SEQUENCE LISTING

<110> VASCULAR BIOGENICS LTD.

<120> METHODS FOR ANTI-TUMOR THERAPY

<130> 3182.091PC01/GLL/C-K/SGM

<150> US 62/833,402
<151> 2019-04-12

<160> 25

<170> PatentIn version 3.5

<210> 1
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide Sequence encoding TNFR1

<400> 1
atgggcctct ccaccgtgcc tgacctgctg ctgccgctgg tgctcctgga gctgttggtg 60

ggaatatacc cctcaggggt tattggactg gtccctcacc taggggacag ggagaagaga 120

gatagtgtgt gtccccaagg aaaatatatc caccctcaaa ataattcgat ttgctgtacc 180

aagtgccaca aaggaaccta cttgtacaat gactgtccag gcccggggca ggatacggac 240

tgcagggagt gtgagagcgg ctccttcacc gcttcagaaa accacctcag acactgcctc 300

agctgctcca aatgccgaaa ggaaatgggt caggtggaga tctcttcttg cacagtggac 360

cgggacaccg tgtgtggctg caggaagaac cagtaccggc attattggag tgaaaacctt 420

ttccagtgct tcaattgcag cctctgcctc aatgggaccg tgcacctctc ctgccaggag 480

aaacagaaca ccgtgtgcac ctgccatgca ggtttctttc taagagaaaa cgagtgtgtc 540

tcctgtagta actgtaagaa aagcctggag tgcacgaagt tgtgcctacc ccagattgag 600

aatgttaagg gcactgagga ctcaggcacc acagtgctgt tgcccctggt cattttcttt 660

ggtctttgcc ttttatccct cctcttcatt ggtttaatgt atcgctacca acggtggaag 720

tccaagctct actccattgt ttgtgggaaa tcgacacctg aaaaagaggg ggagcttgaa 780

ggaactacta ctaagcccct ggccccaaac ccaagcttca gtcccactcc aggcttcacc 840

cccaccctgg gcttcagtcc cgtgcccagt tccaccttca cctccagctc cacctatacc 900

cccggtgact gtcccaactt tgcggctccc cgcagagagg tggcaccacc ctatcagggg 960

gctgacccca tccttgcgac agccctcgcc tccgacccca tccccaaccc ccttcagaag 1020

tgggaggaca gcgcccacaa gccacagagc ctagacactg atgaccccgc gacgctgtac 1080

gccgtggtgg agaacgtgcc cccgttgcgc tggaaggaat tcgtgcggcg cctagggctg 1140

agcgaccacg agatcgatcg gctggagctg cagaacgggc gctgcctgcg cgaggcgcaa 1200

tacagcatgc tggcgacctg gaggcggcgc acgccgcggc gcgaggccac gctggagctg 1260

ctgggacgcg tgctccgcga catggacctg ctgggctgcc tggaggacat cgaggaggcg 1320

ctttgcggcc ccgccgccct cccgcccgcg cccagtcttc tcaga 1365

<210> 2
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of TNFR1

<400> 2

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
100 105 110

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Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
        115                 120                 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
    130                 135                 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
145                 150                 155                 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
                165                 170                 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
            180                 185                 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
        195                 200                 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
    210                 215                 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
225                 230                 235                 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
                245                 250                 255

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
            260                 265                 270

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
        275                 280                 285

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
    290                 295                 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
305                 310                 315                 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
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                325                 330                 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
            340                 345                 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
        355                 360                 365

Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
    370                 375                 380

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
385                 390                 395                 400

Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
                405                 410                 415

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
            420                 425                 430

Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
        435                 440                 445

Pro Ala Pro Ser Leu Leu Arg
    450                 455


<210>  3
<211>  591
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleotide sequence encoding a Ligand Binding Domain of TNFR1

<400>  3
atgggcctct ccaccgtgcc tgacctgctg ctgccgctgg tgctcctgga gctgttggtg       60

ggaatatacc cctcaggggt tattggactg gtccctcacc taggggacag ggagaagaga      120

gatagtgtgt gtccccaagg aaaatatatc caccctcaaa ataattcgat ttgctgtacc      180

aagtgccaca aaggaaccta cttgtacaat gactgtccag gcccggggca ggatacggac      240

tgcagggagt gtgagagcgg ctccttcacc gcttcagaaa accacctcag acactgcctc      300
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agctgctcca aatgccgaaa ggaaatgggt caggtggaga tctcttcttg cacagtggac 360

cgggacaccg tgtgtggctg caggaagaac cagtaccggc attattggag tgaaaacctt 420

ttccagtgct tcaattgcag cctctgcctc aatgggaccg tgcacctctc ctgccaggag 480

aaacagaaca ccgtgtgcac ctgccatgca ggtttctttc taagagaaaa cgagtgtgtc 540

tcctgtagta actgtaagaa aagcctggag tgcacgaagt tgtgcctacc a 591

<210> 4
<211> 197
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a Ligand Binding Domain of TNFR1

<400> 4

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe

```
    130                 135                 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
145                 150                 155                 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
                165                 170                 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
            180                 185                 190

Lys Leu Cys Leu Pro
        195
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<210> 5
<211> 1008
<212> DNA
<213> Artificial Sequence

<220>
<223> full-length FAS

<400> 5

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aaaagtgtta atgcccaagt gactgacatc aactccaagg gattggaatt gaggaagact      120

gttactacag ttgagactca gaacttggaa ggcctgcatc atgatggcca attctgccat      180

aagccctgtc ctccaggtga aaggaaagct agggactgca cagtcaatgg ggatgaacca      240

gactgcgtgc cctgccaaga agggaaggag tacacagaca aagcccattt ttcttccaaa      300

tgcagaagat gtagattgtg tgatgaagga catggcttag aagtggaaat aaactgcacc      360

cggacccaga ataccaagtg cagatgtaaa ccaaactttt tttgtaactc tactgtatgt      420

gaacactgtg acccttgcac caaatgtgaa catggaatca tcaaggaatg cacactcacc      480

agcaacacca agtgcaaaga ggaaggatcc agatctaact tggggtggct ttgtcttctt      540

cttttgccaa ttccactaat tgtttgggtg aagagaaagg aagtacagaa aacatgcaga      600

aagcacagaa aggaaaacca aggttctcat gaatctccaa ctttaaatcc tgaaacagtg      660

gcaataaatt tatctgatgt tgacttgagt aaatatatca ccactattgc tggagtcatg      720

acactaagtc aagttaaagg ctttgttcga aagaatggtg tcaatgaagc caaaatagat      780
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gagatcaaga atgacaatgt ccaagacaca gcagaacaga aagttcaact gcttcgtaat 840

tggcatcaac ttcatggaaa gaaagaagcg tatgacacat tgattaaaga tctcaaaaaa 900

gccaatcttt gtactcttgc agagaaaatt cagactatca tcctcaagga cattactagt 960

gactcagaaa attcaaactt cagaaatgaa atccaaagct tggtctag 1008

<210> 6
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> full-length FAS

<400> 6

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
1 5 10 15

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

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
35 40 45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
50 55 60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65 70 75 80

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

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
100 105 110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
115 120 125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
130 135 140

```
Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145                 150                 155                 160


Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
                165                 170                 175


Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
            180                 185                 190


Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
        195                 200                 205


Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu
    210                 215                 220


Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met
225                 230                 235                 240


Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu
                245                 250                 255


Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu
            260                 265                 270


Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys
        275                 280                 285


Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys
    290                 295                 300


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


Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
                325                 330                 335


<210>  7
<211>  505
<212>  DNA
<213>  Artificial Sequence
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<220>
<223> Effector Domain of FAS

<400> 7
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ttgggtgaag agaaaggaag tacagaaaac atgcagaaag cacagaaagg aaaaccaagg 120

ttctcatgaa tctccaacct taaatcctga aacagtggca ataaatttat ctgatgttga 180

cttgagtaaa tatatcacca ctattgctgg agtcatgaca ctaagtcaag ttaaaggctt 240

tgttcgaaag aatggtgtca atgaagccaa aatagatgag atcaagaatg acaatgtcca 300

agacacagca gaacagaaag ttcaactgct tcgtaattgg catcaacttc atggaaagaa 360

agaagcgtat gacacattga ttaaagatct caaaaaagcc aatctttgta ctcttgcaga 420

gaaaattcag actatcatcc tcaaggacat tactagtgac tcagaaaatt caaacttcag 480

aaatgaaatc caaagcttgg tctag 505

<210> 8
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> Effector Domain of FAS

<400> 8

Gly Ser Arg Ser Asn Leu Gly Trp Leu Cys Leu Leu Leu Leu Pro Ile
1   5   10   15

Pro Leu Ile Val Trp Val Lys Arg Lys Glu Val Gln Lys Thr Cys Arg
            20   25   30

Lys His Arg Lys Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu Asn
        35   40   45

Pro Glu Thr Val Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys Tyr
    50   55   60

Ile Thr Thr Ile Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe
65   70   75   80

Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn

85 90 95

Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn
100 105 110

Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile Lys
115 120 125

Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile Gln Thr
130 135 140

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

Asn Glu Ile Gln Ser Leu Val
165

<210> 9
<211> 1101
<212> DNA
<213> Artificial Sequence

<220>
<223> FAS-chimera

<400> 9
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ggaatatacc cctcaggggt tattggactg gtccctcacc taggggacag ggagaagaga 120

gatagtgtgt gtccccaagg aaaatatatc caccctcaaa ataattcgat ttgctgtacc 180

aagtgccaca aaggaaccta cttgtacaat gactgtccag gcccggggca ggatacggac 240

tgcagggagt gtgagagcgg ctccttcacc gcttcagaaa accacctcag acactgcctc 300

agctgctcca aatgccgaaa ggaaatgggt caggtggaga tctcttcttg cacagtggac 360

cgggacaccg tgtgtggctg caggaagaac cagtaccggc attattggag tgaaaacctt 420

ttccagtgct tcaattgcag cctctgcctc aatgggaccg tgcacctctc ctgccaggag 480

aaacagaaca ccgtgtgcac ctgccatgca ggtttctttc taagagaaaa cgagtgtgtc 540

tcctgtagta actgtaagaa aagcctggag tgcacgaagt tgtgcctacc aagcttagga 600

tccagatcta acttggggtg gctttgtctt cttcttttgc caattccact aattgtttgg 660

gtgaagagaa aggaagtaca gaaaacatgc agaaagcaca gaaaggaaaa ccaaggttct 720

catgaatctc caaccttaaa tcctgaaaca gtggcaataa atttatctga tgttgacttg 780

agtaaatata tcaccactat tgctggagtc atgacactaa gtcaagttaa aggctttgtt 840

cgaaagaatg gtgtcaatga agccaaaata gatgagatca agaatgacaa tgtccaagac 900

acagcagaac agaaagttca actgcttcgt aattggcatc aacttcatgg aaagaaagaa 960

gcgtatgaca cattgattaa agatctcaaa aaagccaatc tttgtactct tgcagagaaa 1020

attcagacta tcatcctcaa ggacattact agtgactcag aaaattcaaa cttcagaaat 1080

gaaatccaaa gcttggtcta g 1101

<210> 10
<211> 366
<212> PRT
<213> Artificial Sequence

<220>
<223> FAS-chimera

<400> 10

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
100 105 110

```
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
        115                 120                 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
    130                 135                 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
145                 150                 155                 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
                165                 170                 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
            180                 185                 190

Lys Leu Cys Leu Pro Ser Leu Gly Ser Arg Ser Asn Leu Gly Trp Leu
        195                 200                 205

Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg Lys
    210                 215                 220

Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly Ser
225                 230                 235                 240

His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu Ser
                245                 250                 255

Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met Thr
            260                 265                 270

Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala
        275                 280                 285

Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln
    290                 295                 300

Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys Glu
305                 310                 315                 320

Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr
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325 330 335

Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp
340 345 350

Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
355 360 365

<210> 11
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> cis-regulatory element

<400> 11
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<210> 12
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> cis-regulatory element

<400> 12
aatgaaaagt atgaagtact ggctccagaa gcaaagtcac cctccag 47

<210> 13
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> cis-regulatory element

<400> 13
gtacttcata cttttcattc caatggggtg actttgcttc tgga 44

<210> 14
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> cis-regulatory element

<400> 14
tccagaagca aagtcacccc attggaatga aaagtatgaa gtac 44

<210> 15
<211> 131
<212> DNA
<213> Artificial Sequence

<220>
<223> cis-regulatory element

<400> 15
ctccagaagc aaagtcaccc cattggaatg aaaagtatga agtacaatga aaagtatgaa 60

gtactggctc cagaagcaaa gtcaccctcc agaagcaaag tcaccccatt ggaatgaaaa 120

gtatgaagta c 131

<210> 16
<211> 131
<212> DNA
<213> Artificial Sequence

<220>
<223> cis-regulatory element

<400> 16
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ggagccagta cttcatactt ttcattgtac ttcatacttt tcattccaat ggggtgactt 120

tgcttctgga g 131

<210> 17
<211> 850
<212> DNA
<213> Artificial Sequence

<220>
<223> Endothelial Cell-Specific PPE-1 Promoter

<400> 17
gtacgtgtac ttctgatcgg cgatactagg gagataagga tgtgcctgac aaaaccacat 60

tgttgttgtt atcattatta tttagttttc cttccttgct aactcctgac ggaatctttc 120

tcacctcaaa tgcgaagtac tttagtttag aaaagacttg gtggaagggg tggtggtgga 180

aaagtagggt gatcttccaa actaatctgg ttccccgccc gccccagtag ctgggattca 240

agagcgaaga gtggggatcg tccccttgtt tgatcagaaa gacataaaag gaaaatcaag 300

tgaacaatga tcagccccac ctccacccca ccccccctgcg cgcgcacaat acaatctatt 360

taattgtact tcatactttt cattccaatg gggtgacttt gcttctggag aaactcttga 420

ttcttgaact ctggggctgg cagctagcaa aaggggaagc gggctgctgc tctctgcagg 480

ttctgcagcg gtctctgtct agtgggtgtt ttctttttct tagccctgcc cctggattgt 540

cagacggcgg gcgtctgcct ctgaagttag ccgtgatttc ctctagagcc gggtcttatc 600

tctggctgca cgttgcctgt gggtgactaa tcacacaata acattgttta gggctggaat 660

gaagtcagag ctgtttaccc ccactctata ggggttcaat ataaaaaggc ggcggagaac 720

tgtccgagtc agaagcgttc ctgcaccggc gctgagagcc tgacccggtc tgctccgctg 780

tccttgcgcg ctgcctcccg gctgcccgcg acgctttcgc cccagtggaa gggccacttg 840

ctgcggccgc 850

<210> 18
<211> 987
<212> DNA
<213> Artificial Sequence

<220>
<223> Endothelial Cell-Specific PPE-1 3X Promoter

<400> 18
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tgttgttgtt atcattatta tttagttttc cttccttgct aactcctgac ggaatctttc 120

tcacctcaaa tgcgaagtac tttagtttag aaaagacttg gtggaagggg tggtggtgga 180

aaagtagggt gatcttccaa actaatctgg ttccccgccc gccccagtag ctgggattca 240

agagcgaaga gtggggatcg tccccttgtt tgatcagaaa gacataaaag gaaaatcaag 300

tgaacaatga tcagccccac ctccacccca ccccccctgcg cgcgcacaat acaatctatt 360

taattgtact tcatactttt cattccaatg gggtgacttt gcttctggag aaactcttga 420

ttcttgaact ctggggctgg cagctagcct ccagaagcaa agtcacccca ttggaatgaa 480

aagtatgaag tacaatgaaa agtatgaagt actggctcca gaagcaaagt caccctccag 540

aagcaaagtc accccattgg aatgaaaagt atgaagtacg ctagcaaaag gggaagcggg 600

ctgctgctct ctgcaggttc tgcagcggtc tctgtctagt gggtgttttc tttttcttag 660

ccctgcccct ggattgtcag acggcgggcg tctgcctctg aagttagccg tgatttcctc 720

tagagccggg tcttatctct ggctgcacgt tgcctgtggg tgactaatca cacaataaca 780

ttgtttaggg ctggaatgaa gtcagagctg tttaccccca ctctataggg gttcaatata 840

aaaaggcggc ggagaactgt ccgagtcaga agcgttcctg caccggcgct gagagcctga 900

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agtggaaggg ccacttgctg cggccgc 987

<210> 19
<211> 35207
<212> DNA
<213> Artificial Sequence

<220>
<223> VB-111 entire construct

<400> 19
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ttgtgacgtg gcgcggggcg tgggaacggg gcgggtgacg tagtagtgtg gcggaagtgt 120

gatgttgcaa gtgtggcgga acacatgtaa gcgacggatg tggcaaaagt gacgtttttg 180

gtgtgcgccg gtgtacacag gaagtgacaa ttttcgcgcg gttttaggcg gatgttgtag 240

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