttc cctag
1335

<210> 4
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> FactorVII

<400> 4
Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
  1   5   10   15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
             20   25   30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
         35   40   45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
     50   55   60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
 65   70   75   80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
                 85   90   95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
            100   105   110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
        115   120   125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
    130   135   140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145   150   155   160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
                165   170   175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
            180   185   190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
        195   200   205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
    210   215   220

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Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225                 230                 235                 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
                245                 250                 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
            260                 265                 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
        275                 280                 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
    290                 295                 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
305                 310                 315                 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
                325                 330                 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
            340                 345                 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
        355                 360                 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
    370                 375                 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385                 390                 395                 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
                405                 410                 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
            420                 425                 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro
        435                 440


<210>    5
<211>    6
<212>    PRT
<213>    Artificial Sequence

<220>
<223>    peptide-SOD1 1-6


<400>    5
Ala Thr Lys Ala Val Cys
  1               5
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<210> 6
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> FVIIEcoRISS F

<400> 6
ccggaattca tggccaacgc gttcctggag gagctgcggc cgggc
45

<210> 7
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> FVII#1XhoIAS R

<400> 7
ccgctcgagt cagcacacgg ccttcgtcgc gggaaatggg gctcgcagga ggactcctgg
60

gc
62

<210> 8
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> FactorVII-ATKAVC DNA

<400> 8
atggtctccc aggccctcag gctcctctgc cttctgcttg ggcttcaggg ctgcctggct
60

gcagtcttcg taacccagga ggaagcccac ggcgtcctgc accggcgccg gcgcgccaac
120

gcgttcctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc
180

tccttcgagg aggcccggga gatcttcaag gacgcggaga ggacgaagct gttctggatt
240

tcttacagtg atggggacca gtgtgcctca agtccatgcc agaatggggg ctcctgcaag
300

gaccagctcc agtcctatat ctgcttctgc ctccctgcct tcgagggccg gaactgtgag
360

acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggctgtga gcagtactgc
420

agtgaccaca cgggcaccaa gcgctcctgt cggtgccacg aggggtactc tctgctggca
480

gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa
540

aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaaggtgtg ccccaaaggg
600

gagtgtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg
660

atcaacacca tctgggtggt ctccgcggcc cactgtttcg acaaaatcaa gaactggagg
720

aacctgatcg cggtgctggg cgagcacgac ctcagcgagc acgacgggga tgagcagagc
780

cggcgggtgg cgcaggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac
840

atcgcgctgc tccgcctgca ccagcccgtg gtcctcactg accatgtggt gcccctctgc
900

ctgcccgaac ggacgttctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc
960

ggctggggcc agctgctgga ccgtggcgcc acggccctgg agctcatggt cctcaacgtg
1020

ccccggctga tgacccagga ctgcctgcag cagtcacgga aggtgggaga ctccccaaat
1080

atcacggagt acatgttctg tgccggctac tcggatggca gcaaggactc ctgcaagggg
1140

gacagtggag gcccacatgc cacccactac cggggcacgt ggtacctgac gggcatcgtc
1200

agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctcccag
1260

tacatcgagt ggctgcaaaa gctcatgcgc tcagagccac gcccaggagt cctcctgcga
1320

gccccatttc ccgcgacgaa ggccgtgtgc tga
1353

<210> 9
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> FactorVII-ATKAVC

<400> 9
Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
  1   5   10   15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
             20   25   30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
         35   40   45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
     50   55   60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
 65   70   75   80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
                 85   90   95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
            100   105   110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
        115   120   125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
    130   135   140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145   150   155   160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
                165   170   175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
            180   185   190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
        195   200   205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
    210   215   220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225   230   235   240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
                245   250   255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
            260   265   270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
        275   280   285

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Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
    290                 295                 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
305                 310                 315                 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
                325                 330                 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
            340                 345                 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
        355                 360                 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
    370                 375                 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385                 390                 395                 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
                405                 410                 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
            420                 425                 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Ala Thr Lys Ala
        435                 440                 445

Val Cys
    450


<210>    10
<211>    6
<212>    PRT
<213>    Artificial Sequence

<220>
<223>    peptide


<400>    10
Gly Gly Gly Gly Ser Cys
  1               5


<210>    11
<211>    62
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    FVII#2XhoIAS R
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<400> 11
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60

gc
62

<210> 12
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> FactorVII-GGGGSC DNA

<400> 12
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60

gcagtcttcg taacccagga ggaagcccac ggcgtcctgc accggcgccg gcgcgccaac
120

gcgttcctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc
180

tccttcgagg aggcccggga gatcttcaag gacgcggaga ggacgaagct gttctggatt
240

tcttacagtg atggggacca gtgtgcctca agtccatgcc agaatggggg ctcctgcaag
300

gaccagctcc agtcctatat ctgcttctgc ctccctgcct tcgagggccg gaactgtgag
360

acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggctgtga gcagtactgc
420

agtgaccaca cgggcaccaa gcgctcctgt cggtgccacg aggggtactc tctgctggca
480

gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa
540

aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaaggtgtg ccccaaaggg
600

gagtgtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg
660

atcaacacca tctgggtggt ctccgcggcc cactgtttcg acaaaatcaa gaactggagg
720

aacctgatcg cggtgctggg cgagcacgac ctcagcgagc acgacgggga tgagcagagc
780

cggcgggtgg cgcaggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac
840

atcgcgctgc tccgcctgca ccagcccgtg gtcctcactg accatgtggt gcccctctgc
900

ctgcccgaac ggacgttctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc
960

ggctggggcc agctgctgga ccgtggcgcc acggccctgg agctcatggt cctcaacgtg
1020

ccccggctga tgacccagga ctgcctgcag cagtcacgga aggtgggaga ctccccaaat
1080

atcacggagt acatgttctg tgccggctac tcggatggca gcaaggactc ctgcaagggg
1140

gacagtggag gcccacatgc cacccactac cggggcacgt ggtacctgac gggcatcgtc
1200

agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctcccag
1260

tacatcgagt ggctgcaaaa gctcatgcgc tcagagccac gcccaggagt cctcctgcga
1320

gccccatttc ccggcggcgg cggctcctgc tga
1353

<210> 13
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> FactorVII-GGGGSC

<400> 13
Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
  1   5   10   15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
             20   25   30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
         35   40   45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
     50   55   60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
 65   70   75   80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
                 85   90   95

```
Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
            100                 105                 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
        115                 120                 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
    130                 135                 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145                 150                 155                 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
                165                 170                 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
            180                 185                 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
        195                 200                 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
    210                 215                 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225                 230                 235                 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
                245                 250                 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
            260                 265                 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
        275                 280                 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
    290                 295                 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
305                 310                 315                 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
                325                 330                 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
            340                 345                 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
        355                 360                 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
    370                 375                 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385                 390                 395                 400
```

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Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
                405                 410                 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
            420                 425                 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Gly Gly Gly Gly
        435                 440                 445

Ser Cys
    450
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<210> 14
<211> 593
<212> PRT
<213> Artificial Sequence

<220>
<223> FactorVII-SOD1 1~149

<400> 14

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Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
  1               5                  10                  15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
             20                  25                  30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
         35                  40                  45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
     50                  55                  60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
 65                  70                  75                  80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
                 85                  90                  95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
            100                 105                 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
        115                 120                 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
    130                 135                 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145                 150                 155                 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
                165                 170                 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
            180                 185                 190
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Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
        195                 200                 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
    210                 215                 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225                 230                 235                 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
                245                 250                 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
            260                 265                 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
        275                 280                 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
    290                 295                 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
305                 310                 315                 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
                325                 330                 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
            340                 345                 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
        355                 360                 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
    370                 375                 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385                 390                 395                 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
                405                 410                 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
            420                 425                 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Ala Thr Lys Ala
        435                 440                 445

Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln Gly Ile Ile Asn Phe
    450                 455                 460

Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val Trp Gly Ser Ile Lys
465                 470                 475                 480

Gly Leu Thr Glu Gly Leu His Gly Phe His Val His Glu Phe Gly Asp
                485                 490                 495
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Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His Phe Asn Pro Leu Ser
500 505 510

Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg His Val Gly Asp Leu
515 520 525

Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala Asp Val Ser Ile Glu
530 535 540

Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys Ile Ile Gly Arg Thr
545 550 555 560

Leu Val Val His Glu Lys Ala Asp Asp Leu Gly Lys Gly Gly Asn Glu
565 570 575

Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser Arg Leu Ala Cys Gly Val
580 585 590

Ile

<210> 15
<211> 1785
<212> DNA
<213> Artificial Sequence

<220>
<223> FactorVII-SOD1 1~149 DNA

<400> 15
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60

gcagtcttcg taacccagga ggaagcccac ggcgtcctgc accggcgccg gcgcgccaac
120

gcgttcctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc
180

tccttcgagg aggcccggga gatcttcaag gacgcggaga ggacgaagct gttctggatt
240

tcttacagtg atggggacca gtgtgcctca agtccatgcc agaatggggg ctcctgcaag
300

gaccagctcc agtcctatat ctgcttctgc ctccctgcct tcgagggccg gaactgtgag
360

acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggctgtga gcagtactgc
420

agtgaccaca cgggcaccaa gcgctcctgt cggtgccacg aggggtactc tctgctggca
480

gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa
540

aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaaggtgtg ccccaaaggg
600

gagtgtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg
660

atcaacacca tctgggtggt ctccgcggcc cactgtttcg acaaaatcaa gaactggagg
720

aacctgatcg cggtgctggg cgagcacgac ctcagcgagc acgacgggga tgagcagagc
780

cggcgggtgg cgcaggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac
840

atcgcgctgc tccgcctgca ccagcccgtg gtcctcactg accatgtggt gcccctctgc
900

ctgcccgaac ggacgttctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc
960

ggctggggcc agctgctgga ccgtggcgcc acggccctgg agctcatggt cctcaacgtg
1020

ccccggctga tgacccagga ctgcctgcag cagtcacgga aggtgggaga ctccccaaat
1080

atcacggagt acatgttctg tgccggctac tcggatggca gcaaggactc ctgcaagggg
1140

gacagtggag gcccacatgc cacccactac cggggcacgt ggtacctgac gggcatcgtc
1200

agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctcccag
1260

tacatcgagt ggctgcaaaa gctcatgcgc tcagagccac gcccaggagt cctcctgcga
1320

gccccatttc ccgcgacgaa ggccgtgtgc gtgctgaagg gcgacggccc agtgcagggc
1380

atcatcaatt tcgagcagaa ggaaagtaat ggaccagtga aggtgtgggg aagcattaaa
1440

ggactgactg aaggcctgca tggattccat gttcatgagt ttggagataa tacagcaggc
1500

tgtaccagtg caggtcctca ctttaatcct ctatccagaa aacacggtgg gccaaaggat
1560

gaagagaggc atgttggaga cttgggcaat gtgactgctg acaaagatgg tgtggccgat
1620

gtgtctattg aagattctgt gatctcactc tcaggagacc attgcatcat tggccgcaca
1680

ctggtggtcc atgaaaaagc agatgacttg ggcaaaggtg gaaatgaaga aagtacaaag
1740

acaggaaacg ctggaagtcg tttggcttgt ggtgtaattg ggtga
1785

<210> 16
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> FVIIEcoRISS F

<400> 16
ccggaattca tggtctccca ggccctcagg ctcc
34

<210> 17
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> FVIISOD1InfAS R

<400> 17
cggccttcgt cgcgggaaat ggggctcgca ggag
34

<210> 18
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> FVIISOD1InfSS F

<400> 18
gagccccatt tcccgcgacg aaggccgtgt gcgt
34

<210> 19
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> SOD1XhoIAS R

<400> 19
ccgctcgagt caaattacac cacaagccaa acga
34

<210> 20
<211> 593
<212> PRT
<213> Artificial Sequence

<220>
<223> FactorVII-SOD1 IPRI

<400> 20
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1 5 10 15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
20 25 30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35 40 45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
180 185 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
195 200 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
210 215 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg

225 230 235 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
245 250 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
260 265 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
275 280 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
290 295 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
305 310 315 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
325 330 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
340 345 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
355 360 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
370 375 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385 390 395 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
405 410 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
420 425 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Ala Thr Lys Ala
435 440 445

Val Cys Ile Pro Arg Ile Asp Gly Pro Val Gln Gly Ile Ile Asn Phe
450 455 460

Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val Trp Gly Ser Ile Lys
465 470 475 480

Gly Leu Thr Glu Gly Leu His Gly Phe His Val His Glu Phe Gly Asp
485 490 495

Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His Phe Asn Pro Leu Ser
500 505 510

Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg His Val Gly Asp Leu
515 520 525

Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala Asp Val Ser Ile Glu
530 535 540

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Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys Ile Ile Gly Arg Thr
545                 550                 555                 560

Leu Val Val His Glu Lys Ala Asp Asp Leu Gly Lys Gly Gly Asn Glu
                565                 570                 575

Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser Arg Leu Ala Cys Gly Val
            580                 585                 590

Ile
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<210> 21
<211> 1785
<212> DNA
<213> Artificial Sequence

<220>
<223> FactorVII-SOD1 IPRI DNA

<400> 21

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60

gcagtcttcg taacccagga ggaagcccac ggcgtcctgc accggcgccg gcgcgccaac
120

gcgttcctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc
180

tccttcgagg aggcccggga gatcttcaag gacgcggaga ggacgaagct gttctggatt
240

tcttacagtg atggggacca gtgtgcctca agtccatgcc agaatggggg ctcctgcaag
300

gaccagctcc agtcctatat ctgcttctgc ctccctgcct tcgagggccg gaactgtgag
360

acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggctgtga gcagtactgc
420

agtgaccaca cgggcaccaa gcgctcctgt cggtgccacg aggggtactc tctgctggca
480

gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa
540

aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaaggtgtg ccccaaaggg
600

gagtgtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg
660

atcaacacca tctgggtggt ctccgcggcc cactgtttcg acaaaatcaa gaactggagg
720

aacctgatcg cggtgctggg cgagcacgac ctcagcgagc acgacgggga tgagcagagc
780

cggcgggtgg cgcaggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac
840

atcgcgctgc tccgcctgca ccagcccgtg gtcctcactg accatgtggt gcccctctgc
900

ctgcccgaac ggacgttctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc
960

ggctggggcc agctgctgga ccgtggcgcc acggccctgg agctcatggt cctcaacgtg
1020

ccccggctga tgacccagga ctgcctgcag cagtcacgga aggtgggaga ctccccaaat
1080

atcacggagt acatgttctg tgccggctac tcggatggca gcaaggactc ctgcaagggg
1140

gacagtggag gcccacatgc cacccactac cggggcacgt ggtacctgac gggcatcgtc
1200

agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctcccag
1260

tacatcgagt ggctgcaaaa gctcatgcgc tcagagccac gcccaggagt cctcctgcga
1320

gccccatttc ccgcgacgaa ggccgtgtgc attccgagga tcgacggccc agtgcagggc
1380

atcatcaatt tcgagcagaa ggaaagtaat ggaccagtga aggtgtgggg aagcattaaa
1440

ggactgactg aaggcctgca tggattccat gttcatgagt ttggagataa tacagcaggc
1500

tgtaccagtg caggtcctca ctttaatcct ctatccagaa aacacggtgg gccaaaggat
1560

gaagagaggc atgttggaga cttgggcaat gtgactgctg acaaagatgg tgtggccgat
1620

gtgtctattg aagattctgt gatctcactc tcaggagacc attgcatcat tggccgcaca
1680

ctggtggtcc atgaaaaagc agatgacttg ggcaaaggtg gaaatgaaga aagtacaaag
1740

acaggaaacg ctggaagtcg tttggcttgt ggtgtaattg ggtga
1785

<210> 22
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> VIISOD1mutSS F

<400> 22
cccgcgacga aggccgtgtg cattccgagg atcgacggcc cagtgcaggg catc
54

<210> 23
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> FVIISOD1mutAS R

<400> 23
gatgccctgc actgggccgt cgatcctcgg aatgcacacg gccttcgtcg cggg
54

<210> 24
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> FactorVII-SOD1 1~25 IPRI

<400> 24
Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
  1   5   10   15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
             20   25   30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
         35   40   45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
     50   55   60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
 65   70   75   80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
                 85   90   95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
            100   105   110

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Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
        115                 120                 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
    130                 135                 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145                 150                 155                 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
                165                 170                 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
            180                 185                 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
        195                 200                 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
    210                 215                 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225                 230                 235                 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
                245                 250                 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
            260                 265                 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
        275                 280                 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
    290                 295                 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
305                 310                 315                 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
                325                 330                 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
            340                 345                 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
        355                 360                 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
    370                 375                 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385                 390                 395                 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
                405                 410                 415
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Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
420 425 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Ala Thr Lys Ala
435 440 445

Val Cys Ile Pro Arg Ile Asp Gly Pro Val Gln Gly Ile Ile Asn Phe
450 455 460

Glu Gln Lys Glu Ser
465

<210> 25
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> FactorVII-SOD1 1~25 IPRI DNA

<400> 25
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60

gcagtcttcg taacccagga ggaagcccac ggcgtcctgc accggcgccg gcgcgccaac
120

gcgttcctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc
180

tccttcgagg aggcccggga gatcttcaag gacgcggaga ggacgaagct gttctggatt
240

tcttacagtg atggggacca gtgtgcctca agtccatgcc agaatggggg ctcctgcaag
300

gaccagctcc agtcctatat ctgcttctgc ctccctgcct tcgagggccg gaactgtgag
360

acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggctgtga gcagtactgc
420

agtgaccaca cgggcaccaa gcgctcctgt cggtgccacg aggggtactc tctgctggca
480

gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa
540

aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaaggtgtg ccccaaaggg
600

gagtgtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg
660

atcaacacca tctgggtggt ctccgcggcc cactgtttcg acaaaatcaa gaactggagg
720

aacctgatcg cggtgctggg cgagcacgac ctcagcgagc acgacgggga tgagcagagc
780

cggcgggtgg cgcaggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac
840

atcgcgctgc tccgcctgca ccagcccgtg gtcctcactg accatgtggt gcccctctgc
900

ctgcccgaac ggacgttctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc
960

ggctggggcc agctgctgga ccgtggcgcc acggccctgg agctcatggt cctcaacgtg
1020

ccccggctga tgacccagga ctgcctgcag cagtcacgga aggtgggaga ctccccaaat
1080

atcacggagt acatgttctg tgccggctac tcggatggca gcaaggactc ctgcaagggg
1140

gacagtggag gcccacatgc cacccactac cggggcacgt ggtacctgac gggcatcgtc
1200

agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctcccag
1260

tacatcgagt ggctgcaaaa gctcatgcgc tcagagccac gcccaggagt cctcctgcga
1320

gccccatttc ccgcgacgaa ggccgtgtgc attccgagga tcgacggccc agtgcagggc
1380

atcatcaatt tcgagcagaa ggaaagttga
1410

<210> 26
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> SOD1-25XhoIAS R

<400> 26
ccgctcgagt caactttcct tctgctcgaa attg
34

<210> 27
<211> 534
<212> PRT
<213> Artificial Sequence

<220>

<223> FVII-SOD1 1-90 IPRI

<400> 27

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Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
  1               5                  10                  15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
             20                  25                  30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
         35                  40                  45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
     50                  55                  60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
 65                  70                  75                  80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
                 85                  90                  95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
            100                 105                 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
        115                 120                 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
    130                 135                 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145                 150                 155                 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
                165                 170                 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
            180                 185                 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
        195                 200                 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
    210                 215                 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225                 230                 235                 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
                245                 250                 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
            260                 265                 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
        275                 280                 285
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```
Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
    290                 295                 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
305                 310                 315                 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
                325                 330                 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
            340                 345                 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
        355                 360                 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
    370                 375                 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385                 390                 395                 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
                405                 410                 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
            420                 425                 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Ala Thr Lys Ala
        435                 440                 445

Val Cys Ile Pro Arg Ile Asp Gly Pro Val Gln Gly Ile Ile Asn Phe
    450                 455                 460

Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val Trp Gly Ser Ile Lys
465                 470                 475                 480

Gly Leu Thr Glu Gly Leu His Gly Phe His Val His Glu Phe Gly Asp
                485                 490                 495

Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His Phe Asn Pro Leu Ser
            500                 505                 510

Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg His Val Gly Asp Leu
        515                 520                 525

Gly Asn Val Thr Ala Asp
    530


<210>    28
<211>    1605
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    FVII-SOD1 1-90 IPRI DNA
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<400> 28
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60

gcagtcttcg taacccagga ggaagcccac ggcgtcctgc accggcgccg gcgcgccaac
120

gcgttcctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc
180

tccttcgagg aggcccggga gatcttcaag gacgcggaga ggacgaagct gttctggatt
240

tcttacagtg atggggacca gtgtgcctca agtccatgcc agaatggggg ctcctgcaag
300

gaccagctcc agtcctatat ctgcttctgc ctccctgcct tcgagggccg gaactgtgag
360

acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggctgtga gcagtactgc
420

agtgaccaca cgggcaccaa gcgctcctgt cggtgccacg aggggtactc tctgctggca
480

gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa
540

aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaaggtgtg ccccaaaggg
600

gagtgtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg
660

atcaacacca tctgggtggt ctccgcggcc cactgtttcg acaaaatcaa gaactggagg
720

aacctgatcg cggtgctggg cgagcacgac ctcagcgagc acgacgggga tgagcagagc
780

cggcgggtgg cgcaggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac
840

atcgcgctgc tccgcctgca ccagcccgtg gtcctcactg accatgtggt gcccctctgc
900

ctgcccgaac ggacgttctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc
960

ggctggggcc agctgctgga ccgtggcgcc acggccctgg agctcatggt cctcaacgtg
1020

ccccggctga tgacccagga ctgcctgcag cagtcacgga aggtgggaga ctccccaaat
1080

atcacggagt acatgttctg tgccggctac tcggatggca gcaaggactc ctgcaagggg
1140

gacagtggag gcccacatgc cacccactac cggggcacgt ggtacctgac gggcatcgtc
1200

agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctcccag
1260

tacatcgagt ggctgcaaaa gctcatgcgc tcagagccac gcccaggagt cctcctgcga
1320

gccccatttc ccgcgacgaa ggccgtgtgc gtgctgaagg gcgacggccc agtgcagggc
1380

atcatcaatt tcgagcagaa ggaaagtaat ggaccagtga aggtgtgggg aagcattaaa
1440

ggactgactg aaggcctgca tggattccat gttcatgagt ttggagataa tacagcaggc
1500

tgtaccagtg caggtcctca ctttaatcct ctatccagaa aacacggtgg gccaaaggat
1560

gaagagaggc atgttggaga cttgggcaat gtgactgctg actga
1605

<210> 29
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> SOD1-90XhoIAS R

<400> 29
ccgctcgagt cagtcagcag tcacattgcc caag
34

<210> 30
<211> 154
<212> PRT
<213> Human SOD1

<400> 30
Ala Thr Lys Ala Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln Gly
  1   5   10   15

Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val Trp
             20   25   30

Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His Gly Phe His Val His
         35   40   45

Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His Phe
     50   55   60

Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg His

```
 65                  70                  75                  80

Val Gly Asp Leu Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala Asp
                 85                  90                  95

Val Ser Ile Glu Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys Ile
            100                 105                 110

Ile Gly Arg Thr Leu Val Val His Glu Lys Ala Asp Asp Leu Gly Lys
        115                 120                 125

Gly Gly Asn Glu Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser Arg Leu
    130                 135                 140

Ala Cys Gly Val Ile Gly Ile Ala Gln Leu
145                 150


<210>    31
<211>    149
<212>    PRT
<213>    Human SOD1 1-149

<400>    31
Ala Thr Lys Ala Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln Gly
  1               5                  10                  15

Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val Trp
             20                  25                  30

Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His Gly Phe His Val His
         35                  40                  45

Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His Phe
     50                  55                  60

Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg His
 65                  70                  75                  80

Val Gly Asp Leu Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala Asp
                 85                  90                  95

Val Ser Ile Glu Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys Ile
            100                 105                 110

Ile Gly Arg Thr Leu Val Val His Glu Lys Ala Asp Asp Leu Gly Lys
        115                 120                 125

Gly Gly Asn Glu Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser Arg Leu
    130                 135                 140

Ala Cys Gly Val Ile
145


<210>    32
<211>    90
<212>    PRT
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<213> Human SOD1 1-90

<400> 32
Ala Thr Lys Ala Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln Gly
  1   5   10   15

Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val Trp
             20   25   30

Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His Gly Phe His Val His
         35   40   45

Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His Phe
     50   55   60

Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg His
 65   70   75   80

Val Gly Asp Leu Gly Asn Val Thr Ala Asp
                 85   90

<210> 33
<211> 25
<212> PRT
<213> Human SOD1 1-25

<400> 33
Ala Thr Lys Ala Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln Gly
  1   5   10   15

Ile Ile Asn Phe Glu Gln Lys Glu Ser
             20   25

<210> 34
<211> 534
<212> PRT
<213> Artificial Sequence

<220>
<223> FVII-SOD1 1-90

<400> 34
Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
  1   5   10   15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
             20   25   30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
         35   40   45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
     50   55   60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile

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 65                  70                  75                  80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
                 85                  90                  95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
            100                 105                 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
        115                 120                 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
    130                 135                 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145                 150                 155                 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
                165                 170                 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
            180                 185                 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
        195                 200                 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
    210                 215                 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225                 230                 235                 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
                245                 250                 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
            260                 265                 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
        275                 280                 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
    290                 295                 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
305                 310                 315                 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
                325                 330                 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
            340                 345                 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
        355                 360                 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
    370                 375                 380
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Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385                 390                 395                 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
                405                 410                 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
            420                 425                 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Ala Thr Lys Ala
        435                 440                 445

Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln Gly Ile Ile Asn Phe
    450                 455                 460

Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val Trp Gly Ser Ile Lys
465                 470                 475                 480

Gly Leu Thr Glu Gly Leu His Gly Phe His Val His Glu Phe Gly Asp
                485                 490                 495

Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His Phe Asn Pro Leu Ser
            500                 505                 510

Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg His Val Gly Asp Leu
        515                 520                 525

Gly Asn Val Thr Ala Asp
    530


<210>    35
<211>    469
<212>    PRT
<213>    Artificial Sequence

<220>
<223>    FVII-SOD1 1-25


<400>    35
Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
  1               5                  10                  15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
             20                  25                  30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
         35                  40                  45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
     50                  55                  60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
 65                  70                  75                  80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
```

```
                85                  90                  95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
            100                 105                 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
        115                 120                 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
    130                 135                 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145                 150                 155                 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
                165                 170                 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
            180                 185                 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
        195                 200                 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
    210                 215                 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225                 230                 235                 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
                245                 250                 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
            260                 265                 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
        275                 280                 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
    290                 295                 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
305                 310                 315                 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
                325                 330                 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
            340                 345                 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
        355                 360                 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
    370                 375                 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385                 390                 395                 400
```

```
Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
                405                 410                 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
            420                 425                 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Ala Thr Lys Ala
        435                 440                 445

Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln Gly Ile Ile Asn Phe
    450                 455                 460

Glu Gln Lys Glu Ser
465
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