SEQUENCE LISTING

<110> Bayer HealthCare LLC
Bauzon, Maxine
Hermiston, Terry

<120> Short Acting Factor VII Peptides

<130> BHC115011 PCT

<150> 61/754,674
<151> 2012-12-24

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<151> 2013-03-15

<160> 18

<170> PatentIn version 3.5

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aaaggggagt gtccatggca ggtcctgttg ttggtgaatg gagctcagtt gtgtgggggg 540

accctgatca acaccatctg ggtggtctcc gcggcccact gtttcgacaa aatcaagaac 600

tggaggaacc tgatcgcggt gctgggcgag cacgacctca gcgagcacga cggggatgag 660

cagagccggc gggtggcgca ggtcatcatc cccagcacgt acgtcccggg caccaccaac 720

cacgacatcg cgctgctccg cctgcaccag cccgtggtcc tcactgacca tgtggtgccc 780

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gtcagcggct ggggccagct gctggaccgt ggcgccacgg ccctggagct catggtcctc 900

aacgtgcccc ggctgatgac ccaggactgc ctgcagcagt cacggaaggt gggagactcc 960

ccacagatca cggagtacat gttctgtgcc ggctactcgg atggcagcaa ggactcctgc 1020

aaggggaca gtggaggccc acatgccacc cactaccggg gcacgtggta cctgacgggc 1080

atcgtcagct ggggccaggg ctgcgcaacc gtgggccact ttggggtgta caccagggtc 1140

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<211> 1218
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid sequence

<400> 12
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tggatttctt acagtgatgg ggaccagtgt gcctcaagtc catgccagaa tgggggctcc 180

tgcaaggacc agctccagtc ctatatctgc ttctgcctcc ctgccttcga gggccggaac 240

tgtgagacgc acaaggatga ccagctgatc tgtgtgaacg agaacggcgg ctgtgagcag 300

tactgcagtg accacacggg caccaagcgc tcctgtcggt gccacgaggg gtactctctg 360

ctggcagacg gggtgtcctg cacacccaca gttgaatatc catgtggaaa aatacctatt 420

ctagaaaaaa gaaatgccag caaaccccaa ggccgaattg tgggggggcaa ggtgtgcccc 480

aaaggggagt gtccatggca ggtcctgttg ttggtgaatg gagctcagtt gtgtgggggg 540

accctgatca acaccatctg ggtggtctcc gcggcccact gtttcgacaa aatcaagaac 600

tggaggaacc tgatcgcggt gctgggcgag cacgacctca gcgagcacga cggggatgag 660

cagagccggc gggtggcgca ggtcatcatc cccagcacgt acgtcccggg caccaccaac 720

cacgacatcg cgctgctccg cctgcaccag cccgtggtcc tcactgacca tgtggtgccc 780

ctctgcctgc ccgaacggac gttctctgag aggacgctgg ccttcgtgcg cttctcattg 840

gtcagcggct ggggccagct gctggaccgt ggcgccacgg ccctggagct catggtcctc 900

aacgtgcccc ggctgatgac ccaggactgc ctgcagcagt cacggaaggt gggagactcc 960

ccaaatatca cggagtacat gttctgtgcc ggctactcgg atggcagcaa ggactcctgc 1020

aaggggggaca gtggaggccc acatgccacc cactaccggg gcacgtggta cctgacgggc 1080

atcgtcagct ggggccaggg ctgcgcaacc gtgggccact ttggggtgta caccagggtc 1140

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ctgcgagccc catttccc 1218

<210> 13
<211> 1218
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid sequence

<400> 13
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cagtgctcct tcgaggaggc ccgggagatc ttcgaagacg aagaggaaac gaagctgttc 120

tggatttctt acagtgatgg ggaccagtgt gcctcaagtc catgccagaa tgggggctcc 180

tgcaaggacc agctccagtc ctatatctgc ttctgcctcc ctgccttcga gggccggaac 240

tgtgagacgc acaaggatga ccagctgatc tgtgtgaacg agaacggcgg ctgtgagcag 300

tactgcagtg accacacggg caccaagcgc tcctgtcggt gccacgaggg gtactctctg 360

ctggcagacg gggtgtcctg cacacccaca gttgaatatc catgtggaaa aatacctatt 420

ctagaaaaaa gacaggccag caaaccccaa ggccgaattg tgggggggcaa ggtgtgcccc 480

aaaggggagt gtccatggca ggtcctgttg ttggtgaatg gagctcagtt gtgtgggggg 540

accctgatca acaccatctg ggtggtctcc gcggcccact gtttcgacaa aatcaagaac 600

tggaggaacc tgatcgcggt gctgggcgag cacgacctca gcgagcacga cggggatgag 660

cagagccggc gggtggcgca ggtcatcatc cccagcacgt acgtcccggg caccaccaac 720

cacgacatcg cgctgctccg cctgcaccag cccgtggtcc tcactgacca tgtggtgccc 780

ctctgcctgc ccgaacggac gttctctgag aggacgctgg ccttcgtgcg cttctcattg 840

gtcagcggct ggggccagct gctggaccgt ggcgccacgg ccctggagct catggtcctc 900

aacgtgcccc ggctgatgac ccaggactgc ctgcagcagt cacggaaggt gggagactcc 960

ccaaatatca cggagtacat gttctgtgcc ggctactcgg atggcagcaa ggactcctgc 1020

aaggggaca gtggaggccc acatgccacc cactaccggg gcacgtggta cctgacgggc 1080

atcgtcagct ggggccaggg ctgcgcaacc gtgggccact ttggggtgta caccagggtc 1140

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ctgcgagccc catttccc 1218

<210> 14
<211> 1218
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid sequence

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tggatttctt acagtgatgg ggaccagtgt gcctcaagtc catgccagaa tgggggctcc 180

tgcaaggacc agctccagtc ctatatctgc ttctgcctcc ctgccttcga gggccggaac 240

tgtgagacgc acaaggatga ccagctgatc tgtgtgaacg agaacggcgg ctgtgagcag 300

tactgcagtg accacacggg caccaagcgc tcctgtcggt gccacgaggg gtactctctg 360

ctggcagacg gggtgtcctg cacacccaca gttgaatatc catgtggaaa aatacctatt 420

ctagaaaaaa gaaatgccag caaaccccaa ggccgaattg tgggggcaa ggtgtgcccc 480

aaaggggagt gtccatggca ggtcctgttg ttggtgaatg gagctcagtt gtgtgggggg 540

accctgatca acaccatctg ggtggtctcc gcggcccact gtttcgacaa aatcaagaac 600

tggaggaacc tgatcgcggt gctgggcgag cacgacctca gcgagcacga cggggatgag 660

cagagccggc gggtggcgca ggtcatcatc cccagcacgt acgtcccggg caccaccaac 720

cacgacatcg cgctgctccg cctgcaccag cccgtggtcc tcactgacca tgtggtgccc 780

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aacgtgcccc ggctgatgac ccaggactgc ctgcagcagt cacggaaggt gggagactcc 960

ccacagatca cggagtacat gttctgtgcc ggctactcgg atggcagcaa ggactcctgc 1020

aaggggaca gtggaggccc acatgccacc cactaccggg gcacgtggta cctgacgggc 1080

atcgtcagct ggggccaggg ctgcgcaacc gtgggccact ttggggtgta caccagggtc 1140

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ctgcgagccc catttccc 1218

<210> 15
<211> 1218
<212> DNA

<213> Artificial Sequence

<220>
<223> Plasmid sequence

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cagtgctcct tcgaggaggc ccgggagatc ttcgaagacg aagaggaaac gaagctgttc 120

tggatttctt acagtgatgg ggaccagtgt gcctcaagtc catgccagaa tgggggctcc 180

tgcaaggacc agctccagtc ctatatctgc ttctgcctcc ctgccttcga gggccggaac 240

tgtgagacgc acaaggatga ccagctgatc tgtgtgaacg agaacggcgg ctgtgagcag 300

tactgcagtg accacacggg caccaagcgc tcctgtcggt gccacgaggg gtactctctg 360

ctggcagacg gggtgtcctg cacacccaca gttgaatatc catgtggaaa aatacctatt 420

ctagaaaaaa gacaggccag caaaccccaa ggccgaattg tgggggcaa ggtgtgcccc 480

aaaggggagt gtccatggca ggtcctgttg ttggtgaatg gagctcagtt gtgtgggggg 540

accctgatca acaccatctg ggtggtctcc gcggcccact gtttcgacaa aatcaagaac 600

tggaggaacc tgatcgcggt gctgggcgag cacgacctca gcgagcacga cggggatgag 660

cagagccggc gggtggcgca ggtcatcatc cccagcacgt acgtcccggg caccaccaac 720

cacgacatcg cgctgctccg cctgcaccag cccgtggtcc tcactgacca tgtggtgccc 780

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ctgcgagccc catttccc 1218

<210> 16
<211> 406
<212> PRT
<213> Homo sapiens

<400> 16

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Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys
20 25 30

Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
35 40 45

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Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
    50                  55                  60

Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
65                  70                  75                  80

Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
                85                  90                  95

Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
            100                 105                 110

Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
        115                 120                 125

Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
    130                 135                 140

Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
145                 150                 155                 160

Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
                165                 170                 175

Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
            180                 185                 190

His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
        195                 200                 205

Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
    210                 215                 220

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
225                 230                 235                 240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
                245                 250                 255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
            260                 265                 270

Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
        275                 280                 285

Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
    290                 295                 300

Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
305                 310                 315                 320
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Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
325 330 335

Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
340 345 350

Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
355 360 365

Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
370 375 380

Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
385 390 395 400

Leu Arg Ala Pro Phe Pro
405

<210> 17
<211> 407
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant human FVII peptide sequence

<220>
<221> misc_feature
<222> (407)..(407)
<223> Xaa can be any naturally occurring amino acid

<400> 17

Ala Asn Ala Phe Leu Glu Glu Leu Arg Gln Gly Ser Leu Glu Arg Glu
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Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Glu
20 25 30

Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
35 40 45

Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
50 55 60

Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
65 70 75 80

Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
85 90 95

Gly Cys Glu Gln Tyr Cys Ser Asp His Asn Gly Thr Lys Arg Ser Cys
100 105 110

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Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
        115                 120                 125

Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
    130                 135                 140

Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
145                 150                 155                 160

Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
                165                 170                 175

Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
            180                 185                 190

His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
        195                 200                 205

Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
    210                 215                 220

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
225                 230                 235                 240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Asn Leu Thr Asp
                245                 250                 255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
            260                 265                 270

Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
        275                 280                 285

Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
    290                 295                 300

Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
305                 310                 315                 320

Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
                325                 330                 335

Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
            340                 345                 350

Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
        355                 360                 365

Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
    370                 375                 380
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Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
385                 390                 395                 400


Leu Arg Ala Pro Phe Pro Xaa
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<210> 18
<211> 406
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant human FVII peptide sequence

<400> 18

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1               5                   10                  15


Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Glu
            20                  25                  30


Asp Glu Glu Glu Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
        35                  40                  45


Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
    50                  55                  60


Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
65                  70                  75                  80


Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
                85                  90                  95


Gly Cys Glu Gln Tyr Cys Ser Asp His Asn Gly Thr Lys Arg Ser Cys
            100                 105                 110


Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
        115                 120                 125


Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
    130                 135                 140


Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
145                 150                 155                 160


Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
                165                 170                 175


Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
            180                 185                 190


His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
        195                 200                 205
```

```
Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
    210                 215                 220

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
225                 230                 235                 240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Asn Leu Thr Asp
                245                 250                 255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
            260                 265                 270

Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
        275                 280                 285

Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
    290                 295                 300

Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
305                 310                 315                 320

Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
                325                 330                 335

Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
            340                 345                 350

Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
        355                 360                 365

Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
    370                 375                 380

Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
385                 390                 395                 400

Leu Arg Ala Pro Phe Pro
                405
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