WILD TYPE FACTOR VII

GCCAACGCGTTCCTGGAGGAGCTGCGGCCGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGAAATGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCAAATATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTACC
TGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTAC
ACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 1)

V1

GCCAACGCGTTCCTGGAGGAGCTGCGGCAGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCGAAGACGCGGAGAGGACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACAACGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGAAATGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGAACCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCAAATATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTACC
TGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTAC
ACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCCT

Figure 1A

V2

GCCAACGCGTTCCTGGAGGAGCTGCGGCAGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCGAAGACGAAGAGGAAACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACAACGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGAAATGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGAACCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCAAATATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTACC
TGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTAC
ACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 3)

pMB113

GCCAACGCGTTCCTGGAGGAGCTGCGGCCGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGAAATGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCAAATATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTACC
TGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTAC
ACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 4)

Figure 1B

pMB114

GCCAACGCGTTCCTGGAGGAGCTGCGGCCGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGACAGGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCAAATATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTACC
TGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTAC
ACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 5)

pMB115

GCCAACGCGTTCCTGGAGGAGCTGCGGCCGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGAAATGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCACAGATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGG
ACTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTAC
CTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTA
CACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 6)

Figure 1C

pMB116

GCCAACGCGTTCCTGGAGGAGCTGCGGCCGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGACAGGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCACAGATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGG
ACTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTAC
CTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTA
CACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 7)

pMB117

GCCAACGCGTTCCTGGAGGAGCTGCGGCAGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCGAAGACGCGGAGAGGACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGAAATGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCAAATATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTACC
TGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTAC
ACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 8)

Figure 1D

pMB118

GCCAACGCGTTCCTGGAGGAGCTGCGGCAGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCGAAGACGCGGAGAGGACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGACAGGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCAAATATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTACC
TGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTAC
ACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 9)

pMB119

GCCAACGCGTTCCTGGAGGAGCTGCGGCAGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCGAAGACGCGGAGAGGACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGAAATGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCACAGATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGG
ACTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTAC
CTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTA
CACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 10)

Figure 1E

pMB120

GCCAACGCGTTCCTGGAGGAGCTGCGGCAGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCGAAGACGCGGAGAGGACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGACAGGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCACAGATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGG
ACTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTAC
CTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTA
CACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 11)

pMB121

GCCAACGCGTTCCTGGAGGAGCTGCGGCAGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCGAAGACGAAGAGGAAACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGAAATGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCAAATATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTACC
TGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTAC
ACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 12)

Figure 1F

pMB122

GCCAACGCGTTCCTGGAGGAGCTGCGGCAGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCGAAGACGAAGAGGAAACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGACAGGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCAAATATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTACC
TGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTAC
ACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 13)

pMB123

GCCAACGCGTTCCTGGAGGAGCTGCGGCAGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCGAAGACGAAGAGGAAACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGAAATGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCACAGATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGG
ACTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTAC
CTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTA
CACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 14)

Figure 1G

pMB124

GCCAACGCGTTCCTGGAGGAGCTGCGGCAGGGCTCCCTGGAGAGGGAGTGCAAGGAGGA
GCAGTGCTCCTTCGAGGAGGCCCGGGAGATCTTCGAAGACGAAGAGGAAACGAAGCTGT
TCTGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCAGAATGGGGGCT
CCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCTGCCTCCCTGCCTTCGAGGGCCGGA
ACTGTGAGACGCACAAGGATGACCAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAG
CAGTACTGCAGTGACCACACGGGCACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACTCT
CTGCTGGCAGACGGGGTGTCCTGCACACCCACAGTTGAATATCCATGTGGAAAAATACCT
ATTCTAGAAAAAAGACAGGCCAGCAAACCCCAAGGCCGAATTGTGGGGGGCAAGGTGTG
CCCCAAAGGGGAGTGTCCATGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGG
GGGGACCCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAAAATCAA
GAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGACCTCAGCGAGCACGACGGGG
ATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATCCCCAGCACGTACGTCCCGGGCACC
ACCAACCACGACATCGCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTG
GTGCCCCTCTGCCTGCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTCGTGCGCTTC
TCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGGCGCCACGGCCCTGGAGCTCATG
GTCCTCAACGTGCCCCGGCTGATGACCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGG
AGACTCCCCACAGATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGG
ACTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGGGCACGTGGTAC
CTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCAACCGTGGGCCACTTTGGGGTGTA
CACCAGGGTCTCCCAGTACATCGAGTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCC
AGGAGTCCTCCTGCGAGCCCCATTTCCC (SEQ ID NO: 15)

Figure 1H

Wild Type Factor VII Peptide

ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGDQCASSPCQNGGS
CKDQLQSYICFCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSL
LADGVSCTPTVEYPCGKIPILEKRNASKPQGRIVGGKVCPKGECPWQVLLLVNGAQLCGG
TLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDEQSRRVAQVIIPSTYVPGTTN
HDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGATALELMVL
NVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTG
IVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFP (SEQ ID NO: 16)

V1 Peptide

ANAFLEELR**Q**GSLERECKEEQCSFEEAREIF**E**DAERTKLFWISYSDGDQCASSPCQNGGS
CKDQLQSYICFCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDH**N**GTKRSCRCHEGYSL
LADGVSCTPTVEYPCGKIPILEKRNASKPQGRIVGGKVCPKGECPWQVLLLVNGAQLCGG
TLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDEQSRRVAQVIIPSTYVPGTTN
HDIALLRLHQPV**N**LTDHVVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGATALELMVL
NVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTG
IVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFP (SEQ ID NO: 17)

V2 Peptide

ANAFLEELR**Q**GSLERECKEEQCSFEEAREIF**EDEEE**TKLFWISYSDGDQCASSPCQNGGS
CKDQLQSYICFCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDH**N**GTKRSCRCHEGYSL
LADGVSCTPTVEYPCGKIPILEKRNASKPQGRIVGGKVCPKGECPWQVLLLVNGAQLCGG
TLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDEQSRRVAQVIIPSTYVPGTTN
HDIALLRLHQPV**N**LTDHVVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGATALELMVL
NVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTG
IVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFP (SEQ ID NO: 18)

Figure 2

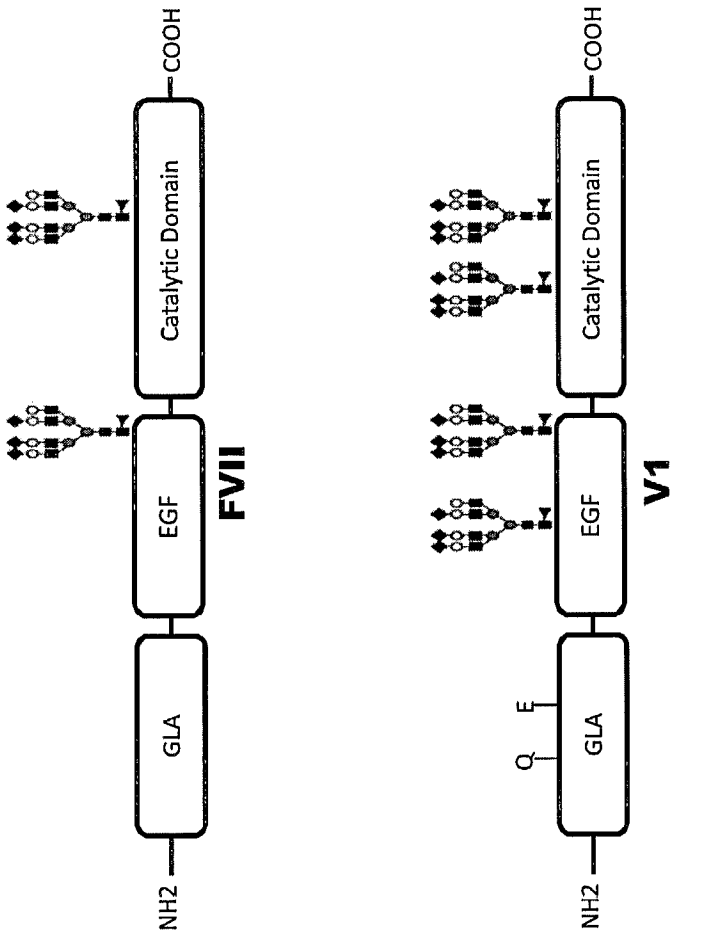
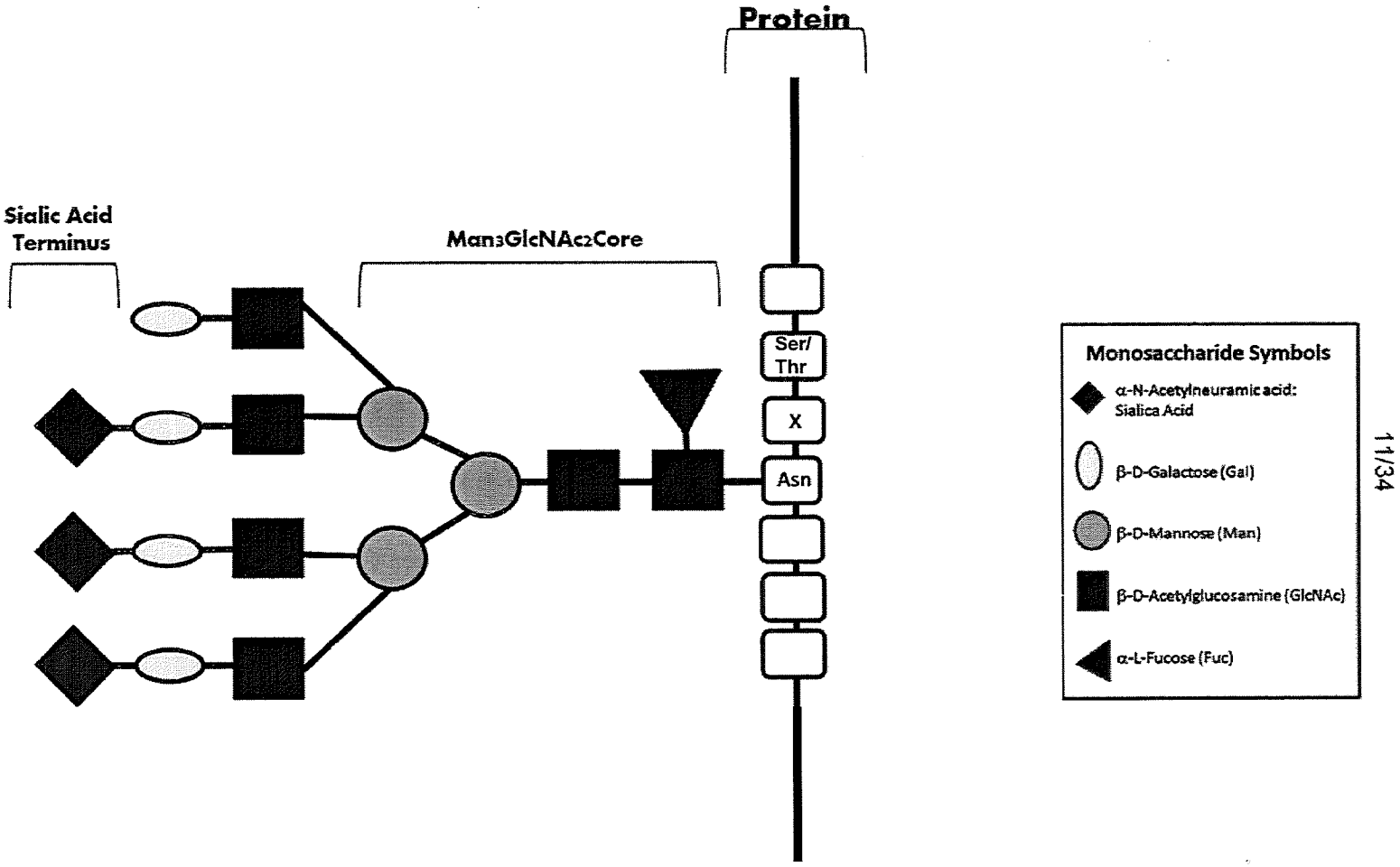

COOH
Catalytic Domain
EGF
GLA
NH2
FVII
COOH
Catalytic Domain
EGF
Q E
GLA
NH2
V1
COOH
Catalytic Domain
EGF
Q E E E
GLA
NH2
V2

Figure 3



Example of a complex N-linked glycan

Figure 4

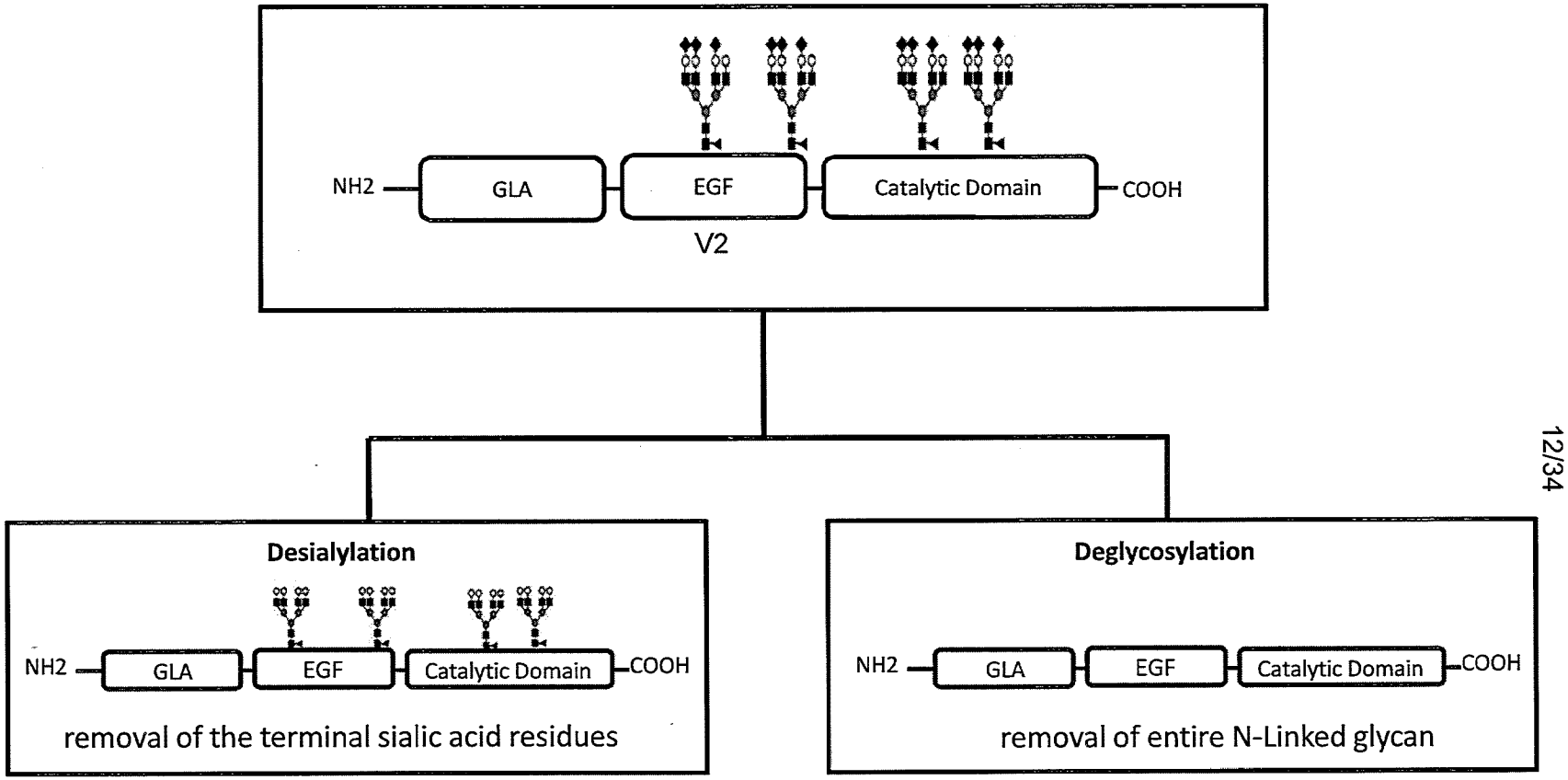
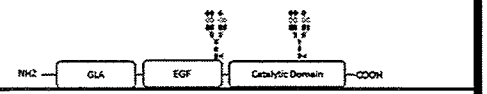
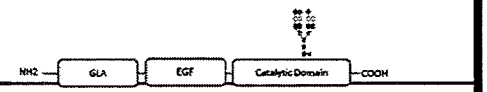
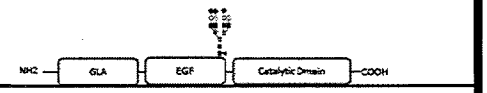
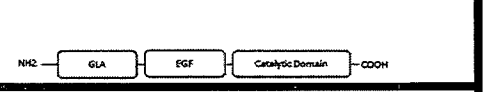
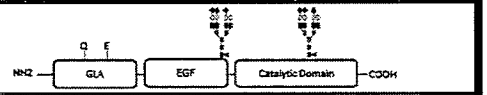
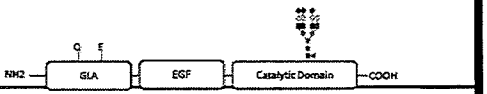
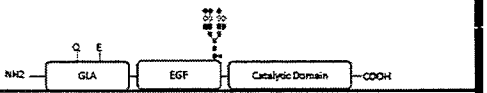
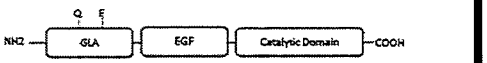
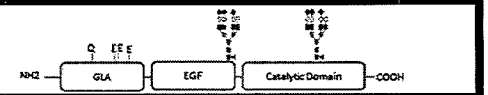
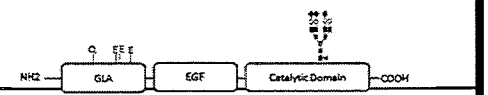
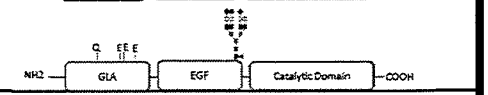
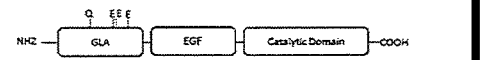

NH2
GLA
EGF
Catalytic Domain
COOH
V2
Desialylation
NH2
GLA
EGF
Catalytic Domain
COOH
removal of the terminal sialic acid residues
Deglycosylation
NH2
GLA
EGF
Catalytic Domain
COOH
removal of entire N-Linked glycan

Figure 5

Figure 6

pMB number	Backbone	N-glycosylation sites	
pMB113	F7wt	N145, N322	
pMB114		N145Q, N322	
pMB115		N145, N322Q	
pMB116		N145Q,N322Q	
pMB117	V1	N145, N322	
pMB118		N145Q, N322	
pMB119		N145, N322Q	
pMB120		N145Q,N322Q	
pMB121	V2	N145, N322	
pMB122		N145Q, N322	
pMB123		N145, N322Q	
pMB124		N145Q,N322Q	

Human FVII-B0189, heavy chain

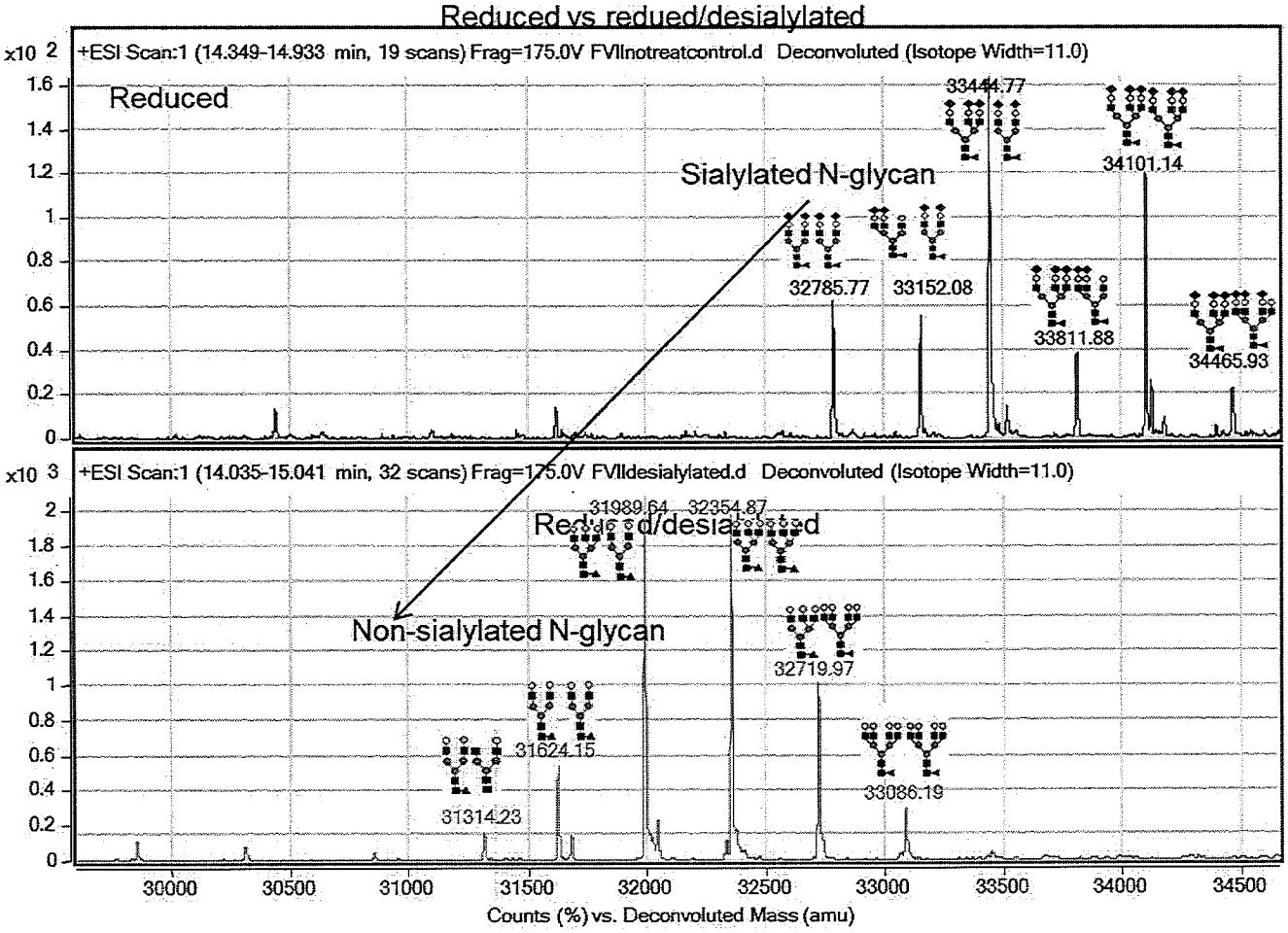
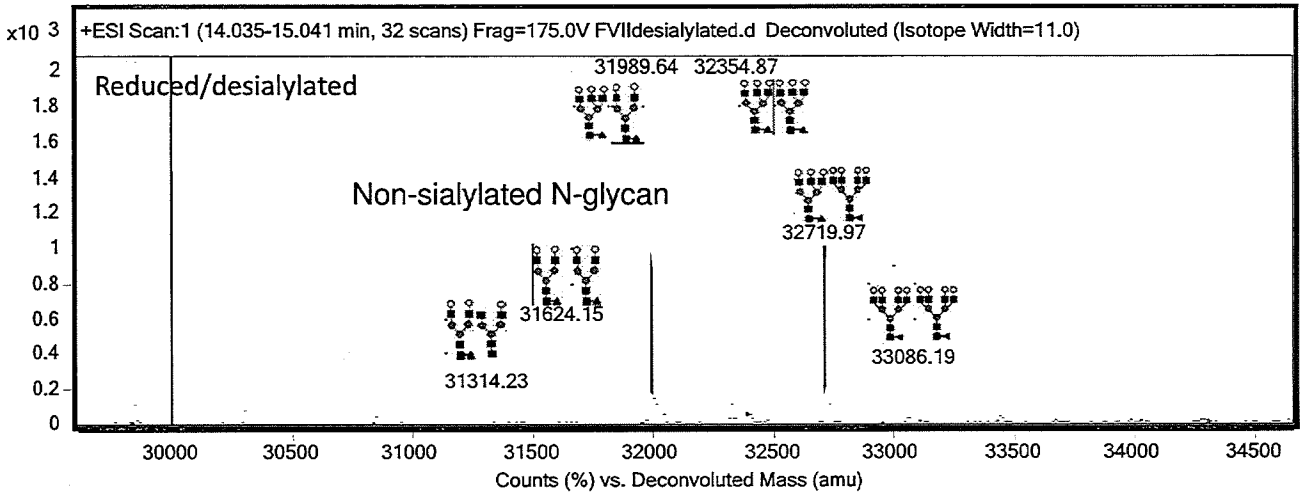


Figure 7


x10 3
+ESI Scan:1 (14.035-15.041 min, 32 scans) Frag=175.0V FVIIdesialylated.d Deconvoluted (Isotope Width=11.0)
Reduced/desialylated
31989.64
32354.87
Non-sialylated N-glycan
32719.97
31624.15
31314.23
33086.19
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
30000
30500
31000
31500
32000
32500
33000
33500
34000
34500
Counts (%) vs. Deconvoluted Mass (amu)

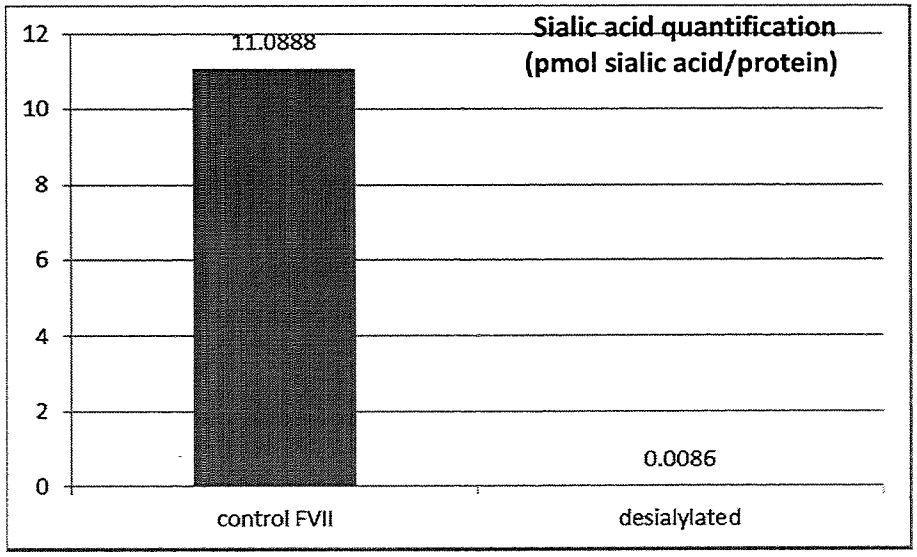

Sialic acid quantification
(pmol sialic acid/protein)
11.0888
0.0086
12
10
8
6
4
2
0
control FVII
desialylated

Figure 8

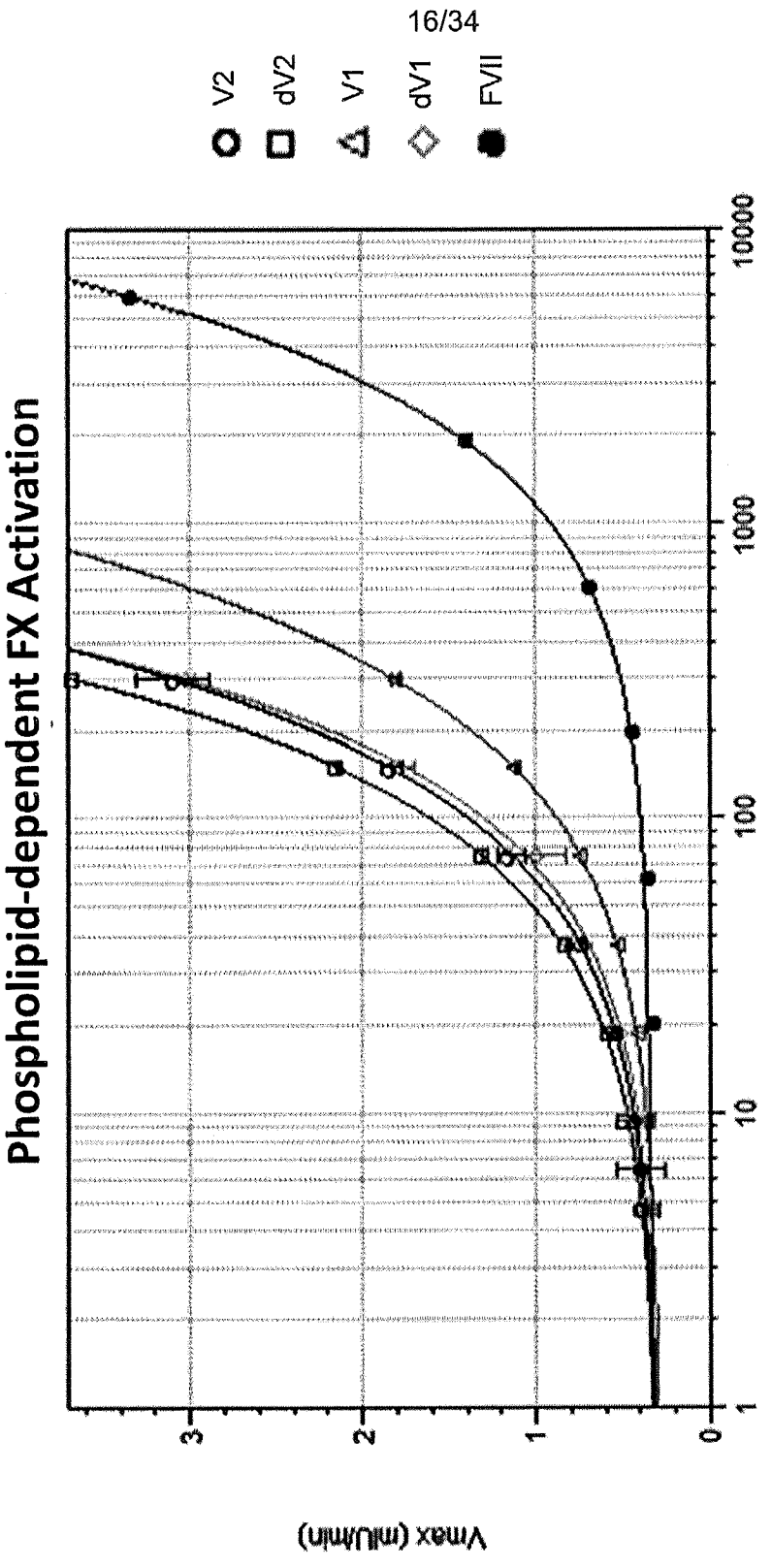
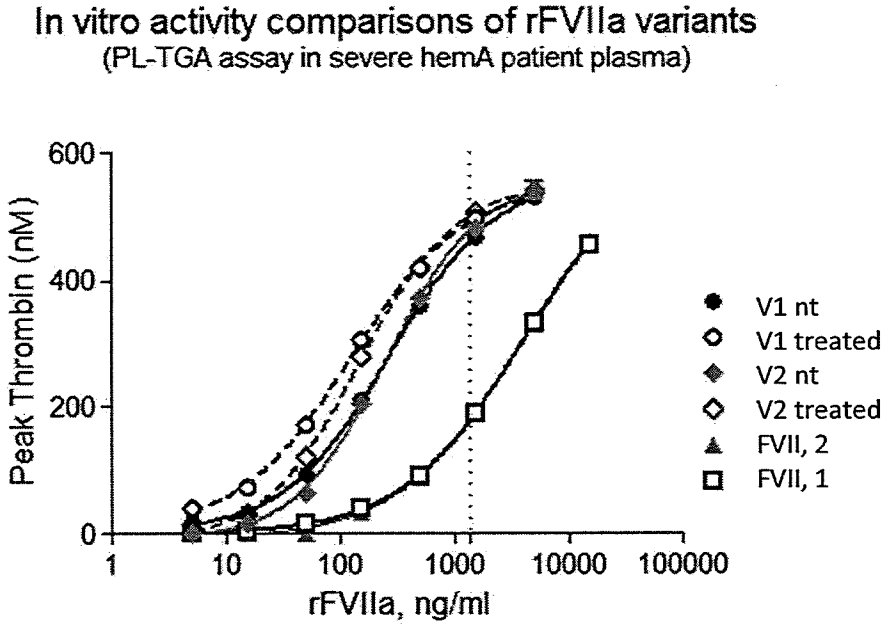

Phospholipid-dependent FX Activation
V2
dV2
V1
dV1
FVII
Vmax (mIU/min)
FVII ng/mL
0
1
2
3
1
10
100
1000
10000

Figure 9



Amount of thrombin generated by 1300 ng/ml of various rFVIIa proteins

	V1 no treatment	V1 treatment	V2 no treatment	V2 treatment	FVII
Peak Thrombin	463 nM	492 nM	480 nM	502 nM	178 nM
Fold Over FVII	2.60	2.76	2.70	2.82	1

Figure 10

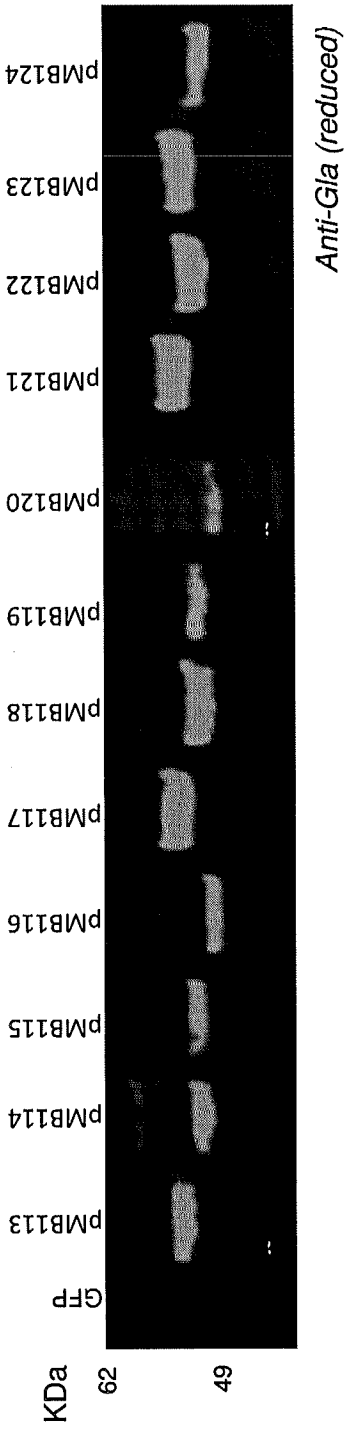
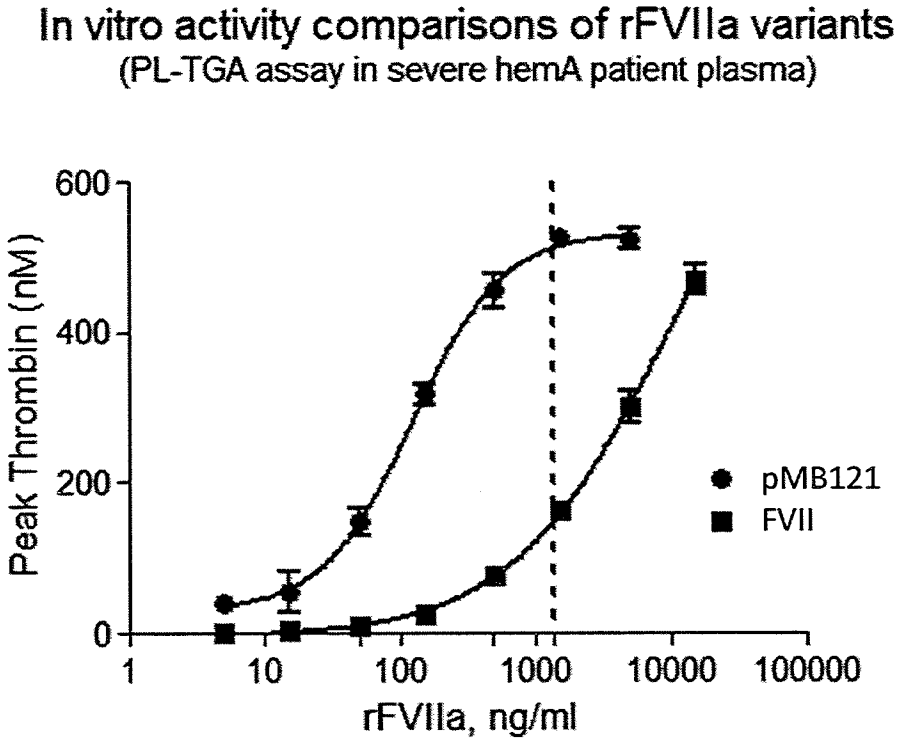

Anti-Gla (reduced)
pMB124
pMB123
pMB122
pMB121
pMB120
pMB119
pMB118
pMB117
pMB116
pMB115
pMB114
pMB113
GFP
KDa
62
49

Figure 11

	FVII Chromo (ng/ml)	FVII ELISA (ng/ml)	Chromo/ELISA ratio
pMB113	740.4	788.2	0.9
pMB114	619.8	601.0	1.0
pMB115	554.2	426.8	1.3
pMB116	498.9	430.0	1.2
pMB117	1248.3	870.8	1.4
pMB118	1272.1	890.5	1.4
pMB119	601.7	346.8	1.7
pMB120	292	236.8	1.2
pMB121	166.3	808.2	0.2
pMB122	155.6	711.9	0.2
pMB123	181.5	514.5	0.4
pMB124	78.9	277.2	0.3

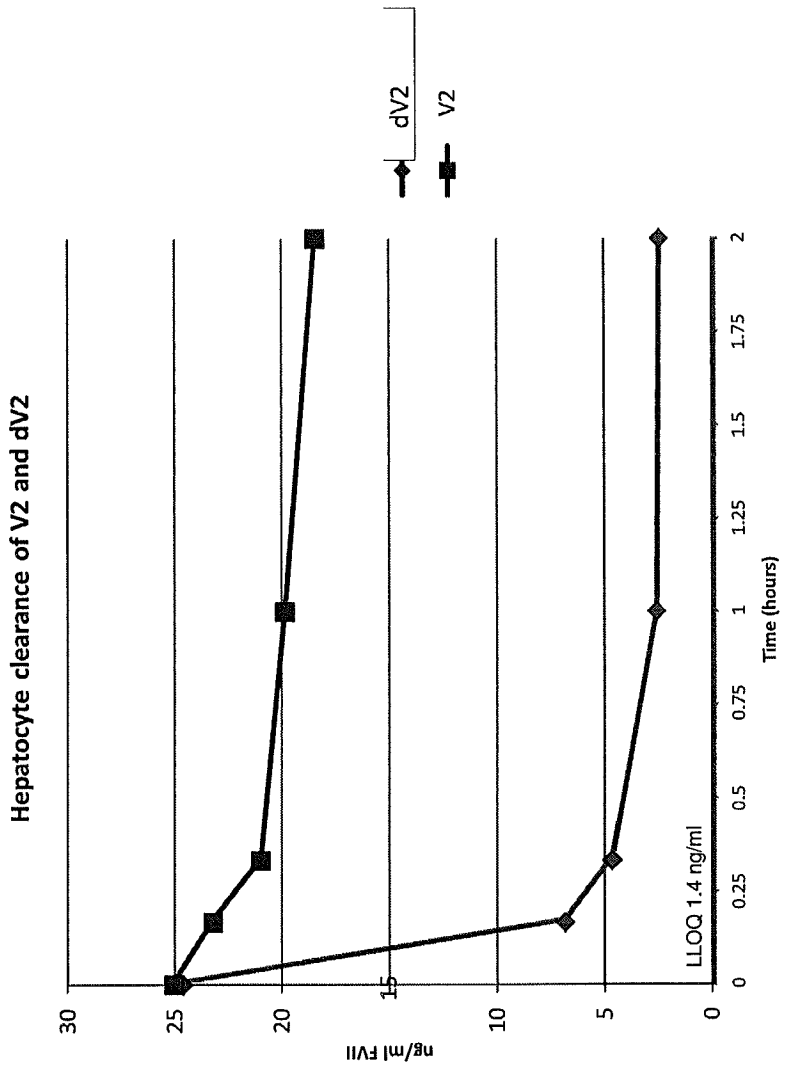
Figure 12



	pMB121	FVII
Peak Thrombin	511 nM	148 nM
Fold Over FVII	3.45	1

Figure 13

Figure 14


Hepatocyte clearance of V2 and dV2
dV2
V2
ng/ml FVII
30
25
20
15
10
5
0
LLOQ 1.4 ng/ml
0
0.25
0.5
0.75
1
1.25
1.5
1.75
2
Time (hours)

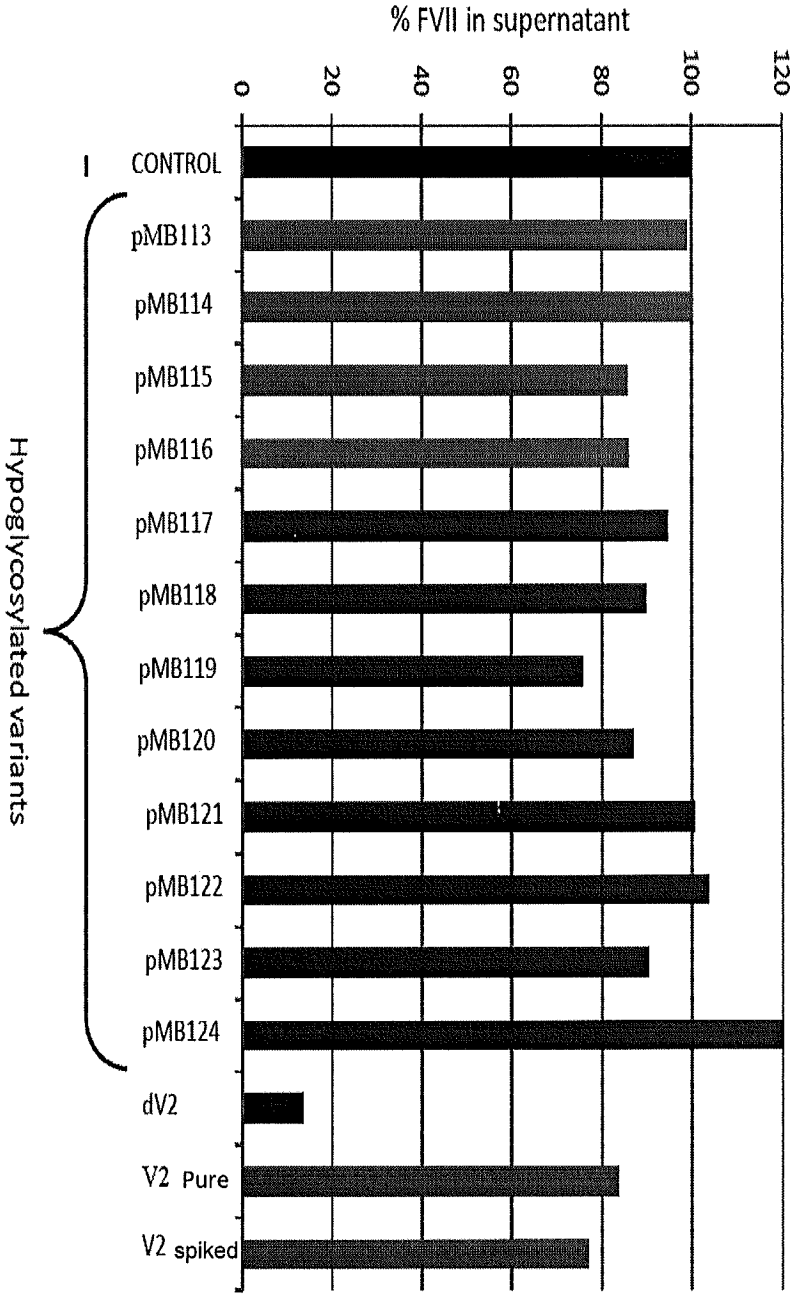
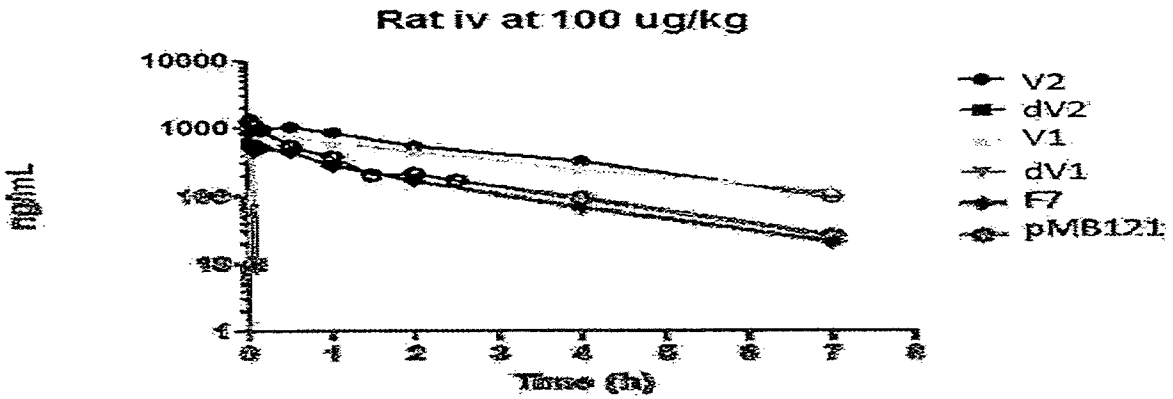

% FVII in supernatant
0
20
40
60
80
100
120
CONTROL
pMB113
pMB114
pMB115
pMB116
pMB117
pMB118
pMB119
pMB120
pMB121
pMB122
pMB123
pMB124
dV2
V2 Pure
V2 spiked
Hypoglycosylated variants

Figure 15

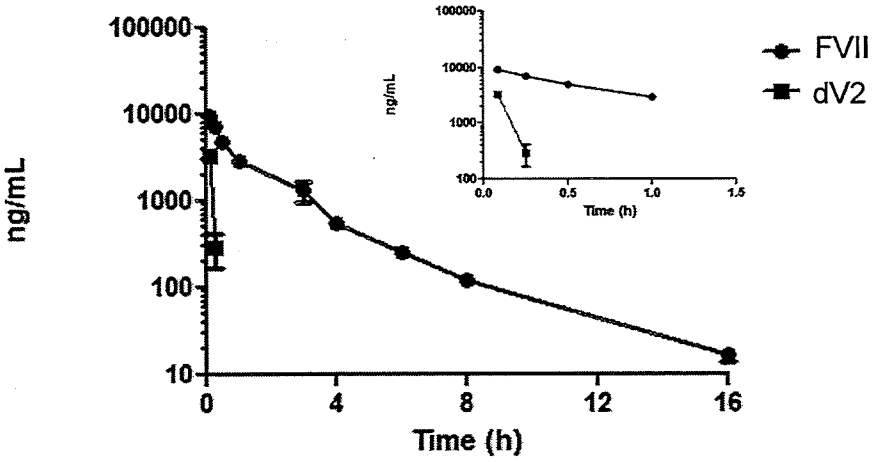


	$T_{1/2}$ (h)	MRT (h)	CL(mL/h/kg)	Vss(Ll/kg)
V2	2.7	3.3	26	80
V1	2.5	3.3	33	109
F7	1.6	2.0	91	181
pMB121	1.6	1.9	68	129
dV2	~ 1 min	n.c.	n.c.	n.c.
dV1	~ 1 min	n.c.	n.c.	n.c.

Figure 16

Figure 17

A) ELISA Assay



	T1/2 (h)	MRT (h)	CL (ml/h/kg)	Vss (ml/kg)
FVII	2.6	1.9	79	152
dV2	~ 3 min	n.c.	n.c.	n.c.

B) soluble TF PTT clotting assay

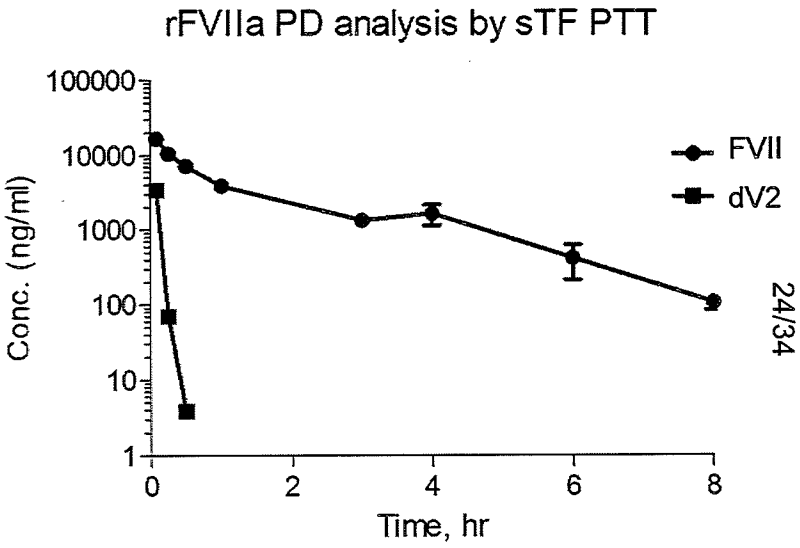
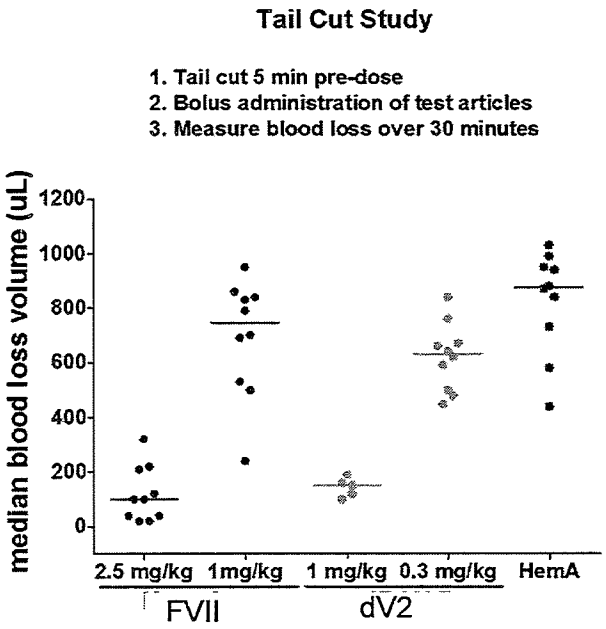
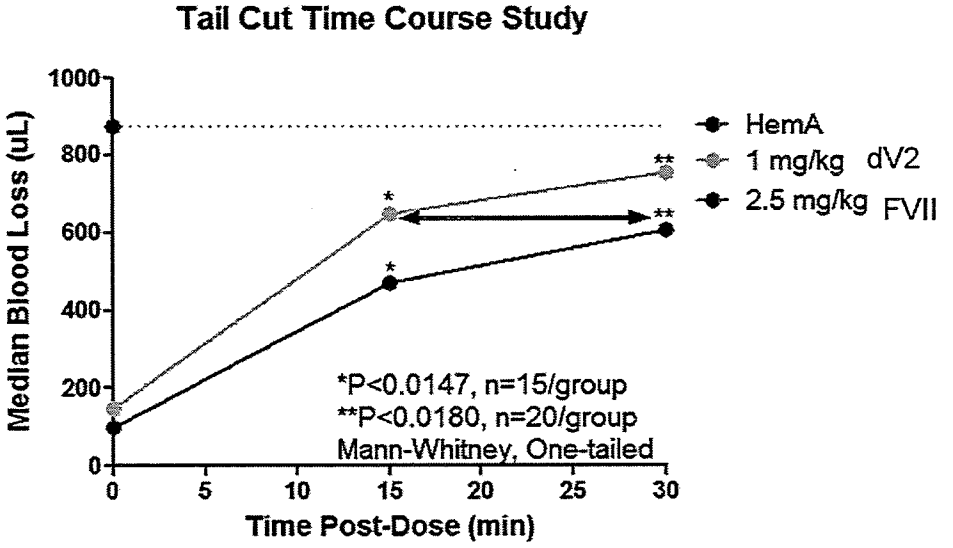


Figure 18

A)


Tail Cut Study
1. Tail cut 5 min pre-dose
2. Bolus administration of test articles
3. Measure blood loss over 30 minutes
median blood loss volume (uL)
1200
1000
800
600
400
200
0
2.5 mg/kg
1mg/kg
1 mg/kg
0.3 mg/kg
HemA
FVII
dV2

B)


Tail Cut Time Course Study
Median Blood Loss (uL)
1000
800
600
400
200
0
0
5
10
15
20
25
30
Time Post-Dose (min)
HemA
1 mg/kg dV2
2.5 mg/kg FVII
*P<0.0147, n=15/group
**P<0.0180, n=20/group
Mann-Whitney, One-tailed

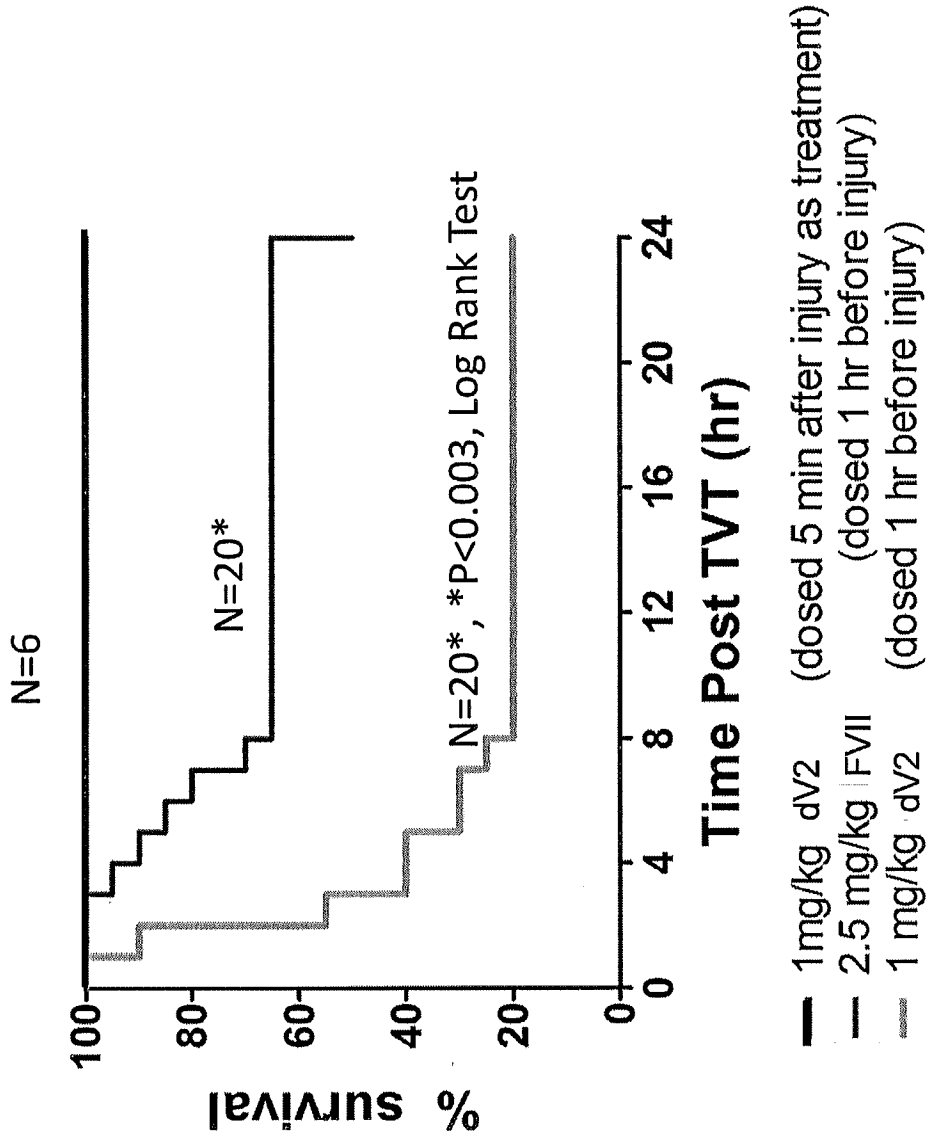

N=6
N=20*
N=20*, *P<0.003, Log Rank Test
% survival
100
80
60
40
20
0
0
4
8
12
16
20
24
Time Post TVT (hr)
1mg/kg dV2 (dosed 5 min after injury as treatment)
2.5 mg/kg FVII (dosed 1 hr before injury)
1 mg/kg dV2 (dosed 1 hr before injury)

Figure 19

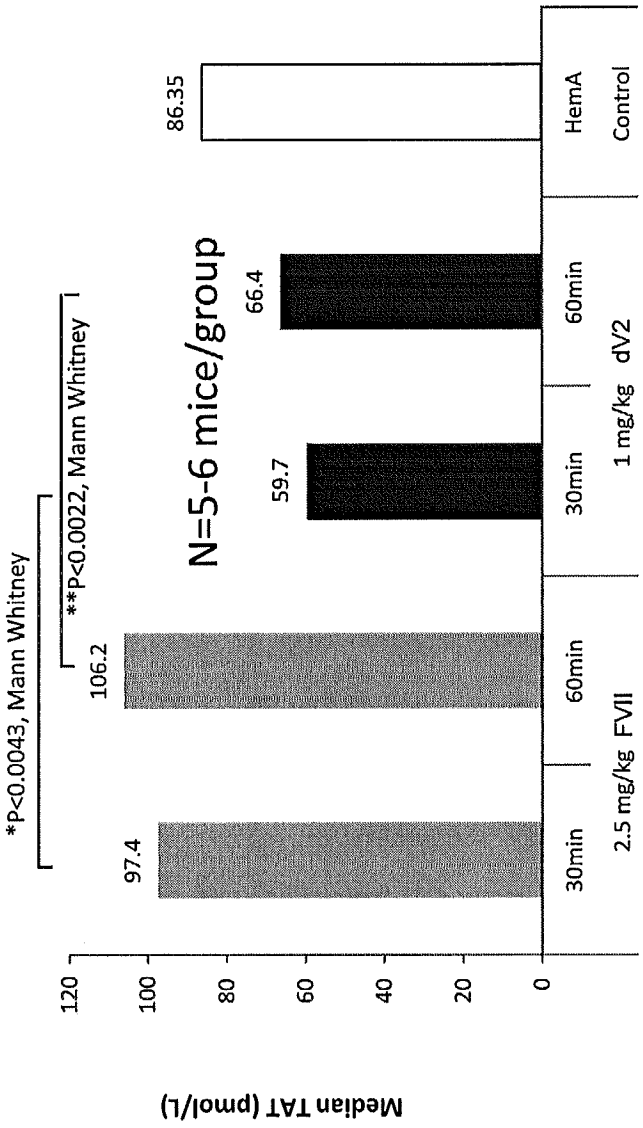

*P<0.0043, Mann Whitney
**P<0.0022, Mann Whitney
N=5-6 mice/group
97.4
106.2
59.7
66.4
86.35
120
100
80
60
40
20
0
Median TAT (pmol/L)
30min
60min
30min
60min
HemA
Control
2.5 mg/kg FVII
1 mg/kg dV2
Time After Dosing

Figure 20

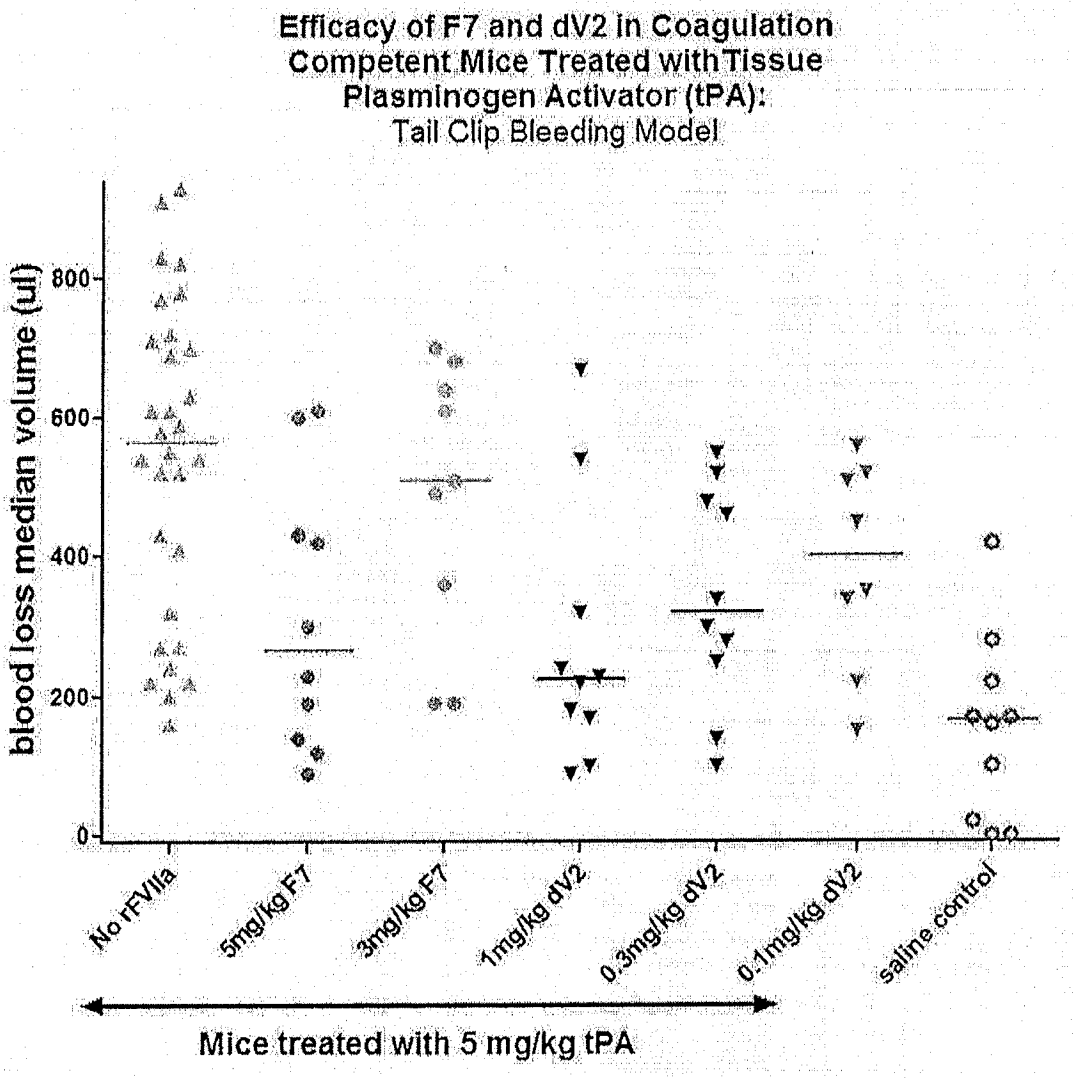
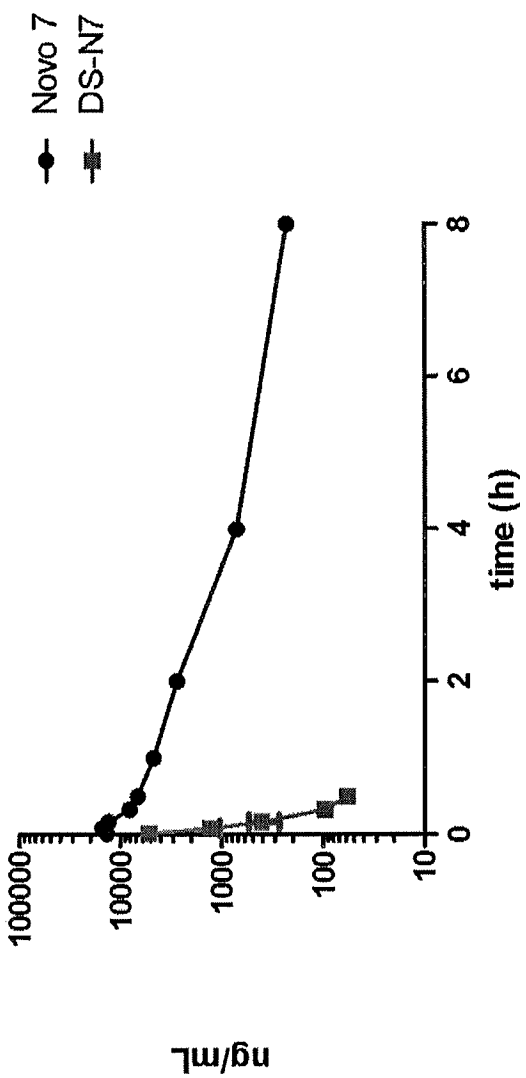

Efficacy of F7 and dV2 in Coagulation Competent Mice Treated with Tissue Plasminogen Activator (tPA): Tail Clip Bleeding Model
blood loss median volume (ul)
800
600
400
200
0
No rFVIIa
5mg/kg F7
3mg/kg F7
1mg/kg dV2
0.3mg/kg dV2
0.1mg/kg dV2
saline control
Mice treated with 5 mg/kg tPA

Figure 21



	T1/2 (h)	MRT (h)	CL (ml/h/kg)	Vss (ml/kg)
F7	1.7	1.9	59	110
dF7	0.12	0.09	2400	210

Figure 22

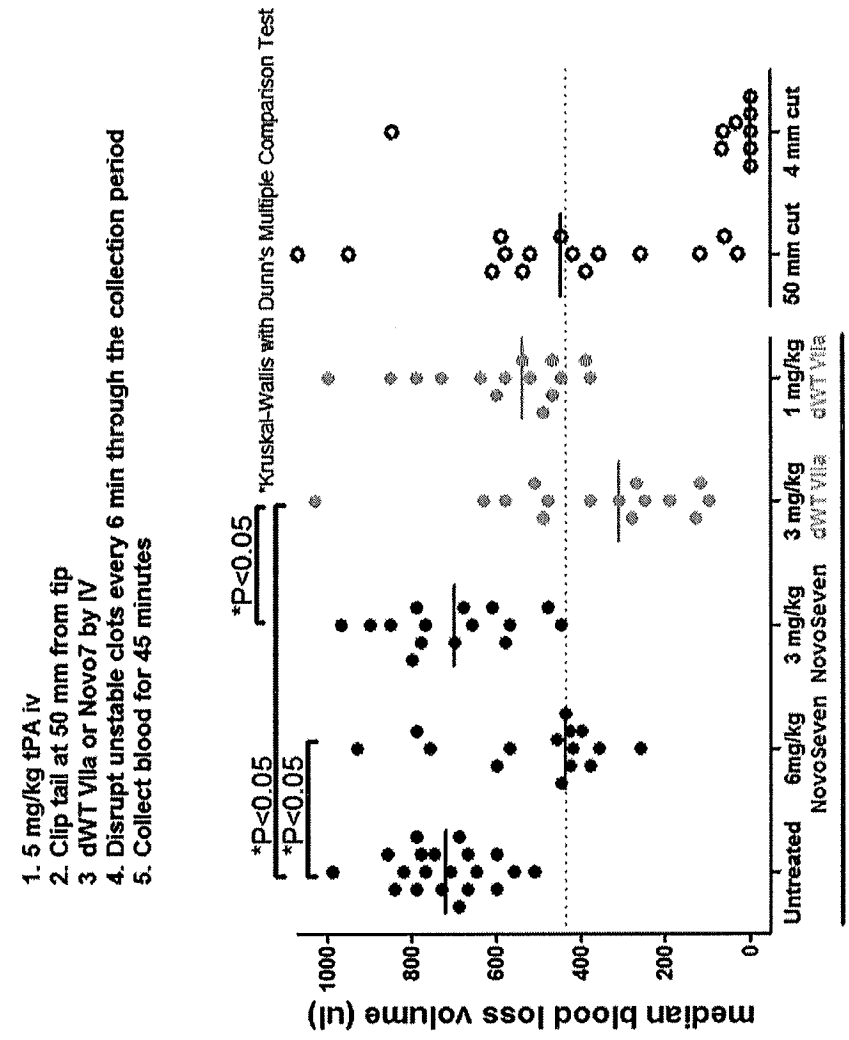
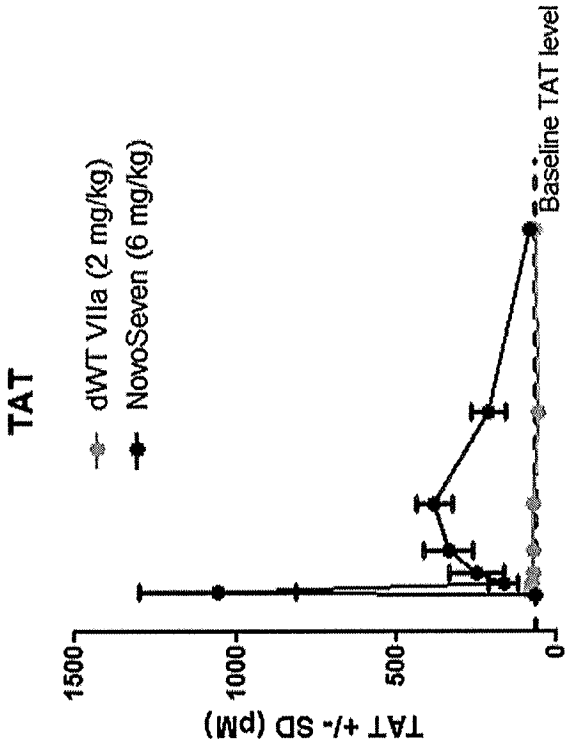

Tail Cut Study
1. 5 mg/kg tPA iv
2. Clip tail at 50 mm from tip
3 dWT VIIa or Novo7 by IV
4. Disrupt unstable clots every 6 min through the collection period
5. Collect blood for 45 minutes
*P<0.05
*P<0.05
*P<0.05
*Kruskal-Wallis with Dunn's Multiple Comparison Test
median blood loss volume (ul)
1000
800
600
400
200
0
Untreated
6mg/kg NovoSeven
3 mg/kg NovoSeven
3 mg/kg dWT VIIa
1 mg/kg dWT VIIa
50 mm cut
4 mm cut
50 mm cut + 5 mg/kg tPA

Figure 23



	AUC above baseline
2 mg/kg dWT VIIa	0
6 mg/kg NovoSeven	1352

Figure 24

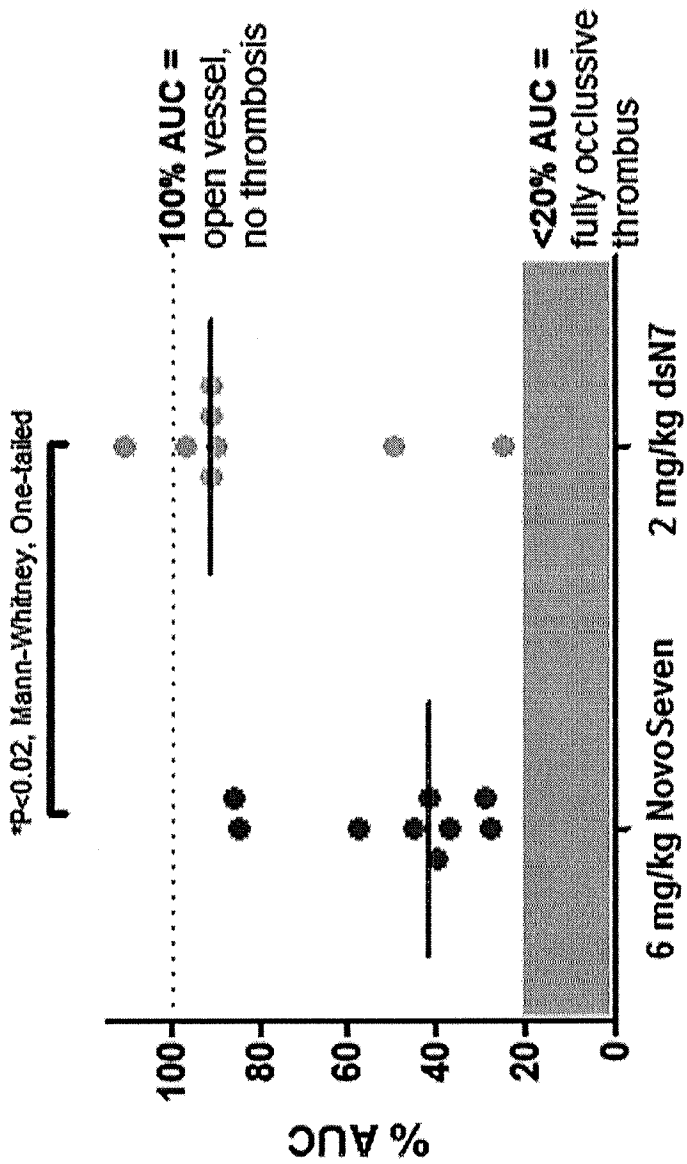

*P<0.02, Mann-Whitney, One-tailed
100% AUC =
open vessel,
no thrombosis
<20% AUC =
fully occlussive
thrombus
% AUC
100
80
60
40
20
0
6 mg/kg NovoSeven
2 mg/kg dsN7

Figure 25

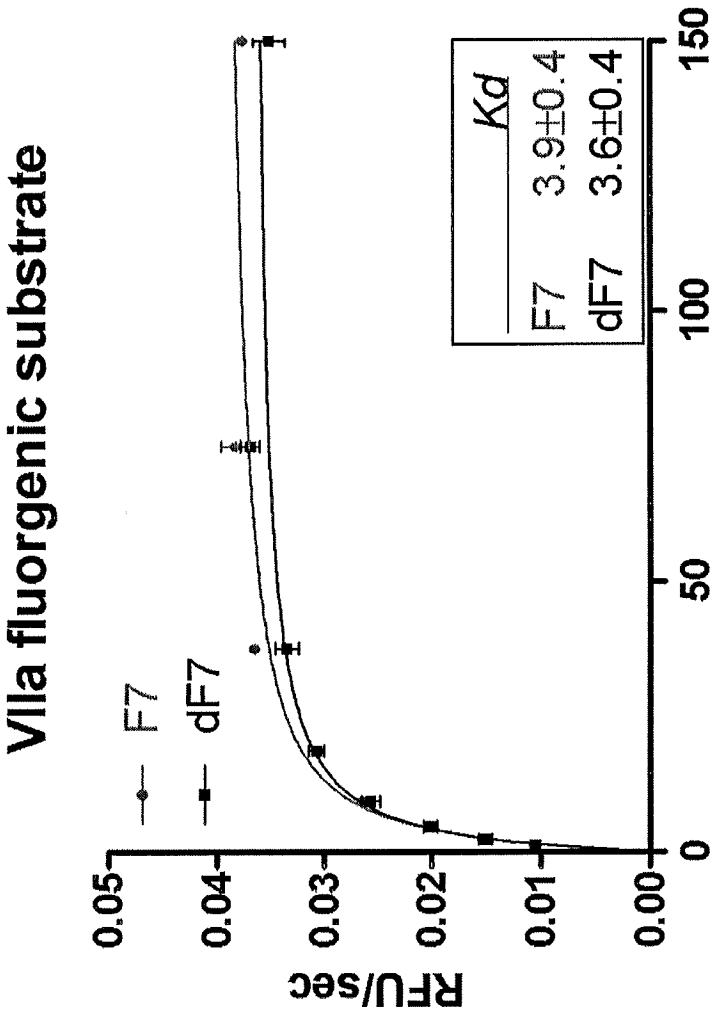

VIIa fluorgenic substrate
F7
dF7
RFU/sec
0.05
0.04
0.03
0.02
0.01
0.00
0
50
100
150
nM sTF
Kd
F7 3.9±0.4
dF7 3.6±0.4

Figure 26

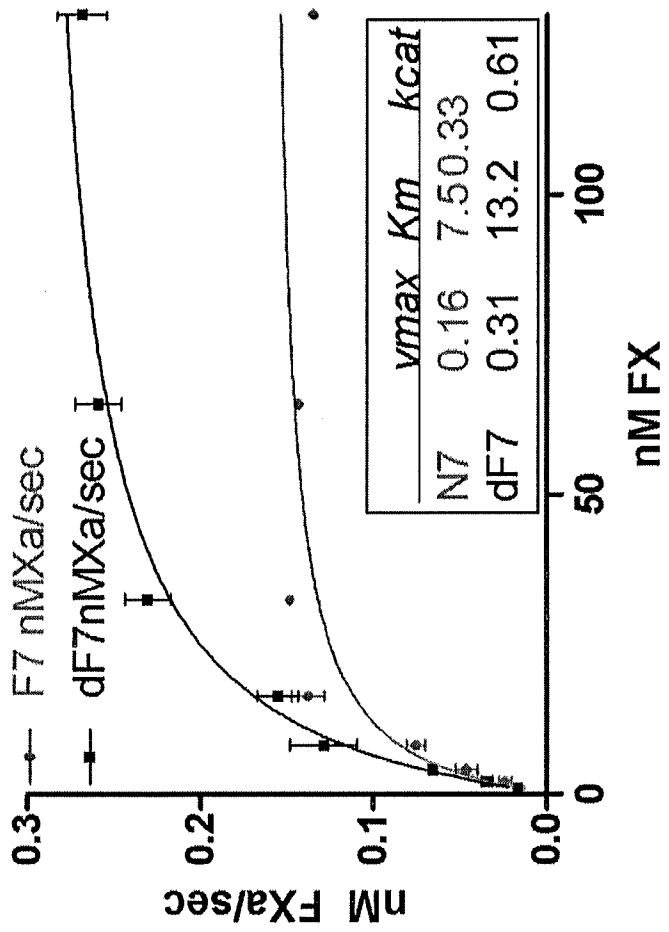

F7 nMXa/sec
dF7nMXa/sec
nM FXa/sec
0.3
0.2
0.1
0.0
0
50
100
nM FX
vmax Km kcat
N7 0.16 7.5 0.33
dF7 0.31 13.2 0.61

Figure 27