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(73) Patenthaver: **Bioverativ Therapeutics Inc., 225 Second Avenue, Waltham, MA 02451, USA**

(72) Opfinder: **CHHABRA, Ekta, Seth, 1550 Worcester Road 128, Framingham, MA 01702, USA**
LIU, Tongyao, 53 Buckman Drive, Lexington, MA 02421, USA
PETERS, Robert, T., 53 Parkinson Street, Needham, MA 02492, USA
KULMAN, John, 88 Creeley Road, Belmont, MA 02478, USA
CHANG, Pei-yun, 27 Liberty Road, Bedford, MA 01730, USA

(74) Fuldmægtig i Danmark: **RWS Group, Europa House, Chiltern Park, Chiltern Hill, Chalfont St Peter, Bucks SL9 9FG, Storbritannien**

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DESCRIPTION

BACKGROUND OF THE INVENTION

[0001] Haemophilia A is a bleeding disorder caused by defects in the gene encoding coagulation factor VIII (FVIII) and affects 1-2 in 10,000 male births. Graw et al., Nat. Rev. Genet. 6(6): 488-501 (2005). Patients affected with hemophilia A can be treated with infusion of purified or recombinantly produced FVIII. All commercially available FVIII products, however, are known to have a half-life of about 8-12 hours, requiring frequent intravenous administration to the patients. *See* Weiner M.A. and Cairo, M.S., Pediatric Hematology Secrets, Lee, M.T., 12. Disorders of Coagulation, Elsevier Health Sciences, 2001; Lillicrap, D. Thromb. Res. 122 Suppl 4:S2-8 (2008). In addition, a number of approaches have been tried in order to extend the FVIII half-life. For example, the approaches in development to extend the half-life of clotting factors include pegylation, glycopegylation, and conjugation with albumin. See Dumont et al., Blood. 119(13): 3024-3030 (Published online Jan. 13, 2012). Regardless of the protein engineering used, however, the long acting FVIII products currently under development are reported to have limited half-lives - only to about 1.5 to 2 hours in preclinical animal models. *See id.* Consistent results have been demonstrated in humans, for example, rFVIIIFc was reported to improve half-life up to ~ 1.7 fold compared with ADVATE® in hemophilia A patients. *See Id.* Therefore, the half-life increases, despite minor improvements, may indicate the presence of other T1/2 limiting factors. *See* Liu, T. et al., 2007 ISTH meeting, abstract #P-M-035; Henrik, A. et al., 2011 ISTH meeting, abstract #P=MO-181; Liu, T. et al., 2011 ISTH meeting abstract #P-WE-131.

[0002] Plasma von Willebrand Factor (VWF) has a half-life of approximately 12 hours (ranging from 9 to 15 hours). http://www.nhlbi.nih.gov/guidelines/vwd/2_scientificoverview.htm (last visited October 22, 2011). The VWF half-life may be affected by a number of factors: glycosylation pattern, ADAMTS-13 (a disintegrin and metalloprotease with thrombospondin motif-13), and various mutations in VWF.

[0003] In plasma, 95-98% of FVIII circulates in a tight non-covalent complex with full-length VWF. The formation of this complex is important for the maintenance of appropriate plasma levels of FVIII in vivo. Lenting et al., Blood. 92(11): 3983-96 (1998); Lenting et al., J. Thromb. Haemost. 5(7): 1353-60 (2007). The full-length wild-type FVIII is mostly present as a heterodimer having a heavy chain (MW 200kD) and a light chain (MW 73kD). When FVIII is activated due to proteolysis at positions 372 and 740 in the heavy chain and at position 1689 in the light chain, the VWF bound to FVIII is removed from the activated FVIII. The activated FVIII, together with activated factor IX, calcium, and phospholipid ("tenase complex"), induces the activation of factor X, generating large amounts of thrombin. Thrombin, in turn, then cleaves fibrinogen to form soluble fibrin monomers, which then spontaneously polymerize to form the soluble fibrin polymer. Thrombin also activates factor XIII, which, together with calcium, serves to crosslink and stabilize the soluble fibrin polymer, forming crosslinked (insoluble) fibrin. The activated FVIII is cleared fast from the circulation by proteolysis.

[0004] Due to the frequent dosing and inconvenience caused by the dosing schedule, there is still a need to develop FVIII products requiring less frequent administration, *i.e.,* a FVIII product that has a half-life longer than the 1.5 to 2 fold half-life limitation.

[0005] WO 2011/060242 describes methods, compositions and kits for preparing FVIII and employing the same. This document also describes VWF polypeptides and nucleic acid molecules encoding VWF polypeptides.

[0006] WO 2011/069164 describes methods of administering FVIII and chimeric and hybrid polypeptides comprising FVIII. It also describes polynucleotides encoding such chimeric and hybrid polypeptides, cells comprising such polynucleotides and methods of producing chimeric and hybrid polypeptides using those cells.

[0007] Schellenberger et al. (Nat. Biotechnol. (2009) 27(12):1186-90) shows that genetic fusion of XTEN to a peptide or protein provides an approach to extend plasma half-life.

BRIEF SUMMARY OF THE INVENTION

[0008] Based on the disclosure that is contained herein, the present invention provides a chimeric protein comprising (i) a von Willebrand Factor (VWF) fragment comprising the D' domain and the D3 domain of VWF, (ii) an extended length polypeptide (XTEN) sequence, (iii) a factor VIII (FVIII) protein, (iv) a first Ig constant region or a portion thereof, and (v) a second Ig constant region or a portion thereof,
wherein the VWF fragment and the XTEN sequence are linked by an optional linker,
wherein the XTEN sequence or the VWF fragment is linked to the first Ig constant region or a portion thereof,
wherein the FVIII protein is linked to the second Ig constant region or a portion thereof, and
wherein the first Ig constant region or a portion thereof is associated with or linked to the second Ig constant region or a portion thereof by a covalent bond.

[0009] In some embodiments, the chimeric protein comprises a formula comprising:

(g) V-L2-X-L1-F1:FVIII-L3-F2;

(h) V-L2-X-L1-F1:F2-L3-FVIII;

(i) F1-L1-X-L2-V:FVIII-L3-F2;

(j) F1-L1-X-L2-V:F2-L3-FVIII;

(k) V-L2-X-L1-F1-L4-FVIII-L3-F2;

(l) F2-L3-FVIII-L4-F1-LL1-X-L2-V;

(m) FVIII-L3-F2-L4-V-L2-X-L1-F1; or

(n) F1-L1-X-L2-V-L4-F2-L3-FVIII,

wherein V is a VWF fragment,

each of L1, L2, and L3 is an optional linker, *e.g.,* a cleavable linker,

L4 is an optional linker, *e.g.,* a processable linker,

FVIII comprises a FVIII protein,

X comprises one or more XTEN sequences,

F1 is a first Ig constant region or a portion thereof,

F2 is a second Ig constant region or a portion thereof, and

(:) is a covalent bond.

[0010] Non-limiting examples of the chimeric proteins may comprise a formula, which comprises:

(1) FVIII(X1)-L1-F1:V-L2-X2-L3-F2;

(2) FVIII(X1)-L1-F1:F2-L3-X2-L2-V;

(3) F1-L1-FVIII(X1):V-L2-X2-L3-F2;

(4) F1-L1-FVIII(X1):F2-L3-X2-L2-V;

(5) FVIII(X1)-L1-F1-L4-V-L2-X2-L3-F2;

(6) FVIII(X1)-L1-F1-L4-F2-L3-X2-L2-V;

(7) F1-L1-FVIII(X1)-L4-V-L2-X2-L3-F2,

or

(8) F1-L1-FVIII(X1)-L4-F2-L3-X2-L2-V,

wherein FVIII(X1) comprises a FVIII protein and one or more XTEN sequences, wherein one or more of the XTEN sequences are linked to the N-terminus or C-terminus of the FVIII protein or inserted immediately downstream of one or more amino acids in the FVIII protein (*e.g.*, one or more XTEN insertion sites);

each of L1, L2, or L3 is an optional linker, *e.g.,* a cleavable linker;

L4 is a linker, a processable linker;

X2 is a second XTEN sequence;

F1 is an Ig constant region or a portion thereof;

F2 an optional additional Ig constant region or a portion thereof, and V is a VWF fragment;

(-) is a peptide bond; and

(:) is a covalent bond.

[0011] One aspect of the invention is that the VWF fragment useful for the chimeric protein does not bind to a VWF clearance receptor, which prevents or inhibits interaction of the FVIII protein with endogenous VWF. The chimeric protein comprising the VWF fragment thus has reduced clearance or is not cleared through a VWF clearance pathway. Another aspect of the invention is that the VWF fragment is capable of protecting the FVIII protein from one or more protease cleavages, protecting the FVIII protein from activation, stabilizing the heavy chain and/or the light chain of the FVIII protein, or preventing clearance of the FVIII protein by one or more scavenger receptors.

[0012] Because of the VWF fragment's ability to prevent or inhibit interaction between the FVIII protein and endogenous VWF, the half-life of the FVIII protein, is extended compared to a FVIII protein without the VWF fragment. In one embodiment, the half-life of the FVIII protein is extended at least about 1.5 times, at least about 2 times, at least about 2.5 times, at least about 3 times, at least about 4 times, at least about 5 times, at least about 6 times, at least about 7 times, at least about 8 times, at least about 9 times, at least about 10 times, at least about 11 times, or at least about 12 times longer than wild type FVIII. In another embodiment, the half-life of the FVIII protein is at least about 10 hours, at least about 11 hours, at least about 12 hours, at least about 13 hours, at least about 14 hours, at least about 15 hours, at least about 16 hours, at least about 17 hours, at least about 18 hours, at least about 19 hours, at least about 20 hours, at least about 21 hours, at least about 22 hours, at least about 23 hours, at least about 24 hours, at least about 36 hours, at least about 48 hours, at least about 60 hours, at least about 72 hours, at least about 84 hours, at least about 96 hours, or at least about 108 hours.

[0013] The Ig constant region or a portion thereof useful in the present invention and the additional Ig constant region or a portion thereof useful in the present invention are identical or different.

[0014] In some aspects, the FVIII protein is linked to an XTEN sequence at the C-terminus or the N-terminus of the FVIII protein or inserted immediately downstream of one or more amino acids in mature native human FVIII (*e.g.,* one or more insertion sites) or any combinations thereof. One or more insertion sites in the FVIII protein can be located within one or more domains of the FVIII protein selected from the group consisting of the A1 domain, the a1 acidic region, the A2 domain, the a2 acidic region, the A3 domain, the B domain, the C1 domain, the C2 domain, and any combinations thereof or between one or more domains of the FVIII protein selected from the group consisting of the A1 domain and a1 acidic region, the a1 acidic region and A2 domain, the A2 domain and a2 acidic region, the a2 acidic region and B domain, the B domain and A3 domain, the A3 domain and C1 domain, the C1 domain and C2 domain, and any combinations thereof or between two domains of the FVIII protein selected from the group consisting of the A1 domain and a1 acidic region, the a1 acidic region and A2 domain, the A2 domain and a2 acidic region, the a2 acidic region and B domain, the B domain and A3 domain, the A3 domain and C1 domain, the C1 domain and C2 domain, and any combinations thereof.

[0015] In one embodiment, the one or more insertion sites are located immediately downstream of one or more amino acids in mature native human FVIII (*e.g.,* SEQ ID NO: **4** [mature FVIII sequence-full length]) selected from the group consisting of the amino acid residues in Table 7, 8, 9, 10, 11, or any combinations thereof.

[0016] In another embodiment, the one or more insertion sites are located in one or more permissive loops of mature native human FVIII. In other embodiments, the one or more insertion sites are located in the a3 region of mature native human FVIII. For example, an XTEN sequence can be inserted immediately downstream of amino acid 1656 corresponding to SEQ ID NO: **4** (full length mature FVIII). In other embodiments, a FVIII protein is linked to at least two XTEN sequences, a first XTEN sequence inserted within the a3 region, and a second XTEN sequence inserted within a permissive loop in the FVIII protein (*e.g.*, A1-1, A1-2, A2-1, A2-2, A3-1, or A3-2). In still other embodiments, a FVIII protein is linked to at least three XTEN sequences, a first XTEN sequence inserted within the a3 region and a second XTEN sequence and a third XTEN sequence inserted within one or two permissive loop in the FVIII protein (*e.g.,* A1-1, A1-2, A2-1, A2-2, A3-1, or A3-2).

[0017] In certain embodiments, the one or more insertion sites for one or more XTEN insertions are immediately downstream of one or more amino acids (numbered relative to mature FVIII sequence) selected from the group consisting of:
(1) amino acid 3, (2) amino acid 18, (3) amino acid 22, (4) amino acid 26, (5) amino acid 32, (6) amino acid 40, (7) amino acid 60, (8) amino acid 65, (9) amino acid 81, (10) amino acid 116, (11) amino acid 119, (12) amino acid 130, (13) amino acid 188, (14) amino acid 211, (15) amino acid 216, (16) amino acid 220, (17) amino acid 224, (18) amino acid 230, (19) amino acid 333, (20) amino acid 336, (21) amino acid 339, (22) amino acid 375, (23) amino acid 399, (24) amino acid 403, (25) amino acid 409, (26) amino acid 416, (26) amino acid 442, (28) amino acid 487, (29) amino acid 490, (30) amino acid 494, (31) amino acid 500, (32) amino acid 518, (33) amino acid 599, (34) amino acid 603, (35) amino acid 713, (36) amino acid 745, (37) amino acid 1656, (38) amino acid 1711, (39) amino acid 1720,
(40) amino acid 1725, (41) amino acid 1749, (42) amino acid 1796,
(43) amino acid 1802, (44) amino acid 1827, (45) amino acid 1861,
(46) amino acid 1896, (47) amino acid 1900, (48) amino acid 1904,
(49) amino acid 1905, (50) amino acid 1910, (51) amino acid 1937,
(52) amino acid 2019, (53) amino acid 2068, (54) amino acid 2111,
(55) amino acid 2120, (56) amino acid 2171, (57) amino acid 2188,
(58) amino acid 2227, (59) amino acid 2277, and
(60) two or more combinations thereof.

[0018] In some embodiments, one XTEN is inserted in the FVIII protein. In some embodiments, two XTENs are inserted in the FVIII protein. In some embodiments, 3 XTENs are inserted in the FVIII protein.

[0019] In a particular example, a first XTEN is inserted immediately downstream of amino acid 26 corresponding to SEQ ID NO: 4, and a second XTEN is inserted immediately downstream of amino acid 1720 corresponding to SEQ ID NO: 4 (full-length mature FVIII). In another example, a first XTEN is inserted immediately downstream of amino acid 403 corresponding to SEQ ID NO: 4, and a second XTEN is inserted immediately downstream of amino acid 1720 corresponding to SEQ ID NO: 4. In some examples, a first XTEN is inserted immediately downstream of amino acid 1656 corresponding to SEQ ID NO: 4, and a second XTEN is inserted immediately downstream of amino acid 1720 corresponding to SEQ ID NO: 4. In other examples, a first XTEN is inserted immediately downstream of amino acid 26 corresponding to SEQ ID NO: 4, a second XTEN is inserted immediately downstream of amino acid 1656 corresponding to SEQ ID NO: 4, and a third XTEN is inserted immediately downstream of amino acid 1720 corresponding to SEQ ID NO: 4. In yet other embodiments, a first XTEN is inserted immediately downstream of amino acid 403 corresponding to SEQ ID NO: 4, a second XTEN is inserted immediately downstream of amino acid 1656 corresponding to SEQ ID NO: 4, and a third XTEN is inserted immediately downstream of amino acid 1720 corresponding to SEQ ID NO: 4. In still other embodiments, a first XTEN is inserted between amino acids 403 and 404 corresponding to SEQ ID NO: 4, a second XTEN is inserted immediately downstream of amino acid 1656 corresponding to SEQ ID NO: 4, and a third XTEN is inserted immediately downstream of amino acid 1720 corresponding to SEQ ID NO: 4. In certain embodiments, a first XTEN is inserted immediately downstream of amino acid 26 corresponding to SEQ ID NO: 4 (full-length mature FVIII), a second XTEN is inserted immediately downstream of amino acid 1720 corresponding to SEQ ID NO: 4, and a third XTEN is inserted immediately downstream of amino acid 1900 corresponding to SEQ ID NO: 4. In some embodiments, a first XTEN is inserted immediately downstream of amino acid 26 corresponding to SEQ ID NO: 4, a second XTEN is inserted immediately downstream of amino acid 1656 corresponding to SEQ ID NO: 2, a third XTEN is inserted immediately downstream of amino acid 1720 corresponding to SEQ ID NO: 4, and a fourth XTEN is inserted immediately downstream of amino acid 1900 corresponding to SEQ ID NO: 4. In another example, an XTEN is inserted immediately downstream of amino acid 745 corresponding to SEQ ID NO: 4. In an additional example, a first XTEN is inserted immediately downstream of amino acid 1656 corresponding to SEQ ID NO: 4 and a second XTEN is inserted immediately downstream of amino acid 1900 corresponding to SEQ ID NO: 4. In some embodiments, a first XTEN is inserted immediately downstream of amino acid 26 corresponding to SEQ ID NO: 4, a second XTEN is inserted immediately downstream of amino acid 1656 corresponding to SEQ ID NO: 4, and a third XTEN is inserted immediately downstream of amino acid 1900 corresponding to SEQ ID NO: 4. In another example, a first XTEN is immediately inserted downstream of amino acid 403 corresponding to SEQ ID NO: 4 and a second XTEN is inserted immediately downstream of amino acid 745 corresponding to SEQ ID NO: 4. In some embodiments, a first XTEN is inserted immediately downstream of amino acid 745 of corresponding to SEQ ID NO: 4, and a second XTEN is inserted immediately downstream of amino acid 1900 corresponding to SEQ ID NO: 4. In some embodiments, a first XTEN is inserted immediately downstream of amino acid 18 corresponding to SEQ ID NO: 4, and a second XTEN is inserted immediately downstream of amino acid 745 corresponding to SEQ ID NO: 4.

[0020] In some embodiments, the FVIII protein is a dual chain FVIII isoform. In some embodiments, the FVIII protein is a single chain FVIII isoform.

[0021] In some embodiments, the XTEN that is inserted is SEQ ID NO: 39 (AE288). In some examples, the XTENs that are inserted are SEQ ID NOs: 38 and 37 (AG144 and AE144). In some examples, the XTENs that are inserted are SEQ ID NOs: 37, 38 and 37 (AE144, AG144, and AE144). In some embodiments. the XTENs that are inserted are SEQ ID NOs: 37 and 40 (AE144 and AE288). In some embodiments, the XTENs that are inserted are AE42 (SEQ ID NO: 36), AE72 (SEQ ID NO: 127), AE144_2A (SEQ IDNO: 128), AE144 3B (SEQ ID NO: 129), AE144_4A (SEQ ID NO: 130), AE144_5A (SEQ IDNO: 131), AE144_6B (SEQ IDNO: 132), AG144 A (SEQ ID NO: 133), AG144_B (SEQ IDNO: 134), AG144_C (SEQ ID NO: 135), AG144_F (SEQ IDNO: 136), AE864 (SEQ ID NO: 43), AE576 (SEQ ID NO: 41), AE288 (SEQ IDNO: 39), AE288_2 (SEQ ID NO: 137), AE144 (SEQ ID NO: 37), AG864 (SEQ ID NO: 44), AG576 (SEQ ID NO: 42), AG288 (SEQ ID NO: 40), AG144 (SEQ ID NO: 38), and any combinations thereof.

[0022] The FVIII protein useful in the invention can comprise B domain or a portion thereof, *e.g.,* SQ B domain deleted FVIII. In one embodiment, the FVIII protein comprises single chain FVIII. In another embodiment, the

single chain FVIII contains at least one amino acid substitution at a residue corresponding to residue 1648, residue 1645, or both of full-length mature Factor VIII polypeptide (SEQ ID NO: 4) or residue 754, residue 751, or both of SQ BDD Factor VIII (SEQ ID NO: 6). In other embodiments, the amino acid substitution is an amino acid other than arginine. In some embodiments, the FVIII protein comprises a heavy chain of FVIII and a light chain of FVIII, wherein the heavy chain and the light chain are associated with each other by a metal bond.

[0023] The FVIII protein can have a low affinity to or does not bind to a low-density lipoprotein receptor-related protein (LRP), *e.g.,* by containing at least one amino acid substitution that lowers the affinity to or eliminates the binding to the LRP. Such at least one amino acid substitution can be at a residue corresponding to residue 471, residue 484, residue 487, residue 490, residue 497, residue 2092, residue 2093 or two or more combinations thereof of full-length mature FVIII. In a particular embodiment, the amino acid substitution at residue 471, 484, or 497 is an amino acid other than arginine, the amino acid substitution at residue 487 is an amino acid other than tyrosine, the amino acid substitution at residue 2092 is an amino acid other than lysine, or the amino acid substitution at residue 2093 is an amino acid other than phenylalanine.

[0024] In some embodiments, the FVIII protein contains at least one amino acid substitution, which induces the FVIII protein to be more stable than a FVIII protein without the substitution. Such substitutions can be located in the A2 domain and the A3 domain of the FVIII protein, *e.g.,* at a residue corresponding to residue 664, residue 1826, residue 662, residue 1828, or two or more combinations thereof of full-length mature FVIII.

[0025] The VWF fragment useful for the present invention comprises a D' domain and D3 domain, which together are capable of binding to FVIII. The VWF fragment can comprise the amino acid sequence of the D' domain is at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to amino acids 764 to 866 of SEQ ID NO: 2 and/or the amino acid sequence of the D3 domain is at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to amino acids 867 to 1240 of SEQ ID NO: 2. In one embodiment, the VWF fragment is a monomer. In another embodiment, the VWF fragment comprises at least two VWF fragments, at least three VWF fragments, at least four VWF fragments, at least five VWF fragments, or at least six VWF fragments. In one embodiment, the two or more VWF fragments may be identical or they may be different. The VWF fragment can comprise an amino acid at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to amino acids 764 to 1240 of SEQ ID NO: 2. The VWF fragment may consist essentially of or consist of amino acids 764 to 1240 of SEQ ID NO: 2. In certain embodiments, the VWF fragment can contain at least one amino acid substitution at a residue corresponding to residue 1099, residue 1142, or both residues 1099 and 1142 of SEQ ID NO: 2. In other embodiments, the VWF fragment further comprises the D1 domain, the D2 domain, or the D1 and D2 domains of VWF.

[0026] The VWF fragment may further comprise a VWF domain selected from the group consisting of the A1 domain, the A2 domain, the A3 domain, the D4 domain, the B1 domain, the B2 domain, the B3 domain, the C1 domain, the C2 domain, the CK domain, one or more fragments thereof, and any combinations thereof. For example, the VWF fragment can consist essentially of or consist of: (1) the D' and D3 domains of VWF or fragments thereof; (2) the D1, D', and D3 domains of VWF or fragments thereof; (3) the D2, D', and D3 domains of VWF or fragments thereof; (4) the D1, D2, D', and D3 domains of VWF or fragments thereof; or (5) the D1, D2, D', D3, and A1 domains of VWF or fragments thereof. In some embodiments, the VWF fragment further comprises a signal peptide of VWF or FVIII which is operably linked to the VWF fragment.

[0027] One or more of the linkers useful in the invention have a length of at least about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1200, 1400, 1600, 1800, or 2000 amino acids. In some embodiments, one or more of the linkers have a length of about 1 to about 2000 amino acids. In one embodiment, one or more of the linkers have a length of at least about 20, 35, 42, 48, 73, 75, 95, 98, 144, 288, 324, 333, 576, or 864 amino acids. In another embodiment, one or more of the linkers comprise a gly/ser peptide, an XTEN sequence, or both. Examples of the gly/ser peptide include, but are not limited to, a formula of $(Gly_4Ser)_n$ (SEQ ID NO: 139) or $S(Gly_4Ser)_n$ (SEQ ID NO: 140), wherein n is a positive integer selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9 and 10. For example, the $(Gly_4Ser)_n$ linker can be $(Gly_4Ser)_3$ (SEQ ID NO: 63) or $(Gly_4Ser)_4$ (SEQ ID NO: 138). In one embodiment, the linker comprises at least one first cleavage site at the N-terminus of

the linker, at least one second cleavage site at the C-terminus of the linker, or both. In another embodiment, the linker comprises 20 amino acids, 35 amino acids, 48 amino acids, 73 amino acids, or 95 amino acids thrombin cleavable linker. The cleavable linkers can comprise one or more of the cleavage sites by a protease selected from the group consisting of factor XIa, factor XIIa, kallikrein, factor VIIa, factor IXa, factor Xa, factor IIa (thrombin), Elastase-2, Granzyme-B, TEV, Enterokinase, Protease 3C, Sortase A, MMP-12, MMP-13, MMP-17, and MMP-20, *e.g.*, TLDPRSFLLRNPNDKYEPFWEDEEK (SEQ ID NO: 8). Non-limiting examples of one or more of the cleavage sites comprise an amino acid sequence selected from the group consisting of RRRR (SEQ ID NO: 9), RKRRKR (SEQ ID NO: 10), RRRRS (SEQ ID NO: 11), TQSFNDFTR (SEQ ID NO: 12), SVSQTSKLTR (SEQ ID NO: 13), DFLAEGGGVR (SEQ ID NO: 14), TTKIKPR (SEQ ID NO: 15), LVPRG (SEQ ID NO: 16), ALRPR (SEQ ID NO: 17), KLTRAET (SEQ ID NO: 18), DFTRVVG (SEQ ID NO: 19), TMTRIVGG (SEQ ID NO: 20), SPFRSTGG (SEQ ID NO: 21), LQVRIVGG (SEQ ID NO: 22), PLGRIVGG (SEQ ID NO:23), IEGRTVGG (SEQ ID NO: 24), LTPRSLLV (SEQ ID NO: 25), LGPVSGVP (SEQ ID NO: 26), VAGDSLEE (SEQ ID NO: 27), GPAGLGGA (SEQ ID NO: 28), GPAGLRGA (SEQ ID NO: 29), APLGLRLR (SEQ ID NO: 30), PALPLVAQ (SEQ ID NO: 31), ENLYFQG (SEQ ID NO: 32), DDDKIVGG (SEQ ID NO: 33), LEVLFQGP (SEQ ID NO: 34), and LPKTGSES (SEQ ID NO: 35). In some embodiments, the first cleavage site and the second cleavage site are identical or different.

[0028] The XTEN sequence useful for the invention can be selected from the group consisting of AE42 (SEQ ID NO: 36), AE144 (SEQ ID NO: 37), AG144 (SEQ ID NO: 38), AE288 (SEQ ID NO: 39), AG288 (SEQ ID NO: 40), AE576 (SEQ ID NO: 41). AG576 (SEQ ID NO: 42), AE864 (SEQ ID NO: 43), AE72 (SEQ ID NO: 127), AE144_2A (SEQ ID NO: 128), AE144_3B (SEQ ID NO: 129), AE144_4A (SEQ ID NO: 130), AE144_5A (SEQ ID NO: 131), AE144_6B (SEQ ID NO: 132), AG144 A (SEQ ID NO: 133), AG144_B (SEQ ID NO: 134), AG144_C (SEQ ID NO:135), AG144_F (SEQ ID NO: 136), AE288_2 (SEQ ID NO: 137), or AG864 (SEQ ID NO: 44). In a particular embodiment, the XTEN sequence comprises AE288 or AG288.

[0029] The chimeric protein of the invention can be polysialylated, pegylated, or hesylated.

[0030] The present invention is also directed to a polynucleotide or a set of polynucleotides encoding the chimeric protein, of the invention. The polynucleotide can further comprise a polynucleotide chain, which encodes PC5 or PC7. In another aspect, the present invention provides a vector comprising the polynucleotide or the set of polynucleotides of the invention and one or more promoter operably linked to the polynucleotide or the set of polynucleotides of the invention. The vector can further comprise an additional vector, which comprises a polynucleotide chain encoding PC5 or PC7. The invention is also drawn to a host cell comprising the polynucleotide or the vector of the invention. The host cell can be a mammalian cell, *e.g.,* HEK293 cell, CHO cell, or BHK cell. In some embodiments, the PC5 or PC7 of the host cell cleaves the D1D2 domains of VWF.

[0031] The invention is also directed to a pharmaceutical composition comprising the chimeric protein, the polynucleotide, the vector, or the host cell, of the invention, and a pharmaceutically acceptable carrier. The composition of the invention thus has an extended half-life compared to wild type FVIII protein. The half-life of the FVIII protein is extended at least about 1.5 times, at least about 2 times, at least about 2.5 times, at least about 3 times, at least about 4 times, at least about 5 times, at least about 6 times, at least about 7 times, at least about 8 times, at least about 9 times, at least about 10 times, at least about 11 times, or at least about 12 times longer than wild type FVIII. The half-life of Factor VIII is at least about 17 hours, at least about 18 hours, at least about 19 hours, at least about 20 hours, at least about 21 hours, at least about 22 hours, at least about 23 hours, at least about 24 hours, at least about 25 hours, at least about 26 hours, at least about 27 hours, at least about 28 hours, at least about 29 hours, at least about 30 hours, at least about 31 hours, at least about 32 hours, at least about 33 hours, at least about 34 hours, at least about 35 hours, at least about 36 hours, at least about 48 hours, at least about 60 hours, at least about 72 hours, at least about 84 hours, at least about 96 hours, or at least about 108 hours.

[0032] The composition of the present invention can be administered by a route selected from the group consisting of topical administration, intraocular administration, parenteral administration, intrathecal administration, subdural administration and oral administration. In one instance, the composition is administered via parenteral administration, *e.g.*, intravenous or subcutaneous administration. The composition of the invention is useful to

treat a bleeding disease or condition in a subject in need thereof. The bleeding disease or condition is selected from the group consisting of a bleeding coagulation disorder, hemarthrosis, muscle bleed, oral bleed, hemorrhage, hemorrhage into muscles, oral hemorrhage, trauma, trauma capitis, gastrointestinal bleeding, intracranial hemorrhage, intra-abdominal hemorrhage, intrathoracic hemorrhage, bone fracture, central nervous system bleeding, bleeding in the retropharyngeal space, bleeding in the retroperitoneal space, bleeding in the illiopsoas sheath and any combinations thereof. In one instance, the subject treated with the chimeric protein is scheduled to undergo a surgery. In another instance, the treatment is prophylactic or on-demand.

[0033] The disclosure is also directed to a method of preventing or inhibiting binding of a FVIII protein with endogenous VWF comprising adding an effective amount of the chimeric protein, the polynucleotide vector, the host cell, or the composition to a subject in need thereof, wherein the VWF fragment binds to the FVIII protein and thus prevents or inhibits binding of endogenous VWF. The present disclosure is further directed to a method of extending or increasing the half-life of the FVIII protein, wherein the method comprises administering an effective amount of the chimeric protein, the polynucleotide, the vector, the host cell, or the composition to a subject in need thereof, wherein the VWF fragment binds to the FVIII protein and thus extends or increases the half-life of the FVIII protein. Also provided is a method of preventing or inhibiting clearance of a FVIII protein from a cell, wherein the method comprises administering an effective amount of the chimeric protein, the polynucleotide, the vector, the host cell, or the composition to a cell comprising a FVIII protein or a polynucleotide encoding the FVIII protein, wherein the protein having VWF activity binds to the FVIII protein. The subject useful for the present methods is an animal, *e.g.*, a human, *e.g.*, a patient suffering from hemophilia A.

[0034] In another aspect, the present invention provides the chimeric protein of the invention, the polynucleotide or the set of polynucleotides of the invention, the host cell of the invention, or the composition of the invention for use in the treatment of a bleeding disease or disorder in a subject in need thereof. The bleeding disease or disorder is selected from the group consisting of a bleeding coagulation disorder, hemarthrosis, muscle bleed, oral bleed, hemorrhage, hemorrhage into muscles, oral hemorrhage, trauma, trauma capitis, gastrointestinal bleeding, intracranial hemorrhage, intra-abdominal hemorrhage, intrathoracic hemorrhage, bone fracture, central nervous system bleeding, bleeding in the retropharyngeal space, bleeding in the retroperitoneal space, and bleeding in the illiopsoas sheath. The treatment can be prophylactic or on-demand. In one embodiment, the effective amount is 0.1 µg/kg to 500 mg/kg.

[0035] In another aspect, the present invention provides a method of making the chimeric protein of the invention, comprising transfecting one or more host cell with the polynucleotide or the vector of the invention and expressing the chimeric protein in the host cell. The present invention and embodiments thereof are set out in the appended claims.

BRIEF DESCRIPTION OF THE DRAWINGS/FIGURES

[0036]

Figure 1A-D. Schematic diagrams of VWF fragments. Fig. 1A shows three exemplary VWF fragments useful for the invention, *e.g.*, VWF-002, VWF-010, and VWF-013. VWF-002 contains amino acids 1 to 477 of SEQ ID NO: 124 (amino acids 764 to 1240 of SEQ ID NO: 2) and is synthesized without the pre/propeptide sequences. VWF-010 contains the D1D2 domains in addition to the D'D3 domains. VWF-013 contains the D1D2D'D3 domains in addition to alanine residues substituting cysteines at residues 336 and 379 of SEQ ID NO: 123 Fig. 1B shows VWF-031, which contains the D1D2D'D3 domains fused to an Ig constant region or a portion thereof, *e.g.,* an Fc region, by a cleavable linker, *e.g.,* a 48 amino acids thrombin cleavable linker. Fig. 1C shows VWF-025, which is a nucleotide sequence encoding D1D2D'D3 domains contained in pLIVE vector, and VWF-029, which is a nucleotide sequence encoding D1D2D'D3 domains with two amino acid substitutions, C336A and C379A, in pLIVE vector. Fig. 1D shows full-length VWF fragment comprising propeptide (the D1 and D2 domains) and mature subunits (the D', D3, A1, A2, A3, D4, B1-3, C1-2 domains). The VWF fragment is about 250 kDa protein and forms multimers (> 20 MDa) by disulfide bonding. The VWF fragment associates with FVIII (95-98%) in non-covalent

complex and then extends half-life of FVIII by protecting FVIII from protease cleavage/activation, stabilizing heavy & light chain, and preventing clearance of FVIII by scavenger receptors. The VWF fragment also can limit half-life of FVIII by clearance of FVIII-VWF complex through VWF receptors and preventing pinocytosis and recycling of rFVIIIFc.

Figure 2. Pharmacokinetic profile of rFVIII-XTEN (rFVIII-AE288 or rFVIII-288AE) in VWF D'D3 expression mice or in FVIII and VWF double knockout (DKO) mice. Figure 2A shows the timeline of hydrodynamic injection (HDI) of the D'D3 domain encoding plasmid DNA (VWF-025) (day -5), intravenous dosing of rFVIII-XTEN AE288 (day 0), and PK sample collection (day 5). Figure 2B shows FVIII activity measured by a FVIII chromogenic assay after IV dosing of rFVIII-XTEN288 in D1D2D'D3 mice (inverted triangle) and rFVIII-XTEN288 in DKO mice (diamond). Fig. 2C shows the D'D3 plasma level (ng/mL) after administration of VWF-025. The X axis represents time in hours.

Figure 3. Schematic diagram of exemplary VWF:FVIII heterodimer constructs. The constructs have the common structure represented as formula FVIII-F1-L1-V-X-L2-F2, but contain examples of different variable linkers. The construct (FVIII-161) shown contains a heterodimeric FVIII (the heavy chain and the light chain are associated by a metal bond) linked to a first Fc region and a VWF fragment, which is the D' and D3 domains of VWF (*i.e.,* amino acids 1 to 477 of SEQ ID NO: 2 with amino acid substitutions C336A and C379A) linked to an XTEN sequence, which is further linked to a cleavable linker and a second Fc region. The XTEN sequence contained in FVIII-161 is an XTEN AE288 sequence, and the linker is a thrombin cleavable linker, which has 35 amino acids. In FVIII-161, the FVIII protein linked to the first Fc region is linked to the VWF fragment by a processable linker. Upon expression, the processable linker can be cleaved by an intracellular processing enzyme, thus making the construct three polypeptide chains associated with each other.

Figure 4 is schematic diagrams of FVIII-VWF heterodimer or monomer examples. FVIII-168, FVIII-175, FVIII-172, FVIII-174, and FVIII170. Construct FVIII-168 comprises a single chain FVIII sequence (having an alanine residue substitute the arginine residues at residues 1645 and 1648) linked to a first Fc region, which is then fused to a VWF fragment linked to a second Fc region by a thrombin cleavable linker, which has 48 amino acids. AE288 XTEN is inserted in the B domain of the single chain FVIII sequence. The linkage between the first Fc region and the VWF fragment comprises a linker that is capable of being cleaved by an intracellular processing enzyme, *i.e.,* processable linker. Construct FVIII-175 comprises a single chain FVIII (having an alanine residue substitute the arginine residues at residues 1645 and 1648) linked to AE288 XTEN and a first Fc region, which is linked to a second Fc region by a linker, *e.g.,* a processable linker. AE288 XTEN is inserted in the B domain of the single chain FVIII sequence. Construct FVIII-172 comprises two polypeptide chains, a first chain comprising a heavy chain FVIII sequence fused to AE288 XTEN, a second chain comprising a light chain FVIII sequence, a first Fc region, a linker (*e.g.,* a processable linker), a VWF fragment, a thrombin cleavable linker (*e.g.,* 48 amino acids), and a second Fc region. Construct FVIII-174 comprises two polypeptide chains, a first chain comprising a heavy chain FVIII sequence fused to AE288 XTEN and a second chain comprises a light chain FVIII, a first Fc region, a linker (*e.g.,* a processable linker), and a second Fc region. Construct FVIII-170 comprises a VWF fragment, AE288 XTEN, a linker (*e.g.,* a thrombin cleavable linker, which is 35 amino acids in length), and a single chain FVIII sequence.

Figure 5. Pharmacokinetic profile of FVIII/VWF heterodimers containing an XTEN sequence in combination with an Fc region. Constructs FVIII-161, FVIII-168, and FVIII-172 were administered to FVIII:VWF double knockout (DKO) mice by Hydrodynamic injection (HDI) at 100ug/mouse dose. Construct FVIII-170 was administered to FVIII:VWF DKO mice by HDI at 50 µg/mouse dose. The post-HDI plasma FVIII activity was analyzed by FVIII chromogenic assay for 24 hr post-HDI. The FVIII activity of the FVIII:VWF heterodimers containing an XTEN sequence and Fc domains was compared with the FVIII activity of BDD-FVIII without the VWF fragment, XTEN sequence, and Fc domains.

Figure 6. Schematic diagrams of FVIII-VWF heterodimer examples co-transfection system. Fig. 6A. Construct FVIII-169 contains the full-length FVIII sequence (with an alanine residue substituting the arginine residues at 1645 and 1648 and with an XTEN sequence inserted in the single chain FVIII sequence), which is linked to an Fc region. VWF-031 contains the D1D2D'D3 fragment (with an alanine residue substituting the cysteine residues at 336 and 379) which is linked to another Fc region with a 48 thrombin cleavable linker. After intracellular processing, construct FVIII-169 produces a full length single chain FVIII (SCFVIII) fused to one Fc fragment and

an XTEN sequence, and construct VWF-031 produces a 477 amino acid D'D3 fragment linked to another Fc fragment. Two covalent bonds can be formed between the Fc fragments that are linked to the SC FVIII or the D'D3 fragment, this in turn allows a non-covalent association of FVIII and D'D3. Fig. 6B. Construct FVIII-173 contains a heterodimeric FVIII sequence, a heavy chain FVIII sequence linked to an XTEN sequence and a light chain FVIII sequence linked to an Fc region. VWF-031 is described above. After intracellular processing, construct FVIII-173 produces a heterodimeric protein, a heavy chain FVIII fused to an XTEN sequence, a light chain FVIII fused to one Fc fragment, and construct VWF-031 produces a 477 amino acid D'D3 fragment linked to another Fc fragment. Two covalent bonds can be formed between the Fc fragments that are linked to the light chain FVIII or the D'D3 fragment, this in turn allows a non-covalent association of FVIII and D'D3.

Figure 7. Binding Affinity of Exemplary FVIII:VWF containing an XTEN sequence and Fc domains to immobilized hVWF in Octet assay. The binding affinity for FVIII-169/VWF-031 and FVIII-057 (rFVIIIFc) fused to immobilized hVWF was tested using biolayer interferometry based measurements (Octet assay). Figure 7A shows binding response in nanomoles of FVIII169 and FVIIIFc drug substance (a positive control) to immobilized hVWF. Figure 7B shows binding response of human IgG1 (a negative control) to immobilized human VWF.

Figure 8. Pharmacokinetic (PK) profile of FVIII-169 in HemA and FVIII:VWF double knockout (DKO) mice. Figure 8A shows the PK profile of FVIII-169/VWF-031 and FVIIIFc in HemA mice. HemA mice were treated with a single intravenous dose of FVIII-169/VWF-031 at 200 IU/kg. Plasma samples collected from the mice were tested by FVIII chromogenic assay. Half-life of FVIII-169/VWF-031 was calculated using WinNonlin program. Figure 8B shows the PK profile of FVIII-169/VWF-031, FVIII-169/Fc, and FVIIIFc in FVIII/VWF DKO mice.

Figure 9. PK profile of FVIII-XTEN variants in D'D3 expressing FVIII/VWF DKO mice. Figure 9A shows comparison of the PK profile of the FVIII-XTEN variants, FVIII with one XTEN, FVIII with two XTENs, and FVIII with three XTENs. One, two, or three XTENs were inserted in various portions of FVIII including C-terminus and B-domain. CT indicates that an XTEN is linked to the C-terminus of FVIII. Insertion site B/CT indicates that one XTEN is inserted between amino acid residue 745 and amino acid residue 746 of the FVIII protein and another XTEN is linked to the C-terminus of the FVIII protein. The amino acid residue numbering corresponds to the SQ BDD FVIII protein sequence. Insertion site 1900/B/CT indicates that a first XTEN is inserted between amino acid residue 1900 and amino acid residue 1901 of FVIII, a second XTEN is inserted between amino acid residue 745 and amino acid residue 746 of FVIII, and a third XTEN is linked to the C-terminus of FVIII. The mouse strain used to administer the FVIII-XTEN variants is a DKO mouse strain expressing D'D3 domains. Figure 9B shows the PK profile of FVIII-XTEN with three XTEN insertions. The FVIII-XTEN (1900/B/CT) variant was administered to either the FVIII/VWF DKO mice or HemA mice. The half-life of FVIII-XTEN (1900/B/CT) is compared.

Figure 10. FVIII activity of FVIIIFc (hollow triangle), FVIII169:Fc (filled circle), and FVIII 1 69:VWF31 (hollow triangle) in mouse DKO plasma measured by chromogenic assay. FVIII:Fc contains a dual-chain FVIII (Heavy chain and Light chain) fused to an Fc dimer (*i.e.,* monomer-dimer hybrid). FVIII169 is described above (containing AE288 in the B domain, immediately downstream of amino acid 745 corresponding to mature FVIII sequence). FVIII169:Fc contains FVIII169 fused to an Fc dimer. FVIII169:VWF31 contains VWF31 in addition to the Fc dimer, FVIII169 fused to the first Fc region and VWF31 fused to the second Fc region, wherein the first Fc region and the second Fc region form a covalent bond, *e.g.,* one or more disulfide bonds.

Figure 11. Effects of Fc, XTEN, and VWF-D'D3 fragments on FVIII half-life extension. BDD-FVIII (REFACTO®) (square), FVIIFc (circle), FVIII169/Fc (triangle), and FVIII169/VWF031 (inverted triangle) were administered to FVIII and VWF double knockout (DKO) mice. The FVIII activity was measured by chromogenic assay, and the half-life was calculated using the WinNonlin-Phoenix program. X-axis shows time, and the Y-axis shows the FVIII plasma activity in mU/mL.

Figure 12A-C. Effects of different XTENs in rFVIII-XTEN/VWF heterodimer in HemA mice. Figure 12A shows the FVIII plasma activity normalized to 5 min value (%) of two XTENs inserted immediately downstream of residues 1900 and 1656 corresponding to mature FVIII sequence (*i.e.,* FVIII-195 (dual chain FVIII isoform) and FVIII-199 (single chain FVIII isoform)), compared to FVIII-169 containing an XTEN immediately downstream of residue 745 corresponding to mature FVIII sequence. FVIII-169/VWF-031 (filled circle), FVIII-199/VWF-031 (filled square), and FVIII-195/VWF031 (hollow square) were administered in HemA mice to measure the FVIII plasma activity. Figure

12B shows the half-life extension effect of the second XTEN insertion immediately downstream of residues 403 (A2 domain) and 745 (B domain) (*i.e.*, FVIII-203) and residues 745 (B domain) and 1900 (A3 domain) (FVIII-204) corresponding to mature FVIII sequence compared to FVIII-169 (an XTEN insertion in B domain only). FVIII-204/VWF031 (filled triangle), FVIII-169/VWF-031 (filled circle), FVIII-203/VWF-031 (filled square), and scBDD-FVIII (hollow diamond) were administered to HemA mice. The X-axis shows FVIII plasma activity normalized to 5 min value (%), and the y-axis shows time in hours. Figure 12C shows the half-life extension effect of the two XTEN insertions immediately downstream of residues 18 (A1 domain) and 745 (B domain) (*i.e.,* FVIII-205) compared to FVIII-169 (a single XTEN insertion in the B domain) and single chain FVIII without any Fc regions or any XTENs (*i.e.,* FVIII-207). Figure 12C additionally shows the half-life extension effect of three XTEN insertions incorporated immediately downstream of residues 26 (A1 domain), 1656 (A3 domain), and 1900 (A3 domain) (*i.e.,* FVIII-201) compared to FVIII-169 (a single XTEN insertion immediately downstream of residue 745).. FVIII-205/VWF-031 (filled square), FVIII-201/VWF-031 (inverted triangle), FVIII-169/VWF-031 (filled circle), and FVIII-207 (hollow diamond) were administered to HemA mice. The FVIII plasma activity normalized to 5 min value (%) (X-axis) was measured over time in hours (Y-axis).

Figure 13. FVIII activity of rFVIII-XTEN/VWF-XTEN heterodimer in FVIII/VWF DKO mice. FVIII activity of plasma samples was analyzed by FVIII chromogenic assay, and the regression curve of plasma FVIII activity (X-axis) as a function of time (Y-axis) was plotted. FVIII-155 (scFVIIIFc without any XTENs) was co-expressed with VWF-034 (VWF-Fc with AE 288 XTEN plus a 35 residue thrombin cleavable linker). The half-life of FVIII-155/VWF-034 was compared with that of FVIII-169/VWF-031, which has a AE 288 XTEN inserted into the B domain junction (immediately downstream of residue 745 corresponding to mature FVIII polypeptide) of FVIII.

Figure 14A-H. Schematic diagrams of various rFVIII-XTEN/VWF constructs. These constructs are also described in other sections herein. Fig. 14A shows single chain B domain deleted FVIII protein (sometimes indicated herein as scBDD-FVIII). The scBDD-FVIII constructs contain two substitutions at residues 1645 and 1648 from Arg to Ala. Figure 14B shows two polypeptide chain construct (FVIII155/VWF031), the first chain comprising single chain FVIII linked to an Fc region without any XTENS and the second chain comprising the VWF D'D3 fragment linked to an Fc region. This construct is used as a control. Fig. 14C shows two polypeptide chain construct (FVIII199/VWF031), the first chain comprising single chain FVIII linked to an Fc region, in which a first XTEN is inserted immediately downstream of residue 1900 corresponding to mature FVIII sequence and a second XTEN is inserted immediately downstream of residue 1656 corresponding to mature FVIII sequence, and the second chain comprising the VWF D'D3 fragment linked to an Fc region. Fig. 14D shows two polypeptide chain construct (FVIII201/VWF031), the first chain comprising single chain FVIII protein linked to an Fc region, in which a first XTEN is inserted immediately downstream of residue 26 corresponding to mature FVIII sequence, a second XTEN is inserted immediately downstream of residue 1656 corresponding to mature FVIII sequence, and a third XTEN is inserted immediately downstream of residue 1900 corresponding to mature FVIII sequence ,and the second chain comprising the VWF D'D3 fragment linked to an Fc region. Fig. 14E shows two polypeptide chain constructs (FVIII169/VWF031), the first chain comprising single chain FVIII protein linked to an Fc region, in which an XTEN is inserted immediately downstream of residue 745 (indicated as "B") corresponding to mature FVIII sequence, and the second chain comprising the VWF D'D3 fragment linked to an Fc region. Fig. 14F shows two polypeptide chain construct (FVIII203/VWF031), the first chain comprising single chain FVIII protein, in which a first XTEN is inserted at residue 745 ("B") corresponding to mature FVIII sequence and a second XTEN is inserted at residue 1900 corresponding to mature FVIII sequence, and the second chain comprising the VWF D'D3 fragment linked to an Fc region. Fig. 14G shows two polypeptide chain construct (FVIII204/VWF031), the first chain comprising single chain FVIII protein linked to an Fc region, in which a first XTEN is inserted immediately downstream of residue 403 corresponding to mature FVIII sequence and a second XTEN is inserted immediately downstream of residue 745 ("B") corresponding to mature FVIII sequence, and a second chain comprising the VWF D'D3 fragment linked to an Fc region. Fig. 14H shows two polypeptide chain construct (FVIII205/VWF031), the first chain comprising single chain FVIII, in which a first XTEN is inserted immediately downstream of residue 18 corresponding to mature FVIII sequence and a second XTEN is inserted immediately downstream of residue 745 ("B") corresponding to mature FVIII sequence, and the second chain comprising the VWF D'D3 fragment linked to an Fc region.

Figure 15. FVIII activity of rFVIII-XTEN/VWF and BDD-FVIII in FVIII/VWF DKO mice. FVIII activity of plasma

samples was analyzed by FVIII chromogenic assay, and the regression curve of plasma FVIII activity (X-axis) as a function of time (Y-axis) was plotted. The half-life of rFVIII-XTEN/VWF (FVIII-205/VWF-031) was compared with that of BDD-FVIII and rFVIIIFc.

Figure 16. Efficacy of FVIII-XTEN-Fc:VWF-Fc heterodimers in HemA mice using tail clip bleeding model. The HemA mice tail clip bleeding model was used to compare the efficacy of FVIII169/VWF034, FVIII205/VWF031, and BDD-FVIII. The median blood loss in ml for 200 IU/kg of FVIII169/VWF034 and FVIII205/VWF031 is compared with 200 IU/kg of BDD-FVIII, 65 IU/kg of BDD-FVIII, 20 IU/kg of BDD-FVIII, and vehicle.

DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

[0037] It is to be noted that the term "a" or "an" entity refers to one or more of that entity; for example, "a nucleotide sequence," is understood to represent one or more nucleotide sequences. As such, the terms "a" (or "an"), "one or more," and "at least one" can be used interchangeably herein.

[0038] The term "polynucleotide" or "nucleotide" is intended to encompass a singular nucleic acid as well as plural nucleic acids, and refers to an isolated nucleic acid molecule or construct, *e.g.*, messenger RNA (mRNA) or plasmid DNA (pDNA). In certain embodiments, a polynucleotide comprises a conventional phosphodiester bond or a non-conventional bond (*e.g.,* an amide bond, such as found in peptide nucleic acids (PNA)). The term "nucleic acid" refers to any one or more nucleic acid segments, *e.g.*, DNA or RNA fragments, present in a polynucleotide. By "isolated" nucleic acid or polynucleotide is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. For example, a recombinant polynucleotide encoding a Factor VIII polypeptide contained in a vector is considered isolated for the purposes of the present invention. Further examples of an isolated polynucleotide include recombinant polynucleotides maintained in heterologous host cells or purified (partially or substantially) from other polynucleotides in a solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of polynucleotides of the present invention. Isolated polynucleotides or nucleic acids according to the present invention further include such molecules produced synthetically. In addition, a polynucleotide or a nucleic acid can include regulatory elements such as promoters, enhancers, ribosome binding sites, or transcription termination signals.

[0039] As used herein, a "coding region" or "coding sequence" is a portion of polynucleotide which consists of codons translatable into amino acids. Although a "stop codon" (TAG, TGA, or TAA) is typically not translated into an amino acid, it may be considered to be part of a coding region, but any flanking sequences, for example promoters, ribosome binding sites, transcriptional terminators, introns, and the like, are not part of a coding region. The boundaries of a coding region are typically determined by a start codon at the 5' terminus, encoding the amino terminus of the resultant polypeptide, and a translation stop codon at the 3' terminus, encoding the carboxyl terminus of the resulting polypeptide. Two or more coding regions of the present invention can be present in a single polynucleotide construct, *e.g.*, on a single vector, or in separate polynucleotide constructs, *e.g.*, on separate (different) vectors. It follows, then, that a single vector can contain just a single coding region, or comprise two or more coding regions, *e.g.,* a single vector can separately encode a binding domain-A and a binding domain-B as described below. In addition, a vector, polynucleotide, or nucleic acid of the invention can encode heterologous coding regions, either fused or unfused to a nucleic acid encoding a binding domain of the invention. Heterologous coding regions include without limitation specialized elements or motifs, such as a secretory signal peptide or a heterologous functional domain.

[0040] Certain proteins secreted by mammalian cells are associated with a secretory signal peptide which is cleaved from the mature protein once export of the growing protein chain across the rough endoplasmic reticulum

has been initiated. Those of ordinary skill in the art are aware that signal peptides are generally fused to the N-terminus of the polypeptide, and are cleaved from the complete or "full-length" polypeptide to produce a secreted or "mature" form of the polypeptide. In certain embodiments, a native signal peptide or a functional derivative of that sequence that retains the ability to direct the secretion of the polypeptide that is operably associated with it. Alternatively, a heterologous mammalian signal peptide, *e.g.,* a human tissue plasminogen activator (TPA) or mouse B-glucuronidase signal peptide, or a functional derivative thereof, can be used.

[0041] The term "downstream" refers to a nucleotide sequence that is located 3' to a reference nucleotide sequence. In certain embodiments, downstream nucleotide sequences relate to sequences that follow the starting point of transcription. For example, the translation initiation codon of a gene is located downstream of the start site of transcription.

[0042] The term "upstream" refers to a nucleotide sequence that is located 5' to a reference nucleotide sequence. In certain embodiments, upstream nucleotide sequences relate to sequences that are located on the 5' side of a coding region or starting point of transcription. For example, most promoters are located upstream of the start site of transcription.

[0043] As used herein, the term "regulatory region" refers to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding region, and which influence the transcription, RNA processing, stability, or translation of the associated coding region. Regulatory regions may include promoters, translation leader sequences, introns, polyadenylation recognition sequences, RNA processing sites, effector binding sites and stem-loop structures. If a coding region is intended for expression in a eukaryotic cell, a polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

[0044] A polynucleotide which encodes a gene product, *e.g.,* a polypeptide, can include a promoter and/or other transcription or translation control elements operably associated with one or more coding regions. In an operable association a coding region for a gene product, *e.g.,* a polypeptide, is associated with one or more regulatory regions in such a way as to place expression of the gene product under the influence or control of the regulatory region(s). For example, a coding region and a promoter are "operably associated" if induction of promoter function results in the transcription of mRNA encoding the gene product encoded by the coding region, and if the nature of the linkage between the promoter and the coding region does not interfere with the ability of the promoter to direct the expression of the gene product or interfere with the ability of the DNA template to be transcribed. Other transcription control elements, besides a promoter, for example enhancers, operators, repressors, and transcription termination signals, can also be operably associated with a coding region to direct gene product expression.

[0045] A variety of transcription control regions are known to those skilled in the art. These include, without limitation, transcription control regions which function in vertebrate cells, such as, but not limited to, promoter and enhancer segments from cytomegaloviruses (the immediate early promoter, in conjunction with intron-A), simian virus 40 (the early promoter), and retroviruses (such as Rous sarcoma virus). Other transcription control regions include those derived from vertebrate genes such as actin, heat shock protein, bovine growth hormone and rabbit β-globin, as well as other sequences capable of controlling gene expression in eukaryotic cells. Additional suitable transcription control regions include tissue-specific promoters and enhancers as well as lymphokine-inducible promoters (*e.g.*, promoters inducible by interferons or interleukins).

[0046] Similarly, a variety of translation control elements are known to those of ordinary skill in the art. These include, but are not limited to ribosome binding sites, translation initiation and termination codons, and elements derived from picornaviruses (particularly an internal ribosome entry site, or IRES, also referred to as a CITE sequence).

[0047] The term "expression" as used herein refers to a process by which a polynucleotide produces a gene product, for example, an RNA or a polypeptide. It includes without limitation transcription of the polynucleotide into

messenger RNA (mRNA), transfer RNA (tRNA), small hairpin RNA (shRNA), small interfering RNA (siRNA) or any other RNA product, and the translation of an mRNA into a polypeptide. Expression produces a "gene product." As used herein, a gene product can be either a nucleic acid, *e.g.,* a messenger RNA produced by transcription of a gene, or a polypeptide which is translated from a transcript. Gene products described herein further include nucleic acids with post transcriptional modifications, *e.g.*, polyadenylation or splicing, or polypeptides with post translational modifications, *e.g.*, methylation, glycosylation, the addition of lipids, association with other protein subunits, or proteolytic cleavage.

[0048] A "vector" refers to any vehicle for the cloning of and/or transfer of a nucleic acid into a host cell. A vector may be a replicon to which another nucleic acid segment may be attached so as to bring about the replication of the attached segment. A "replicon" refers to any genetic element (*e.g.*, plasmid, phage, cosmid, chromosome, virus) that functions as an autonomous unit of replication *in vivo, i.e.,* capable of replication under its own control. The term "vector" includes both viral and nonviral vehicles for introducing the nucleic acid into a cell *in vitro, ex vivo* or *in vivo.* A large number of vectors are known and used in the art including, for example, plasmids, modified eukaryotic viruses, or modified bacterial viruses. Insertion of a polynucleotide into a suitable vector can be accomplished by ligating the appropriate polynucleotide fragments into a chosen vector that has complementary cohesive termini.

[0049] Vectors may be engineered to encode selectable markers or reporters that provide for the selection or identification of cells that have incorporated the vector. Expression of selectable markers or reporters allows identification and/or selection of host cells that incorporate and express other coding regions contained on the vector. Examples of selectable marker genes known and used in the art include: genes providing resistance to ampicillin, streptomycin, gentamycin, kanamycin, hygromycin, bialaphos herbicide, sulfonamide, and the like; and genes that are used as phenotypic markers, *i.e.,* anthocyanin regulatory genes, isopentanyl transferase gene, and the like. Examples of reporters known and used in the art include: luciferase (Luc), green fluorescent protein (GFP), chloramphenicol acetyltransferase (CAT), -galactosidase (LacZ), -glucuronidase (Gus), and the like. Selectable markers may also be considered to be reporters.

[0050] The term "plasmid" refers to an extra-chromosomal element often carrying a gene that is not part of the central metabolism of the cell, and usually in the form of circular double-stranded DNA molecules. Such elements may be autonomously replicating sequences, genome integrating sequences, phage or nucleotide sequences, linear, circular, or supercoiled, of a single- or double-stranded DNA or RNA, derived from any source, in which a number of nucleotide sequences have been joined or recombined into a unique construction which is capable of introducing a promoter fragment and DNA sequence for a selected gene product along with appropriate 3' untranslated sequence into a cell.

[0051] Eukaryotic viral vectors that can be used include, but are not limited to, adenovirus vectors, retrovirus vectors, adeno-associated virus vectors, and poxvirus, *e.g.*, vaccinia virus vectors, baculovirus vectors, or herpesvirus vectors. Non-viral vectors include plasmids, liposomes, electrically charged lipids (cytofectins), DNA-protein complexes, and biopolymers.

[0052] A "cloning vector" refers to a "replicon," which is a unit length of a nucleic acid that replicates sequentially and which comprises an origin of replication, such as a plasmid, phage or cosmid, to which another nucleic acid segment may be attached so as to bring about the replication of the attached segment. Certain cloning vectors are capable of replication in one cell type, *e.g.*, bacteria and expression in another, *e.g.*, eukaryotic cells. Cloning vectors typically comprise one or more sequences that can be used for selection of cells comprising the vector and/or one or more multiple cloning sites for insertion of nucleic acid sequences of interest.

[0053] The term "expression vector" refers to a vehicle designed to enable the expression of an inserted nucleic acid sequence following insertion into a host cell. The inserted nucleic acid sequence is placed in operable association with regulatory regions as described above.

[0054] Vectors are introduced into host cells by methods well known in the art, *e.g.*, transfection, electroporation,

microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, lipofection (lysosome fusion), use of a gene gun, or a DNA vector transporter.

[0055] "Culture," "to culture" and "culturing," as used herein, means to incubate cells under *in vitro* conditions that allow for cell growth or division or to maintain cells in a living state. "Cultured cells," as used herein, means cells that are propagated *in vitro.*

[0056] As used herein, the term "polypeptide" is intended to encompass a singular "polypeptide" as well as plural "polypeptides," and refers to a molecule composed of monomers (amino acids) linearly linked by amide bonds (also known as peptide bonds). The term "polypeptide" refers to any chain or chains of two or more amino acids, and does not refer to a specific length of the product. Thus, peptides, dipeptides, tripeptides, oligopeptides, "protein," "amino acid chain," or any other term used to refer to a chain or chains of two or more amino acids, are included within the definition of "polypeptide," and the term "polypeptide" can be used instead of, or interchangeably with any of these terms. The term "polypeptide" is also intended to refer to the products of post-expression modifications of the polypeptide, including without limitation glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, or modification by non-naturally occurring amino acids. A polypeptide can be derived from a natural biological source or produced recombinant technology, but is not necessarily translated from a designated nucleic acid sequence. It can be generated in any manner, including by chemical synthesis.

[0057] An "isolated" polypeptide or a fragment, variant, or derivative thereof refers to a polypeptide that is not in its natural milieu. No particular level of purification is required. For example, an isolated polypeptide can simply be removed from its native or natural environment. Recombinantly produced polypeptides and proteins expressed in host cells are considered isolated for the purpose of the invention, as are native or recombinant polypeptides which have been separated, fractionated, or partially or substantially purified by any suitable technique.

[0058] Also included in the present invention are fragments or variants of polypeptides, and any combination thereof. The term "fragment" or "variant" when referring to polypeptide binding domains or binding molecules of the present invention include any polypeptides which retain at least some of the properties (*e.g.*, FcRn binding affinity for an FcRn binding domain or Fc variant, coagulation activity for an FVIII variant, or FVIII binding activity for the VWF fragment) of the reference polypeptide. Fragments of polypeptides include proteolytic fragments, as well as deletion fragments, in addition to specific antibody fragments discussed elsewhere herein, but do not include the naturally occurring full-length polypeptide (or mature polypeptide). Variants of polypeptide binding domains or binding molecules of the present invention include fragments as described above, and also polypeptides with altered amino acid sequences due to amino acid substitutions, deletions, or insertions. Variants can be naturally or non-naturally occurring. Non-naturally occurring variants can be produced using art-known mutagenesis techniques. Variant polypeptides can comprise conservative or non-conservative amino acid substitutions, deletions or additions.

[0059] The term "VWF fragment" or "VWF fragments" used herein means any VWF fragments that interact with FVIII and retain at least one or more properties that are normally provided to FVIII by full-length VWF, *e.g.*, preventing premature activation to FVIIIa, preventing premature proteolysis, preventing association with phospholipid membranes that could lead to premature clearance, preventing binding to FVIII clearance receptors that can bind naked FVIII but not VWF-bound FVIII, and/or stabilizing the FVIII heavy chain and light chain interactions.

[0060] A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art, including basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.,* aspartic acid, glutamic acid), uncharged polar side chains (*e.g.,* glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, if an amino acid in a polypeptide is replaced with another

amino acid from the same side chain family, the substitution is considered to be conservative. In another embodiment, a string of amino acids can be conservatively replaced with a structurally similar string that differs in order and/or composition of side chain family members.

[0061] As known in the art, "sequence identity" between two polypeptides is determined by comparing the amino acid sequence of one polypeptide to the sequence of a second polypeptide. When discussed herein, whether any particular polypeptide is at least about 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, or 100% identical to another polypeptide can be determined using methods and computer programs/software known in the art such as, but not limited to, the BESTFIT program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711). BESTFIT uses the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981), to find the best segment of homology between two sequences. When using BESTFIT or any other sequence alignment program to determine whether a particular sequence is, for example, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full-length of the reference polypeptide sequence and that gaps in homology of up to 5% of the total number of amino acids in the reference sequence are allowed.

[0062] As used herein, an "amino acid corresponding to" or an "equivalent amino acid" in a VWF sequence or a FVIII protein sequence is identified by alignment to maximize the identity or similarity between a first VWF or FVIII sequence and a second VWF or FVIII sequence. The number used to identify an equivalent amino acid in a second VWF or FVIII sequence is based on the number used to identify the corresponding amino acid in the first VWF or FVIII sequence.

[0063] As used herein, the term "insertion site" refers to a position in a FVIII polypeptide, or fragment, variant, or derivative thereof, which is immediately upstream of the position at which a heterologous moiety can be inserted. An "insertion site" is specified as a number, the number being the number of the amino acid in mature native FVIII (SEQ ID NO:4) to which the insertion site corresponds, which is immediately N-terminal to the position of the insertion. For example, the phrase "a3 comprises an XTEN at an insertion site which corresponds to amino acid 1656 of SEQ ID NO: 4" indicates that the heterologous moiety is located between two amino acids corresponding to amino acid 1656 and amino acid 1657 of SEQ ID NO: 4.

[0064] The phrase "immediately downstream of an amino acid" as used herein refers to position right next to the terminal carboxyl group of the amino acid. Similarly, the phrase "immediately upstream of an amino acid" refers to the position right next to the terminal amine group of the amino acid. Therefore, the phrase "between two amino acids of an insertion site" as used herein refers to a position in which an XTEN or any other polypeptide is inserted between two adjacent amino acids. Thus, the phrases "inserted immediately downstream of an amino acid" and "inserted between two amino acids of an insertion site" are used synonymously with "inserted at an insertion site."

[0065] The terms "inserted," "is inserted," "inserted into" or grammatically related terms, as used herein refers to the position of an XTEN in a chimeric polypeptide relative to the analogous position in native mature human FVIII. As used herein the terms refer to the characteristics of the recombinant FVIII polypeptide relative to native mature human FVIII, and do not indicate, imply or infer any methods or process by which the chimeric polypeptide was made. For example, in reference to a chimeric polypeptide provided herein, the phrase "an XTEN is inserted into immediately downstream of residue 745 of the FVIII polypeptide" means that the chimeric polypeptide comprises an XTEN immediately downstream of an amino acid which corresponds to amino acid 745 in native mature human FVIII, *e.g.,* bounded by amino acids corresponding to amino acids 745 and 746 of native mature human FVIII.

[0066] A "fusion" or "chimeric" protein comprises a first amino acid sequence linked to a second amino acid sequence with which it is not naturally linked in nature. The amino acid sequences which normally exist in separate proteins can be brought together in the fusion polypeptide, or the amino acid sequences which normally exist in the same protein can be placed in a new arrangement in the fusion polypeptide, *e.g.*, fusion of a Factor VIII domain of the invention with an Ig Fc domain. A fusion protein is created, for example, by chemical synthesis, or by creating and translating a polynucleotide in which the peptide regions are encoded in the desired

relationship. A chimeric protein can further comprises a second amino acid sequence associated with the first amino acid sequence by a covalent, non-peptide bond or a non-covalent bond.

[0067] As used herein, the term "half-life" refers to a biological half-life of a particular polypeptide *in vivo*. Half-life may be represented by the time required for half the quantity administered to a subject to be cleared from the circulation and/or other tissues in the animal. When a clearance curve of a given polypeptide is constructed as a function of time, the curve is usually biphasic with a rapid α-phase and longer β-phase. The α-phase typically represents an equilibration of the administered Fc polypeptide between the intra- and extra-vascular space and is, in part, determined by the size of the polypeptide. The β-phase typically represents the catabolism of the polypeptide in the intravascular space. In some embodiments, FVIII and chimeric proteins comprising FVIII are monophasic, and thus do not have an alpha phase, but just the single beta phase. Therefore, in certain embodiments, the term half-life as used herein refers to the half-life of the polypeptide in the β-phase. The typical β-phase half-life of a human antibody in humans is 21 days.

[0068] The term "linked" as used herein refers to a first amino acid sequence or nucleotide sequence covalently or non-covalently joined to a second amino acid sequence or nucleotide sequence, respectively. The first amino acid or nucleotide sequence can be directly joined or juxtaposed to the second amino acid or nucleotide sequence or alternatively an intervening sequence can covalently join the first sequence to the second sequence. The term "linked" means not only a fusion of a first amino acid sequence to a second amino acid sequence at the C-terminus or the N-terminus, but also includes insertion of the whole first amino acid sequence (or the second amino acid sequence) into any two amino acids in the second amino acid sequence (or the first amino acid sequence, respectively). In one embodiment, the first amino acid sequence can be linked to a second amino acid sequence by a peptide bond or a linker. The first nucleotide sequence can be linked to a second nucleotide sequence by a phosphodiester bond or a linker. The linker can be a peptide or a polypeptide (for polypeptide chains) or a nucleotide or a nucleotide chain (for nucleotide chains) or any chemical moiety (for both polypeptide and polynucleotide chains). The term "linked" is also indicated by a hyphen (-).

[0069] As used herein the term "associated with" refers to a covalent or non-covalent bond formed between a first amino acid chain and a second amino acid chain. In one embodiment, the term "associated with" means a covalent, non-peptide bond or a non-covalent bond. This association can be indicated by a colon, *i.e.,* (:). In another embodiment, it means a covalent bond except a peptide bond. For example, the amino acid cysteine comprises a thiol group that can form a disulfide bond or bridge with a thiol group on a second cysteine residue. In most naturally occurring IgG molecules, the CH1 and CL regions are associated by a disulfide bond and the two heavy chains are associated by two disulfide bonds at positions corresponding to 239 and 242 using the Kabat numbering system (position 226 or 229, EU numbering system). Examples of covalent bonds include, but are not limited to, a peptide bond, a metal bond, a hydrogen bond, a disulfide bond, a sigma bond, a pi bond, a delta bond, a glycosidic bond, an agnostic bond, a bent bond, a dipolar bond, a Pi backbond, a double bond, a triple bond, a quadruple bond, a quintuple bond, a sextuple bond, conjugation, hyperconjugation, aromaticity, hapticity, or antibonding. Non-limiting examples of non-covalent bond include an ionic bond (*e.g.*, cation-pi bond or salt bond), a metal bond, an hydrogen bond (*e.g.*, dihydrogen bond, dihydrogen complex, low-barrier hydrogen bond, or symmetric hydrogen bond), van der Walls force, London dispersion force, a mechanical bond, a halogen bond, aurophilicity, intercalation, stacking, entropic force, or chemical polarity.

[0070] The term "monomer-dimer hybrid" used herein refers to a chimeric protein comprising a first polypeptide chain and a second polypeptide chain, which are associated with each other by a disulfide bond, wherein the first chain comprises a clotting factor, *e.g.*, Factor VIII, and a first Fc region and the second chain comprises, consists essentially of, or consists of a second Fc region without the clotting factor. The monomer-dimer hybrid construct thus is a hybrid comprising a monomer aspect having only one clotting factor and a dimer aspect having two Fc regions.

[0071] As used herein, the term "cleavage site" or "enzymatic cleavage site" refers to a site recognized by an enzyme. Certain enzymatic cleavage sites comprise an intracellular processing site. In one embodiment, a polypeptide has an enzymatic cleavage site cleaved by an enzyme that is activated during the clotting cascade,

such that cleavage of such sites occurs at the site of clot formation. Exemplary such sites include, *e.g.*, those recognized by thrombin, Factor XIa or Factor Xa. Exemplary FXIa cleavage sites include, *e.g.*, TQSFNDFTR (SEQ ID NO: 45) and SVSQTSKLTR (SEQ ID NO: 46). Exemplary thrombin cleavage sites include, *e.g.*, DFLAEGGGVR (SEQ ID NO: 47), TTKIKPR (SEQ ID NO: 48), LVPRG (SEQ ID NO: 49) and ALRPR (amino acids 1 to 5 of SEQ ID NO: 50). Other enzymatic cleavage sites are known in the art.

[0072] As used herein, the term "processing site" or "intracellular processing site" refers to a type of enzymatic cleavage site in a polypeptide which is a target for enzymes that function after translation of the polypeptide. In one embodiment, such enzymes function during transport from the Golgi lumen to the trans-Golgi compartment. Intracellular processing enzymes cleave polypeptides prior to secretion of the protein from the cell. Examples of such processing sites include, *e.g.,* those targeted by the PACE/furin (where PACE is an acronym for Paired basic Amino acid Cleaving Enzyme) family of endopeptidases. These enzymes are localized to the Golgi membrane and cleave proteins on the carboxyterminal side of the sequence motif Arg-[any residue]-(Lys or Arg)-Arg. As used herein the "furin" family of enzymes includes, *e.g.*, PCSK1 (also known as PC1/Pc3), PCSK2 (also known as PC2), PCSK3 (also known as furin or PACE), PCSK4 (also known as PC4), PCSK5 (also known as PC5 or PC6), PCSK6 (also known as PACE4), or PCSK7 (also known as PC7/LPC, PC8, or SPC7). Other processing sites are known in the art.

[0073] In constructs that include more than one processing or cleavage site, it will be understood that such sites may be the same or different.

[0074] The term "Furin" refers to the enzymes corresponding to EC No. 3.4.21.75. Furin is subtilisin-like proprotein convertase, which is also known as PACE (Paired basic Amino acid Cleaving Enzyme). Furin deletes sections of inactive precursor proteins to convert them into biologically active proteins. During its intracellular transport, pro-peptide of VWF can be cleaved from mature VWF molecule by a Furin enzyme. In some embodiments, Furin cleaves the D1D2 from the D'D3 of VWF. In other embodiments, a nucleotide sequence encoding Furin can be expressed together with the nucleotide sequence encoding a VWF fragment so that D1D2 domains can be cleaved off intracellularly by Furin.

[0075] In constructs that include more than one processing or cleavage site, it will be understood that such sites may be the same or different.

[0076] A "processable linker" as used herein refers to a linker comprising at least one intracellular processing site, which is described elsewhere herein.

[0077] Hemostatic disorder, as used herein, means a genetically inherited or acquired condition characterized by a tendency to hemorrhage, either spontaneously or as a result of trauma, due to an impaired ability or inability to form a fibrin clot. Examples of such disorders include the hemophilias. The three main forms are hemophilia A (factor VIII deficiency), hemophilia B (factor IX deficiency or "Christmas disease") and hemophilia C (factor XI deficiency, mild bleeding tendency). Other hemostatic disorders include, *e.g.*, Von Willebrand disease, Factor XI deficiency (PTA deficiency), Factor XII deficiency, deficiencies or structural abnormalities in fibrinogen, prothrombin, Factor V, Factor VII, Factor X or factor XIII, Bernard-Soulier syndrome, which is a defect or deficiency in GPIb. GPIb, the receptor for VWF, can be defective and lead to lack of primary clot formation (primary hemostasis) and increased bleeding tendency), and thrombasthenia of Glanzman and Naegeli (Glanzmann thrombasthenia). In liver failure (acute and chronic forms), there is insufficient production of coagulation factors by the liver; this may increase bleeding risk.

[0078] The chimeric molecules of the invention can be used prophylactically. As used herein the term "prophylactic treatment" refers to the administration of a molecule prior to a bleeding episode. In one embodiment, the subject in need of a general hemostatic agent is undergoing, or is about to undergo, surgery. The chimeric protein of the invention can be administered prior to or after surgery as a prophylactic. The chimeric protein of the invention can be administered during or after surgery to control an acute bleeding episode. The surgery can include, but is not limited to, liver transplantation, liver resection, dental procedures, or stem cell transplantation.

[0079] The chimeric protein of the invention is also used for on-demand treatment. The term "on-demand treatment" refers to the administration of a chimeric molecule in response to symptoms of a bleeding episode or before an activity that may cause bleeding. In one aspect, the on-demand treatment can be given to a subject when bleeding starts, such as after an injury, or when bleeding is expected, such as before surgery. In another aspect, the on-demand treatment can be given prior to activities that increase the risk of bleeding, such as contact sports.

[0080] As used herein the term "acute bleeding" refers to a bleeding episode regardless of the underlying cause. For example, a subject may have trauma, uremia, a hereditary bleeding disorder (*e.g.*, factor VII deficiency) a platelet disorder, or resistance owing to the development of antibodies to clotting factors.

[0081] Treat, treatment, treating, as used herein refers to, *e.g.,* the reduction in severity of a disease or condition; the reduction in the duration of a disease course; the amelioration of one or more symptoms associated with a disease or condition; the provision of beneficial effects to a subject with a disease or condition, without necessarily curing the disease or condition, or the prophylaxis of one or more symptoms associated with a disease or condition. In one embodiment, the term "treating" or "treatment" means maintaining a FVIII trough level at least about 1 IU/dL, 2 IU/dL, 3 IU/dL, 4 IU/dL, 5 IU/dL, 6 IU/dL, 7 IU/dL, 8 IU/dL, 9 IU/dL, 10 IU/dL, 11 IU/dL, 12 IU/dL, 13 IU/dL, 14 IU/dL, 15 IU/dL, 16 IU/dL, 17 IU/dL, 18 IU/dL, 19 IU/dL, or 20 IU/dL in a subject by administering a chimeric protein or a VWF fragment of the invention. In another embodiment, treating or treatment means maintaining a FVIII trough level between about 1 and about 20 IU/dL, about 2 and about 20 IU/dL, about 3 and about 20 IU/dL, about 4 and about 20 IU/dL, about 5 and about 20 IU/dL, about 6 and about 20 IU/dL, about 7 and about 20 IU/dL, about 8 and about 20 IU/dL, about 9 and about 20 IU/dL, or about 10 and about 20 IU/dL. Treatment or treating of a disease or condition can also include maintaining FVIII activity in a subject at a level comparable to at least about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, or 20% of the FVIII activity in a non-hemophiliac subject. The minimum trough level required for treatment can be measured by one or more known methods and can be adjusted (increased or decreased) for each person.

CHIMERIC PROTEINS

[0082] The present invention is directed to extending the half-life of a Factor VIII protein using a VWF fragment and an XTEN sequence by preventing or inhibiting a FVIII half-life limiting factor, *i.e.,* endogenous VWF, from associating with the FVIII protein. Endogenous VWF associates with about 95% to about 98% of FVIII in non-covalent complexes. While endogenous VWF is a FVIII half-life limiting factor, endogenous VWF bound to a FVIII protein is also known to protect FVIII in various ways. For example, full length VWF (as a multimer having about 250 kDa) can protect FVIII from protease cleavage and FVIII activation, stabilize the FVIII heavy chain and/or light chain, and prevent clearance of FVIII by scavenger receptors. But, at the same time, endogenous VWF limits the FVIII half-life by preventing pinocytosis and by clearing FVIII-VWF complex from the system through the VWF clearance pathway. It is believed, while not bound by a theory, that endogenous VWF is a half-life limiting factor that prevents the half-life of a FVIII protein fused to a half-life extender from being longer than about two-fold that of wild-type FVIII. Therefore, the present invention is directed to preventing or inhibiting interaction between endogenous VWF and a FVIII protein using a VWF fragment, thereby increasing a half-life of the FVIII protein by using an XTEN sequence alone or an XTEN sequence in combination with an Ig constant region or a portion thereof. The XTEN sequence can be linked to the FVIII protein or the VWF fragment. The FVIII protein associated with the VWF fragment is thus cleared from the circulation more slowly by one or more VWF clearance receptors and then can have the full half-life extension of the XTEN sequence or the XTEN sequence in combination of the Ig constant region, as compared to wild type FVIII or a FVIII protein without the VWF fragment.

[0083] In one embodiment, a VWF fragment is associated (or linked) with the FVIII protein by a covalent bond. In some instances, the physical blockage or chemical association (*e.g.*, non-covalent bonding) between the VWF fragment and the FVIII protein may not be strong enough to provide a stable complex comprising the FVIII protein

and the VWF fragment in the presence of endogenous VWF. For example, a VWF fragment forming a non-covalent bond with a FVIII protein without any other connections may readily be dissociated *in vivo* from the FVIII protein in the presence of endogenous VWF, replacing the VWF fragment (*e.g.,* recombinant VWF, *i.e.,* rVWF) with endogenous VWF. Therefore, the FVIII protein non-covalently bound to endogenous VWF would undergo the VWF clearance pathway and be readily cleared from the system. In order to prevent the dissociation of the VWF fragment with the FVIII protein, the association or linkage between the FVIII protein and the VWF fragment is a covalent bond, *e.g.,* a peptide bond, or a disulfide bond. In certain embodiments, the association (*i.e.,* linkage) is a peptide bond or a linker between the FVIII protein and the VWF fragment ("FVIII/VWF linker"). Non-limiting examples of the linker are described elsewhere herein. In some embodiments, the VWF fragment is a polypeptide comprising, consisting essentially of, or consisting of at least about 10, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2500, 3000, or 4000 amino acids. Non-limiting examples of the VWF fragment are described elsewhere herein.

[0084] In certain embodiments, the VWF fragment chemically (*e.g.*, non-covalently) binds to or physically blocks one or more VWF binding sites on a FVIII protein. The VWF binding site on a FVIII protein is located within the A3 domain or the C2 domain of the FVIII protein. In still other embodiments, the VWF binding site on a FVIII protein is located within the A3 domain and C2 domain. For example, the VWF binding site on a FVIII protein can correspond to amino acids 1669 to 1689 and/or 2303 to 2332 of SEQ ID NO: 4 [full-length mature FVIII].

[0085] The disclosure also provides a chimeric protein (comprising a FVIII protein and a VWF fragment) further comprising one or more XTEN sequences, which provide additional half-life extension properties. The one or more XTEN sequences can be inserted within the FVIII protein or the VWF fragment or linked to the N-terminus or the C-terminus of the FVIII protein or the VWF fragment. The disclosure also includes a FVIII protein linked to an XTEN sequence (a first half-life extending moiety) and an Ig constant region or a portion thereof (a second half-life extending moiety) so that the two half-life extending moieties extend the half-life of the FVIII protein through two different mechanisms.

[0086] In some instances, a chimeric protein comprises a FVIII protein linked to a first Ig constant region or a portion thereof (*e.g.,* a first FcRn binding partner), a VWF fragment linked to a second Ig constant region or a portion thereof (*e.g.,* a second FcRn binding partner), and one or more XTEN sequences inserted or linked to the FVIII protein or the VWF fragment, wherein the VWF fragment prevents the FVIII half-life limiting factor (*e.g.*, endogenous VWF) from binding to the FVIII protein, wherein the first and second Ig constant regions or portions thereof forms a covalent bond, *e.g.,* a disulfide bond, and the one or more XTEN sequences extends the half-life of the FVIII protein.

[0087] In certain instances, a chimeric protein of the disclosure comprises a FVIII protein linked to a VWF fragment by an optional linker (*i.e.,* FVIII/VWF linker) and one or more XTEN sequences inserted or linked to the FVIII protein or the VWF fragment, wherein the VWF fragment prevents the FVIII half-life limiting factor (*e.g.*, endogenous VWF) from binding to the FVIII protein and the one or more XTEN sequences extends the half-life of the FVIII protein. In one instance, the optional linker (FVIII/VWF linker) comprises a sortase recognition motif. In another instance, the optional linker (FVIII/VWF linker) comprises a cleavable site. Examples of the cleavage linker (*i.e.,* linker containing one or more cleavage site) are described elsewhere herein.

[0088] The chimeric protein of the present disclosure includes, but is not limited to:

1. (1) a VWF fragment comprising a D' domain and a D3 domain, an XTEN sequence, and FVIII, wherein the XTEN sequence is linked to the VWF fragment;
2. (2) a FVIII protein, an XTEN sequence, and an Ig constant region or a portion thereof, wherein the FVIII protein is linked to an XTEN sequence and the Ig constant region or a portion thereof, or
3. (3) a FVIII protein, an XTEN sequence, and a VWF fragment, wherein the XTEN sequence is linked to the FVIII protein at the C-terminus or N-terminus or inserted immediately downstream of one or more amino acids (*e.g.,* one or more XTEN insertion sites) of FVIII, and the VWF fragment and the FVIII protein are associated with each other.

(1) Von Willebrand Factor (VWF) fragment linked to XTEN, and FVIII

[0089] The present disclosure is directed to a chimeric protein comprising (i) a VWF fragment comprising a D' domain and a D3 domain of VWF, (ii) an XTEN sequence, and (iii) a FVIII protein, wherein (i), (ii), and (iii) are linked to or associated with each other. The VWF fragment linked to the XTEN sequence, as a part of a chimeric protein in the present invention, associates with the FVIII protein, thus preventing or inhibiting interaction between endogenous VWF and the FVIII protein. In certain instances, the VWF fragment, which is capable of preventing or inhibiting binding of the FVIII protein with endogenous VWF, can at the same time have at least one VWF-like FVIII protecting property. Examples of the VWF-like FVIII protecting properties include, but are not limited to, protecting FVIII from protease cleavage and FVIII activation, stabilizing the FVIII heavy chain and/or light chain, and preventing clearance of FVIII by scavenger receptors. As a result, the VWF fragment can prevent clearance of the FVIII protein through the VWF clearance pathway, thus reducing clearance of FVIII from the circulatory system. In some instances, the VWF fragments of the present invention bind to or are associated with a FVIII protein and/or physically or chemically block the VWF binding site on the FVIII protein. The FVIII protein associated with the VWF fragment is thus cleared from the circulation more slowly, as compared to wild type FVIII or FVIII not associated with the VWF fragment.

[0090] In one instance, the disclosure is directed to a chimeric protein comprising (i) a VWF fragment comprising the D' domain and the D3 domain of VWF, (ii) an XTEN sequence, and (iii) a FVIII protein, wherein the XTEN sequence is linked to the VWF fragment (*e.g.,* (a1) V-X or (a2) X-V, wherein V comprises a VWF fragment and X comprises an XTEN sequence), and the VWF fragment is linked to or associated with the FVIII protein. In another instance, the VWF fragment and the XTEN sequence can be linked by a linker (*e.g.,* (a3) V-L-X or (a4) X-L-V) or a peptide bond. The linker can be a cleavable linker, *e.g.,* a thrombin cleavable linker, which can be cleaved at the site of coagulation. In other instances, the VWF fragment, the XTEN sequence, and the FVIII protein are placed in a single polypeptide chain. In still other instances, the chimeric protein comprises two polypeptide chains, a first chain comprising the VWF fragment and the XTEN sequence and a second chain comprising the FVIII protein. In yet other instances, the chimeric protein comprises three polypeptide chains, a first chain comprising the VWF fragment and the XTEN sequence, a second chain comprising a light chain of FVIII and a third chain comprising a heavy chain of FVIII, wherein the first chain and the second chain are associated with each other (*e.g.,* covalent bond, *e.g.,* disulfide bond), and the second chain and the third chain are associated with each other (*e.g.*, metal bond). In still other instances, the XTEN sequence can be linked to the N-terminus or the C-terminus of the VWF fragment or inserted immediately downstream of one or more amino acids in the VWF fragment.

[0091] In certain instances, a chimeric protein of the disclosure comprises a formula comprising:

(a) V-X-FVIII,

(b) FVIII-X-V,

(c) V-X:FVIII,

(d) X-V:FVIII,

(e) FVIII:V-X,

(f) FVIII:X-V,

or

(a5) X-V-FVIII,

wherein V comprises a VWF fragment,

X comprises one or more XTEN sequences,

FVIII comprises a FVIII protein;

(-) represents a peptide bond or one or more amino acids; and

(:) is a chemical association or a physical association. In one instance, (:) represents a chemical association, *e.g.*, at least one non-peptide bond. In another instance, the chemical association, *i.e.,* (:) is a covalent bond. In other instances, the chemical association, *i.e.,* (:) is a non-covalent interaction, *e.g.,* an ionic interaction, a hydrophobic interaction, a hydrophilic interaction, a Van der Waals interaction, or a hydrogen bond. In other instances, (:) is a non-peptide covalent bond. In still other instances, (:) is a peptide bond. In yet other instances, (:) represents a physical association between two sequences, wherein a portion of a first sequence is in close proximity to a second sequence such that the first sequence shields or blocks a portion of the second sequence from interacting with another moiety, and further that this physical association is maintained without allowing the second sequence to interact with other moieties. The orientation of the polypeptide formulas herein is listed from N-terminus (left) to C-terminus (right). For example, formula V-X-FVIII means formula NH2-V-X-FVIII -COOH. In one instance, the formulas described herein can comprise any additional sequences between the two moieties. For example, formula V-X-FVIII can further comprise any sequences at the N-terminus of V between V and X, between X and FVIII, or at the C-terminus of FVIII unless otherwise specified. In another instance, the hyphen (-) indicates a peptide bond.

[0092] In other instances, a chimeric protein of the disclosure comprises a formula comprising:

(a) V(X1)-X2-FVIII,

(b) FVIII-X2-V(X1),

(c) V(X1):FVIII,

(d) FVIII:V(X1),

or

(a5) X2-V(X1)-FVIII,

wherein V(X1) comprises a VWF fragment and a first XTEN sequence (X1),

wherein the XTEN sequence is inserted immediately downstream of one or more amino acids in the VWF fragment,

X2 comprises one or more optional XTEN sequences,

FVIII comprises a FVIII protein;

(-) is a peptide bond or one or more amino acids; and

(:) is a chemical association or a physical association.

[0093] In some instances, a chimeric protein comprises (i) a VWF fragment comprising a D' domain and a D3 domain of VWF, (ii) an XTEN sequence, (iii) a FVIII protein, (iv) a first optional linker, and (v) a second optional linker, wherein the XTEN sequence is linked to the VWF fragment and/or to the FVIII protein by the linker. In certain instances, a chimeric protein comprises a formula comprising:

(b1) V-L1-X-L2-FVIII,

(b2) FVIII-L2-X-L1-V,

(b3) V-L1-X:FVIII,

(b4) X-L1-V:FVIII,

(b5) FVIII:V-L1-X,

(b6) FVIII:X-L1-V,

(b7) X-L1-V-L2-FVIII, or

(b8) FVIII-L2-V-L1-X,

wherein V comprises a VWF fragment,

X comprises one or more XTEN sequences,

FVIII comprises a FVIII protein,

L1 comprises a first optional linker, *e.g.,* a first cleavable linker,

L2 comprises a second optional linker, *e.g.,* a second cleavable linker or an optional processable linker;

(-) is a peptide bond or one or amino acids; and

(:) is a chemical association or a physical association. In one instance, (:) represents a chemical association, *e.g.*, at least one non-peptide bond. In another instance, the chemical association, *i.e.,* (:) is a covalent bond. In other instances, the chemical association, *i.e.,* (:) is a non-covalent interaction, *e.g.,* an ionic interaction, a hydrophobic interaction, a hydrophilic interaction, a Van der Waals interaction, or a hydrogen bond. In other instances, (:) is a non-peptide covalent bond. In still other instances, (:) is a peptide bond. In yet other instances, (:) represents a physical association between two sequences, wherein a portion of a first sequence is in close proximity to a second sequence such that the first sequence shields or blocks a portion of the second sequence from interacting with another moiety, and further that this physical association is maintained without allowing the second sequence to interact with other moieties. The orientation of the polypeptide formulas herein is listed from N-terminus (left) to C-terminus (right). For example, formula (b1) V-L1-X-L2-FVIII means formula NH2-V-L1-X-L2-FVIII-COOH. In one instance, the formulas described herein can comprise any additional sequences between the two moieties. In another instance, the hyphen (-) indicates a peptide bond.

[0094] Another instance of the present disclosure is to provide a FVIII chimeric protein having reduced or no interactions with a FVIII half-life limiting factor, *e.g.*, endogenous VWF, and at the same time maximizing the half-life of the FVIII protein using an XTEN sequence (a first half-life extender) in combination with a second half-life extender or a moiety providing a covalent bond between the FVIII protein and the VWF fragment, *e.g.*, an Ig constant region or a portion thereof. In one instance, a chimeric protein of the disclosure comprises (i) a VWF fragment comprising a D' domain and a D3 domain of VWF, (ii) an XTEN sequence, (iii) a FVIII protein, and (iv) an

Ig constant region or a portion thereof (also referred to herein as F), wherein (1) the VWF fragment is linked to the XTEN sequence by an optional linker, *e.g.,* a cleavable linker, (2) the VWF fragment is associated with or linked to the FVIII protein by an additional optional linker, *e.g.,* a cleavable linker, and (3) the Ig constant region or a portion thereof is linked to the VWF fragment, the XTEN sequence, or the FVIII protein. A chimeric protein of the invention comprises (i) a VWF fragment comprising a D' domain and a D3 domain of VWF, (ii) an XTEN sequence, (iii) a FVIII protein, (iv) an Ig constant region or a portion thereof (F1 or a first Ig constant region or a portion thereof), and (v) an additional Ig constant region or a portion thereof (F2 or a second Ig constant region or a portion thereof), wherein (1) the VWF fragment is linked to the XTEN sequence by an optional linker, *e.g.,* a cleavable linker, (2) the XTEN sequence or the VWF fragment is linked to the Ig constant region or a portion thereof, (3) the FVIII is linked to the additional Ig constant region or a portion thereof, and (4) the Ig constant region or a portion thereof is associated with or linked to the additional Ig constant region or a portion thereof, by a covalent bond, *e.g.,* a disulfide bond. In another embodiment, the association or linkage between the two Ig constant regions or a portion thereof is a processable linker, wherein the processable linker is intracellularly processed by a protease. For example, the chimeric protein comprises a formula comprising:

(g) V-L2-X-L1-F1: FVIII-L3-F2;

(h) V-L2-X-L1-F1:F2-L3-FVIII;

(i) F-L1-X-L2-V: FVIII-L3-F2;

(j) F-L1-X-L2-V:F2-L3-FVIII;

(k) V-L2-X-L1-F1-L4-FVIII-L3-F2;

(l) F2-L3-FVIII-L4-F1-LL1-X-L2-V;

(m) FVIII-L2-F2-L4-V-L2-X-L1-F1;

or

(n) F1-L1-X-L2-V-L4-F2-L2-FVIII,

wherein V comprises a VWF fragment,

each of L1 and L3 comprises an optional linker,

L2 comprises an optional linker, *e.g.,* a cleavable linker,

L4 is an optional linker, *e.g.,* a processable linker,

FVIII comprises a FVIII protein,

X comprises one or more XTEN sequences,

F1 comprises the first Ig constant region or a portion thereof,

F2 comprises the second Ig constant region or a portion thereof;

(-) is a peptide bond or one or more amino acids; and

(:) is a covalent bond.

[0095] In some embodiments, the FVIII protein in any constructs or formulas disclosed herein can further

comprises at least one, at least two, at least three, at least four, at least five, or at least six XTEN sequences, each of the XTEN sequences inserted immediately downstream of one or more amino acids in the FVIII protein or linked to the N-terminus or the C-terminus of the FVIII protein. Non-limiting examples of the XTEN insertion sites are disclosed elsewhere herein.

[0096] In one embodiment, (:) represents covalent bond. In other embodiments, (:) is a non-peptide covalent bond. In still other embodiments, (:) is a peptide bond. The orientation of the polypeptide formulas herein is listed from N-terminus (left) to C-terminus (right). For example, formula (n) F1-L1-X-L2-V-L4-F2-L2-FVIII means formula NH2-F1-L1-X-L2-V-L4-F2-L2-FVIII -COOH. In one embodiment, the formulas described herein can comprise any additional sequences between the two moieties. In another embodiment, the hyphen (-) indicates a peptide bond.

[0097] In one embodiment, either or both of the Ig constant region or a portion thereof (sometimes indicated herein by "F" or "F1") and the additional Ig constant region or a portion thereof (sometimes indicated herein by "F2") linked to the VWF fragment or the FVIII protein can extend the half-life of the VWF fragment, the FVIII protein, or both. In another embodiment, the Ig constant region or a portion thereof (sometimes indicated herein by "F" or "F1") and the additional Ig constant region or a portion thereof (sometimes indicated herein by "F2"), each of which are linked to the VWF fragment and the FVIII protein, provides a bond stronger than the non-covalent bond between the FVIII protein and the VWF fragment, *i.e.,* a covalent bond, *e.g.,* a disulfide bond, thereby preventing endogenous VWF from replacing the VWF fragment *in vivo.* F1 or F2 can comprise an Fc region or an FcRn binding partner. In other embodiments, either or both of F1 and F2 linked to the VWF fragment and/or the FVIII protein form a covalent bond (*e.g.,* a disulfide bond) between F1 and F2, thereby placing the VWF fragment and the FVIII protein in close proximity to prevent interaction of the FVIII protein with the VWF fragment. In some embodiments, F1 and F2 are identical or different. Non-limiting examples of F1 and F2 can be selected from the group consisting of a CH1 domain, a CH2 domain, a CH3 domain, a CH4 domain, a hinge domain, any functional fragments, derivatives, or analogs thereof, and two or more combinations thereof. In one embodiment, F1, F2, or both comprise at least one CH1 domain, at least one CH2 domain, at least one CH3 domain, at least one CH4 domain, or the functional fragments, derivatives, or analogs thereof. In another embodiment, F1, F2, or both comprise at least one hinge domain or portion thereof and at least one CH2 domain or portion thereof (*e.g.,* in the hinge-CH2 orientation). In other embodiments, F1, F2, or both comprise at least one CH2 domain or portion thereof and at least one CH3 domain or portion thereof (*e.g.,* in the CH2-CH3 orientation.) Examples of the combination include, but are not limited to, a CH2 domain, a CH3 domain, and a hinge domain, which are also known as an Fc region (or Fc domain), *e.g.*, a first Fc region or a first FcRn binding partner for F1 and a second Fc region or a second FcRn binding partner for F2. In other embodiments, F1 is linked to the VWF fragment by a linker, and/or F2 is linked to the FVIII protein by a linker. In some embodiments, F1 and/or F2 comprises, consisting essentially of, or consisting of a hinge region. Additional non-limiting examples of the Fc regions or the FcRn binding partners are described elsewhere herein.

[0098] In certain embodiments, a chimeric protein of the invention comprises two polypeptide chains, a first polypeptide chain comprising, consisting essentially of, or consisting of a VWF fragment comprising a D' domain and a D3 domain, an XTEN sequence, a first Ig constant region or a portion thereof (*e.g.,* a first Fc region), and an optional linker between the VWF fragment and the XTEN sequence or the XTEN sequence or the first Ig constant region or a portion thereof and a second polypeptide chain comprising, consisting essentially of, or consisting of a FVIII protein and a second Ig constant region or a portion thereof (*e.g.,* a second Fc region). The linker between the VWF fragment and the first Ig constant region or a portion thereof can be a cleavable linker, *e.g.,* a thrombin cleavable linker, which can be cleaved at the site of coagulation. The first polypeptide chain and the second polypeptide chain are associated with each other. The association between the first chain and the second chain prevents replacement of the first chain comprising the VWF fragment with endogenous VWF *in vivo.* The association between the first chain and the second chain is a covalent bond. In a particular embodiment, the covalent bond is a disulfide bond. In some embodiments, the FVIII protein in the second chain further comprises one or more XTEN sequences linked to the C-terminus or N-terminus of the FVIII protein or inserted immediately downstream of one or more amino acids (*e.g.,* at least one insertion site disclosed herein) in the FVIII protein. Non-limiting examples of the insertion sites are described elsewhere herein.

[0099] In other embodiments, a chimeric protein of the invention comprises three polypeptide chains, wherein a first polypeptide chain comprises, consists essentially of, or consists of a heavy chain of a FVIII protein, a second polypeptide chain comprises, consists essentially of, or consists of a light chain of a FVIII protein fused to a first Ig constant region or a portion thereof (*e.g.,* a first Fc region), and a third polypeptide chain comprises, consists essentially of, or consists of a VWF fragment comprising a D' domain and a D3 domain, an XTEN sequence, a second Ig constant region or a portion thereof (*e.g.,* a second Fc region), and an optional linker between the XTEN sequence and the second Ig constant region or a portion thereof or the VWF fragment and the XTEN sequence. The linker in the third chain can be a cleavable linker, which is cleaved at the site of coagulation, *e.g.*, a thrombin cleavage site. In some embodiments, the heavy chain FVIII or the light chain FVIII is linked to one or more XTEN sequences, which can be linked to the N-terminus, the C-terminus, or inserted within one or more insertion sites within the FVIII sequence. Non-limiting examples of the insertion sites are disclosed elsewhere herein.

[0100] In yet other instances, a chimeric protein of the disclosure comprises two polypeptide chains, a first polypeptide chain comprising, consisting essentially of, or consisting of a heavy chain of a FVIII protein and a second polypeptide chain comprising, consisting essentially of, or consisting of a light chain of a FVIII protein, a first Ig constant region or a portion thereof (*e.g.,* a first Fc region), a first linker (*e.g.,* a processable linker, which contains one or more protease cleavage sites comprising one or more intracellular processing sites), a VWF fragment, a second linker (*e.g.,* a thrombin cleavable linker), an XTEN sequence, and a second Ig constant region or a portion thereof (*e.g.,* a second Fc region), wherein the light chain of the FVIII protein is linked to the first Ig constant region or a portion thereof (*e.g.,* the first Fc region), which is further linked to the VWF fragment by the first linker, and wherein the VWF fragment is linked to the XTEN sequence, which is further linked to the second Ig constant region or a portion thereof by the second linker. In certain instances, the first linker is a processable linker, and the second linker is a cleavable linker. Upon expression, the chimeric protein can be processed by an intracellular processing enzyme, which cleaves the processable linker, and thus the chimeric protein can comprise, consists essentially of, or consists of three polypeptide chains. In addition, the VWF fragment can be cleaved off at the site of coagulation due to the cleavable linker.

[0101] In certain embodiments, a chimeric protein of the invention comprises one polypeptide chain, which comprises a single chain FVIII protein, a first Ig constant region or a portion thereof (*e.g.,* a first Fc region), a first linker (*e.g.,* a processable linker), a VWF fragment, an XTEN sequence, a second linker (*e.g.,* a thrombin cleavable linker), and a second Ig constant region or a portion thereof (*e.g.,* a second Fc region), wherein the single chain FVIII protein is linked to the first Ig constant region or a portion thereof, which is also linked to the VWF fragment by the first linker, and the VWF fragment is linked to the XTEN sequence, which is further linked to the second Ig constant region or a portion thereof. In one embodiment, the VWF fragment and the XTEN sequence are linked by the second linker. In another embodiment, the XTEN sequence and the second Ig constant region or a portion thereof are linked by the second linker. In other embodiments, the second chain further comprises a third linker. The single polypeptide chain can thus comprise the VWF fragment linked to the XTEN sequence by the second linker and the XTEN linked to the second Ig constant region or a portion thereof by the third linker. The second linker and the third linker can be identical or different. In one embodiment, the first linker is a processable linker. In another embodiment, the second linker or the third linker is a cleavable linker comprising one or two cleavable sites. In a specific embodiment, the second linker is a thrombin cleavable linker. The linkers useful in the invention are described elsewhere herein.

(2) FVIII, XTEN, and Fc

[0102] A chimeric protein of the disclosure also comprises (i) a FVIII protein, (ii) an XTEN sequence (a first half-life extender), and (iii) an Ig constant region or a portion thereof (a second half-life extender), in which the XTEN sequence is linked to the FVIII protein by an optional linker and the Ig constant region or a portion thereof by an additional optional linker. The XTEN sequence and the Ig constant region or a portion thereof can be used together to extend half-life of the FVIII protein. In one instance, the chimeric protein is a monomer. In another

instance, the chimeric protein is a dimer (a homodimer or a heterodimer).

[0103] The present disclosure is also directed to a chimeric protein comprising (i) a FVIII protein, (ii) an XTEN sequence, (iii) an Ig constant region or a portion thereof (*i.e.,* a first Ig constant region or a portion thereof, "F," or "F1"), and (iv) an additional Ig constant region or a portion thereof (*i.e.,* a second Ig constant region or a portion thereof or "F2"). In one instance, the XTEN sequence is linked to the FVIII protein at the C-terminus or the N-terminus or inserted immediately downstream of one or more amino acids in the FVIII protein (*e.g.*, one or more XTEN insertion sites), the FVIII protein is linked to the first Ig constant region or a portion thereof, and the first Ig constant region or a portion thereof and the second Ig constant region or a portion thereof are associated with or linked to each other by an optional linker. In certain aspects, the chimeric protein is a monomer-dimer hybrid, which comprises a first polypeptide chain and a second polypeptide chain, wherein the first polypeptide chain comprises a FVIII protein, an XTEN sequence, and a first Ig constant region or a portion thereof, and the second polypeptide chain comprises, consists essentially of, or consists of a second Ig constant region or a portion thereof without the FVIII protein and wherein the first chain and the second chain are associated with each other. The association between the Ig constant region or a portion thereof (*e.g.,* the first Fc region) and the additional Ig constant region or a portion thereof (*e.g.,* a second Fc region) is a chemical association or a physical association. In certain instances, the chemical association is a covalent bond. In other instances, the chemical association is a non-covalent interaction, *e.g.*, an ionic interaction, a hydrophobic interaction, a hydrophilic interaction, a Van der Waals interaction, or a hydrogen bond. In other instances, the association is a non-peptide covalent bond. In still other instances, the association is a peptide bond.

[0104] In other instances, the chimeric protein is a single polypeptide chain comprising a FVIII protein, an XTEN sequence, a first Ig constant region or a portion thereof, a linker, *e.g.,* a processable linker, and a second Ig constant region or a portion thereof, wherein the single polypeptide chain is processed after expression by an intracellular enzyme and becomes two polypeptide chains.

[0105] In one instance, the Ig constant region or a portion thereof (sometimes indicated herein by "F" or "F1") linked to the FVIII protein can extend the half-life of the FVIII protein together with the XTEN sequence. In another instance, the Ig constant region or a portion thereof ("F" or "F1") is an Fc region or an FcRn binding partner described elsewhere herein.

[0106] In other instances, the additional Ig constant region or a portion thereof (sometimes indicated herein by "F2" or a second Ig constant region or a portion thereof) associated with or linked to the first Ig constant region or a portion thereof can also extend the half-life of the FVIII protein. In other instances, the second Ig constant region or a portion thereof ("F2") together with the first Ig constant region or a portion thereof and the XTEN sequence can extend the half-life of the FVIII protein. The additional Ig constant region or a portion thereof can be an Fc region or an FcRn binding partner described elsewhere herein.

[0107] In certain instances, the second Ig constant region or a portion thereof associated with the first Ig constant region or a portion thereof is further linked to a VWF fragment described elsewhere herein and an optional XTEN sequence.

[0108] In some instances, either or both of the Ig constant region or a portion thereof ("F" or "F1" or a first Ig constant region or a portion thereof) and an additional Ig constant region or a portion thereof (*i.e.,* a second Ig constant region or a portion thereof or "F2") (indicated in this paragraph as "the Ig constant regions or portion thereof") can include, but not limited to, a CH1 domain, a CH2 domain, a CH3 domain, a CH4 domain, a hinge domain, any functional fragments, derivatives, or analogs thereof or two or more combinations thereof. In one instance, the Ig constant region or a portion thereof comprises at least one CH1 domain, at least one CH2 domain, at least one CH3 domain, at least one CH4 domain, or the functional fragments, derivatives, or analogues thereof. In another instance, the Ig constant region or a portion thereof comprises at least one hinge domain or portion thereof and at least one CH2 domain or portion thereof (*e.g.,* in the hinge-CH2 orientation). In other instances, the Ig constant domain or portion thereof comprises at least one CH2 domain or portion thereof and at least one CH3 domain or portion thereof (*e.g.,* in the CF2-CH3 orientation). Examples of the combination include,

but are not limited to, a CH2 domain, a CH3 domain, and a hinge domain, which are also known as an Fc region (or Fc domain), *e.g.*, first Fc region. Additional examples of the Ig constant regions or portion thereof are described elsewhere herein.

[0109] The chimeric protein of the disclosure can have an extended half-life of the FVIII protein compared to wild-type FVIII. In one embodiment, the half-life of the FVIII protein is extended at least about 1.5 times, at least about 2 times, at least about 2.5 times, at least about 3 times, at least about 4 times, at least about 5 times, at least about 6 times, at least about 7 times, at least about 8 times, at least about 9 times, at least about 10 times, at least about 11 times, or at least about 12 times longer than the half-life of wild type FVIII. In another embodiment, the half-life of the FVIII protein is at least about 10 hours, at least about 11 hours, at least about 12 hours, at least about 13 hours, at least about 14 hours, at least about 15 hours, at least about 16 hours, at least about 17 hours, at least about 18 hours, at least about 19 hours, at least about 20 hours, at least about 21 hours, at least about 22 hours, at least about 23 hours, at least about 24 hours, at least about 36 hours, at least about 48 hours, at least about 60 hours, at least about 72 hours, at least about 84 hours, at least about 96 hours, or at least about 108 hours.

(3) FVIII, XTEN, and VWF

[0110] In one instance, a chimeric protein of the present disclosure comprises (i) a FVIII protein, (ii) an XTEN sequence, and (iii) a VWF fragment comprising a D' domain and a D3 domain of VWF, wherein the FVIII protein is linked to the XTEN sequence and wherein the FVIII protein is associated with or linked to the VWF fragment. In one instance, the VWF fragment of the chimeric protein described herein is not capable of binding to a VWF clearance receptor. In another instance, the VWF fragment is capable of protecting the FVIII protein from one or more protease cleavages, protecting the FVIII protein from activation, stabilizing the heavy chain and/or the light chain of the FVIII protein, or preventing clearance of the FVIII protein by one or more scavenger receptors. In other instances, the VWF fragment prevents or inhibits binding of endogenous VWF to the VWF binding site in the FVIII protein. The VWF binding site can be located in the A3 domain or the C2 domain of the FVIII protein or both the A3 domain and the C2 domain. In a specific instance, the VWF binding site comprises the amino acid sequence corresponding to amino acids 1669 to 1689 and/or amino acids 2303 to 2332 of SEQ ID NO: 2.

[0111] In another instance, a chimeric protein comprises (i) a FVIII protein, (ii) an XTEN sequence, (iii) a VWF fragment, which comprises a D' domain and a D3 domain of VWF, and (iv) an Ig constant region or a portion thereof, wherein the XTEN sequence is linked to the FVIII protein at the C-terminus or the N-terminus or inserted immediately downstream of one or more amino acids (*e.g.*, one or more XTEN insertion sites disclosed herein) in the FVIII protein, the VWF fragment is linked to or associated with the FVIII protein or the XTEN sequence, and the Ig constant region or a portion thereof is linked to the FVIII protein, the XTEN sequence, the VWF fragment, or any combinations thereof. The Ig constant region or a portion thereof useful for chimeric proteins of the disclosure is described elsewhere herein. In one instance, the Ig constant region or a portion thereof is capable of extending the half-life of a FVIII protein. In another instance, the Ig constant region or a portion thereof comprises a first Fc region or a first FcRn binding partner. In yet other instances, the Ig constant region or a portion thereof is linked to the FVIII protein by an optional linker. In still other instances, the linker comprises a cleavable linker. The chimeric protein can be a single polypeptide chain, *i.e.,* a monomer (*i.e.*, a single chain), containing (i), (ii), (iii), and (iv) or two chains containing a first chain comprising (i) and (ii) and a second chain comprising (iii) and (iv). In other instances, the chimeric protein is a dimer (*e.g.*, a homodimer or a heterodimer). In one instance, the chimeric protein comprises two chains, each comprising (i), (ii), (iii), and (iv).

[0112] In certain instances, a chimeric protein comprises (i) a FVIII protein, (ii) an XTEN sequence, (iii) a VWF fragment, which comprises a D' domain and a D3 domain of VWF, (iv) an Ig constant region or a portion thereof (sometimes also indicated as "F," "a first Ig constant region or a portion thereof", or "F2"), and (v) an additional Ig constant region or a portion thereof (sometimes also indicated as "F2" or "a second Ig constant region or a portion thereof'), wherein (1) the FVIII protein is linked to the XTEN sequence at the C-terminus or N-terminus of the FVIII protein or inserted immediately downstream of one or more amino acids (*e.g.*, one or more XTEN insertion sites

disclosed herein) in the FVIII protein, (2) either the XTEN sequence or the FVIII protein is linked to the Ig constant region or a portion thereof, (3) the VWF fragment is linked to the second Ig constant region or a portion thereof, and (4) the Ig constant region or a portion thereof is associated with the second Ig constant region or a portion thereof. In one instance, the Ig constant region or a portion thereof linked to the FVII protein or the XTEN sequence is further linked to the VWF fragment by a linker, *e.g.*, a processable linker. In another instance, the additional Ig constant region or a portion thereof useful for chimeric proteins of the disclosure can further be linked to the FVIII protein or the Ig constant region or a portion thereof by an optional linker, *e.g.*, a processable linker. In some instances, a pair of the Ig constant region or a portion thereof and the additional Ig constant region or a portion thereof, each of which are linked to the VWF fragment and the FVIII protein, provides a bond stronger than the non-covalent bond between the FVIII protein and the VWF fragment, *i.e.*, a covalent bond, *e.g.*, a disulfide bond, thereby preventing endogenous VWF from replacing the VWF fragment *in vivo*. In other instances, either or both of the Ig constant region or a portion thereof and the additional Ig constant region or a portion thereof are capable of extending a half-life of the FVIII protein or the VWF fragment. In other instances, the additional Ig constant region or a portion thereof comprises a second Fc region or an FcRn binding partner. The Ig constant region or a portion thereof and the additional Ig constant region or a portion thereof in the chimeric proteins are identical or different.

[0113] In certain instances, the Ig constant region or a portion thereof and the additional Ig constant region or a portion thereof are associated by a chemical association or a physical association. In one instance, the chemical association, *i.e.*, (:), is at least one non-peptide bond. In certain instance, the chemical association, *i.e.*, (:), is a covalent bond. In other instance, the chemical association, *i.e.*, (:), is a non-covalent interaction, *e.g.*, an ionic interaction, a hydrophobic interaction, a hydrophilic interaction, a Van der Waals interaction, or a hydrogen bond. In other instance, (:) is a non-peptide covalent bond. In still other instance, (:) is a peptide bond. In yet other instance, (:) represents a physical association between two sequences, wherein a portion of a first sequence is in close proximity to a second sequence such that the first sequence shields or blocks a portion of the second sequence from interacting with another moiety. In some instances, the association between the Ig constant region or a portion thereof and the additional Ig constant region or a portion thereof can be a covalent bond, *e.g.*, a disulfide bond, which prevents replacement the VWF fragment or the polypeptide containing the VWF fragment with endogenous VWF. Therefore, preventing interaction between the FVIII protein and endogenous VWF reduces or eliminates this half-life limiting factor for the FVIII protein, and thus the half-life of the FVIII protein is extended compared to a FVIII protein without the VWF protein or wild-type FVIII.

[0114] In other aspects, a chimeric protein comprises a formula comprising:

(1) FVIII(X1)-L1-F1:V-L2-X2-L3-F2;

(2) FVIII(X1)-L1-F1 :F2-L3-X2-L2-V;

(3) F1-L1-FVIII(X1):V-L2-X2-L3-F2;

(4) F1-L1-FVIII(X1):F2-L3-X2-L2-V;

(5) FVIII(X1)-L1-F1-L4-V-L2-X2-L3-F2;

(6) FVIII(X1)-L1-F1-L4-F2-L3-X2-L2-V;

(7) F1-L1-FVIII(X1)-L4-V-L2-X2-L3-F2,

or

(8) F1-L1-FVIII(X1)-L4- F2-L3-X2-L2-V,

wherein FVIII(X1) comprises a FVIII protein and one or more XTEN sequences, wherein the one or more XTEN sequence are linked to the N-terminus or C-terminus of the FVIII protein or inserted immediately downstream of one or more amino acids (*e.g.*, one or more XTEN insertion sites disclosed herein) in the FVIII protein;

each of L1, L2, or L3 comprises an optional linker, *e.g.*, a cleavable linker;

L4 is a linker, *e.g.*, a processable linker;

X2 comprises one or more optional XTEN sequences;

F1 comprises the first Ig constant region or a portion thereof;

F2 comprises the second Ig constant region or a portion thereof, and

V comprises a VWF fragment;

(-) is a peptide bond or one or more amino acids; and

(:) comprises a covalent bond. In other embodiments, (:) is a non-peptide covalent bond. In still other embodiments, (:) is a peptide bond. The orientation of the polypeptide formulas herein is listed from N-terminus (left) to C-terminus (right). For example, formula V-X-FVIII means formula NH2-V-X-FVIII -COOH. In one embodiment, the formulas described herein can comprise any additional sequences between the two moieties. For example, formula V-X-FVIII can further comprise any sequences at the N-terminus of V between V and X, between X and FVIII, or at the C-terminus of FVIII unless otherwise specified. In another embodiment, the hyphen (-) indicates a peptide bond.

[0115] In one aspect, the chimeric protein comprises two polypeptide chains, (A) a first chain comprising (i) a single chain FVIII protein (ii) an XTEN sequence, and (iii) a first Ig constant region or a portion thereof, *e.g.*, a first Fc region or FcRn binding partner, wherein the XTEN sequence is linked to the FVIII protein at the N-terminus or C-terminus or inserted immediately downstream of one or more amino acids of the FVIII protein (*e.g.*, one or more XTEN insertion sites disclosed herein) and the first Ig constant region or a portion thereof is linked to the XTEN sequence when the XTEN sequence is linked to the FVIII protein at the N-terminus or the C-terminus or the FVIII protein when the XTEN sequence is inserted within the FVIII protein, and (B) a second chain comprising (iv) a VWF fragment comprising a D' domain and a D3 domain, (v) a linker, and (vi) a second Ig constant region or a portion thereof, *e.g.*, a second Fc region or a second FcRn binding partner, wherein the VWF fragment is linked to the linker, *e.g.*, a cleavable linker, which is further linked to the second Ig constant region or a portion thereof, and wherein the first polypeptide chain and the second polypeptide chain are associated with each other by a covalent bond, *e.g.*, a disulfide bond. In one embodiment, the linker is a cleavable linker described elsewhere herein, *e.g.*, a thrombin cleavable linker. The second chain comprises one or more XTEN sequences between (iv) and (v) or (v) and (vi).

[0116] In other aspects, the chimeric protein comprises one polypeptide chain comprising (i) a single chain FVIII protein (ii) an XTEN sequence, (iii) a first Ig constant region or a portion thereof, *e.g.*, a first Fc region or a first FcRn binding partner, (iv) a first linker, (v) a VWF fragment comprising a D' domain and a D3 domain, (vi) a second linker, and (vii) a second Ig constant region or a portion thereof, *e.g.*, a second Fc region or a second FcRn binding partner, wherein (i) to (vii) are linked in the order or in any orders. In one embodiment, the first linker is a processable linker, which can be intracellularly processed or cleaved after expression and makes the single polypeptide chain into two polypeptide chains. In another embodiment, the second linker is a cleavable linker described herein, *e.g.,* a thrombin cleavable linker. The XTEN sequence used herein can be linked to the FVIII protein by an optional linker at the N-terminus or the C terminus of the FVIII protein or inserted immediately downstream of one or more amino acids (*e.g.*, one or more XTEN insertion sites) in the FVIII protein.

[0117] In certain instances, a chimeric protein comprises three polypeptide chains, (A) a first polypeptide chain comprising (i) a heavy chain of a FVIII protein and (ii) an XTEN sequence, which are linked to each other and (B)

a second polypeptide chain comprising (iii) a light chain of the FVIII protein and (iv) a first Ig constant region or a portion thereof, *e.g.*, a first Fc region or a first FcRn binding partner, which are linked to each other, and (C) a third polypeptide chain comprising (v) a VWF fragment comprising a D' domain and a D3 domain, (vi) a linker, and (vii) a second Ig constant region or a portion thereof, *e.g.*, a second Fc region or a second FcRn binding partner, wherein the second chain is associated with the first chain and the third chain. In one instance, the association between the first chain and the second chain is a chemical association or a physical association. For example, the association between the first chain and the second chain can be a metal bond. In another instance, the association between the second chain and the third chain is also a chemical association or a physical association, *e.g.*, a covalent bond or a non-covalent bond. In certain instances, the association between the second chain and the third chain is through the two Ig constant regions or a portion thereof and is a disulfide bond. The bonding between the second chain and the third chain prevents or inhibits binding of the FVIII protein with endogenous VWF, thus preventing the FVIII protein being cleared by the VWF clearance pathway. In some instances, the linker is a processable linker, which is intracellularly cleaved after expression in a host cell. The XTEN sequence used herein is linked to the FVIII protein by an optional linker at the N-terminus or C terminus of the FVIII protein or inserted immediately downstream of one or more amino acids (*e.g.*, one or more XTEN insertion sites) in the FVIII protein.

[0118] In certain instances, the VWF fragment is directly linked to the FVIII protein, which comprises one or more XTENs, by a peptide bond or a linker. As one way of linking the VWF fragment and the FVIII protein, in which one or more XTENs are inserted or linked, through a direct link (*e.g.* a peptide bond) or a linker, an enzymatic ligation (*e.g.*, sortase) can be employed. For example, sortase refers to a group of prokaryotic enzymes that modify surface proteins by recognizing and cleaving a carboxyl-terminal sorting signal. For most substrates of sortase enzymes, the recognition signal consists of the motif LPXTG (Leu-Pro-any-Thr-Gly (SEQ ID NO: 51), then a highly hydrophobic transmembrane sequence, then a cluster of basic residues such as arginine. Cleavage occurs between the Thr and Gly, with transient attachment through the Thr residue to the active site Cys residue of a ligation partner, followed by transpeptidation that attaches the protein covalently to the cell wall. In some instances, the ligation partner contains Gly(n). In other instances, the chimeric protein further comprises a sortase recognition motif. In some instances, the VWF fragment is attached to FVIII comprising one or more XTENs inserted within or linked to using sortase mediated *in vitro* protein ligation.

[0119] In one instance, a VWF fragment linked to a sortase recognition motif by an optional linker can be fused to a FVIII protein linked to Gly(n) by a sortase, wherein n can be any integer and wherein one or more XTENs are inserted within or linked to the FVIII protein. A ligation construct comprises the VWF fragment (N-terminal portion of the construct) and the FVIII protein, in which one or more XTENs are inserted or linked (C-terminal portion of the construct), wherein the sortase recognition motif is inserted in between. Another ligation construct comprises the VWF fragment (N-terminal portion of the construct, the linker, the sortase recognition motif, and the FVIII protein, in which one or more XTENs are inserted or linked (C-terminal portion of the construct). In another instance, a FVIII protein linked to a sortase recognition motif by an optional linker can be fused to a VWF fragment linked to Gly(n) by a sortase, wherein n is any integer. A resulting ligation construct comprises the FVIII protein (N-terminal portion of the construct), in which one or more XTENs are inserted or linked, and the VWF fragment (C-terminal portion of the construct), wherein the sortase recognition motif is inserted in between. Another resulting ligation construct comprises the FVIII protein (N-terminal portion of the construct), in which one or more XTENs are inserted or linked, the linker, the sortase recognition motif, and the VWF fragment (C-terminal portion of the construct). In other instances, a VWF fragment linked to a sortase recognition motif by a first optional linker can be fused to a heterologous moiety, *e.g.*, an immunoglobulin constant region or a portion thereof, *e.g.*, an Fc region, linked to a thrombin cleavage site by a second optional linker. A resulting construct can comprise the VWF fragment (N-terminal portion), the first linker, the sortase recognition motif, the protease cleavage site, the second optional linker, and the heterologous moiety.

[0120] In some instances, the VWF fragment is associated with the FVIII protein. The association between the VWF fragment and the FVIII protein can be a chemical association or a physical association. The chemical association can be a non-covalent interaction, *e.g.*, an ionic interaction, a hydrophobic interaction, a hydrophilic interaction, a Van der Waals interaction, or a hydrogen bond. In yet other instances, the association between the

FVIII protein and the VWF fragment is a physical association between two sequences, *e.g.*, due to an additional association between the sequence having the FVIII protein and the sequence having the VWF fragment, wherein a portion of a first sequence is in close proximity to a second sequence such that the first sequence shields or blocks a portion of the second sequence from interacting with another moiety.

[0121] As a result of preventing or inhibiting endogenous VWF interaction with the FVIII protein by the VWF fragment, the chimeric protein described herein have an extended half-life compared to wild-type FVIII or the corresponding chimeric protein without the VWF fragment. In one embodiment, the half-life of the FVIII protein is extended at least about 1.5 times, at least about 2 times, at least about 2.5 times, at least about 3 times, at least about 4 times, at least about 5 times, at least about 6 times, at least about 7 times, at least about 8 times, at least about 9 times, at least about 10 times, at least about 11 times, or at least about 12 times longer than a FVIII protein without the VWF fragment. In another embodiment, the half-life of the FVIII protein is at least about 10 hours, at least about 11 hours, at least about 12 hours, at least about 13 hours, at least about 14 hours, at least about 15 hours, at least about 16 hours, at least about 17 hours, at least about 18 hours, at least about 19 hours, at least about 20 hours, at least about 21 hours, at least about 22 hours, at least about 23 hours, at least about 24 hours, at least about 36 hours, at least about 48 hours, at least about 60 hours, at least about 72 hours, at least about 84 hours, at least about 96 hours, or at least about 108 hours. In a particular embodiment, the half-life of the FVIII protein is extended at least 10 hours, at least about 11 hours, at least about 12 hours, at least about 13 hours, at least about 14 hours, at least about 15 hours, at least about 16 hours, at least about 17 hours, at least about 18 hours, at least about 19 hours, at least about 20 hours, at least about 21 hours, at least about 22 hours, at least about 23 hours, at least about 24 hours, at least about 25 hours, at least about 26 hours, or at least about 27 hours in HemA mice.

A) Von Willebrand Factor (VWF) Fragments

[0122] VWF (also known as F8VWF) is a large multimeric glycoprotein present in blood plasma and produced constitutively in endothelium (in the Weibel-Palade bodies), megakaryocytes (α-granules of platelets), and subendothelian connective tissue. The basic VWF monomer is a 2813 amino acid protein. Every monomer contains a number of specific domains with a specific function, the D'/D3 domain (which binds to Factor VIII), the A1 domain (which binds to platelet GPIb-receptor, heparin, and/or possibly collagen), the A3 domain (which binds to collagen), the C1 domain (in which the RGD domain binds to platelet integrin αIIbβ3 when this is activated), and the "cysteine knot" domain at the C-terminal end of the protein (which VWF shares with platelet-derived growth factor (PDGF), transforming growth factor-β (TGFβ) and β-human chorionic gonadotropin (βHCG).

[0123] The term "a VWF fragment" as used herein includes, but is not limited to, functional VWF fragments comprising a D' domain and a D3 domain, which are capable of inhibiting binding of endogenous VWF to FVIII. In one embodiment, the VWF fragment binds to the FVIII protein. In another embodiment, the VWF fragment blocks the VWF binding site on the FVIII protein, thereby inhibiting interaction of the FVIII protein with endogenous VWF. The VWF fragments include derivatives, variants, mutants, or analogues that retain these activities of VWF.

[0124] The 2813 monomer amino acid sequence for human VWF is reported as Accession Number_NP_000543.2_ in Genbank. The nucleotide sequence encoding the human VWF is reported as Accession Number_NM_000552.3_ in Genbank. The nucleotide sequence of human VWF is designated as SEQ ID NO: 1. SEQ ID NO: 2 is the amino acid sequence encoded by SEQ ID NO: 1. Each domain of VWF is listed in Table 1.

TABLE 1. VWF Sequences

VWF domains	Amino acid Sequence
VWF Signal Peptide (Amino acids 1 to 22 of SEQ ID NO: 2)	1 MIPARFAGVL LALALILPGT LC 22
VWF D1D2 region (Amino	

VWF domains	Amino acid Sequence
acids 23 to 763 of SEQ ID NO: 2)	23 AEGTRGRS STARCSLFGS DFVNTFDGSM 51 YSFAGYCSYL LAGGCQKRSF SIIGDFQNGK RVSLSVYLGE FFDIHLFVNG 101 TVTQGDQRVS MPYASKGLYL ETEAGYYKLS GEAYGFVARI DGSGNFQVLL 151 SDRYFNKTCG LCGNFNIFAE DDFMTQEGTL TSDPYDFANS WALSSGEQWC 201 ERASPPSSSC NISSGEMQKG LWEQCQLLKS TSVFARCHPL VDPEPFVALC 251 EKTLCECAGG LECACPALLE YARTCAQEGM VLYGWTDHSA CSPVCPAGME 301 YRQCVSPCAR TCQSLHINEM CQERCVDGCS CPEGQLLDEG LCVESTECPC 351 VHSGKRYPPG TSLSRDCNTC ICRNSQWICS NEECPGECLV TGQSHFKSFD 401 NRYFTFSGIC QYLLARDCQD HSFSIVIETV
	QCADDRDAVC TRSVTVRLPG 451 LHNSLVKLKH GAGVAMDGQD IQLPLLKGDL RIQHTVTASV RLSYGEDLQM 501 DWDGRGRLLV KLSPVYAGKT CGLCGNYNGN QGDDFLTPSG LAEPRVEDFG 551 NAWKLHGDCQ DLQKQHSDPC ALNPRMTRFS EEACAVLTSP TFEACHRAVS 601 PLPYLRNCRY DVCSCSDGRE CLCGALASYA AACAGRGVRV AWREPGRCEL 651 NCPKGQVYLQ CGTPCNLTCR SLSYPDEECN EACLEGCFCP PGLYMDERGD 701 CVPKAQCPCY YDGEIFQPED IFSDHHTMCY CEDGFMHCTM SGVPGSLLPD 751 AVLSSPLSHR SKR 763
VWF D' Domain	764 SLSCRPP MVKLVCPADN LRAEGLECTK TCQNYDLECM 801 SMGCVSGCLC PPGMVRHENR CVALERCPCF HQGKEYAPGE TVKIGCNTCV 851 CRDRKWNCTD HVCDAT 866
VWF D3 Domain	867 CSTI GMAHYLTFDG LKYLFPGECQ YVLVQDYCGS 901 NPGTFRILVG NKGCSHPSVK CKKRVTILVE GGEIELFDGE VNVKRPMKDE 951 THFEVVESGR YIILLLGKAL SVVWDRHLSI SVVLKQTYQE KVCGLCGNFD 1001 GIQNNDLTSS NLQVEEDPVD FGNSWKVSSQ CADTRKVPLD SSPATCHNNI 1051 MKQTMVDSSC RILTSDVFQD CNKLVDPEPY LDVCIYDTCS CESIGDCACF 1101 CDTIAAYAHV CAQHGKVVTW RTATLCPQSC EERNLRENGY ECEWRYNSCA 1151 PACQVTCQHP EPLACPVQCV EGCHAHCPPG KILDELLQTC VDPEDCPVCE 1201 VAGRRFASGK KVTLNPSDPE HCQICHCDVV NLTCEACQEP 1240
VWF A1 Domain	1241 GGLVVPPTDA

VWF domains	Amino acid Sequence
	1251 PVSPTTLYVE DISEPPLHDF YCSRLLDLVF LLDGSSRLSE AEFEVLKAFV 1301 VDMMERLRIS QKWVRVAVVE YHDGSHAYIG LKDRKRPSEL RRIASQVKYA 1351 GSQVASTSEV LKYTLFQIFS KIDRPEASRI ALLLMASQEP QRMSRNFVRY 1401 VQGLKKKKVI VIPVGIGPHA NLKQIRLIEK
	QAPENKAFVL SSVDELEQQR 1451 DEIVSYLCDL APEAPPPTLP PDMAQVTVG 1479
	1480 P GLLGVSTLGP KRNSMVLDVA 1501 FVLEGSDKIG EADFNRSKEF MEEVIQRMDV GQDSIHVTVL QYSYMVTVEY 1551 PFSEAQSKGD ILQRVREIRY QGGNRTNTGL ALRYLSDHSF LVSQGDREQA 1600 1601 PNLVYMVTGN PASDEIKRLP GDIQVVPIGV GPNANVQELE RIGWPNAPIL 1651 IQDFETLPRE APDLVLQRCC SGEGLQIPTL SPAPDCSQPL DVILLLDGSS 1701 SFPASYFDEM KSFAKAFISK ANIGPRLTQV SVLQYGSITT IDVPWNVVPE 1751 KAHLLSLVDV MQREGGPSQI GDALGFAVRY LTSEMHGARP GASKAVVILV 1801 TDVSVDSVDA AADAARSNRV TVFPIGIGDR YDAAQLRILA GPAGDSNVVK 1851 LQRIEDLPTM VTLGNSFLHK LCSGFVRICM DEDGNEKRPG DVWTLPDQCH 1901 TVTCQPDGQT LLKSHRVNCD RGLRPSCPNS QSPVKVEETC GCRWTCPCVC 1951 TGSSTRHIVT FDGQNFKLTG SCSYVLFQNK EQDLEVILHN GACSPGARQG 2001 CMKSIEVKHS ALSVEXHSDM EVTVNGRLVS VPYVGGNMEV NVYGAIMHEV 2051 RFNHLGHIFT FTPQNNEFQL QLSPKTFASK TYGLCGICDE NGANDFMLRD 2101 GTVTTDWKTL VQEWTVQRPG QTCQPILEEQ CLVPDSSHCQ VLLLPLFAEC 2151 HKVLAPATFY AICQQDSCHQ EQVCEVIASY AHLCRTNGVC VDWRTPDFCA 2201 MSCPPSLVYN HCEHGCPRHC DGNVSSCGDH PSEGCFCPPD KVMLEGSCVP 2251 EEACTQCIGE DGVQHQFLEA WVPDHQPCQI CTCLSGRKVN CTTQPCPTAK 2301 APTCGLCEVA RLRQNADQCC PEYECVCDPV SCDLPPVPHC ERGLQPTLTN 2351 PGECRPNFTC ACRKEECKRV SPPSCPPHRL PTLRKTQCCD EYECACNCVN 2401 STVSCPLGYL ASTATNDCGC TTTTCLPDKV CVHRSTIYPV GQFWEEGCDV 2451 CTCTDMEDAV MGLRVAQCSQ KPCEDSCRSG FTYVLHEGEC CGRCLPSACE 2501 VVTGSPRGDS QSSWKSVGSQ WASPENPCLI NECVRVKEEV FIQQRNVSCP 2551 QLEVPVCPSG FQLSCKTSAC CPSCRCERME ACMLNGTVIG PGKTVMIDVC
	2601 TTCRCMVQVG VISGFKLECR KTTCNPCPLG YKEENNTGEC CGRCLPTACT 2651 IQLRGGQIMT LKRDETLQDG CDTHFCKVNE RGEYFWEKRV TGCPPFDEHK 2701 CLAEGGKIMK IPGTCCDTCE EPECNDITAR

VWF domains	Amino acid Sequence
	LQYVKVGSCK SEVEVDIHYC 2751 QGKCASKAMY SIDINDVQDQ CSCCSPTRTE PMQVALHCTN GSVVYHEVLN 2801 AMECKCSPRK CSK
	Nucleotide Sequence (SEQ ID NO: 1)
Full-length VWF	1 ATGATTCCTG CCAGATTTGC CGGGGTGCTG CTTGCTCTGG CCCTCATTTT 51 GCCAGGGACC CTTTGTGCAG AAGGAACTCG CGGCAGGTCA TCCACGGCCC 101 GATGCAGCCT TTTCGGAAGT GACTTCGTCA ACACCTTTGA TGGGAGCATG 151 TACAGCTTTG CGGGATACTG CAGTTACCTC CTGGCAGGGG GCTGCCAGAA 201 ACGCTCCTTC TCGATTATTG GGGACTTCCA GAATGGCAAG AGAGTGAGCC 251 TCTCCGTGTA TCTTGGGGAA TTTTTTGACA TCCATTTGTT TGTCAATGGT 301 ACCGTGACAC AGGGGGACCA AAGAGTCTCC ATGCCCTATG CCTCCAAAGG 351 GCTGTATCTA GAAACTGAGG CTGGGTACTA CAAGCTGTCC GGTGAGGCCT 401 ATGGCTTTGT GGCCAGGATC GATGGCAGCG GCAACTTTCA AGTCCTGCTG 451 TCAGACAGAT ACTTCAACAA GACCTGCGGG CTGTGTGGCA ACTTTAACAT 501 CTTTGCTGAA GATGACTTTA TGACCCAAGA AGGGACCTTG ACCTCGGACC 551 CTTATGACTT TGCCAACTCA TGGGCTCTGA GCAGTGGAGA ACAGTGGTGT 601 GAACGGGCAT CTCCTCCCAG CAGCTCATGC AACATCTCCT CTGGGGAAAT 651 GCAGAAGGGC CTGTGGGAGC AGTGCCAGCT TCTGAAGAGC ACCTCGGTGT 701 TTGCCCGCTG CCACCCTCTG GTGGACCCCG AGCCTTTTGT GGCCCTGTGT 751 GAGAAGACTT TGTGTGAGTG TGCTGGGGGG CTGGAGTGCG CCTGCCCTGC 801 CCTCCTGGAG TACGCCCGGA CCTGTGCCCA GGAGGGAATG GTGCTGTACG 851 GCTGGACCGA CCACAGCGCG TGCAGCCCAG TGTGCCCTGC TGGTATGGAG 901 TATAGGCAGT GTGTGTCCCC TTGCGCCAGG ACCTGCCAGA GCCTGCACAT 951 CAATGAAATG TGTCAGGAGC
	GATGCGTGGA TGGCTGCAGC TGCCCTGAGG 1001 GACAGCTCCT GGATGAAGGC CTCTGCGTGG AGAGCACCGA GTGTCCCTGC 1051 GTGCATTCCG GAAAGCGCTA CCCTCCCGGC ACCTCCCTCT CTCGAGACTG 1101 CAACACCTGC ATTTGCCGAA ACAGCCAGTG GATCTGCAGC AATGAAGAAT 1151 GTCCAGGGGA GTGCCTTGTC ACTGGTCAAT CCCACTTCAA GAGCTTTGAC 1201 AACAGATACT TCACCTTCAG TGGGATCTGC CAGTACCTGC TGGCCCGGGA 1251 CTTGCCAGGAC CACTCCTTCT CCATTGTCAT TGAGACTGTC CAGTGTGCTG 1301 ATGACCGCGA CGCTGTGTGC ACCCGCTCCG TCACCGTCCG GCTGCCTGGC 1351 CTGCACAACA GCCTTGTGAA ACTGAAGCAT GGGGCAGGAG TTGCCATGGA 1401 TGGCCAGGAC ATCCAGCTCC CCCTCCTGAA AGGTGACCTC CGCATCCAGC 1451 ATACAGTGAC GGCCTCCGTG CGCCTCAGCT ACGGGGAGGA CCTGCAGATG

	Nucleotide Sequence (SEQ ID NO: 1)
	1501 GACTGGGATG GCCGCGGGAG GCTGCTGGTG AAGCTGTCCC CCGTCTATGC 1551 CGGGAAGACC TGCGGCCTGT GTGGGAATTA CAATGGCAAC CAGGGCGACG 1601 ACTTCCTTAC CCCCTCTGGG CTGGCCRGAGC CCCGGGTGGA GGACTTCGGG 1651 AACGCCTGGA AGCTGCACGG GGACTGCCAG GACCTGCAGA AGCAGCACAG 1701 CGATCCCTGC GCCCTCAACC CGCGCATGAC CAGGTTCTCC GAGGAGGCGT 1751 GCGCGGTCCT GACGTCCCCC ACATTCGAGG CCTGCCATCG TGCCGTCAGC 1801 CCGCTGCCCT ACCTGCGGAA CTGCCGCTAC GACGTGTGCT CCTGCTCGGA 1851 CGGCCGCGAG TGCCTGTGCG GCGCCCTGGC CAGCTATGCC GCGGCCTGCG 1901 CGGGGAGAGG CGTGCGCGTC GCGTGGCGCG AGCCAGGCCG CTGTGAGCTG 1951 AACTGCCCGA AAGGCCAGGT GTACCTGCAG TGCGGGACCC CCTGCAACCT 2001 GACCTGCCGC TCTCTCTCTT ACCCGGATGA GGAATGCAAT GAGGCCTGCC 2051 TGGAGGGCTG CTTCTGCCCC CCAGGGCTCT ACATGGATGA GAGGGGGGAC 2101 TGCGTGCCCA AGGCCCAGTG CCCCTGTTAC TATGACGGTG AGATCTTCCA 2151 GCCAGAAGAC ATCTTCTCAG ACCATCACAC CATGTGCTAC TGTGAGGATG 2201 GCTTCATGCA CTGTACCATG AGTGGAGTCC CCGGAAGCTT GCTGCCTGAC
	2251 GCTGTCCTCA GCAGTCCCCT GTCTCATCGC AGCAAAAGGA GCCTATCCTG 2301 TCGGCCCCCC ATGGTCAAGC TGGTGTGTCC CGCTGACAAC CTGCGGGCTG 2351 AAGGGCTCGA GTGTACCAAA ACGTGCCAGA ACTATGACCT GGAGTGCATG 2401 AGCATGGGCT GTGTCTCTGG CTGCCTCTGC CCCCCGGGCA TGGTCCGGCA 2451 TGAGAACAGA TGTGTGGCCC TGGAAAGGTG TCCCTGCTTC CATCAGGGCA 2501 AGGAGTATCC CCCTCCACAA ACAGTGAAGA TTGGCTGCAA CACTTGTGTC 2551 TGTCGGGACC GGAAGTGGAA CTGCACAGAC CATGTGTGTG ATGCCACGTG 2601 CTCCACGATC GGCATGGCCC ACTACCTCAC CTTCGACGGG CTCAAATACC 2651 TGTTCCCCGG GGAGTGCCAG TACGTTCTGG TGCAGGATTA CTGCGGCAGT 2701 AACCCTGGGA CCTTTCGGAT CCTACTCCCG AATAAGCCAT GCAGCCACCC 2751 CTCAGTGAAA TGCAAGAAAC CCGTCACCAT CCTCGTCCAC CGACCAGACA 2801 TTGAGCTGTT TGACGGGGAG GTGAATGTCA AGAGGCCCAT GAAGGATGAG 2851 ACTCACTTTG AGGTGGTGGA GTCTGGCCCG TACATCATTC TGCTGCTGGG 2901 CAAAGCCCTC TCCGTGGTCT GGGACCGCCA CCTGAGCATC TCCGTGGTCC 2951 TGAAGCAGAC ATACCAGGAG AAAGTGTGTG GCCTGTGTGG GAATTTTGAT 3001 GGCATCCAGA ACAATGACCT CACCAGCAGC AACCTCCAAG TGGAGGAAGA 3051 CCCTGTGGAC TTTGGGAACT CCTCGAAAGT GAGCTCGCAG TGTGCTGACA 3101 CCAGAAAAGT GCCTCTGGAC TCATCCCCTG CCACCTGCCA TAACAACATC 3151 ATGAAGCAGA CGATGGTGGA TTCCTCCTGT AGAATCCTTA CCAGTGACGT 3201 CTTCCAGGAC TGCAACAAGC TGGTGGACCC CGAGCCATAT CTGGATGTCT 3251 GCATTTACGA CACCTGCTCC TGTCAGTCCA TTCGCGACTG CGCCTGCTTC

	Nucleotide Sequence (SEQ ID NO: 1)
	3301 TGCGACACCA TTGCTGCCTA TGCCCACGTG TGTGCCCAGC ATGGCAAGGT 3351 GGTGACCTGG AGGACGGCCA CATTGTGCCC CCAGAGCTGC GAGGAGAGGA 3401 ATCTCCGGGA GAACGGGTAT GAGTGTGAGT GGCGCTATAA CAGCTGTGCA 3451 CCTGCCTGTC AAGTCACGTG TCAGCACCCT GAGCCACTGG CCTGCCCTGT 3501 GCAGTGTGTG GAGGGCTGCC
	ATGCCCACTG CCCTCCAGGG AAAATCCTGG 3551 ATGAGCTTTT GCAGACCTGC GTTGACCCTG AAGACTGTCC AGTGTGTGAG 3601 GTGGCTGGCC GGCGTTTTGC CTCAGGAAAG AAAGTCACCT TGAATCCCAG 3651 TGACCCTGAG CACTGCCAGA TTTGCCACTG TGATGTTGTC AACCTCACCT 3701 GTGAAGCCTG CCAGGAGCCG GGAGGCCTGG TGGTGCCTCC CACAGATGCC 3751 CCGGTGAGCC CCACCACTCT GTATGTGGAG GACATCTCCG AACCGCCGTT 3801 GCACGATTTC TACTGCAGCA GGCTACTGGA CCTGGTCTTC CTGCTGGATG 3851 GCTCCTCCAG GCTGTCCGAG GCTGAGTTTG AAGTGCTGAA GGCCTTTGTG 3901 GTGGACATGA TGGAGCGGCT GCGCATCTCC CAGAAGTGGG TCCGCGTGGC 3951 CGTGGTGGAG TACCACGACG GCTCCCACGC CTACATCGGG CTCAAGGACC 4001 GGAAGCGACC GTCAGAGCTG CGGCGCATTG CCAGCCAGGT GAAGTATGCG 4051 GGCAGCCAGG TGGCCTCCAC CAGCGAGGTC TTGAAATACA CACTGTTCCA 4101 AATCTTCAGC AAGATCGACC GCCCTGAAGC CTCCCGCATC GCCCTGCTCC 4151 TGATGGCCAG CCAGGAGCCC CAACGGATGT CCCGGAACTT TGTCCGCTAC 4201 GTCCAGGGCC TGAAGAAGAA GAAGGTCATT GTGATCCCGG TGGGCATTGG 4251 GCCCCATGCC AACCTCAAGC AGATCCGCCT CATCGAGAAG CAGGCCCCTG 4301 AGAACAAGGC CTTCGTGCTG AGCAGTGTGG ATGAGCTGGA GCAGCAAAGG 4351 GACGAGATCG TTAGCTACCT CTGTGACCGT GCCCCTGAAG CCCCTCCTCC 4401 TACTCTGCCC CCCGACATGG CACAAGTCAC TGTGGGCCCG GGGCTCTTGG 4451 GGGTTTCGAC CCTGGGGCCC AAGAGGAACT CCATGGTTCT GGATGTGGCG 4501 TTCGTCCTGG AAGGATCGGA CAAAATTGGT GAAGCCGACT TCAACAGGAG 4551 CAAGGAGTTC ATGGAGGAGG TGATTCAGCG GATGCATGTG GGCCAGGACA 4601 GCATCCACGT CACGGTGCTG CAGTACTCCT ACATGGTGAC CGTGGAGTAC 4651 CCCTTCAGCG AGGCACAGTC CAAAGGGGAC ATCCTGCAGC GGGTGCGAGA 4701 GATCCGCTAC CAGGGCGGCA ACAGGACCAA CACTGGGCTG GCCCTGCGGT 4751 ACCTCTCTGA CCACAGCTTC TTGGTCAGCC ACCGTGACCG CGACCAGGCC
	4801 CCCAACCTGG TCTACATGGT CACCGGAAAT CCTGCCTCTG ATGAGATCAA 4851 GAGGCTGCCT GGAGACATCC AGGTGGTGCC CATTGGAGTG GGCCCTAATG 4901 CCAACGTGCA GGAGCTGGAG AGGATTGGCT GGCCCAATGC CCCTATCCTC 4951 ATCCAGGACT TTGAGACGCT CCCCCGAGAG GCTCCTGACC TGGTGCTGCA 5001 GAGGTGCTGC TCCGGAGAGG

	Nucleotide Sequence (SEQ ID NO: 1)
	GGCTGCAGAT CCCCACCCIC TCCCCTGCAC 5051 CIGACTGCAG CCAGCCCCTG GACGTGATCC TTCTCCTGGA TGGCTCCTCC 5101 AGTTTCCCAG CTTCTTATTT TGATGAAATG AAGACTTTCG CCAAGGCTTI 5151 CATTTCAAAA GCCAATATAG GGCCTCGTCT CACTCAGGIG TCAGTGCTGC 5201 AGTATGGAAG CATCACCACC ATTGACGTGC CATGGAACGT GGTCCCGGAG 5251 AAAGCCCATT TGCTGAGCCT TGTGGACGTC ATGCAGCGGG AGGGAGGCCC 5301 CAGCCAAATC GGGGATGCCT TGGGCTTTGC TGTGCGATAC TIGACTTCAG 5351 AAATGCATGG TGCCAGGCCG GGAGCCTCAA AGGCGGTGGT CATCCTGGTC 5401 ACGGACGTCT CTGTGGATTC AGTGGATGCA GCAGCTGAIG CCGCCAGGTC 5451 CAACAGAGTG ACAGTGTTCC CTATTGGAAT TGGAGATCGC TACGATGCAG 5501 CCCAGCTACG GATCTTGGCA GGCCCAGCAG GCGACTCCAA CGTGGTGAAG 5551 CICCAGCGAA TCGAAGACCT CCCTACCATG GTCACCTTGG GCAATTCCTI 5601 CCTCCACAAA CTGTGCTCTG GATTTGTTAG GATTTGCAIG GATGAGGATG 5651 GGAATGAGAA GAGGCCCGGG GACGTCTGGA CCTTGCCAGA CCAGTGCCAC 5701 ACCGTGACTT GCCAGCCAGA TGGCCAGACC TTGCTGAAGA GTCATCGGGT 5751 CAACTGTGAC CGGGGGCTGA GGCCTTCGTG CCCTAACAGC CAGTCCCCTG 5801 TTAAAGTGGA AGAGACCTGT GGCTGCCGCT GGACCTGCCC CTGYGTGTGC 5851 ACAGGCAGCT CCACTCGGCA CATCGTGACC TTTGATGGGC AGAATTTCAA 5901 GCTGACTGGC AGCTGTTCTT ATGTCCTATT TCAAAACAAG GAGCAGGACC 5951 TGGAGGTGAT TCTCCATAAT GGTGCCTGCA GCCCTGGAGC AAGGCAGGGC 6001 TGCATGAAAT CCATCGAGGT GAAGCACAGT GCCCTCTCCG TCGAGSTGCA 6051 CAGTGACATG GAGGTGACGG
	TGAATGGGAG ACTGGTCTCT GTTCCTTACG 6101 TGGGTGGGAA CATGGAAGTC AACGTTTATG GTGCCATCAT GCATGAGGTC 6151 AGATTCAATC ACCTTGGTCA CATCTTCACA TTCACTCCAC AAAACAATGA 6201 GTTCCAACTG CAGCTCAGCC CCAAGACTTT TGCTTCAAAG ACGTATGGTC 6251 TGTGTGGGAT CTGTCATGAG AACGGAGCCA ATGACTTCAT GCTGAGGGAT 6301 GGCACAGTCA CCACAGACTG GAAAACACCT GTTCAGGAAT GGACTGTGCA 6351 GCGGCCAGGG CAGACGTGCC AGCCCATCCT GGAGGAGCAG TGTCTTGTCC 6401 CCGACAGCTC CCACTGCCAG GTCCTCCTCT TACCACTGIT TGCTGAATGC 6451 CACAAGGTCC TGGCTCCAGC CACATTCTAT GCCATCTGCC AGCAGGACAG 6501 TTGCCACCAG GAGCAAGTGT GTGAGGTGAT CGCCTCTTAT GCCCACCTCI 6551 GTCGGACCAA CGGGGTCTGC GTTGACTGGA GGACACCTGA TTTCTGTGCI 6601 AIGTCATGCC CACCATCTCT GGTCTACAAC CACTGTGAGC ATGGCTGTCC 6651 CCGGCACTGT GATGGCAACG TGAGCTCCTG TGGGGACCAT CCCTCCGAAG 6701 GCTGTTTCTG CCCTCCAGAT AAAGTCATGT TGGAAGGCAG CTGTGTCCCI 6751 GAAGAGGCCT GCACTCAGTG CATTGGTGAG GATGGAGTCC AGCACCAGTI 6801 CCTGGAAGCC TGGGTCCCGG

	Nucleotide Sequence (SEQ ID NO: 1)
	ACCACCAGCC CTGTCAGATC TGCACATGCC 6851 TCAGCGGGCG GAAGGTCAAC TGCACAACGC AGCCCTGCCC CACGGCCAAA 6901 GCTCCCACGT GTGGCCTGTG TGAAGTAGCC CGCCTCCGCC AGAATGCAGA 6951 CCAGTGCTGC CCCGAGTATG AGTGTGTGTG TGACCCAGTG AGCTGTGACC 7001 TGCCCCCAGT GCCTCACTGT GAACGTGGCC TCCAGCCCAC ACTGACCAAC 7051 CCTGGCGAGT GCAGACCCAA CTTCACCTGC GCCTGCAGGA AGGAGGAGTG 7101 CAAAAGAGTG TCCCCACCCT CCTGCCCCCC GCACCGTTTG CCCACCCTTC 7151 GGAAGACCCA GTGCTGTGAT GAGTATGAGT GTGCCTGCAA CTGTGTCAAC 7201 TCCACAGTGA GCTGTCCCCT TGGGTACTTG GCCTCAACCG CCACCAATGA 7251 CTGTGGCTGT ACCACAACCA CCTGCCTTCC CGACAAGGTG TGTGTCCACC 7301 GAAGCACCAT CTACCCTGTG GGCCAGTTCT GGGAGGAGCG CTGCGATGTG
	7351 TGCACCTGCA CCGACATGGA GGATGCCGTG ATGGGCCTCC GCGTGGCCCA 7401 GTGCTCCCAG AAGCCCTGTG AGGACAGCTG TCGGTCGGGC TTCACTTACG 7451 TTCTGCATGA AGGCGAGTGC TGTGGAAGGT GCCTGCCATC TGCCTGTGAG 7501 GTGGTGACTG GCTCACCGCG GGGGGACTCC CAGTCTTCCT GGAAGAGTGT 7551 CGGCTCCCAG TGGGCCTCCC CGGAGAACCC CTGCCTCATC AATGAGTGTG 7601 TCCGAGTGAA GGAGGAGGTC TTTATACAAC AAAGGAACGT CTCCTGCCCC 7651 CAGCTGGAGG TCCCTGTCTG CCCCTCGGGC TTTCAGCTGA GCTGTAAGAC 7701 CTCAGCGTGC TGCCCAAGCT GTCGCTGTGA GCGCATGGAG GCCTGCATGC 7751 TCAATGGCAC TGTCATTGGG CCCGGGAAGA CTGTGATGAT CGATGTGTGC 7801 ACGACCTGCC GCTGCATGGT GCAGGTGGGG GTCATCTCTG GATTCAAGCT 7851 GGAGTGCAGG AAGACCACCT GCAACCCCTG CCCCCTGGGT TACAAGGAAG 7901 AAAATAACAC AGGTGAATGT TGTGGGAGAT GTTTGCCTAC GGCTTGCACC 7951 ATTCAGCTAA GAGGAGGACA GATCATGACA CTGAAGCGTG ATGAGACGCT 8001 CCAGGATGGC TGTGATACTC ACTTCTGCAA GGTCAATGAG AGAGGAGAGT 8051 ACTTCTGGGA GAAGAGGGTC ACAGGCTGCC CACCCTTTGA TGAACACAAG 8101 TGTCTTGCTG AGGGAGGTAA AATTATGAAA ATTCCAGGCA CCTGCTGTGA 8151 CACATGTGAG GAGCCTGAGT GCAACGACAT CACTGCCAGG CTGCAGTATG 8201 TCAAGGTGGG AAGCTGTAAG TCTGAAGTAG AGGTGGATAT CCACTACTGC 8251 CAGGGCAAAT GTGCCAGCAA AGCCATGTAC TCCATTGACA TCAACGATGT 8301 GCAGGACCAG TGCTCCTGCT GCTCTCCGAC ACGGACGGAG CCCATGCAGG 8351 TGGCCCTGCA CTGCACCAAT GGCTCTGTTG TGTACCATGA GGTTCTCAAT 8401 GCCATGGAGT GCAAATGCTC CCCCAGGAAG TGCAGCAAGT GA

[0125] The VWF fragment as used herein can be a VWF fragment comprising a D' domain and a D3 domain of VWF, wherein the VWF fragment binds to Factor VIII (FVIII) and inhibits binding of endogenous VWF (full-length VWF) to FVIII. The VWF fragment comprising the D' domain and the D3 domain can further comprise a VWF domain selected from the group consisting of an A1 domain, an A2 domain, an A3 domain, a D1 domain, a D2 domain, a D4 domain, a B1 domain, a B2 domain, a B3 domain, a C1 domain, a C2 domain, a CK domain, one or more fragments thereof, and any combinations thereof. In one embodiment, a VWF fragment comprises, consists essentially of, or consists of: (1) the D' and D3 domains of VWF or fragments thereof; (2) the D1, D', and D3 domains of VWF or fragments thereof; (3) the D2, D', and D3 domains of VWF or fragments thereof; (4) the D1, D2, D', and D3 domains of VWF or fragments thereof; or (5) the D1, D2, D', D3, and A1 domains of VWF or fragments thereof. The VWF fragment described herein does not contain a site binding to a VWF clearance receptor. In another embodiment, the VWF fragment described herein is not amino acids 764 to 1274 of SEQ ID NO: 2. The VWF fragment can comprise any other sequences linked to or fused to the VWF fragment. For example, a VWF fragment described herein can further comprise a signal peptide.

[0126] In one embodiment, the VWF fragment binds to or is associated with a FVIII protein. By binding to or associating with a FVIII protein, a VWF fragment of the invention protects FVIII from protease cleavage and FVIII activation, stabilizes the heavy chain and light chain of FVIII, and prevents clearance of FVIII by scavenger receptors. In another embodiment, the VWF fragment binds to or associates with a FVIII protein and blocks or prevents binding of the FVIII protein to phospholipid and activated Protein C. By preventing or inhibiting binding of the FVIII protein with endogenous, full-length VWF, the VWF fragment of the invention reduces the clearance of FVIII by VWF clearance receptors and thus extends half-life of the FVIII protein. In one embodiment, the half-life extension of a FVIII protein is thus due to the binding of or associating with the VWF fragment lacking a VWF clearance receptor binding site to the FVIII protein and shielding or protecting of the FVIII protein by the VWF fragment from endogenous VWF which contains the VWF clearance receptor binding site. The FVIII protein bound to or protected by the VWF fragment can also allow recycling of a FVIII protein. By eliminating the VWF clearance pathway receptor binding sites contained in the full length VWF molecule, the FVIII/VWF heterodimers of the invention are shielded from the VWF clearance pathway, further extending FVIII half-life.

[0127] In one embodiment, a VWF fragment comprises the D' domain and the D3 domain of VWF, wherein the D' domain is at least 60%, 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to amino acids 764 to 866 of SEQ ID NO: 2, wherein the VWF fragment prevents binding of endogenous VWF to FVIII. In another embodiment, a VWF fragment comprises the D' domain and the D3 domain of VWF, wherein the D3 domain is at least 60%, 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to amino acids 867 to 1240 of SEQ ID NO: 2, wherein the VWF fragment prevents binding of endogenous VWF to FVIII. In some embodiments, a VWF fragment described herein comprises, consists essentially of, or consists of the D' domain and D3 domain of VWF, which are at least 60%, 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to amino acids 764 to 1240 of SEQ ID NO: 2, wherein the VWF fragment prevents binding of endogenous VWF to FVIII. In other embodiments, a VWF fragment comprises, consists essentially of, or consists of the D1, D2, D', and D3 domains at least 60%, 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to amino acids 23 to 1240 of SEQ ID NO: 2, wherein the VWF fragment prevents binding of endogenous VWF to FVIII. In still other embodiments, the VWF fragment further comprises a signal peptide operably linked thereto.

[0128] In some embodiments, a VWF fragment consists essentially of or consists of (1) the D'D3 domain, the D1D'D3 domain, D2D'D3 domain, or D1D2D'D3 domain and (2) an additional VWF sequence up to about 10 amino acids (*e.g.*, any sequences from amino acids 764 to 1240 of SEQ ID NO: 2 to amino acids 764 to 1250 of SEQ ID NO: 2), up to about 15 amino acids (*e.g.*, any sequences from amino acids 764 to 1240 of SEQ ID NO: 2 to amino acids 764 to 1255 of SEQ ID NO: 2), up to about 20 amino acids (*e.g.*, any sequences from amino acids 764 to 1240 of SEQ ID NO: 2 to amino acids 764 to 1260 of SEQ ID NO: 2), up to about 25 amino acids (*e.g.*, any sequences from amino acids 764 to 1240 of SEQ ID NO: 2 to amino acids 764 to 1265 of SEQ ID NO: 2), or up to about 30 amino acids (*e.g.*, any sequences from amino acids 764 to 1240 of SEQ ID NO: 2 to amino acids 764 to 1260 of SEQ ID NO: 2). In a particular embodiment, the VWF fragment comprising or consisting essentially of the D' domain and the D3 domain is neither amino acids 764 to 1274 of SEQ ID NO: 2 nor the full-length mature VWF.

In some embodiments, the D1D2 domain is expressed in trans with the D'D3 domain. In some embodiments, the D1D2 domain is expressed in cis with the D'D3 domain.

[0129] In other embodiments, the VWF fragment comprising the D'D3 domains linked to the D1D2 domains further comprises an intracellular cleavage site, *e.g.*, (a cleavage site by PACE (furin) or PC5), allowing cleavage of the D1D2 domains from the D'D3 domains upon expression. Non-limiting examples of the intracellular cleavage site are disclosed elsewhere herein.

[0130] In yet other embodiments, a VWF fragment comprises the D' domain and the D3 domain, but does not comprise an amino acid sequence selected from the group consisting of (1) amino acids 1241 to 2813 of SEQ ID NO: 2, (2) amino acids 1270 to amino acids 2813 of SEQ ID NO: 2, (3) amino acids 1271 to amino acids 2813 of SEQ ID NO: 2, (4) amino acids 1272 to amino acids 2813 of SEQ ID NO: 2, (5) amino acids 1273 to amino acids 2813 of SEQ ID NO: 2, (6) amino acids 1274 to amino acids 2813 of SEQ ID NO: 2, and any combinations thereof.

[0131] In still other embodiments, a VWF fragment comprises, consists essentially of, or consists of an amino acid sequence corresponding to the D' domain, D3 domain, and A1 domain, wherein the amino acid sequence is at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to amino acid 764 to 1479 of SEQ ID NO: 2, wherein the VWF fragment prevents binding of endogenous VWF to FVIII. In a particular embodiment, the VWF fragment is not amino acids 764 to 1274 of SEQ ID NO: 2.

[0132] In some embodiments, a VWF fragment comprises the D' domain and the D3 domain, but does not comprise at least one VWF domain selected from the group consisting of (1) an A1 domain, (2) an A2 domain, (3) an A3 domain, (4) a D4 domain, (5) a B1 domain, (6) a B2 domain, (7) a B3 domain, (8) a C1 domain, (9) a C2 domain, (10) a CK domain, (11) a CK domain and C2 domain, (12) a CK domain, a C2 domain, and a C1 domain, (13) a CK domain, a C2 domain, a C1 domain, a B3 domain, (14) a CK domain, a C2 domain, a C1 domain, a B3 domain, a B2 domain, (15) a CK domain, a C2 domain, a C1 domain, a B3 domain, a B2 domain, and a B1 domain, (16) a CK domain, a C2 domain, a C1 domain, a B3 domain, a B2 domain, a B1 domain, and a D4 domain, (17) a CK domain, a C2 domain, a C1 domain, a B3 domain, a B2 domain, a B1 domain, a D4 domain, and an A3 domain, (18) a CK domain, a C2 domain, a C1 domain, a B3 domain, a B2 domain, a B1 domain, a D4 domain, an A3 domain, and an A2 domain, (19) a CK domain, a C2 domain, a C1 domain, a B3 domain, a B2 domain, a B1 domain, a D4 domain, an A3 domain, an A2 domain, and an A1 domain, and (20) any combinations thereof.

[0133] In yet other embodiments, the VWF fragment comprises the D'D3 domains and one or more domains or modules. Examples of such domains or modules include, but are not limited to, the domains and modules disclosed in Zhour et al., Blood published online April 6, 2012: DOI 10.1182/blood-2012-01-405134. For example, the VWF fragment can comprise the D'D3 domain and one or more domains or modules selected from the group consisting of A1 domain, A2 domain, A3 domain, D4N module, VWD4 module, C8-4 module, TIL-4 module, C1 module, C2 module, C3 module, C4 module, C5 module, C5 module, C6 module, and any combinations thereof.

[0134] In still other embodiments, the VWF fragment is linked to a heterologous moiety, wherein the heterologous moiety is linked to the N-terminus or the C-terminus of the VWF fragment or inserted immediately downstream of one or more amino acids (*e.g.*, one or more XTEN insertion sites) in the FVIII protein in the VWF fragment. For example, the insertion sites for the heterologous moiety in the VWF fragment can be in the D' domain, the D3 domain, or both. The heterologous moiety can be a half-life extender.

[0135] In certain embodiments, a VWF fragment forms a multimer, *e.g.*, dimer, trimer, tetramer, pentamer, hexamer, heptamer, or the higher order multimers. In other embodiments, the VWF fragment is a monomer having only one VWF fragment. In some embodiments, the VWF fragment can have one or more amino acid substitutions, deletions, additions, or modifications. In one embodiment, the VWF fragment can include amino acid substitutions, deletions, additions, or modifications such that the VWF fragment is not capable of forming a disulfide bond or forming a dimer or a multimer. In another embodiment, the amino acid substitution is within the D' domain and the D3 domain. In a particular embodiment, a VWF fragment contains at least one amino acid

substitution at a residue corresponding to residue 1099, residue 1142, or both residues 1099 and 1142 of SEQ ID NO: 2. The at least one amino acid substitution can be any amino acids that are not occurring naturally in the wild type VWF. For example, the amino acid substitution can be any amino acids other than cysteine, *e.g.*, Isoleucine, Alanine, Leucine, Asparagine, Lysine, Aspartic acid, Methionine, Phenylalanine, Glutamic acid, Threonine, Glutamine, Tryptophan, Glycine, Valine, Proline, Serine, Tyrosine, Arginine, or Histidine. In another example, the amino acid substitution has one or more amino acids that prevent or inhibit the VWF fragments from forming multimers.

[0136] In certain embodiments, the VWF fragment useful herein can be further modified to improve its interaction with FVIII, *e.g.*, to improve binding affinity to FVIII. As a non-limiting example, the VWF fragment comprises a serine residue at the residue corresponding to amino acid 764 of SEQ ID NO: 2 and a lysine residue at the residue corresponding to amino acid 773 of SEQ ID NO: 2. Residues 764 and/or 773 can contribute to the binding affinity of the VWF fragments to FVIII. In other embodiments, the VWF fragments useful for the invention can have other modifications, *e.g.*, the protein can be pegylated, glycosylated, hesylated, or polysialylated.

B) XTEN Sequences

[0137] As used here "XTEN sequence" refers to extended length polypeptides with non-naturally occurring, substantially non-repetitive sequences that are composed mainly of small hydrophilic amino acids, with the sequence having a low degree or no secondary or tertiary structure under physiologic conditions. As a chimeric protein partner, XTENs can serve as a carrier, conferring certain desirable pharmacokinetic, physicochemical and pharmaceutical properties when linked to a VWF fragment or a FVIII sequence of the invention to create a chimeric protein. Such desirable properties include but are not limited to enhanced pharmacokinetic parameters and solubility characteristics. As used herein, "XTEN" specifically excludes antibodies or antibody fragments such as single-chain antibodies or Fc fragments of a light chain or a heavy chain.

[0138] In some embodiments, the XTEN sequence of the invention is a peptide or a polypeptide having greater than about 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1200, 1400, 1600, 1800, or 2000 amino acid residues. In certain embodiments, XTEN is a peptide or a polypeptide having greater than about 20 to about 3000 amino acid residues, greater than 30 to about 2500 residues, greater than 40 to about 2000 residues, greater than 50 to about 1500 residues, greater than 60 to about 1000 residues, greater than 70 to about 900 residues, greater than 80 to about 800 residues, greater than 90 to about 700 residues, greater than 100 to about 600 residues, greater than 110 to about 500 residues, or greater than 120 to about 400 residues.

[0139] The XTEN sequence of the invention can comprise one or more sequence motif of 9 to 14 amino acid residues or an amino acid sequence at least 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the sequence motif, wherein the motif comprises, consists essentially of, or consists of 4 to 6 types of amino acids selected from the group consisting of glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P). *See* US 2010-0239554 A1.

[0140] In some embodiments, the XTEN comprises non-overlapping sequence motifs in which about 80%, or at least about 85%, or at least about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, or about 99% or about 100% of the sequence consists of multiple units of non-overlapping sequences selected from a single motif family selected from Table 2A, resulting in a family sequence. As used herein, "family" means that the XTEN has motifs selected only from a single motif category from Table 2A; *i.e.*, AD, AE, AF, AG, AM, AQ, BC, or BD XTEN, and that any other amino acids in the XTEN not from a family motif are selected to achieve a needed property, such as to permit incorporation of a restriction site by the encoding nucleotides, incorporation of a cleavage sequence, or to achieve a better linkage to FVIII or VWF. In some embodiments of XTEN families, an XTEN sequence comprises multiple units of non-overlapping sequence motifs of the AD motif family, or of the AE motif family, or of the AF motif family, or of the AG motif family, or of the AM motif family, or of the AQ motif family, or of the BC family, or of the BD family, with the

resulting XTEN exhibiting the range of homology described above. In other embodiments, the XTEN comprises multiple units of motif sequences from two or more of the motif families of Table 2A. These sequences can be selected to achieve desired physical/chemical characteristics, including such properties as net charge, hydrophilicity, lack of secondary structure, or lack of repetitiveness that are conferred by the amino acid composition of the motifs, described more fully below. In the embodiments hereinabove described in this paragraph, the motifs incorporated into the XTEN can be selected and assembled using the methods described herein to achieve an XTEN of about 36 to about 3000 amino acid residues.

Table 2A. XTEN Sequence Motifs of 12 Amino Acids and Motif Families

Motif Family*	MOTIF SEQUENCE
AD	GESPGGSSGSES
AD	GSEGSSGPGESS
AD	GSSESGSSEGGP
AD	GSGGEPSESGSS
AE, AM	GSPAGSPTSTEE
AE, AM, AQ	GSEPATSGSETP
AE, AM, AQ	GTSESATPESGP
AE, AM, AQ	GTSTEPSEGSAP
AF, AM	GSTSESPSGTAP
AF, AM	GTSTPESGSASP
AF, AM	GTSPSGESSTAP
AF, AM	GSTSSTAESPGP
AG, AM	GTPGSGTASSSP
AG, AM	GSSTPSGATGSP
AG, AM	GSSPSASTGTGP
AG, AM	GASPGTSSTGSP
AQ	GEPAGSPTSTSE
AQ	GTGEPSSTPASE
AQ	GSGPSTESAPTE
AQ	GSETPSGPSETA
AQ	GPSETSTSEPGA
AQ	GSPSEPTEGTSA
BC	GSGASEPTSTEP
BC	GSEPATSGTEPS
BC	GTSEPSTSEPGA
BC	GTSTEPSEPGSA
BD	GSTAGSETSTEA
BD	GSETATSGSETA
BD	GTSESATSESGA
BD	GTSTEASEGSAS
• Denotes individual motif sequences that, when used together in various permutations, results in a "family sequence"	

[0141] XTEN can have varying lengths for insertion into or linkage to FVIII or VWF. In one embodiment, the length of the XTEN sequence(s) is chosen based on the property or function to be achieved in the fusion protein.

Depending on the intended property or function, XTEN can be short or intermediate length sequence or longer sequence that can serve as carriers. In certain embodiments, the XTEN include short segments of about 6 to about 99 amino acid residues, intermediate lengths of about 100 to about 399 amino acid residues, and longer lengths of about 400 to about 1000 and up to about 3000 amino acid residues. Thus, the XTEN inserted into or linked to FVIII or VWF can have lengths of about 6, about 12, about 36, about 40, about 42, about 72, about 96, about 144, about 288, about 400, about 500, about 576, about 600, about 700, about 800, about 864, about 900, about 1000, about 1500, about 2000, about 2500, or up to about 3000 amino acid residues in length. In other embodiments, the XTEN sequences is about 6 to about 50, about 50 to about 100, about 100 to 150, about 150 to 250, about 250 to 400, about 400 to about 500, about 500 to about 900, about 900 to 1500, about 1500 to 2000, or about 2000 to about 3000 amino acid residues in length. The precise length of an XTEN inserted into or linked to FVIII or VWF can vary without adversely affecting the activity of the FVIII or VWF. In one embodiment, one or more of the XTEN used herein has 36 amino acids, 42 amino acids, 72 amino acids, 144 amino acids, 288 amino acids, 576 amino acids, or 864 amino acids in length and can be selected from one or more of the XTEN family sequences; *i.e.*, AD, AE, AF, AG, AM, AQ, BC or BD.

[0142] In some embodiments, the XTEN sequence used in the invention is at least 60%, 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence selected from the group consisting of AE42, AG42, AE48, AM48, AE72, AG72, AE108, AG108, AE144, AF144, AG144, AE180, AG180, AE216, AG216, AE252, AG252, AE288, AG288, AE324, AG324, AE360, AG360, AE396, AG396, AE432, AG432, AE468, AG468, AE504, AG504, AF504, AE540, AG540, AF540, AD576, AE576, AF576, AG576, AE612, AG612, AE624, AE648, AG648, AG684, AE720, AG720, AE756, AG756, AE792, AG792, AE828, AG828, AD836, AE864, AF864, AG864, AM875, AE912, AM923, AM1318, BC864, BD864, AE948, AE1044, AE1140, AE1236, AE1332, AE1428, AE1524, AE1620, AE1716, AE1812, AE1908, AE2004A, AG948, AG1044, AG1140, AG1236, AG1332, AG1428, AG1524, AG1620, AG1716, AG1812, AG1908, and AG2004. *See* US 2010-0239554 A1.

[0143] In one embodiment, the XTEN sequence is at least 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence selected from the group consisting of AE42 (SEQ ID NO: 36), AE72 (SEQ ID NO: 127), AE144_2A (SEQ IDNO: 128), AE144_3B (SEQ ID NO: 129), AE144_4A (SEQ ID NO: 130), AE144_5A (SEQ IDNO: 131), AE144_6B (SEQ IDNO: 132), AG144 A (SEQ ID NO: 133), AG144_B (SEQ IDNO: 134), AG144_C (SEQ ID NO: 135), AG144_F (SEQ IDNO: 136), AE864 (SEQ ID NO: 43), AE576 (SEQ ID NO: 41), AE288 (SEQ IDNO: 39), AE288_2 (SEQ ID NO: 137), AE144 (SEQ ID NO: 37), AG864 (SEQ ID NO: 44), AG576 (SEQ ID NO: 42), AG288 (SEQ ID NO: 40), AG144 (SEQ ID NO: 38), and any combinations thereof.

[0144] In some embodiments, less than 100% of amino acids of an XTEN are selected from glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P), or less than 100% of the sequence consists of the sequence motifs from Table 2A or the XTEN sequences of Table 2B. In such embodiments, the remaining amino acid residues of the XTEN are selected from any of the other 14 natural L-amino acids, but may be preferentially selected from hydrophilic amino acids such that the XTEN sequence contains at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or at least about 99% hydrophilic amino acids. The content of hydrophobic amino acids in the XTEN utilized in the conjugation constructs may be less than 5%, or less than 2%, or less than 1% hydrophobic amino acid content. Hydrophobic residues that are less favored in construction of XTEN include tryptophan, phenylalanine, tyrosine, leucine, isoleucine, valine, and methionine. Additionally, XTEN sequences may contain less than 5% or less than 4% or less than 3% or less than 2% or less than 1% or none of the following amino acids: methionine (for example, to avoid oxidation), or asparagine and glutamine (to avoid desamidation).

[0145] In another embodiment, the XTEN sequence is selected from the group consisting of AE42 (SEQ ID NO: 36), AE72 (SEQ ID NO: 127), AE144_2A (SEQ IDNO: 128), AE144_3B (SEQ ID NO: 129), AE144_4A (SEQ ID NO: 130), AE144_5A (SEQ IDNO: 131), AE144_6B (SEQ IDNO: 132), AG144_A (SEQ ID NO: 133), AG144_B (SEQ IDNO: 134), AG144_C (SEQ ID NO: 135), AG144_F (SEQ IDNO: 136), AE864 (SEQ ID NO: 43), AE576 (SEQ ID NO: 41), AE288 (SEQ IDNO: 39), AE288_2 (SEQ ID NO: 137), AE144 (SEQ ID NO: 37), AG864 (SEQ ID NO: 44), AG576 (SEQ ID NO: 42), AG288 (SEQ ID NO: 40), AG144 (SEQ ID NO: 38), and any combinations thereof. In a specific embodiment, the XTEN sequence is AE288. The amino acid sequences for certain XTEN sequences of the invention are shown in Table 2B.

TABLE 2B. XTEN Sequences

XTEN	Amino Acid Sequence
AE42 SEQ ID NO: 36	GAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPASS
AE72 SEQ ID NO: 127	GAPTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPA TSGSETPGTSESATPESGPGTSTEPSEGSAPGASS
AE144 SEQ ID NO:37	GSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSPAGSPTSTE EGTSTEPSEG SAPGSEPATSGSETPGSEPATSGSETPGSEPATSGSETPGTSTEPSE GSAPGTSESA PESGPGSEPATSGSETPGTSTEPSEGSAP
AE144_2A (SEQ ID NO: 128)	TSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAP GTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPES GPG
AE144_ 3B (SEQ ID NO: 129)	SPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGP GTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSA PGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APG
AE144_4A (SEQ ID NO: 130)	TSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETP GTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTE EGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGS APG
AE144_5A (SEQ ID NO: 131)	TSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETP GTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESG PGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTST
	EEG
AE144_6B (SEQ ID NO: 132)	TSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGP GSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSA PGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGS APG
AG144 SEQ ID NO:38	GTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTG PGASPGTSST GSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSS TGSPGSSPSA STGTGPGTPGSGTASSSPGSSTPSGATGSP
AG144_A (SEQ ID NO: 133)	GASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSST GSP

XTEN	Amino Acid Sequence
AG144_B (SEQ ID NO: 134)	GTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATG SPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSST GSP
AG144_C (SEQ ID NO: 135)	GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGS PGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTG SPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSST GSP
AG144_F (SEQ ID NO: 136)	GSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGT GPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSST GSP
AE288 SEQ ID NO:39	GTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSET PGTSESATPESG PGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSE TPGTSESATPES GPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPE SGPGTSESATPE SGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSTEPSE GSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPS EGSAP
AE288_2 (SEQ ID NO: 137)	GSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESG PGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGS APGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEG SAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSG SETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSP TSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEP SEGSAP
AG288 SEQ ID NO:40	PGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG
	SPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGAT GSPGSSPSASTG TGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGA TGSPGSSPSAST GTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSG ATGSPGSSPSAS TGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGS
AE576 SEQ ID N0:41	GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSA PGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSE TPGSPAGSPTST EEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTS TEEGTSTEPSEG SAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATP ESGPGSEPATSG SETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESAT PESGPGSPAGSP TSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEP

XTEN	Amino Acid Sequence
	SEGSAPGTSTEP SEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTE PSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGSEP ATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSP AGSPTSTEEGSP AGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAP
AG576 SEQ ID NO:42	PGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGT GPGSSTPSGATG SPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSST GSPGTPGSGTAS SSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSAST GTGPGTPGSGTA SSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSG ATGSPGSSTPSG ATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPS GATGSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGSST PSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSS TPSGATGSPGSS TPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGT PGSGTASSSPGS STPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGS
AE864 SEQ ID NO:43	GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSA
	PGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSE TPGSPAGSPTST EEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTS TEEGTSTEPSEG SAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATP ESGPGSEPATSG SETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESAT PESGPGSPAGSP TSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEP SEGSAPGTSTEP SEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTE PSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGSEP ATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSP AGSPTSTEEGSP AGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGT SESATPESGPGS EPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPG TSTEPSEGSAPG SPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGP GSPAGSPTSTEE GSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESG PGTSESATPESG PGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGS APGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP
AG864 SEQ ID NO:44	GASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGS PGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASS

XTEN	Amino Acid Sequence
	SPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGAT GSPGASPGTSST GSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSAST GTGPGSSTPSGA TGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTS STGSPGTPGSGT ASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSA STGTGPGTPGSG TASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTP SGATGSPGSSTP SGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSST PSGATGSPGSST PSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGAS PGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGT PGSGTASSSPGS STPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPG SSTPSGATGSPG SSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSP GTPGSGTASSSP
	GSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGS PGASPGTSSTGS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGT GPGTPGSGTASS SPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSP

[0146] In further embodiments, the XTEN sequence used in the invention affects the physical or chemical property, *e.g.*, pharmacokinetics, of the chimeric protein of the present invention. The XTEN sequence used in the present invention can exhibit one or more of the following advantageous properties: conformational flexibility, enhanced aqueous solubility, high degree of protease resistance, low immunogenicity, low binding to mammalian receptors, or increased hydrodynamic (or Stokes) radii. In a specific embodiment, the XTEN sequence linked to a FVIII protein in this invention increases pharmacokinetic properties such as longer terminal half-life or increased area under the curve (AUC), so that the chimeric protein described herein stays *in vivo* for an increased period of time compared to wild type FVIII. In further embodiments, the XTEN sequence used in this invention increases pharmacokinetic properties such as longer terminal half-life or increased area under the curve (AUC), so that FVIII protein stays *in vivo* for an increased period of time compared to wild type FVIII.

[0147] A variety of methods and assays can be employed to determine the physical/chemical properties of proteins comprising the XTEN sequence. Such methods include, but are not limited to analytical centrifugation, EPR, HPLC-ion exchange, HPLC-size exclusion, HPLC-reverse phase, light scattering, capillary electrophoresis, circular dichroism, differential scanning calorimetry, fluorescence, HPLC-ion exchange, HPLC-size exclusion, IR, NMR, Raman spectroscopy, refractometry, and UV/Visible spectroscopy. Additional methods are disclosed in Amau et al., Prot Expr and Purif 48, 1-13 (2006).

[0148] Additional examples of XTEN sequences that can be used according to the present invention and are disclosed in US Patent Publication Nos. 2010/0239554 A1, 2010/0323956 A1, 2011/0046060 A1, 2011/0046061 A1, 2011/0077199 A1, or 2011/0172146 A1, or International Patent Publication Nos. WO 2010091122 A1, WO 2010144502 A2, WO 2010144508 A1, WO 2011028228 A1, WO 2011028229 A1, or WO 2011028344 A2.

C) Factor VIII (FVIII) Protein

[0149] "A FVIII protein" as used herein means a functional FVIII polypeptide in its normal role in coagulation,

unless otherwise specified. The term a FVIII protein includes a functional fragment, variant, analog, or derivative thereof that retains the function of full-length wild-type Factor VIII in the coagulation pathway. "A FVIII protein" is used interchangeably with FVIII polypeptide (or protein) or FVIII. Examples of the FVIII functions include, but not limited to, an ability to activate coagulation, an ability to act as a cofactor for factor IX, or an ability to form a tenase complex with factor IX in the presence of Ca^{2+} and phospholipids, which then converts Factor X to the activated form Xa. The FVIII protein can be the human, porcine, canine, rat, or murine FVIII protein. In addition, comparisons between FVIII from humans and other species have identified conserved residues that are likely to be required for function (Cameron et al., Thromb. Haemost. 79:317-22 (1998); US 6,251,632).

[0150] A number of tests are available to assess the function of the coagulation system: activated partial thromboplastin time (aPTT) test, chromogenic assay, ROTEM assay, prothrombin time (PT) test (also used to determine INR), fibrinogen testing (often by the Clauss method), platelet count, platelet function testing (often by PFA-100), TCT, bleeding time, mixing test (whether an abnormality corrects if the patient's plasma is mixed with normal plasma), coagulation factor assays, antiphospholipid antibodies, D-dimer, genetic tests (*e.g.*, factor V Leiden, prothrombin mutation G20210A), dilute Russell's viper venom time (dRVVT), miscellaneous platelet function tests, thromboelastography (TEG or Sonoclot), thromboelastometry (TEM®, *e.g.*, ROTEM®), or euglobulin lysis time (ELT).

[0151] The aPTT test is a performance indicator measuring the efficacy of both the "intrinsic" (also referred to the contact activation pathway) and the common coagulation pathways. This test is commonly used to measure clotting activity of commercially available recombinant clotting factors, *e.g.*, FVIII or FIX. It is used in conjunction with prothrombin time (PT), which measures the extrinsic pathway.

[0152] ROTEM analysis provides information on the whole kinetics of haemostasis: clotting time, clot formation, clot stability and lysis. The different parameters in thromboelastometry are dependent on the activity of the plasmatic coagulation system, platelet function, fibrinolysis, or many factors which influence these interactions. This assay can provide a complete view of secondary haemostasis.

[0153] The FVIII polypeptide and polynucleotide sequences are known, as are many functional fragments, mutants and modified versions. Examples of human FVIII sequences (full-length) are shown below.

TABLE 3. Amino Acid Sequence of Full-length Factor VIII

(Full-length FVIII (FVIII signal peptide underlined; FVIII heavy chain is double underlined; B domain is italicized; and FVIII light chain is in plain text)
Signal Peptide: (SEQ ID NO: 3)
MQIELSTCFFLCLLRFCFS

Mature Factor VIII (SEQ ID NO: 4)*

ATRRYYLGAVELSWDYMQSDLGELPVDARFPPRVPKSFPFNTSVVYKKTLFVEFT
DHLFNIAKPRPPWMGLLGPTIQAEVYDTVVITLKNMASHPVSLHAVGVSYWKASE
GAEYDDQTSQREKEDDKVFPGGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLV
KDLNSGLIGALLVCREGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDR
DAASARAWPKMHTVNGYVNRSLPGLIGCHRKSVYWHVIGMGTTPEVHSIFLEGHT
FLVRNHRQASLEISPITFLTAQTLLMDLGQFLLFCHISSHQHDGMEAYVKVDSCP
EEPQLRMKNNEEAEDYDDDLTDSEMDVVRFDDDNSPSFIQIRSVAKKHPKTWVHY
IAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGRKYKKVRFMAYTDETFKTRE
AIQHESGILGPLLYGEVGDTLLIIFKNQASRPYNIYPHGITDVRPLYSRRLPKGV
KHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYYSSFVNMERDLASGLIGP
LLICYKESVDQRGNQIMSDKRNVILFSVFDENRSWYLTENIQRFLPNPAGVQLED
PEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKH
KMVYEDTLTLFPFSGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNT
GDYYEDSYEDISAYLLSKNNAIEPRSFSQNSRHPSTRQKQFNATTIPENDIEKTD
PWFAHRTPMPKIQNVSSSDLLMLLRQSPTPHGLSLSDLQEAKYETFSDDPSPGAI
DSNNSLSEMTHFRPQLHHSGDMVFTPESGLQLRLNEKLGTTAATELKKLDFKVSS
TSNNLISTIPSDNLAAGTDNTSSLGPPSMPVHYDSQLDTTLFGKKSSPLTESGGP
LSLSEENNDSKLLESGLMNSQESSWGKNVSSTESGRLFKGKRAHGPALLTKDNAL
FKVSISLLKTNKTSNNSATNRKTHIDGPSLLIENSPSVWQNILESDTEFKKVTPL
IHDRMLMDKNATALRLNHMSNKTTSSKNMEMVQQKKEGPIPPDAQNPDMSFFKML
FLPESARWIQRTHGKNSLNSGQGPSPKQLVSLGPEKSVEGQNFLSEKNKVVVGKG
EFTKDVGLKEMVFPSSRNLFLTNLDNLHENNTHNQEKKIQEEIEKKETLIQENVV
LPQIHTVTGTKNFMKNLFLLSTRQNVEGSYDGAYAPVLQDFRSLNDSTNRTKKHT
AHFSKKGEEENLEGLGNQTKQIVEKYACTTRISPNTSQQNFVTQRSKRALKQFRL
PLEETELEKRIIVDDTSTQWSKNMKHLTPSTLTQIDYNEKEKGAITQSPLSDCLT
RSHSIPQANRSPLPIAKVSSFPSIRPIYLTRVLFQDNSSHLPAASYRKKDSGVQE
SSHFLQGAKKNNLSLAILTLEMTGDQREVGSLGTSATNSVTYKKVENTVLPKPDL
PKTSGKVELLPKVHIYQKDLFPTETSNGSPGHLDLVEGSLLQGTEGAIKWNEANR
PGKVPFLRVATESSAKTPSKLLDPLAWDNHYGTQIPKEEWKSQEKSPEKTAFKKK
DTILSLNACESNHAIAAINEGQNKPEIEVTWAKQGRTERLCSQNPPVLKRHQREI
TRTTLQSDQEEIDYDDTISVEMKKEDFDIYDEDENQSPRSFQKKTRHYFIAAVER
LWDYGMSSSPHVLRNRAQSGSVPQFKKVVFQEFTDGSFTQPLYRGELNEHLGLLG

PYIRAEVEDNIMVTFRNQASRPYSFYSSLISYEEDQRQGAEPRKNFVKPNETKTY
FWKVQHHMAPTKDEFDCKAWAYFSDVDLEKDVHSGLIGPLLVCHTNTLNPAHGRQ
VTVQEFALFFTIFDETKSWYFTENMERNCRAPCNIQMEDPTFKENYRFHAINGYI
MDTLPGLVMAQDQRIRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMALYNLYP
GVFETVEMLPSKAGIWRVECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDF
QITASGQYGQWAPKLARLHYSGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGAR
QKFSSLYISQFIIMYSLDGKKWQTYRGNSTGTLMVFFGNVDSSGIKHNIFNPPII
ARYIRLHPTHYSIRSTLRMELMGCDLNSCSMPLGMESKAISDAQITASSYFTNMF
ATWSPSKARLHLQGRSNAWRPQVNNPKEWLQVDFQKTMKVTGVTTQGVKSLLTSM
YVKEFLISSSQDGHQWTLFFQNGKVKVFQGNQDSFTPVVNSLDPPLLTRYLRIHP
QSWVHQIALRMEVLGCEAQDLY

TABLE 4. Nucleotide Sequence Encoding Full-Length FVIII (SEQ ID NO: 5)*

```
 661                                                    ATG
   CAAATAGAGC TCTCCACCTG
 721   CTTCTTTCTG TGCCTTTTGC GATTCTGCTT TAGTGCCACC
   AGAAGATACT ACCTGGGTGC
 781   AGTGGAACTG TCATGGGACT ATATGCAAAG TGATCTCGGT
   GAGCTGCCTG TGGACGCAAG
 841   ATTTCCTCCT AGAGTGCCAA AATCTTTTCC ATTCAACACC
   TCAGTCGTGT ACAAAAAGAC
 901   TCTGTTTGTA GAATTCACGG ATCACCTTTT CAACATCGCT
   AAGCCAAGGC CACCCTGGAT
 961   GGGTCTGCTA GGTCCTACCA TCCAGGCTGA GGTTTATGAT
   ACAGTGGTCA TTACACTTAA
1021   GAACATGGCT TCCCATCCTG TCAGTCTTCA TGCTGTTGGT
   GTATCCTACT GGAAAGCTTC
1081   TGAGGGAGCT GAATATGATG ATCAGACCAG TCAAAGGGAG
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1081  TGAGGCAGCT CAATATGATC ATCAGACCAG TCAAAGGGAG
      AAAGAAGATG ATAAAGTCTT
1141  CCCTGGTGGA AGCCATACAT ATGTCTGGCA GGTCCTGAAA
      GAGAATGGTC CAATGGCCTC
1201  TGACCCACTG TGCCTTACCT ACTCATATCT TTCTCATGTG
      GACCTGGTAA AAGACTTGAA
1261  TTCAGGCCTC ATTGGAGCCC TACTAGTATG TAGAGAAGGG
      AGTCTGGCCA AGGAAAAGAC
1321  ACAGACCTTG CACAAATTTA TACTACTTTT TGCTGTATTT
      GATGAAGGGA AAAGTTGGCA
1381  CTCAGAAACA AAGAACTCCT TGATGCAGGA TAGGGATGCT
      GCATCTGCTC GGGCCTGGCC
1441  TAAAATGCAC ACAGTCAATG GTTATGTAAA CAGGTCTCTG
      CCAGGTCTGA TTGGATGCCA
1501  CAGGAAATCA GTCTATTGGC ATGTGATTGG AATGGGCACC
      ACTCCTGAAG TGCACTCAAT

1561  ATTCCTCGAA GGTCACACAT TTCTTGTGAG GAACCATCGC
      CAGGCGTCCT TGGAAATCTC
1621  GCCAATAACT TTCCTTACTG CTCAAACACT CTTGATGGAC
      CTTGGACAGT TTCTACTGTT
1681  TTGTCATATC TCTTCCCACC AACATGATGG CATGGAAGCT
      TATGTCAAAG TAGACAGCTG
1741  TCCAGAGGAA CCCCAACTAC GAATGAAAAA TAATGAAGAA
      GCGGAAGACT ATGATGATGA
1801  TCTTACTGAT TCTCAAATGC ATCTCCTCAG GTTTGATGAT
      GACAACTCTC CTTCCTTTAT
1861  CCAAATTCGC TCAGTTGCCA AGAAGCATCC TAAAACTTGG
      GTACATTACA TTGCTGCTGA
1921  AGAGGAGGAC TGGGACTATG CTCCCTTAGT CCTCGCCCCC
      GATGACAGAA GTTATAAAAG
1981  TCAATATTTG AACAATGGCC CTCAGCGGAT TGGTAGGAAG
      TACAAAAAAG TCCGATTTAT
2041  GGCATACACA GATGAAACCT TTAAGACTCG TGAAGCTATT
      CAGCATGAAT CAGGAATCTT
2101  GGGACCTTTA CTTTATGGGG AAGTTGGAGA CACACTGTTG
      ATTATATTTA AGAATCAAGC
2161  AAGCAGACCA TATAACATCT ACCCTCACGG AATCACTGAT
      GTCCCTCCTT TGTATTCAAC
2221  GAGATTACCA AAAGGTGTAA AACATTTGAA GGATTTTCCA
      ATTCTGCCAG GAGAAATATT
2281  CAAATATAAA TGGACAGTGA CTGTACAAGA TGGGCCAACT
      AAATCAGATC CTCGGTGCCT
2341  GACCCGCTAT TACTCTAGTT TCGTTAATAT GGAGAGAGAT
      CTAGCTTCAG GACTCATTGG
2401  CCCTCTCCTC ATCTGCTACA AAGAATCTGT AGATCAAAGA
      GGAAACCAGA TAATGTCAGA
2461  CAAGAGGAAT GTCATCCTGT TTTCTGTATT TGATGAGAAC
      CGAAGCTGGT ACCTCACAGA
2521  GAATATACAA CGCTTTCTCC CCAATCCAGC TGGAGTGCAG
      CTTGAGGATC CAGAGTTCCA
2581  AGCCTCCAAC ATCATGCACA GCATCAATGG CTATGTTTTT
      GATAGTTTGC AGTTGTCAGT
2641  TTGTTTGCAT GAGGTGGCAT ACTGGTACAT TCTAAGCATT
      GGAGCACAGA CTGACTTCCT
2701  TTCTGTCTTC TTCTCTGGAT ATACCTTCAA ACACAAAATG
      GTCTATGAAG ACACACTCAC
2761  CCTATTCCCA TTCTCAGGAG AAACTGTCTT CATGTCGATG
      GAAAACCCAG GTCTATGGAT
2821  TCTGGGGTGC CACAACTCAG ACTTTCGGAA CAGAGGCATG
      ACCGCCTTAC TGAAGGTTTC
2881  TAGTTGTGAC AAGAACACTG GTGATTATTA CGAGGACAGT
      TATGAAGATA TTTCAGCATA
2941  CTTGCTGAGT AAAAACAATG CCATTGAACC AAGAAGCTTC
      TCCCACAATT CAACACACCC
3001  TAGCACTAGG CAAAAGCAAT TTAATGCCAC CACAATTCCA
      GAAAATGACA TAGAGAAGAC

3061  TGACCCTTGG TTTGCACACA GAACACCTAT GCCTAAAATA
      CAAAATGTCT CCTCTAGTGA
3121  TTTGTTGATG CTCTTGCGAC AGAGTCCTAC TCCACATGGG
      CTATCCTTAT CTGATCTCCA
3181  AGAAGCCAAA TATGAGACTT TTTCTGATGA TCCATCACCT
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GGAGCAATAG ACAGTAATAA
3241 CAGCCTGTCT GAAATGACAC ACTTCAGGCC ACAGCTCCAT
CACAGTGGGG ACATGGTATT
3301 TACCCCTGAG TCAGCCCTCC AATTAAGATT AAATGACAAA
CTGGGGACAA CTGCAGCAAC
3361 AGAGTTGAAG AAACTTGATT TCAAAGTTTC TAGTACATCA
AATAATCTGA CTTCAACAAT
3421 TCCATCAGAC AATTTGGCAG CAGGTACTGA TAATACAAGT
TCCTTAGGAC CCCCAAGTAT
3481 GCCAGTTCAT TATGATAGTC AATTAGATAC CACTCCATTT
GGCAAAAAGT CATCTCCCCT
3541 TACTGAGTCT GGTGGACCTC TGAGCTTGAG TGAAGAAAAT
AATGATTCAA AGTTGTTAGA
3601 ATCAGGTTTA ATGAATAGCC AAGAAAGTTC ATGGGGAAAA
AATGTATCGT CAACAGAGAG
3661 TGGTAGGTTA TTTAAAGGGA AAAGAGCTCA TGGACCTGCT
TTGTTGACTA AAGATAATGC
3721 CTTATTCAAA GTTAGCATCT CTTTGTTAAA GACAAACAAA
ACTTCCAATA ATTCAGCAAC
3781 TAATAGAAAG ACTCACATTG ATGGCCCATC ATTATCAATT
GAGAATAGTC CATCAGTCTG
3841 GCAAAATATA TTAGAAAGTG ACACTGAGTT TAAAAAAGTG
ACACCTTTGA CTCATGACAG
3901 AATGCTTATG GACAAAAATG CTACAGCTTT GAGGCCAAAT
CATATGTCAA ATAAAACTAC
3961 TTCATCAAAA AACATGGAAA TGGTCCAACA GAAAAAAGAG
GGCCCCATTC CACCAGATGC
4021 ACAAAATCCA GATATGTCGT TCTTTAAGAT GCTATCCTTG
CCAGAATCAG CAAGGTGGAT
4081 ACAAAGGACT CATGGAAAGA ACTCTCTGAA CTCTGGGCAA
GGCCCCAGTC CAAAGCAATT
4141 AGTATCCTTA GGACCAGAAA AATCTGTGGA AGGTCAGAAT
TTCTTGTCTG AGAAAAACAA
4201 AGTGGTAGTA GGAAAGGGTG AATTTACAAA GGACGCAGGA
CTCAAAGAGA CGGTTTTTCC
4261 AAGCAGCAGA AACCTATTTC TTACTAACTT GGATAATTTA
CATGAAAATA ATACACACAA
4321 TCAAGAAAAA AAAATTCAGG AAGAAATAGA AAAGAAGGAA
ACATTAATCC AAGAGAATGT
4381 AGTTTTGCCT CAGATACATA CAGTGACTGG CACTAAGAAT
TTCATGAAGA ACCTTTTCTT
4441 ACTGAGCACT AGGCAAAATG TAGAAGGTTC ATATGACGGG
GCATATGCTC CAGTACTTCA
4501 AGATTTTAGG TCATTAAATG ATTCAACAAA TAGAACAAAG
AAACACACAG CTCATTTCTC

4561 AAAAAAAGGG GAGGAAGAAA ACTTGGAAGG CTTGGGAAAT
CAAACCAAGC AAATTGTAGA
4621 GAAATATGCA TGCACCACAA GGATATCTCC TAATACAAGC
CAGCAGAATT CTGTCACGCA
4681 ACGTAGTAAG AGAGCTTTGA AACAATTCAG ACTCCCACTA
GAAGAAACAG AACTTGAAAA
4741 AAGGATAATT GTGGATGACA CCTCAACCCA GTGGTCCAAA
AACATGAAAC ATTTGACCCC
4801 CAGCACCCTC ACACAGATAC ACTACAATGA CAACGACAAA
GGGGCCATTA CTCAGTCTCC
4861 CTTATCAGAT TGCCTTACGA GGAGTCATAG CATCCCTCAA
GCAAATAGAT CTCCATTACC
4921 CATTGCAAAG GTATCATCAT TTCCATCTAT TAGACCTATA
TATCTGACCA GGGTCCTATT
4981 CCAAGACAAC TCTTCTCATC TTCCAGCAGC ATCTTATAGA
AAGAAAGATT CTGGGGTCCA
5041 AGAAAGCAGT CATTTCTTAC AAGGAGCCAA AAAAAATAAC
CTTTCTTTAG CCATTCTAAC
5101 CTTGGAGATG ACTGGTGATC AAAGAGAGGT TGGCTCCCTG
GGGACAAGTG CCACAAATTC
5161 AGTCACATAC AAGAAAGTTG AGAACACTGT TCTCCCGAAA
CCACACTTGC CCAAAACATC
5221 TGGCAAAGTT GAATTGCTTC CAAAAGTTCA CATTTATCAG
AAGGACCTAT CCCCTACGGA
5281 AACTAGCAAT GGGTCTCCTG GCCATCTGGA TCTCGTGGAA
GGGAGCCTTC CTCAGGGAAC
5341 AGAGGGAGCG ATTAAGTGGA ATGAAGCAAA CAGACCTGGA
AAAGTTCCCT CTCTGAGAGT

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5401  AGCAACAGAA AGCTCTGCAA AGACTCCCTC CAAGCTATTG
   GATCCTCTTG CTTGGGATAA
5461  CCACTATGGT ACTCAGATAC CAAAAGAAGA GTGGAAATCC
   CAAGAGAAGT CACCAGAAAA
5521  AACAGCTTTT AAGAAAAAGG ATACCATTTT GTCCCTGAAC
   GCTTGTGAAA GCAATCATGC
5581  AATAGCAGCA ATAAATGACC CACAAAATAA CCCCGAAATA
   GAAGTCACCT GGGCAAAGCA
5641  AGGTAGGACT GAAAGGCTGT GCTCTCAAAA CCCACCAGTC
   TTGAAACGCC ATCAACGGGA
5701  AATAACTCGT ACTACTCTTC AGTCAGATCA AGAGGAAATT
   GACTATGATG ATACCATATC
5761  AGTTGAAAIG AAGAAGGAAG ATTTTGACAT TTATGATGAG
   GATGAAAATC AGAGCCCCCG
5821  CAGCTTTCAA AAGAAAACAC GACACTATTT TATTGCTGCA
   GTGGAGAGGC CCTGGGATTA
5881  TGGGATGAGT AGCTCCCCAC ATGTTCTAAG AAACAGGGCT
   CAGAGTGGCA GTGTCCCTCA
5941  GTTCAAGAAA GTTGTTTTCC AGGAATTTAC TGATGGCTCC
   TTTACTCAGC CCTTATACCG
6001  TGGAGAACTA AATGAACATT TGGGACTCCT GGGGCCATAT
   ATAAGAGCAG AAGTTGAAGA

6061  TAATATCATG GTAACTTTCA GAAATCAGGC CTCTCGTCCC
   TATTCCTTCT ATTCTAGCCT
6121  TATTTCTTAT GAGGAAGATC AGAGGCAAGG AGCAGAACCT
   AGAAAAAACT CTGTCAAGCC
6181  TAATGAAACC AAAACTTACT TTTGGAAAGT GCAACATCAT
   ATGGCACCCA CTAAAGATGA
6241  GTTTGACTGC AAAGCCTGGG CTTATTTCTC TGATGCTGAC
   CTGGAAAAAG ATGTGCACTC
6301  ACGCCTCATT GCACCCCTTC TGCTCTGCCA CACTAACACA
   CTGAACCCTG CTCATGGGAG
6361  ACAAGTGACA GTACAGGAAT TTGCTCTGTT TTTCACCATC
   TTTGATGAGA CCAAAAGCTG
6421  GTACTTCACT GAAAATATGG AAAGAAACTG CAGGGCTCCC
   TGCAATATCC AGATGGAAGA
6481  TCCCACTTTT AAAGAGAATT ATCGCTTCCA TGCAATCAAT
   GGCTACATAA CGGATACACT
6541  ACCTGGCTTA GTAATGGCTC AGGATCAAAG GATTCGATGG
   TATCTGCTCA GCATGGGCAG
6601  CAATGAAAAC ATCCATTCTA TTCATTTCAG TGGACATGTG
   TTCACTGTAC GAAAAAAAGA
6661  GGAGTATAAA ATGGCACTGT ACAATCTCTA TCCAGGTGTT
   TTTGAGACAG CGGAAATGTT
6721  ACCATCCAAA GCTGGAATTT GGCGGGTGGA ATGCCCTATT
   GGCGAGCATC CACATGCTGG
6781  GATGAGCACA CTTTTTCTGG TGTACAGCAA TAAGTGTCAG
   ACTCCCCTGG GAATGGCTTC
6841  TGGACACATT AGAGATTTTC AGATTACAGC TTCAGGACAA
   TATGGACAGT GGGCCCCAAA
6901  GCTGGCCAGA CTTCATTATT CCGGATCAAT CAATGCCTGG
   AGCACCAAGG AGCCCTTTTC
6961  TTGGATCAAG GTGGATCTGT TGGCACCAAT GATTATTCAC
   GGCATCAAGA CCCAGGGTGC
7021  CCGTCAGAAG TTCTCCAGCC TCTACATCTC TCAGTCTATC
   ATCATGTATA GTCTTGATGG
7081  GAAGAAGTGG CAGACTTATC GAGGAAATTC CACTGGAACC
   TTAATGGTCT CCTTTGGCAA
7141  TGTGGATTCA TCTGGGATAA AACACAATAT TTTTAACCCT
   CCAATTATTG CTCGATACAT
7201  CCGTTTGCAC CCAACTCATT ATAGCATTCG CAGCACTCTT
   CGCATGGAGT CGATGGGCTG
7261  TGATTTAAAT AGTTGCAGCA TGCCATTGGG AATGGAGAGT
   AAAGCAATAT CAGATGCACA
7321  GATTACTGCT TCATCCTACT TTACCAATAT GTTTGCCACC
   TGGTCTCCTT CAAAAGCTCG
7381  ACTTCACCIC CAAGGGAGGA GTAATGCCTG GAGACCTCAG
   GTGAATAATC CAAAAGAGTG
7441  GCTGCAAGTG GACTTCCAGA AGACAATGAA AGTCACAGGA
   GTAACTACTC AGGGAGTAAA
7501  ATCTCTGCIT ACCAGCATGT ATGTGAAGGA GTTCCCCATC
   TCCAGCAGTC AAGATGGCCA
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7561  TCAGTGGACT CTCTTTTTTC AGAATGGCAA AGTAAAGGTT
   TTTCAGGGAA ATCAAGACTC
7621  CTTCACACCT GTGGTGAACT CTCTAGACCC ACCGTTACTG
   ACTCGCTACC TTCGAATTCA
7681  CCCCCAGAGT TGGGTGCACC AGATTGCCCT GAGGATGGAG
   GTTCTGGGCT GCGAGGCACA
7741  GGACCTCTAC
```

*The underlined nucleic acids encode a signal peptide.

[0154] FVIII polypeptides include full-length FVIII, full-length FVIII minus Met at the N-terminus, mature FVIII (minus the signal sequence), mature FVIII with an additional Met at the N-terminus, and/or FVIII with a full or partial deletion of the B domain. In certain embodiments, FVIII variants include B domain deletions, whether partial or full deletions.

[0155] The sequence of native mature human FVIII is presented as SEQ ID NO: 4. A native FVIII protein has the following formula: A1-a1-A2-a2-B-a3-A3-C1-C2, where A1, A2, and A3 are the structurally-related "A domains," B is the "B domain," C1 and C2 are the structurally-related "C domains," and a1, a2 and a3 are acidic spacer regions. Referring to the primary amino acid sequence position in SEQ ID NO:4, the A1 domain of human FVIII extends from Ala1 to about Arg336, the a1 spacer region extends from about Met337 to about Val374, the A2 domain extends from about Ala375 to about Tyr719, the a2 spacer region extends from about Glu720 to about Arg740, the B domain extends from about Ser741 to about Arg 1648, the a3 spacer region extends from about Glu1649 to about Arg1689, the A3 domain extends from about Ser1690 to about Leu2025, the C1 domain extends from about Gly2026 to about Asn2072, and the C2 domain extends from about Ser2073 to Tyr2332. Other than specific proteolytic cleavage sites, designation of the locations of the boundaries between the domains and regions of FVIII can vary in different literature references. The boundaries noted herein are therefore designated as approximate by use of the term "about."

[0156] The human FVIII gene was isolated and expressed in mammalian cells (Toole, J. J., et al., Nature 312:342-347 (1984); Gitschier, J., et al., Nature 312:326-330 (1984); Wood, W. I., et al., Nature 312:330-337 (1984); Vehar, G. A., et al., Nature 312:337-342 (1984); WO 87/04187; WO 88/08035; WO 88/03558; and U.S. Pat. No. 4,757,006). The FVIII amino acid sequence was deduced from cDNA as shown in U.S. Pat. No. 4,965,199. In addition, partially or fully B-domain deleted FVIII is shown in U.S. Pat. Nos. 4,994,371 and 4,868,112. In some embodiments, the human FVIII B-domain is replaced with the human Factor V B-domain as shown in U.S. Pat. No. 5,004,803. The cDNA sequence encoding human Factor VIII and amino acid sequence are shown in SEQ ID NOs: 4 and 5, respectively, of US Application Publ. No. 2005/0100990.

[0157] The porcine FVIII sequence is published in Toole, J. J., et al., Proc. Natl. Acad. Sci. USA 83:5939-5942 (1986). Further, the complete porcine cDNA sequence obtained from PCR amplification of FVIII sequences from a pig spleen cDNA library has been reported in Healey, J. F., et al., Blood 88:4209-4214 (1996). Hybrid human/porcine FVIII having substitutions of all domains, all subunits, and specific amino acid sequences were disclosed in U.S. Pat. No. 5,364,771 by Lollar and Runge, and in WO 93/20093. More recently, the nucleotide and corresponding amino acid sequences of the A1 and A2 domains of porcine FVIII and a chimeric FVIII with porcine A1 and/or A2 domains substituted for the corresponding human domains were reported in WO 94/11503. U.S. Pat. No. 5,859,204, Lollar, J. S., also discloses the porcine cDNA and deduced amino acid sequences. U.S. Pat. No. 6,458,563 discloses a B-domain-deleted porcine FVIII.

[0158] U.S. Pat. No. 5,859,204 to Lollar, J. S. reports functional mutants of FVIII having reduced antigenicity and reduced immunoreactivity. U.S. Pat. No. 6,376,463 to Lollar, J. S. also reports mutants of FVIII having reduced immunoreactivity. US Appl. Publ. No. 2005/0100990 to Saenko et al. reports functional mutations in the A2 domain of FVIII.

[0159] In one embodiment, the FVIII (or FVIII portion of a chimeric protein) may be at least 50%, 60%, 70%, 80%,

90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a FVIII amino acid sequence of amino acids 1 to 1438 of SEQ ID NO: 6 or amino acids 1 to 2332 of SEQ ID NO: **4** (without a signal sequence) or a FVIII amino acid sequence of amino acids 1 to 19 of SEQ ID NO: 3 and 1 to 1438 of SEQ ID NO: 6 or amino acids 1 to 19 of SEQ ID NO: 3 and amino acids 1 to 2332 of SEQ ID NO: **4** (with a signal sequence), wherein the FVIII has a clotting activity, *e.g.*, activates Factor IX as a cofactor to convert Factor X to activated Factor X. The FVIII (or FVIII portion of a chimeric protein) may be identical to a FVIII amino acid sequence of amino acids 1 to 1438 of SEQ ID NO: 6 or amino acids 1 to 2332 of SEQ ID NO: **4** (without a signal sequence). The FVIII may further comprise a signal sequence.

[0160] The "B-domain" of FVIII, as used herein, is the same as the B-domain known in the art that is defined by internal amino acid sequence identity and sites of proteolytic cleavage, *e.g.*, residues Ser741-Arg1648 of full-length human FVIII. The other human FVIII domains are defined by the following amino acid residues: A1, residues Ala1-Arg372; A2, residues Ser373-Arg740; A3, residues Ser1690-Asn2019; C1, residues Lys2020-Asn2172; C2, residues Ser2173-Tyr2332. The A3-C1-C2 sequence includes residues Ser1690-Tyr2332. The remaining sequence, residues Glu1649-Arg1689, is usually referred to as the a3 acidic region. The locations of the boundaries for all of the domains, including the B-domains, for porcine, mouse and canine FVIII are also known in the art. In one embodiment, the B domain of FVIII is deleted ("B-domain-deleted factor VIII" or "BDD FVIII"). An example of a BDD FVIII is REFACTO® (recombinant BDD FVIII), which has the same sequence as the Factor VIII portion of the sequence in Table 5. (BDD FVIII heavy chain is double underlined; B domain is italicized; and BDD FVIII light chain is in plain text). A nucleotide sequence encoding the amino acid sequence set forth in Table 5 (SEQ ID NO: 7) is shown in Table 6.

TABLE 5. Amino Acid Sequence of B-domain Deleted Factor VIII (BDD FVIII)

BDD FVIII (SEQ ID NO: 6)

ATRRYYLGAVELSWDYMQSDLGELPVDARFPPRVPKSFPFNTSVVYKKTLFVEFT
DHLFNIAKPRPPWMGLLGPTIQAEVYDTVVITLKNMASHPVSLHAVGVSYWKASE
GAEYDDQTSQREKEDDKVFPGGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLV
KDLNSGLIGALLVCREGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDR
DAASARAWPKMHTVNGYVNRSLPGLIGCHRKSVYWHVIGMGTTPEVHSIFLEGHT
FLVRNHRQASLEISPITFLTAQTLLMDLGQFLLFCHISSHQHDGMEAYVKVDSCP
EEPQLRMKNNEEAEDYDDDLTDSEMDVVRFDDDNSPSFIQIRSVAKKHPKTWVHY
IAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGRKYKKVRFMAYTDETFKTRE
AIQHESGILGPLLYGEVGDTLLIIFKNQASRPYNIYPHGITDVRPLYSRRLPKGV
KHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYYSSFVNMERDLASGLIGP
LLICYKESVDQRGNQIMSDKRNVILFSVFDENRSWYLTENIQRFLPNPAGVQLED
PEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKH
KMVYEDTLTLFPFSGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNT
GDYYEDSYEDISAYLLSKNNAIEPR*SFSQNPPVLKRHQR*EITRTTLQSDQEEIDY
DDTISVEMKKEDFDIYDEDENQSPRSFQKKTRHYFIAAVERLWDYGMSSSPHVLR

NRAQSGSVPQFKKVVFQEFTDGSFTQPLYRGELNEHLGLLGPYIRAEVEDNIMVT
FRNQASRPYSFYSSLISYEEDQRQGAEPRKNFVKPNETKTYFWKVQHHMAPTKDE
FDCKAWAYFSDVDLEKDVHSGLIGPLLVCHTNTLNPAHGRQVTVQEFALFFTIFD
ETKSWYFTENMERNCRAPCNIQMEDPTFKENYRFHAINGYIMDTLPGLVMAQDQR
IRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMALYNLYPGVFETVEMLPSKAG
IWRVECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDFQITASGQYGQWAPK
LARLHYSGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFSSLYISQFIIM
YSLDGKKWQTYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPTHYSIR
STLRMELMGCDLNSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQG
RSNAWRPQVNNPKEWLQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGH
QWTLFFQNGKVKVFQGNQDSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVL
GCEAQDLY

TABLE 6. Nucleotide Sequence Encoding BDD FVIII (SEQ ID NO: 7)*

```
661                                   A TGCAAATAGA
  GCTCTCCACC TGCTTCTTTC
721  TGTGCCTTTT GCGATTCTGC TTTAGTGCCA CCAGAAGATA
  CTACCTGGGT GCAGTGGAAC
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 781  TGTCATGGGA CTATATGCAA AGTGATCTCG GTGAGCTGCC
  TGTGGACGCA AGATTTCCTC
 841  CTAGAGTGCC AAAATCTTTT CCATTCAACA CCTCAGTCGT
  GTACAAAAAG ACTCTGTTTG
 901  TAGAATTCAC GGATCACCTT TTCAACATCG CTAAGCCAAG
  GCCACCCTGG ATGGGTCTGC
 961  TAGGTCCTAC CATCCAGGCT GAGGTTTATG ATACAGTGGT
  CATTACACTT AAGAACATGG
1021  CTTCCCATCC TGTCAGTCTT CATGCTGTTG GTGTATCCTA
  CTGGAAAGCT TCTGAGGGAG
1081  CTGAATATGA TGATCAGACC AGTCAAAGGG AGAAAGAAGA
  TGATAAAGTC TTCCCTGGTG
1141  GAAGCCATAC ATATGTCTGG CAGGTCCTGA AAGAGAATGG
  TCCAATGGCC TCTGACCCAC
1201  TGTGCCTTAC CTACTCATAT CTTTCTCATG TGGACCTGGT
  AAAAGACTTG AATTCAGGCC
1261  TCATTGGAGC CCTACTAGTA TGTAGAGAAG GGAGTCTGGC
  CAAGGAAAAG ACACAGACCT
1321  TGCACAAATT TATACTACTT TTTGCTGTAT TTGATGAAGG
  GAAAAGTTGG CACTCAGAAA
1381  CAAAGAACTC CTTGATGCAG GATAGGGATG CTGCATCTGC
  TCGGGCCTGG CCTAAAATGC
1441  ACACAGTCAA TGGTTATGTA AACAGGTCTC TGCCAGGTCT
  GATTGGATGC CACAGGAAAT
1501  CAGTCTATTG GCATGTGATT GGAATGGGCA CCACTCCTGA
  AGTGCACTCA ATATTCCTCG
1561  AAGGTCACAC ATTTCTTGTG AGGAACCATC GCCAGGCGTC
  CTTGGAAATC TCGCCAATAA
1621  CTTTCCTTAC TGCTCAAACA CTCTTGATGG ACCTTGGACA
  GTTTCTACTG TTTTGTCATA

1681  TCTCTTCCCA CCAACATGAT GGCATGGAAG CTTATGTCAA
  AGTAGACAGC TGTCCAGAGG
1741  AACCCCAACT ACGAATGAAA AATAATGAAG AAGCGGAAGA
  CTATGATGAT GATCTTACTG
1801  ATTCTGAAAT GGATGTGGTC AGGTTTGATG ATGACAACTC
  TCCTTCCTTT ATCCAAATTC
1861  GCTCAGTTGC CAAGAAGCAT CCTAAAACTT GGGTACATTA
  CATTGCTGCT GAAGAGGAGG
1921  ACTGGGACTA TGCTCCCTTA GTCCTCGCCC CCGATGACAG
  AAGTTATAAA AGTCAATATT
1981  TGAACAATGG CCCTCAGCGG ATTGGTAGGA AGTACAAAAA
  AGTCCGATTT ATGGCATACA
2041  CAGATGAAAC CTTTAAGACT CGTGAAGCTA TTCAGCATGA
  ATCAGGAATC TTGGGACCTT
2101  TACTTTATGG GGAAGTTGGA GACACACTGT TGATTATATT
  TAAGAATCAA GCAAGCAGAC
2161  CATATAACAT CTACCCTCAC GGAATCACTG ATGTCCGTCC
  TTTGTATTCA AGGAGATTAC
2221  CAAAAGGTGT AAAACATTTG AAGGATTTTC CAATTCTGCC
  AGGAGAAATA TTCAAATATA
2281  AATGGACAGT GACTGTAGAA GATGGGCCAA CTAAATCAGA
  TCCTCGGTGC CTGACCCGCT
2341  ATTACTCTAG TTTCGTTAAT ATGGAGAGAG ATCTAGCTTC
  AGGACTCATT GGCCCTCTCC
2401  TCATCTGCTA CAAAGAATCT GTAGATCAAA GAGGAAACCA
  GATAATGTCA GACAAGAGGA
2461  ATGTCATCCT GTTTTCTGTA TTTGATGAGA ACCGAAGCTG
  GTACCTCACA GAGAATATAC
2521  AACGCTTTCT CCCCAATCCA GCTGGAGTGC AGCTTGAGGA
  TCCAGAGTTC CAAGCCTCCA
2581  ACATCATGCA CAGCATCAAT GGCTATGTTT TTGATAGTTT
  GCAGTTGTCA GTTTGTTTGC
2641  ATGAGGTGGC ATACTGGTAC ATTCTAAGCA TTGGAGCACA
  GACTGACTTC CTTTCTGTCT
2701  TCTTCTCTGG ATATACCTTC AAACACAAAA TGGTCTATGA
  AGACACACTC ACCCTATTCC
2761  CATTCTCAGG AGAAACTGTC TTCATGTCGA TGGAAAACCC
  AGGTCTATGG ATTCTGGGGT
2821  GCCACAACTC AGACTTTCGG AACAGAGGCA TGACCGCCTT
  ACTGAAGGTT TCTAGTTGTG
2881  ACAAGAACAC TGGTGATTAT TACGACGACA GTTATGAAGA
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   TATTTCAGCA TACTTGCTGA
2941  GTAAAAACAA TGCCATTGAA CCAAGAAGCT TCTCTCAAAA
   CCCACCAGTC TTGAAACGCC
3001  ATCAACGGGA AATAACTCGT ACTACICTTC AGTCAGATCA
   AGAGGAAATT GACTATGATG
3061  ATACCATATC AGTTGAAATG AAGAAGGAAG ATTTTGACAT
   TTATGATGAG GATGAAAATC
3121  AGAGCCCCCG CAGCTTTCAA AAGAAAACAC GACACTATTT
   TATTGCTGCA GTGGAGAGGC

3181  TCTGGGATTA TGGGATGAGT AGCTCCCCAC ATGTTCTAAG
   AAACAGGGCT CAGAGTGGCA
3241  GTGTCCCTCA GTTCAAGAAA GTTGTTTTCC AGGAACTTAC
   TGATGGCTCC CTTACTCAGC
3301  CCTTATACCG TGGAGAACTA AATGAACATT TGGGACTCCT
   GGGGCCATAT ATAAGAGCAG
3361  AAGTTGAAGA TAATATCATG GTAACTTTCA GAAATCAGGC
   CTCTCGTCCC CATTCCTTCT
3421  ATTCTAGCCT TATTTCTTAT GAGGAAGATC AGAGGCAAGG
   AGCAGAACCT AGAAAAAACT
3481  TTGTCAAGCC TAATGAAACC AAAACTTACT TTTGGAAAGT
   GCAACATCAT ATGGCACCCA
3541  CTAAAGATGA GTTTGACTGC AAAGCCTGGG CTTATCTCTC
   TGATGTTGAC CTGGAAAAAG
3601  ATGTGCACIC AGGCCTGATT GGACCCCTTC TGGTCCGCCA
   CACTAACACA CTGAACCCTG
3661  CTCATGGGAG ACAAGTGACA GTACAGGAAT TTGCTCTGTT
   TTTCACCATC CTTGATGAGA
3721  CCAAAAGCTG GTACTTCACT GAAAATATGG AAAGAAACTG
   CAGGGCTCCC TGCAATATCC
3781  AGATGGAAGA TCCCACTTTT AAAGAGAATT ATCGCCTCCA
   TGCAATCAAT GCCTACATAA
3841  TGGATACACT ACCTGGCTTA GTAATGGCTC AGGATCAAAG
   GATTCGATGG CATCTGCTCA
3901  GCATGGGCAG CAATGAAAAC ATCCATTCTA TTCATCTCAG
   TGGACATGTG CTCACTGTAC
3961  GAAAAAAAGA GGAGTATAAA ATGGCACTGT ACAATCTCTA
   TCCAGGTGTT CTTGAGACAG
4021  TGGAAATGIT ACCATCCAAA GCTGGAATTT GGCGGGTGGA
   ATGCCTTATT GGCGAGCATC
4081  TACATGCTGG GATGAGCACA CTTTTTCTGG TGTACAGCAA
   TAAGTGTCAG ACTCCCCTGG
4141  GAATGGCTTC TGGACACATT AGAGATTTTC AGATTACAGC
   TTCAGGACAA CATGGACAGT
4201  GGGCCCCAAA GCTGGCCAGA CTTCATTATT CCGGACCAAT
   CAATGCCTGG AGCACCAAGG
4261  AGCCCTTTTC TTGGATCAAG GTGGATCTGT TGGCACCAAT
   GATTATTCAC GGCATCAAGA
4321  CCCAGGGTGC CCGTCAGAAG TTCTCCAGCC TCTACATCTC
   TCAGTTTATC ATCATGTATA
4381  GTCTTGATGG GAAGAAGTGG CAGACTTATC GAGGAAATTC
   CACTGGAACC CTAATGGTCT
4441  TCTTTGGCAA TGTGGATTCA TCTGGGATAA AACACAATAT
   TTTTAACCCT CCAATTATTG
4501  CTCGATACAT CCGTTTGCAC CCAACTCATT ATAGCATTCG
   CAGCACTCTT CGCATGGAGT
4561  TGATGGGCTG TGATTTAAAT AGTTGCAGCA TGCCATTGGG
   AATCGAGACT AAAGCAATAT
4621  CAGATGCACA GATTACTGCT TCATCCTACT TTACCAATAT
   GTTTGCCACC CGGTCTCCTT

   4681  CAAAAGCTCG ACTTCACCTC CAAGGGAGGA GTAATGCCTG
      GAGACCTCAG GTGAATAATC
   4741  CAAAAGAGTG GCTGCAAGTG GACTTCCAGA AGACAATGAA
      AGTCACAGGA GTAACTACTC
   4801  AGGGAGTAAA ATCTCTGCTT ACCAGCATGT ATGTGAAGGA
      GTTCCTCATC TCCAGCAGTC
   4861  AAGATGGCCA TCAGTGGACT CTCTTTTTTC AGAATGGCAA
      AGTAAAGGTT TTTCAGGGAA
   4921  ATCAAGACTC CTTCACACCT GTGGTGAACT CTCTAGACCC
      ACCGTTACTG ACTCGCTACC
   4981  TTCGAATTCA CCCCCAGAGT TGGGTGCACC AGATTGCCCT
      GAGGATGGAG GTTCTGGGCT
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5041 GCGAGGCACA GGACCTCTAC

*The underlined nucleic acids encode a signal peptide.

[0161] A "B-domain-deleted FVIII" may have the full or partial deletions disclosed in U.S. Pat. Nos. 6,316,226, 6,346,513, 7,041,635, 5,789,203, 6,060,447, 5,595,886, 6,228,620, 5,972,885, 6,048,720, 5,543,502, 5,610,278, 5,171,844, 5,112,950, 4,868,112, and 6,458,563. In some embodiments, a B-domain-deleted FVIII sequence of the present invention comprises any one of the deletions disclosed at col. 4, line 4 to col. 5, line 28 and Examples 1-5 of U.S. Pat. No. 6,316,226 (also in US 6,346,513). In another embodiment, a B-domain deleted Factor VIII is the S743/Q1638 B-domain deleted Factor VIII (SQ BDD FVIII) (*e.g.*, Factor VIII having a deletion from amino acid 744 to amino acid 1637, *e.g.*, Factor VIII having amino acids 1-743 and amino acids 1638-2332 of SEQ ID NO: *4, i.e.*, SEQ ID NO: 6). In some embodiments, a B-domain-deleted FVIII of the present invention has a deletion disclosed at col. 2, lines 26-51 and examples 5-8 of U.S. Patent No. 5,789,203 (also US 6,060,447, US 5,595,886, and US 6,228,620). In some embodiments, a B-domain-deleted Factor VIII has a deletion described in col. 1, lines 25 to col. 2, line 40 of US Patent No. 5,972,885; col. 6, lines 1-22 and example 1 of U.S. Patent no. 6,048,720; col. 2, lines 17-46 of U.S. Patent No. 5,543,502; col. 4, line 22 to col. 5, line 36 of U.S. Patent no. 5,171,844; col. 2, lines 55-68, figure 2, and example 1 of U.S. Patent No. 5,112,950; col. 2, line 2 to col. 19, line 21 and table 2 of U.S. Patent No. 4,868,112; col. 2, line 1 to col. 3, line 19, col. 3, line 40 to col. 4, line 67, col. 7, line 43 to col. 8, line 26, and col. 11, line 5 to col. 13, line 39 of U.S. Patent no. 7,041,635; or col. 4, lines 25-53, of U.S. Patent No. 6,458,563. In some embodiments, a B-domain-deleted FVIII has a deletion of most of the B domain, but still contains amino-terminal sequences of the B domain that are essential for *in vivo* proteolytic processing of the primary translation product into two polypeptide chain, as disclosed in WO 91/09122. In some embodiments, a B-domain-deleted FVIII is constructed with a deletion of amino acids 747-1638, *i.e.,* virtually a complete deletion of the B domain. Hoeben R.C., et al. J. Biol. Chem. 265 (13): 7318-7323 (1990). A B-domain-deleted Factor VIII may also contain a deletion of amino acids 771-1666 or amino acids 868-1562 of FVIII. Meulien P., et al. Protein Eng. 2(4): 301-6 (1988). Additional B domain deletions that are part of the invention include: deletion of amino acids 982 through 1562 or 760 through 1639 (Toole et al., Proc. Natl. Acad. Sci. U.S.A. (1986) 83, 5939-5942)), 797 through 1562 (Eaton, et al. Biochemistry (1986) 25:8343-8347)), 741 through 1646 (Kaufman (PCT published application No. WO 87/04187)), 747-1560 (Sarver, et al., DNA (1987) 6:553-564)), 741 through 1648 (Pasek (PCT application No.88/00831)), or 816 through 1598 or 741 through 1648 (Lagner (Behring Inst. Mitt. (1988) No 82:16-25, EP 295597)). In other embodiments, BDD FVIII includes a FVIII polypeptide containing fragments of the B-domain that retain one or more N-linked glycosylation sites, *e.g.*, residues 757, 784, 828, 900, 963, or optionally 943, which correspond to the amino acid sequence of the full-length FVIII sequence. Examples of the B-domain fragments include 226 amino acids or 163 amino acids of the B-domain as disclosed in Miao, H.Z., et al., Blood 103(a): 3412-3419 (2004), Kasuda, A, et al., J. Thromb. Haemost. 6: 1352-1359 (2008), and Pipe, S.W., et al., J. Thromb. Haemost. 9: 2235-2242 (2011) (*i.e.*, the first 226 amino acids or 163 amino acids of the B domain are retained). In still other embodiments, BDD FVIII further comprises a point mutation at residue 309 (from Phe to Ser) to improve expression of the BDD FVIII protein. *See* Miao, H.Z., et al., Blood 103(a): 3412-3419 (2004). In still other embodiments, the BDD FVIII includes a FVIII polypeptide containing a portion of the B-domain, but not containing one or more furin cleavage sites *(e.g.,* Arg1313 and Arg 1648). *See* Pipe, S.W., et al., J. Thromb. Haemost. 9: 2235-2242 (2011). Each of the foregoing deletions may be made in any FVIII sequence.

[0162] In some embodiments, the FVIII has a partial B-domain. In some embodiments, the FVIII protein with a partial B-domain is FVIII 198 (SEQ ID NO: 89). FVIII198 is a partial B-domain containing single chain FVIIIFc molecule-226N6. 226 represents the N-terminus 226 amino acid of the FVIII B-domain, and N6 represents six N-glycosylation sites in the B-domain.

[0163] In one embodiment, FVIII is cleaved right after arginine at amino acid 1648 (in full-length Factor VIII or SEQ ID NO: 4), amino acid 754 (in the S743/Q1638 B-domain deleted Factor VIII or SEQ ID NO: 6), or the corresponding arginine residue (in other variants), thereby resulting in a heavy chain and a light chain. In another embodiment, FVIII comprises a heavy chain and a light chain, which are linked or associated by a metal ion-mediated non-covalent bond.

[0164] In other embodiments, FVIII is a single chain FVIII that has not been cleaved right after Arginine at amino acid 1648 (in full-length FVIII or SEQ ID NO: 4), amino acid 754 (in the S743/Q1638 B-domain-deleted FVIII or SEQ ID NO: 6), or the corresponding Arginine residue (in other variants). A single chain FVIII may comprise one or more amino acid substitutions. In one embodiment, the amino acid substitution is at a residue corresponding to residue 1648, residue 1645, or both of full-length mature Factor VIII polypeptide (SEQ ID NO: 4) or residue 754, residue 751, or both of SQ BDD Factor VIII (SEQ ID NO: 6). The amino acid substitution can be any amino acids other than arginine, *e.g.*, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, valine, alanine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, proline, selenocysteine, serine, tyrosine, histidine, ornithine, pyrrolysine, or taurine.

[0165] FVIII can further be cleaved by thrombin and then activated as FVIIIa, serving as a cofactor for activated Factor IX (FIXa). And the activated FIX together with activated FVIII forms a Xase complex and converts Factor X to activated Factor X (FXa). For activation, FVIII is cleaved by thrombin after three Arginine residues, at amino acids 372, 740, and 1689 (corresponding to amino acids 372, 740, and 795 in the B-domain deleted FVIII sequence), the cleavage generating FVIIIa having the 50kDa A1, 43kDa A2, and 73kDa A3-C1-C2 chains. In one embodiment, the FVIII protein useful for the present invention is non-active FVIII. In another embodiment, the FVIII protein is an activated FVIII.

[0166] The protein having FVIII polypeptide linked to or associated with the VWF fragment can comprise a sequence at least 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 4 or 6, wherein the sequence has the FVIII clotting activity, *e.g.*, activating Factor IX as a cofactor to convert Factor X to activated Factor X (FXa).

[0167] "Hybrid" or "chimeric" polypeptides and proteins, as used herein, includes a combination of a first polypeptide chain, *e.g.*, the VWF fragment, optionally fused to a first Ig constant region or a portion thereof, with a second polypeptide chain, *e.g.*, a FVIII protein linked to an XTEN sequence, optionally fused to a second Ig constant region or a portion thereof, thereby forming a heterodimer. In another embodiment, the first polypeptide and the second polypeptide in a hybrid are associated with each other via disulfide or other covalent bond(s). Hybrids are described, for example, in US 2004/101740 and US 2006/074199. In another embodiment, the first polypeptide comprises a VWF fragment-XTEN-Fc fusion protein, and the second polypeptide comprises FVIII-Fc fusion protein, making the hybrid a heterodimer. In yet other embodiments, the first polypeptide comprises a VWF fragment-XTEN-Fc fusion protein, and the second polypeptide comprises FVIII(X)-Fc fusion protein. The first polypeptide and the second polypeptide are associated through a covalent bond, *e.g.*, a disulfide bond, between the first Fc region and the second Fc region. The first polypeptide and the second polypeptide can further be associated with each other by binding between the VWF fragment and the FVIII protein.

[0168] A FVIII protein useful in the present invention can include FVIII having one or more additional XTEN sequences, which do not affect the FVIII coagulation activity. Such XTEN sequences can be fused to the C-terminus or N-terminus of the FVIII protein or inserted between one or more of the two amino acid residues in the FVIII protein wherein the insertions do not affect the FVIII coagulation activity or FVIII function. In one embodiment, the insertions improve pharmacokinetic properties of the FVIII protein (*e.g.*, half-life). In another embodiment, the insertions can be multiple insertions, *e.g.*, more than two, three, four, five, six, seven, eight, nine, or ten insertions. Examples of the insertion sites include, but are not limited to, the sites listed in Tables 7, 8, 9, 10, 11, 12, 13, 14, 15 or any combinations thereof.

[0169] The FVIII protein linked to one or more XTEN sequences can be represented as FVIII(X), FVIII(X1), $FVIIU_{(a\rightarrow b)}X\text{-}FVIII_{(a\rightarrow b)}$, wherein $FVIII_{(a\rightarrow b)}$ comprises, consists essentially of, or consists of a first portion of a FVIII protein from amino acid residue "a" to amino acid residue "b"; X or XI comprises, consists essentially of, or consists of one or more XTEN sequences, $FVIII_{(c\rightarrow d)}$ comprises, consists essentially of, or consists of a second portion of a FVIII protein from amino acid residue "c" to amino acid residue "d";

1. a is the N-terminal amino acid residue of the first portion of the FVIII protein,
2. b is the C-terminal amino acid residue of the first portion of the FVIII protein but is also the N-terminal amino

acid residue of the two amino acids of an insertion site in which the XTEN sequence is inserted,

3. c is the N-terminal amino acid residue of the second portion of the FVIII protein but is also the C-terminal amino acid residue of the two amino acids of an insertion site in which the XTEN sequence is inserted, and
4. d is the C-terminal amino acid residue of the FVIII protein, and

wherein the first portion of the FVIII protein and the second portion of the FVIII protein are not identical to each other and are of sufficient length together such that the FVIII protein has a FVIII coagulation activity.

[0170] In one embodiment, the first portion of the FVIII protein and the second portion of the FVIII protein are fragments of SEQ ID NO: **4** [full length mature FVIII sequence] or SEQ ID NO: 6 [B-domain deleted FVIII], *e.g.*, N-terminal portion and C-terminal portion, respectively. In certain embodiments, the first portion of the FVIII protein comprises the A1 domain and the A2 domain of the FVIII protein. The second portion of the FVIII protein comprises the A3 domain, the C1 domain, and optionally the C2 domain. In yet other embodiments, the first portion of the FVIII protein comprises the A1 domain and A2 domain, and the second portion of the FVIII protein comprises a portion of the B domain, the A3 domain, the C1 domain, and optionally the C2 domain. In still other embodiments, the first portion of the FVIII protein comprises the A1 domain, A2 domain, and a portion of the B domain of the FVIII protein, and the second portion of the FVIII protein comprises the A3 domain, the C1 domain, and optionally the C2 domain. In still other embodiments, the first portion of the FVIII protein comprises the A1 domain, A2 domain, and a first portion of the B domain of the FVIII protein. The second portion of the FVIII protein comprises a second portion of the B domain, the A3 domain, the C1 domain, and optionally the C2 domain. In some embodiments, the two amino acids ("b" and "c") can be any one or more of the amino acid residues insertion sites shown in Tables 7, 8, 9, 10, 11, 12, 13, 14, and 15. For example, "b" can be the amino acid residue immediately upstream of the site in which one or more XTEN sequences are inserted or linked, and "c" can be the amino acid residue immediately downstream of the site in which the one or more XTEN sequences are inserted or linked. In some embodiments, "a" is the first mature amino acid sequence of a FVIII protein, and "d" is the last amino acid sequence of a FVIII protein. For example, $FVIII_{(a \rightarrow b)}$ can be an amino acid sequence at least 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to amino acids 1 to 745 of SEQ ID NO: 6 [B domain deleted FVIII amino acid sequence] or SEQ ID NO: **4** [full length FVIII] and $FVIII_{(c \rightarrow d)}$ can be amino acids 746 to 1438 of SEQ ID NO: 6 or amino acids 1641 to 2332 of SEQ ID NO: **4**, respectively.

[0171] In some aspects, the insertion site in the FVIII protein is located in one or more domains of the FVIII protein, which is the N-terminus, the A1 domain, the A2 domain, the A3 domain, the B domain, the C1 domain, the C2 domain, the C-terminus, or two or more combinations thereof or between two domains of the FVIII protein, which are the A1 domain and a1 acidic region, and the a1 acidic region and A2 domain, the A2 domain and a2 acidic region, the a2 acidic region and B domain, the B domain and A3 domain, and the A3 domain and C1 domain, the C1 domain and C2 domain, or any combinations thereof. For example, the insertion sites in which the XTEN sequence can be inserted are selected from the group consisting of the N-terminus and A1 domain, the N-terminus and A2 domain, the N-terminus and A3 domain, the N-terminus and B domain, the N-terminus and C1 domain, the N-terminus and C2 domain, the N-terminus and the C-terminus, the A1 and A2 domains, the A1 and A3 domains, the A1 and B domains, the A1 and C1 domains, the A1 and C2 domains, the A1 domain and the C-terminus, the A2 and A3 domains, the A2 and B domains, the A2 and C1 domains, the A2 and C2 domains, the A2 domain and the C-terminus, the A3 and B domains, the A3 and C1 domains, the A3 and C2 domains, the A3 domain and the C-terminus, the B and C1 domains, the B and C2 domains, the B domain and the C-terminus, the C1 and C2 domains, the C1 and the C-terminus, the C2 domain, and the C-terminus, and two or more combinations thereof. Non-limiting examples of the insertion sites are listed in Tables 7, 8, 9, 10, 11, 12, 13, 14, and 15.

[0172] The FVIII protein, in which the XTEN sequence is inserted immediately downstream of one or more amino acids (*e.g.*, one or more XTEN insertion sites) in the FVIII protein or linked at the C-terminus or the N-terminus, retains the FVIII activity after linkage to or insertion by the XTEN sequence. The XTEN sequence can be inserted in the FVIII protein once or more than once, twice, three times, four times, five times, or six times such that the insertions do not affect the FVIII activity (*i.e.*, the FVIII protein still retains the coagulation property).

[0173] The FVIII protein useful in the present invention can be linked to one or more XTEN polypeptides at the N-terminus or C-terminus of the FVIII protein by an optional linker or inserted immediately downstream of one or more amino acids (*e.g.*, one or more XTEN insertion sites) in the FVIII protein by one or more optional linkers. In one embodiment, the two amino acid residues in which the XTEN sequence is inserted or the amino acid residue to which the XTEN sequence is linked correspond to the two or one amino acid residues of SEQ ID NO: 4 [full length mature FVIII] selected from the group consisting of the residues in Table 7, Table 8, Table 9, and Table 10 and any combinations thereof.

[0174] In other embodiments, at least one XTEN sequence is inserted in any one or more XTEN insertion sites disclosed herein or any combinations thereof. In one aspect, at least one XTEN sequence is inserted in one or more XTEN insertion sites disclosed in one or more amino acids disclosed in Table 7.

TABLE 7: Exemplary XTEN Insertion Sites

No.	XTEN Insertion Point*	Insertion Residue	FVIII BDD Downstream Sequence	FVIII Domain
1	0	(N-terminus)	ATR	A1
2	3	R	RYY	A1
3	17	M	QSD	A1
4	18	Q	SDL	A1
5	22	G	ELP	A1
6	24	L	PVD	A1
7	26	V	DAR	A1
8	28	A	RFP	A1
9	32	P	RVP	A1
10	38	F	PFN	A1
11	40	F	NTS	A1
12	41	N	TSV	A1
13	60	N	IAK	A1
14	61	I	AKP	A1
15	65	R	PPW	A1
16	81	Y	DTV	A1
17	111	G	AEY	A1
18	116	D	QTS	A1
19	119	S	QRE	A1
20	120	Q	REK	A1
21	128	V	FPG	A1
22	129	F	PGG	A1
23	130	P	GGS	A1
24	182	G	SLA	A1
25	185	A	KEK	A1
26	188	K	TQT	A1
27	205	G	KSW	A1
28	210	S	ETK	A1
29	211	E	TKN	A1
30	216	L	MQD	A1
31	220	R	DAA	A1

No.	XTEN Insertion Point*	Insertion Residue	FVIII BDD Downstream Sequence	FVIII Domain
32	222	A	ASA	A1
33	223	A	SAR	A1
34	224	S	ARA	A1
35	230	K	MHT	A1
36	243	P	GLI	A1
37	244	G	LIG	A1
38	250	R	KSV	A1
39	318	D	GME	A1
40	333	P	QLR	A1
42	334	Q	LRM	A1
43	336	R	MKN	a1
44	339	N	NEE	a1
45	345	D	YDD	a1
46	357	V	VRF	a1
47	367	S	FIQ	a1
48	370	S	RPY	a1
49	375	A	KKH	A2
50	376	K	KHP	A2
51	378	H	PKT	A2
52	399	V	LAP	A2
53	403	D	DRS	A2
54	405	R	SYK	A2
55	409	S	QYL	A2
56	416	P	QRI	A2
57	434	E	TFK	A2
58	438	T	REA	A2
59	441	A	IQH	A2
60	442	I	QHE	A2
61	463	I	IFK	A2
62	487	Y	SRR	A2
63	490	R	LPK	A2
64	492	P	KGV	A2
65	493	K	GVK	A2
66	494	G	VKH	A2
67	500	D	FPI	A2
68	506	G	EIF	A2
69	518	E	DGP	A2
70	556	K	ESV	A2
71	565	Q	IMS	A2
72	566	I	MSD	A2
73	598	P	AGV	A2

No.	XTEN Insertion Point*	Insertion Residue	FVIII BDD Downstream Sequence	FVIII Domain
74	599	A	GVQ	A2
75	603	L	EDP	A2
76	616	S	ING	A2
77	686	G	LWI	A2
78	713	K	NTG	A2
79	719	Y	EDS	A2
80	730	L	LSK	A2
81	733	K	NNA	A2
82	745	N	PPV**	B
83	1640	P	PVL	B
84	1652	R	TTL	B
85	1656	Q	SDQ	A3
86	1685	N	QSP	A3
87	1711	M	SSS	A3
88	1713	S	SPH	A3
89	1720	N	RAQ	A3
90	1724	s	GSV	A3
91	1725	G	SVP	A3
92	1726	S	VPQ	A3
93	1741	G	SFT	A3
94	1744	T	QPL	A3
95	1749	R	GEL	A3
96	1773	V	TFR	A3
97	1792	Y	EED	A3
98	1793	E	EDQ	A3
99	1796	Q	RQG	A3
100	1798	Q	GAE	A3
101	1799	G	AEP	A3
102	1802	P	RKN	A3
103	1803	R	KNF	A3
104	1807	V	KPN	A3
105	1808	K	PNE	A3
106	1827	K	DEF	A3
107	1844	E	KDV	A3
108	1861	N	TLN	A3
109	1863	L	NPA	A3
110	1896	E	RNC	A3
111	1900	R	APC	A3
112	1904	N	IQM	A3
113	1905	I	QME	A3
114	1910	P	TFK	A3

No.	XTEN Insertion Point*	Insertion Residue	FVIII BDD Downstream Sequence	FVIII Domain
115	1920	A	ING	A3
116	1937	D	QRI	A3
117	1981	G	VFE	A3
118	2019	N	KCQ	A3
119	2020	K	CQT	C1
120	2044	G	QWA	C1
121	2068	F	SWI	C1
122	2073	V	DLL	C1
123	2090	R	QKF	C1
124	2092	K	FSS	C1
125	2093	F	SSL	C1
126	2111	K	WQT	C1
127	2115	Y	RGN	C1
128	2120	T	GTL	C1
129	2125	V	FFG	C1
130	2171	L	NSC	C1
131	2173	S	CSM	C2
132	2188	A	QIT	C2
133	2223	V	NNP	C2
134	2224	N	NPK	C2
135	2227	K	EWL	C2
136	2268	G	HQW	C2
137	2277	N	GKV	C2
138	2278	G	KVK	C2
139	2290	F	TPV	C2
140	2332	Y	C terminus of FVIII	CT

* Indicates an insertion point for XTEN based on the amino acid number of mature full-length human FVIII, wherein the insertion could be either on the N- or C-terminal side of the indicated amino acid.

[0175] In some embodiments, one or more XTEN sequences are inserted within about six amino acids up or down from amino acids 32, 220, 224, 336, 339, 399, 416, 603, 1656, 1711, 1725, 1905, or 1910, corresponding to SEQ ID NO: 4 or any combinations thereof.

TABLE 8. Exemplary XTEN Insertion Ranges

No.	XTEN Insertion Point	Insertion Residue	FVIII BDD Downstrea m Sequence	FVIII Domain	Distance from insertion residue*
9	32	P	RVP	A1	-3, +6
31	220	R	DAA	A1	-
34	224	S	ARA	A1	+5
43	336	R	MKN	a1	-1, +6
44	339	N	NEE	a1	-4, +5
52	399	V	LAP	A2	-6, +3

No.	XTEN Insertion Point	Insertion Residue	FVIII BDD Downstrea m Sequence	FVIII Domain	Distance from insertion residue*
56	416	P	QRI	A2	+6
75	603	L	EDP	A2	6, +6
85	1656	Q	SDQ	B	-3, +6
87	1711	M	SSS	A3	-6, +1
91	1725	G	SVP	A3	+6
113	1905	I	QME	A3	+6
114	1910	P	TFK	A3	-5, +6

*Distance from insertion residue refers to the relative number of amino acids away from the N-terminus (negative numbers) or C-terminus (positive numbers) of the designated insertion residue (residue "0") where an insertion may be made. The designation "-x" refers to an insertion site which is x amino acids away on the N-terminal side of the designated insertion residue. Similarly, the designation "+x" refers to an insertion site which is x amino acids away on the C-terminal side of the designated insertion residue.
For example, "-1, +2" indicates that the insertion is made at the N-terminus or C-terminus of amino acid residues denoted -1, 0, +1 or +2.

[0176] In other embodiments, one or more XTEN sequences are inserted immediately down stream of one or more amino acids corresponding to the full-length mature human FVIII selected from the group consisting of one or more insertion sites in Table 9.

TABLE 9. Exemplary XTEN Insertion Sites or Ranges

No.	XTEN Insertion Point Range*	First Insertion Residue	FVIII Domain
3	18-32	Q	A1
8	40	F	A1
18	211-224	E	A1
27	336-403	R	A1, A2
43	599	A	A2
47	745-1640	N	B
50	1656-1728	Q	B, a3, A3
57	1796-1804	R	A3
65	1900-1912	R	A3
81	2171-2332	L	C1, C2

* indicates range of insertion sites numbered relative to the amino acid number of mature human FVIII

[0177] In yet other embodiments, one or more XTENs are inserted in the B domain of FVIII. In one example, an XTEN is inserted between amino acids 740 and 1640 corresponding to SEQ ID NO: 4, wherein the FVIII sequence between amino acids 740 and 1640 is optionally not present. In another example, an XTEN is inserted between amino acids 741 and 1690 corresponding to SEQ ID NO: 4, wherein the FVIII sequence between amino acids 740 and 1690 is optionally not present. In other examples, an XTEN is inserted between amino acids 741 and 1648 corresponding to SEQ ID NO: 4, wherein the FVIII sequence between amino acids 741 and 1648 is optionally not present. In yet other examples, an XTEN is inserted between amino acids 743 and 1638 corresponding to SEQ ID NO: 4, wherein the FVIII sequence between amino acids 743 and 1638 is optionally not present. In still other examples, an XTEN is inserted between amino acids 745 and 1656 corresponding to SEQ ID NO: 4, wherein the FVIII sequence between amino acids 745 and 1656 is optionally not present. In some examples, an XTEN is

inserted between amino acids 745 and 1657 corresponding to SEQ ID NO: **4**, wherein the FVIII sequence between amino acids 745 and 1657 is optionally not present. In certain examples, an XTEN is inserted between amino acids 745 and 1667 corresponding to SEQ ID NO: **4**, wherein the FVIII sequence between amino acids 745 and 1667 is optionally not present. In still other examples, an XTEN is inserted between amino acids 745 and 1686 corresponding to SEQ ID NO: **4**, wherein the FVIII sequence between amino acids 745 and 1686 is optionally not present. In some other examples, an XTEN is inserted between amino acids 747 and 1642 corresponding to SEQ ID NO: **4**, wherein the FVIII sequence between amino acids 747 and 1642 is optionally not present. In still other examples, an XTEN is inserted between amino acids 751 and 1667 corresponding to SEQ ID NO: **4**, wherein the FVIII sequence between amino acids 751 and 1667 is optionally not present.

[0178] In some embodiments, one or more XTENs are inserted in one or more amino acids immediately downstream of an amino acid of an insertion site selected from the group consisting of the amino acid residues in Table 10.

TABLE 10: FVIII XTEN insertion sites and construct designations

Construct Number	Domain	Upstream Residue No.*	Downstream Residue No.*	Upstream Sequence	Downstream Sequence
F8X-1	A1	3	4	ATR	RYY
F8X-2	A1	18	19	YMQ	SDL
F8X-3	A1	22	23	DLG	ELP
F8X-4	A1	26	27	LPV	DAR
F8X-5	A1	40	41	FPF	NTS
F8X-6	A1	60	61	LFN	IAK
F8X-7	A1	116	117	YDD	QTS
F8X-8	A1	130	131	VFP	GGS
F8X-9	A1	188	189	KEK	TQT
F8X-10	A1	216	217	NSL	MQD
F8X-11	A1	230	231	WPK	MHT
F8X-12	A1	333	334	EEP	QLR
F8X-13	A2	375	376	SVA	KKH
F8X-14	A2	403	404	APD	DRS
F8X-15	A2	442	443	EAI	QHE
F8X-16	A2	490	491	RRL	PKG
F8X-17	A2	518	519	TVE	DGP
F8X-18	A2	599	600	NPA	GVQ
F8X-19	A2	713	714	CDK	NTG
F8X-20	BD	745	746	SQN	PPV
F8X-21	BD	745	746	SQN	PPV
F8X-22	BD**	745	746	SQN	PPV
F8X-23	A3	1720	1721	APT	KDE
F8X-24	A3	1796	1797	EDQ	RQG
F8X-25	A3	1802	1803	AEP	RKN
F8X-26	A3	1827	1828	PTK	DEF
F8X-27	A3	1861	1862	HTN	TLN
F8X-28	A3	1896	1897	NME	RNC
F8X-29	A3	1900	1901	NCR	APC
F8X-30	A3	1904	1905	PCN	IQM

Construct Number	Domain	Upstream Residue No.*	Downstream Residue No.*	Upstream Sequence	Downstream Sequence
F8X-31	A3	1937	1938	AQD	QRI
F8X-32	C1	2019	2020	YSN	KCQ
F8X-33	C1	2068	2069	EPF	SWI
F8X-34	C1	2111	2112	GKK	WQT
F8X-35	C1	2120	2121	NST	GTL
F8X-36	C2	2171	2172	CDL	NSC
F8X-37	C2	2188	2189	SDA	QIT
F8X-38	C2	2227	2228	NPK	EWL
F8X-39	C2	2277	2278	FQN	GKV
F8X-40	CT	2332	NA	DLY	NA
F8X-41	CT	2332	NA	DLY	NA
F8X-42	A1	3	4	ATR	ATR
pSD0001	A2	403	404		
pSD0002	A2	599	600		
pSD0021	N-term	0	1		
pSD0022	A1	32	33		
pSD0023	A1	65	66		
pSD0024	A1	81	82		
pSD0025	A1	119	120		
pSD0026	A1	211	212		
pSD0027	A1	220	221		
pSD0028	A1	224	225		
pSD0029	A1	336	337		
pSD0030	A1	339	340		
pSD0031	A2	378	379		
pSD0032	A2	399	400		
pSD0033	A2	409	410		
pSD0034	A2	416	417		
pSD0035	A2	487	488		
pSD0036	A2	494	495		
pSD0037	A2	500	501		
pSD0038	A2	603	604		
pSD0039	A3	1656	1657		
pSD0040	A3	1711	1712		
pSD0041	A3	1725	1726		
pSD0042	A3	1749	1750		
pSD0043	A3	1905	1906		
pSD0044	A3	1910	1911		
pDS0062	A3	1900	1901		

* Indicates the amino acid number of the mature FVIII protein

[0179] In one embodiment, the one or more XTEN insertion sites are located within one or more surface-exposed, flexible loop structure of the FVIII protein (*e.g.*, a permissive loop). For example, at least one XTEN sequence can be inserted in each FVIII "A" domain comprising at least two "permissive loops" into which at least one XTEN polypeptide can be inserted without eliminating procoagulant activity of the recombinant protein, or the ability of the recombinant proteins to be expressed in vivo or *in vitro* in a host cell. The permissive loops are regions that allow insertion of at least one XTEN sequence with, among other attributes, high surface or solvent exposure and high conformational flexibility. The A1 domain comprises a permissive loop-1 (A1-1) region and a permissive loop-2 (A1-2) region, the A2 domain comprises a permissive loop-1 (A2-1) region and a permissive loop-2 (A2-2) region, the A3 domain comprises a permissive loop-1 (A3-1) region and a permissive loop-2 (A3-2) region.

[0180] In one aspect, a first permissive loop in the FVIII A1 domain (A1-1) is located between beta strand 1 and beta strand 2, and a second permissive loop in the FVIII A2 domain (A1-2) is located between beta strand 11 and beta strand 12. A first permissive loop in the FVIII A2 domain (A2-1) is located between beta strand 22 and beta strand 23, and a second permissive loop in the FVIII A2 domain (A2-2) is located between beta strand 32 and beta strand 33. A first permissive loop in the FVIII A3 domain (A3-1) is located between beta strand 38 and beta strand 39, and a second permissive loop in the FVIII A3 (A3-2) is located between beta strand 45 and beta strand 46. In certain aspects, the surface-exposed, flexible loop structure comprising A1-1 corresponds to a region in native mature human FVIII from about amino acid 15 to about amino acid 45 of SEQ IDNO: **4**, *e.g.,* from about amino acid 18 to about amino acid 41 of SEQ ID NO: **4**. In other aspects, the surface-exposed, flexible loop structure comprising A1-2 corresponds to a region in native mature human FVIII from about amino acid 201 to about amino acid 232 of SEQ ID NO: **4**, *e.g.,* from about amino acid 218 to about amino acid 229 of SEQ ID NO: **4**. In yet other aspects, the surface-exposed, flexible loop structure comprising A2-1 corresponds to a region in native mature human FVIII from about amino acid 395 to about amino acid 421 of SEQ ID NO: **4**, *e.g.* from about amino acid 397 to about amino acid 418 of SEQ ID NO: **4**. In still other embodiments, the surface-exposed, flexible loop structure comprising A2-2 corresponds to a region in native mature human FVIII from about amino acid 577 to about amino acid 635 of SEQ ID NO: **4**, *e.g.,* from about amino acid 595 to about amino acid 607 of SEQ ID NO: **4**. In certain aspects the surface-exposed, flexible loop structure comprising A3-1 corresponds to a region in native mature human FVIII from about amino acid 1705 to about amino acid 1732 of SEQ ID NO: **4**, *e.g.,* from about amino acid 1711 to about amino acid 1725 of SEQ ID NO: **4**. In yet other aspects, the surface-exposed, flexible loop structure comprising A3-2 corresponds to a region in native mature human FVIII from about amino acid 1884 to about amino acid 1917 of SEQ ID NO: **4**, *e.g.,* from about amino acid 1899 to about amino acid 1911 of SEQ ID NO: **4**.

[0181] In another embodiment, the one or more amino acids in which at least one XTEN sequence is inserted is located within a3 domain, *e.g.*, amino acids 1649 to 1689, corresponding to full-length mature FVIII polypeptide. In a particular embodiment, an XTEN sequence is inserted between amino acids 1656 and 1657 of SEQ ID NO: **4** (full-length mature FVIII). In a specific embodiment, a FVIII protein comprising an XTEN sequence inserted immediately downstream of amino acid 1656 corresponding to SEQ ID NO: **4** further comprises a deletion from amino acid 745 to amino acid 1656 corresponding to SEQ ID NO: **4**.

[0182] In some embodiments, the one or more insertion sites for one or more XTEN insertions are immediately downstream of one or more amino acids selected from the group consisting of: (1) amino acid 3, (2) amino acid 18, (3) amino acid 22, (4) amino acid 26, (5) amino acid 32, (6) amino acid 40, (7) amino acid 60, (8) amino acid 65, (9) amino acid 81, (10) amino acid 116, (11) amino acid 119, (12) amino acid 130, (13) amino acid 188, (14) amino acid 211, (15) amino acid 216, (16) amino acid 220, (17) amino acid 224, (18) amino acid 230, (19) amino acid 333, (20) amino acid 336, (21) amino acid 339, (22) amino acid 375, (23) amino acid 399, (24) amino acid 403, (25) amino acid 409, (26) amino acid 416, (26) amino acid 442, (28) amino acid 487, (29) amino acid 490, (30) amino acid 494, (31) amino acid 500, (32) amino acid 518, (33) amino acid 599, (34) amino acid 603, (35) amino acid 713, (36) amino acid 745, (37) amino acid 1656, (38) amino acid 1711, (39) amino acid 1720, (40) amino acid 1725, (41) amino acid 1749, (42) amino acid 1796, (43) amino acid 1802, (44) amino acid 1827, (45) amino acid 1861, (46) amino acid 1896, (47) amino acid 1900, (48) amino acid 1904, (49) amino acid 1905, (50) amino acid 1910, (51) amino acid 1937, (52) amino acid 2019, (53) amino acid 2068, (54) amino acid 2111, (55)

amino acid 2120, (56) amino acid 2171, (57) amino acid 2188, (58) amino acid 2227, (59) amino acid 2277, and (60) two or more combinations thereof.

[0183] In one embodiment, a FVIII protein useful for the invention comprises two XTEN sequences, a first XTEN sequence inserted into a first XTEN insertion site and a second XTEN inserted into a second XTEN insertion site. Non-limiting examples of the first XTEN insertion site and the second XTEN insertion site are listed in Table 11.

TABLE 11. Exemplary Insertion Sites for Two XTENs

Insertion 1		Insertion 2	
Insertion Site	Domain	Insertion Site	Domain
745	B	2332	CT
26	A1	403	A2
40	A1	403	A2
18	A1	403	A2
26	A1	599	A2
40	A1	599	A2
18	A1	599	A2
1720	A3	1900	A3
1725	A3	1900	A3
1711	A3	1905	A3
1720	A3	1905	A3
1725	A3	1905	A3
1656	A3	26	A1
1656	A3	18	A1
1656	A3	40	A1
1656	A3	399	A2
1656	A3	403	A2
1656	A3	1725	A3
1656	A3	1720	A3
1900	A3	18	A1
1900	A3	26	A1
1900	A3	40	A1
1905	A3	18	A1
1905	A3	40	A1
1905	A3	26	A1
1910	A3	26	A1
18	A1	399	A2
26	A1	399	A2
40	A1	399	A2
18	A1	403	A2
1656	A3	1900	A3
1656	A3	1905	A3
1711	A3	40	A1
1711	A3	26	A1
1720	A3	26	A1

Insertion 1		Insertion 2	
Insertion Site	Domain	Insertion Site	Domain
1720	A3	40	A1
1720	A3	18	A1
1725	A3	26	A1
1725	A3	40	A1
1725	A3	18	A1
1720	A3	403	A2
1720	A3	399	A2
1711	A3	403	A2
1720	A3	403	A2
1725	A3	403	A2
1725	A3	399	A2
1711	A3	403	A2
1900	A3	399	A2
1900	A3	403	A2
1905	A3	403	A2
1905	A3	399	A2
1910	A3	403	A2

[0184] The two XTENs inserted or linked to the FVIII protein can be identical or different. In some embodiments, a FVIII protein useful for the invention comprises two XTEN sequences inserted in the FVIII protein, a first XTEN sequence inserted immediately downstream of amino acid 745 corresponding to SEQ ID NO: 4, and a second XTEN sequence inserted immediately downstream of amino acid 2332 corresponding to SEQ ID NO: 4 (the C-terminus). In other embodiments, the first XTEN sequence is inserted immediately downstream of amino acid 18, 26, 40, 1656, or 1720 corresponding to SEQ ID NO: 4, and a second XTEN sequence inserted immediately downstream of amino acid 403 corresponding to SEQ ID NO: 4. In yet other embodiments, the first XTEN sequence is inserted immediately downstream of amino acid 18, 26, or 40 corresponding to SEQ ID NO: 4, and a second XTEN sequence inserted immediately downstream of amino acid 599 corresponding to SEQ ID NO: 4. In still other embodiments, the first XTEN sequence is inserted immediately downstream of amino acid 1656 corresponding to SEQ ID NO: 4, and a second XTEN sequence inserted immediately downstream of amino acid 18, 26, 40, 399, 403, 1725, 1720, 1900, 1905, or 2332 corresponding to SEQ ID NO: 4. In certain embodiments, the first XTEN sequence is inserted immediately downstream of amino acid 1900 corresponding to SEQ ID NO: 4, and a second XTEN sequence inserted immediately downstream of amino acid 18, 26, or 40 corresponding to SEQ ID NO: 4. In some embodiments, the first XTEN sequence is inserted immediately downstream of amino acid 18, 26, or 40 corresponding to SEQ ID NO: 4, and a second XTEN sequence inserted immediately downstream of amino acid 399 corresponding to SEQ ID NO: 4. In other embodiments, the first XTEN sequence is inserted immediately downstream of amino acid 1720 corresponding to SEQ ID NO: 4, and a second XTEN sequence inserted immediately downstream of amino acid 18, 26, or 40 corresponding to SEQ ID NO: 4. In still other embodiments, the first XTEN sequence is inserted immediately downstream of amino acid 1720 corresponding to SEQ ID NO: 4, and a second XTEN sequence inserted immediately downstream of amino acid 18 corresponding to SEQ ID NO: 4. In a particular embodiment, the FVIII protein comprising two XTEN sequences, a first XTEN sequence inserted immediately downstream of amino acid 745 corresponding to SEQ ID NO: 4 and a second XTEN sequence inserted immediately downstream of amino acid 2332 corresponding to SEQ ID NO: 4, wherein the FVIII protein further has a deletion from amino acid 745 corresponding to SEQ ID NO: 4 to amino acid 1685 corresponding to SEQ ID NO: 4, a mutation or substitution at amino acid 1680 corresponding to SEQ ID NO: 4, *e.g.,* Y1680F, a mutation or substitution at amino acid 1648 corresponding to SEQ ID NO: 4, *e.g.,* R1648A, or at

least two mutations or substitutions at amino acid 1648 corresponding to SEQ ID NO: 4, *e.g.,* R1648A, and amino acid 1680 corresponding to SEQ ID NO: 4, *e.g.,* Y1680F. In a specific embodiment, the FVIII protein comprises two XTEN sequences, a first XTEN inserted immediately downstream of amino acid 1656 corresponding to SEQ ID NO: 4 and a second XTEN sequence inserted immediately downstream of amino acid 2332 of SEQ ID NO: 4, wherein the FVIII protein further has a deletion from amino acid 745 to amino acid 1656 corresponding to SEQ ID NO: 4.

[0185] In certain embodiments, a FVIII protein comprises three XTEN sequences, a first XTEN sequence inserted into a first XTEN insertion site, a second XTEN sequence inserted into a second XTEN sequence, and a third XTEN sequence inserted into a third XTEN insertion site. The first, second, or third XTEN sequences can be identical or different. The first, second, and third insertion sites can be selected from the group of any one of the insertion sites disclosed herein. In some embodiments, the FVIII protein comprising three XTEN sequences can further comprise a mutation or substitution, e.g., amino acid 1648 corresponding to SEQ ID NO: 4, *e.g.,* R1648A. For example, non-limiting examples of the first, second, and third XTEN insertion sites are listed in Table 12.

TABLE 12. Exemplary Insertion Sites for Three XTENs

Insertion 1		Insertion 2		Insertion 3	
Insertion Site	Domain	Insertion Site	Domain	Insertion Site	Domain
26	A1	403	A2	1656	A3
26	A1	403	A2	1720	A3
26	A1	403	A2	1900	A3
26	A1	1656	A3	1720	A3
26	A1	1656	A3	1900	A3
26	A1	1720	A3	1900	A3
403	A2	1656	A3	1720	A3
403	A2	1656	A3	1900	A3
403	A2	1720	A3	1900	A3
1656	A3	1720	A3	1900	A3
745	B	1900		2332	CT
18	A1	745	B	2332	CT
26	A1	745	B	2332	CT
40	A1	745	B	2332	CT
18	A1	745	B	2332	CT
40	A1	745	B	2332	CT
403	A2	745	B	2332	CT
399	A2	745	B	2332	CT
1725	A3	745	B	2332	CT
1720	A3	745	B	2332	CT
1711	A3	745	B	2332	CT
1900	A3	745	B	2332	CT
1905	A3	745	B	2332	CT
1910	A3	745	B	2332	CT

[0186] In some embodiments, a FVIII protein comprises three XTEN sequences, a first XTEN sequence inserted immediately downstream of amino acid 26 corresponding to SEQ ID NO: 4, a second XTEN sequence inserted downstream of amino acid 403 corresponding to SEQ ID NO: 4, and a third XTEN sequence inserted downstream of amino acid 1656, 1720, or 1900 corresponding to SEQ ID NO: 4. In other embodiments, the first XTEN

sequence is inserted immediately downstream of amino acid 26 corresponding to SEQ ID NO: 4, a second XTEN sequence is inserted downstream of amino acid 1656 corresponding to SEQ ID NO: 4, and a third XTEN sequence is inserted downstream of amino acid 1720 or 1900 corresponding to SEQ ID NO: 4. In yet other embodiments, the first XTEN sequence is inserted immediately downstream of amino acid 26 corresponding to SEQ ID NO: 4, a second XTEN sequence is inserted downstream of amino acid 1720 corresponding to SEQ ID NO: 4, and a third XTEN sequence is inserted downstream of amino acid 1900 corresponding to SEQ ID NO: 4. In still other embodiments, the first XTEN sequence is inserted immediately downstream of amino acid 403 corresponding to SEQ ID NO: 4, a second XTEN sequence is inserted downstream of amino acid 1656 corresponding to SEQ ID NO: 4, and a third XTEN sequence is inserted downstream of amino acid 1720 or 1900 corresponding to SEQ ID NO: 4. In other embodiments, the first XTEN sequence is inserted immediately downstream of amino acid 403 or 1656 corresponding to SEQ ID NO: 4, a second XTEN sequence is inserted downstream of amino acid 1720 corresponding to SEQ ID NO: 4, and a third XTEN sequence is inserted downstream of amino acid 1900 corresponding to SEQ ID NO: 4. In other embodiments, the first XTEN sequence is inserted immediately downstream of amino acid 18, 26, 40, 399, 403, 1711, 1720, 1725, 1900, 1905, or 1910 corresponding to SEQ ID NO: 4, a second XTEN sequence is inserted downstream of amino acid 745 corresponding to SEQ ID NO: 4, and a third XTEN sequence is inserted downstream of amino acid 2332 corresponding to SEQ ID NO: 4.

[0187] In other embodiments, a FVIII protein in the invention comprises four XTEN sequences, a first XTEN sequence inserted into a first insertion site, a second XTEN sequence inserted into a second insertion site, a third XTEN sequence inserted into a third insertion site, and a fourth XTEN sequence inserted into a fourth insertion site. The first, second, third, and fourth XTEN sequences can be identical, different, or combinations thereof. In some embodiments, the FVIII protein comprising four XTEN sequences can further comprise a mutation or substitution, *e.g.*, amino acid 1648 corresponding to SEQ ID NO: 4, *e.g.,* R1648A. Non-limiting examples of the first, second, third, and fourth XTEN insertion sites are listed in Table 13.

TABLE 13. Exemplary Insertion Sites for Four XTENs

Insertion 1		Insertion 2		Insertion 3		Insertion 4	
Insertion Site	Domain	Insertion Site	Domain	Insertion Site	Domain	Insertion Site	Domain
26	A1	403	A2	1656	a3	1720	A3
26	A1	403	A2	1656	a3	1900	A3
26	A1	403	A2	1720	A3	1900	A3
26	A1	1656	a3	1720	A3	1900	A3
403	A2	1656	a3	1720	A3	1900	A3
0040	A1	0403	A2	745	B	2332	CT
0040	A1	0403	A2	745	B	2332	CT
0018	A1	0409	A2	745	B	2332	CT
0040	A1	0409	A2	745	B	2332	CT
0040	A1	0409	A2	745	B	2332	CT
0018	A1	0409	A2	745	B	2332	CT
0040	A1	1720	A3	745	B	2332	CT
0026	A1	1720	A3	745	B	2332	CT
0018	A1	1720	A3	745	B	2332	CT
0018	A1	1720	A3	745	B	2332	CT
0018	A1	1720	A3	745	B	2332	CT
0026	A1	1720	A3	745	B	2332	CT
0018	A1	1720	A3	745	B	2332	CT
0018	A1	1900	A3	745	B	2332	CT
0018	A1	1900	A3	745	B	2332	CT

Insertion 1		Insertion 2		Insertion 3		Insertion 4	
Insertion Site	Domain	Insertion Site	Domain	Insertion Site	Domain	Insertion Site	Domain
0026	A1	1900	A3	745	B	2332	CT
0040	A1	1900	A3	745	B	2332	CT
0040	A1	1905	A3	745	B	2332	CT
0018	A1	1905	A3	745	B	2332	CT
0040	A1	1905	A3	745	B	2332	CT
0026	A1	1905	A3	745	B	2332	CT
0018	A1	1905	A3	745	B	2332	CT
0018	A1	1905	A3	745	B	2332	CT
0018	A1	1910	A3	745	B	2332	CT
0018	A1	1910	A3	745	B	2332	CT
0040	A1	1910	A3	745	B	2332	CT
0026	A1	1910	A3	745	B	2332	CT
0018	A1	1910	A3	745	B	2332	CT
0026	A1	1910	A3	745	B	2332	CT
0040	A1	1910	A3	745	B	2332	CT
0018	A1	1910	A3	745	B	2332	CT
0409	A2	1720	A3	745	B	2332	CT
0403	A2	1720	A3	745	B	2332	CT
0409	A2	1720	A3	745	B	2332	CT
0403	A2	1720	A3	745	B	2332	CT
0403	A2	1720	A3	745	B	2332	CT
0403	A2	1900	A3	745	B	2332	CT
0403	A2	1900	A3	745	B	2332	CT
0409	A2	1900	A3	745	B	2332	CT
0403	A2	1900	A3	745	B	2332	CT
0403	A2	1900	A3	745	B	2332	CT
0409	A2	1900	A3	745	B	2332	CT
0409	A2	1905	A3	745	B	2332	CT
0403	A2	1905	A3	745	B	2332	CT
0403	A2	1905	A3	745	B	2332	CT
0403	A2	1905	A3	745	B	2332	CT
0409	A2	1905	A3	745	B	2332	CT
0403	A2	1905	A3	745	B	2332	CT
0409	A2	1910	A3	745	B	2332	CT
0403	A2	1910	A3	745	B	2332	CT
0403	A2	1910	A3	745	B	2332	CT
0403	A2	1910	A3	745	B	2332	CT
0403	A2	1910	A3	745	B	2332	CT
1720	A3	1900	A3	745	B	2332	CT
1720	A3	1905	A3	745	B	2332	CT
1720	A3	1910	A3	745	B	2332	CT

Insertion 1		Insertion 2		Insertion 3		Insertion 4	
Insertion Site	Domain	Insertion Site	Domain	Insertion Site	Domain	Insertion Site	Domain
1720	A3	1910	A3	745	B	2332	CT
0403	A2	1656	a3	1720	A3	2332	CT
0403	A2	1656	a3	1900	A3	2332	CT
0403	A2	1720	A3	1900	A3	2332	CT
1656	a3	1720	A3	1900	A3	2332	CT
0018	A1	0403	A2	1656	a3	2332	CT
0018	A1	0403	A2	1720	A3	2332	CT
0018	A1	0403	A2	1900	A3	2332	CT
0018	A1	1656	a3	1720	A3	2332	CT
0018	A1	1656	a3	1900	A3	2332	CT
0018	A1	1720	A3	1900	A3	2332	CT
0018	A1	0403	A2	0745	B	2332	CT
0018	A1	0745	B	1720	A3	2332	CT
0018	A1	0745	B	1900	A3	2332	CT
0403	A2	0745	B	1720	A3	2332	CT
0403	A2	0745	B	1900	A3	2332	CT
0745	B	1720	A3	1900	A3	2332	CT
0188	A1	1900	A3	0745	B	2332	CT
0599		1900	A3	0745	B	2332	CT
2068		1900	A3	0745	B	2332	CT
2171		1900	A3	0745	B	2332	CT
2227		1900	A3	0745	B	2332	CT
2277		1900	A3	0745	B	2332	CT

[0188] In some embodiments, a FVIII protein comprises five XTEN sequences, a first XTEN sequence inserted into a first insertion site, a second XTEN sequence inserted into a second insertion site, a third XTEN sequence inserted into a third XTEN insertion site, a fourth XTEN sequence inserted into a fourth XTEN insertion site, and a fifth XTEN sequence inserted into a fifth XTEN insertion site. The first, second, third, fourth, of fifth XTEN sequences can be identical, different, or combinations thereof. Non-limiting examples of the first, second, third, fourth, and fifth insertion sites are listed in Table 14.

TABLE 14. Exemplary Insertion Sites for Five XTENs

XTEN Insertion 1	XTEN insertion 2	XTEN Insertion 3	XTEN Insertion 4	XTEN Insertion 5
0403	1656	1720	1900	2332
0018	0403	1656	1720	2332
0018	0403	1656	1900	2332
0018	0403	1720	1900	2332
0018	1656	1720	1900	2332
0018	0403	0745	1720	2332
0018	0403	0745	1900	2332
0018	0745	1720	1900	2332
0403	0745	1720	1900	2332

[0189] In certain embodiments, a FVIII protein comprises six XTEN sequences, a first XTEN sequence inserted into a first XTEN insertion site, a second XTEN sequence inserted into a second XTEN insertion site, a third XTEN sequence inserted into a third XTEN insertion site, a fourth XTEN sequence inserted into a fourth XTEN insertion site, a fifth XTEN sequence inserted into a fifth XTEN insertion site, and a sixth XTEN sequence inserted into a sixth XTEN insertion site. The first, second, third, fourth, fifth, or sixth XTEN sequences can be identical, different, or combinations thereof. Examples of the six XTEN insertion sites include, but are not limited to the insertion sites listed in Table 15.

TABLE 15. Exemplary XTEN Insertion Sites for Six XTENs

XTEN Insertion 1	XTEN insertion 2	XTEN Insertion 3	XTEN Insertion 4	XTEN Insertion 5	XTEN Insertion 6
0018	0403	1656	1720	1900	2332
0018	0403	0745	1720	1900	2332

[0190] In a particular example, a first XTEN is inserted between amino acids 26 and 27 corresponding to SEQ ID NO: **4**, and a second XTEN is inserted between amino acids 1720 and 1721 corresponding to SEQ ID NO: **4** (full-length mature FVIII). In another example, a first XTEN is inserted between amino acids **403** and **404** corresponding to SEQ ID NO: **4**, and a second XTEN is inserted between amino acids 1720 and 1721 corresponding to SEQ ID NO: **4**. In some examples, a first XTEN is inserted between amino acids 1656 and 1657 corresponding to SEQ ID NO: **4**, and a second XTEN is inserted between amino acids 1720 and 1721 corresponding to SEQ ID NO: **4**. In other examples, a first XTEN is inserted between amino acids 26 and 27 corresponding to SEQ ID NO: **4**, a second XTEN is inserted between amino acids 1656 and 1657 corresponding to SEQ ID NO: **4**, and a third XTEN is inserted between amino acids 1720 and 1721 corresponding to SEQ ID NO: **4**. In yet other embodiments, a first XTEN is inserted between amino acids **403** and **404** corresponding to SEQ ID NO: **4**, a second XTEN is inserted between amino acids 1656 and 1657 corresponding to SEQ ID NO: **4**, and a third XTEN is inserted between amino acids 1720 and 1721 corresponding to SEQ ID NO: **4**. In still other embodiments, a first XTEN is inserted between amino acids **403** and **404** corresponding to SEQ ID NO: **4**, a second XTEN is inserted between amino acids 1656 and 1657 corresponding to SEQ ID NO: **4**, and a third XTEN is inserted between amino acids 1720 and 1721 corresponding to SEQ ID NO: **4**. In certain embodiments, a first XTEN is inserted between amino acids 26 and 27 corresponding to SEQ ID NO: **4**, a second XTEN is inserted between amino acids 1720 and 1721 corresponding to SEQ ID NO: **4**, and a third XTEN is inserted between amino acids 1900 and 1901 corresponding to SEQ ID NO: **4**. In some embodiments, a first XTEN is inserted between amino acids 26 and 27 corresponding to SEQ ID NO: **4**, a second XTEN is inserted between amino acids 1656 and 1657 corresponding to SEQ ID NO: **4**, a third XTEN is inserted between amino acids 1720 and 1721 corresponding to SEQ ID NO: **4**, and a fourth XTEN is inserted between 1900 and 1901 corresponding to SEQ ID NO: **4**.

[0191] In a particular embodiment, an XTEN sequence is inserted between amino acids 745 and 746 of a full-length Factor VIII or the corresponding insertion site of the B-domain deleted Factor VIII.

[0192] In some embodiments, a chimeric protein of the invention comprises two polypeptide sequences, a first polypeptide sequence comprising an amino acid sequence at least about 80%, 90%, 95%, or 100% identical to a sequence selected from FVIII-161 (SEQ ID NO: 101), FVIII-169 (SEQ ID NO: 103), FVIII-170 (SEQ ID NO: 102), FVIII-173 (SEQ ID NO: 104); FVIII-195 (SEQ ID NO: 105); FVIII-196 (SEQ ID NO: 106), FVIII-199 (SEQ ID NO: 107), FVIII-201 (SEQ ID NO: 108); FVIII-203 (SEQ ID NO: 109), FVIII-204 (SEQ ID NO: 110), FVIII-205 (SEQ ID NO: 111), FVIII-266 (SEQ ID NO:112), FVIII-267 (SEQ ID NO: 113), FVIII-268 (SEQ ID NO: 114), FVIII-269 (SEQ ID NO: 115), FVIII-271 (SEQ ID NO: 116), or FVIII-272 (SEQ ID NO: 117) and a second polypeptide sequence comprising an amino acid sequence at least about 80%, 90%, 95%, or 100% identical to a sequence selected from VWF031 (SEQ ID NO: 118), VWF034 (SEQ ID NO: 119), or VWF-036 (SEQ ID NO: 120).

D) Ig Constant Region or a portion thereof

[0193] The VWF fragment or the FVIII protein linked to an XTEN sequence in the present disclosure can further comprise an Ig constant region or a portion thereof. The Ig constant region or a portion thereof can improve pharmacokinetic or pharmacodynamic properties of the VWF fragment or the FVIII protein in combination with the XTEN sequence. In certain embodiments, the Ig constant region or a portion thereof extends a half-life of a molecule fused to the Ig constant region or a portion thereof.

[0194] An Ig constant region is comprised of domains denoted CH (constant heavy) domains (CH1, CH2, etc.). Depending on the isotype, (*i.e.* IgG, IgM, IgA, IgD, or IgE), the constant region can be comprised of three or four CH domains. Some isotypes (*e.g.* IgG) constant regions also contain a hinge region. *See* Janeway et al. 2001, Immunobiology, Garland Publishing, N.Y., N.Y.

[0195] An Ig constant region or a portion thereof for producing the chimeric protein of the present invention may be obtained from a number of different sources. In some embodiments, an Ig constant region or a portion thereof is derived from a human Ig. It is understood, however, that the Ig constant region or a portion thereof may be derived from an Ig of another mammalian species, including for example, a rodent (*e.g.* a mouse, rat, rabbit, guinea pig) or non-human primate (*e.g.* chimpanzee, macaque) species. Moreover, the Ig constant region or a portion thereof may be derived from any Ig class, including IgM, IgG, IgD, IgA, and IgE, and any Ig isotype, including IgG1, IgG2, IgG3, and IgG4. In one embodiment, the human isotype IgG1 is used.

[0196] A variety of the Ig constant region gene sequences (*e.g.,* human constant region gene sequences) are available in the form of publicly accessible deposits. Constant region domains sequence can be selected having a particular effector function (or lacking a particular effector function) or with a particular modification to reduce immunogenicity. Many sequences of antibodies and antibody-encoding genes have been published and suitable Ig constant region sequences (*e.g.,* hinge, CH2, and/or CH3 sequences, or portions thereof) can be derived from these sequences using art recognized techniques. The genetic material obtained using any of the foregoing methods may then be altered or synthesized to obtain polypeptides of the present invention. It will further be appreciated that the scope of this invention encompasses alleles, variants and mutations of constant region DNA sequences.

[0197] The sequences of the Ig constant region or a portion thereof can be cloned, *e.g.,* using the polymerase chain reaction and primers which are selected to amplify the domain of interest. To clone a sequence of the Ig constant region or a portion thereof from an antibody, mRNA can be isolated from hybridoma, spleen, or lymph cells, reverse transcribed into DNA, and antibody genes amplified by PCR. PCR amplification methods are described in detail in U.S. Pat. Nos. 4,683,195; 4,683,202; 4,800,159; 4,965,188; and in, *e.g.,* "PCR Protocols: A Guide to Methods and Applications" Innis et al. eds., Academic Press, San Diego, CA (1990); Ho et al. 1989. Gene 77:51; Horton et al. 1993. Methods Enzymol. 217:270). PCR may be initiated by consensus constant region primers or by more specific primers based on the published heavy and light chain DNA and amino acid sequences. As discussed above, PCR also may be used to isolate DNA clones encoding the antibody light and heavy chains. In this case the libraries may be screened by consensus primers or larger homologous probes, such as mouse constant region probes. Numerous primer sets suitable for amplification of antibody genes are known in the art (*e.g.,* 5' primers based on the N-terminal sequence of purified antibodies (Benhar and Pastan. 1994. Protein Engineering 7:1509); rapid amplification of cDNA ends (Ruberti, F. et al. 1994. J. Immunol. Methods 173:33); antibody leader sequences (Larrick et al. 1989 Biochem. Biophys. Res. Commun. 160:1250). The cloning of antibody sequences is further described in Newman et al., U.S. Pat. No. 5,658,570, filed January 25, 1995.

[0198] An Ig constant region used herein can include all domains and the hinge region or portions thereof. In one embodiment, the Ig constant region or a portion thereof comprises CH2 domain, CH3 domain, and a hinge region, *i.e.,* an Fc region or an FcRn binding partner.

[0199] As used herein, the term "Fc region" is defined as the portion of a polypeptide which corresponds to the Fc region of native Ig, *i.e.,* as formed by the dimeric association of the respective Fc domains of its two heavy chains.

A native Fc region forms a homodimer with another Fc region. In contrast, the term "genetically-fused Fc region" or "single-chain Fc region" (scFc region), as used herein, refers to a synthetic dimeric Fc region comprised of Fc domains genetically linked within a single polypeptide chain (*i.e.*, encoded in a single contiguous genetic sequence).

[0200] In one embodiment, the "Fc region" refers to the portion of a single Ig heavy chain beginning in the hinge region just upstream of the papain cleavage site (*i.e.* residue 216 in IgG, taking the first residue of heavy chain constant region to be 114) and ending at the C-terminus of the antibody. Accordingly, a complete Fc domain comprises at least a hinge domain, a CH2 domain, and a CH3 domain.

[0201] The Fc region of an Ig constant region, depending on the Ig isotype can include the CH2, CH3, and CH4 domains, as well as the hinge region. Chimeric proteins comprising an Fc region of an Ig bestow several desirable properties on a chimeric protein including increased stability, increased serum half-life (see Capon et al., 1989, Nature 337:525) as well as binding to Fc receptors such as the neonatal Fc receptor (FcRn) (U.S. Pat. Nos. 6,086,875, 6,485,726, 6,030,613; WO 03/077834; US2003-0235536A1).

[0202] An Ig constant region or a portion thereof can be an FcRn binding partner. FcRn is active in adult epithelial tissues and expressed in the lumen of the intestines, pulmonary airways, nasal surfaces, vaginal surfaces, colon and rectal surfaces (U.S. Pat. No. 6,485,726). An FcRn binding partner is a portion of an Ig that binds to FcRn.

[0203] The FcRn receptor has been isolated from several mammalian species including humans. The sequences of the human FcRn, monkey FcRn, rat FcRn, and mouse FcRn are known (Story et al. 1994, J. Exp. Med. 180:2377). The FcRn receptor binds IgG (but not other Ig classes such as IgA, IgM, IgD, and IgE) at relatively low pH, actively transports the IgG transcellularly in a luminal to serosal direction, and then releases the IgG at relatively higher pH found in the interstitial fluids. It is expressed in adult epithelial tissue (U.S. Pat. Nos. 6,485,726, 6,030,613, 6,086,875; WO 03/077834; US2003-0235536A1) including lung and intestinal epithelium (Israel et al. 1997, Immunology 92:69) renal proximal tubular epithelium (Kobayashi et al. 2002, Am. J. Physiol. Renal Physiol. 282:F358) as well as nasal epithelium, vaginal surfaces, and biliary tree surfaces.

[0204] FcRn binding partners useful in the present invention encompass molecules that can be specifically bound by the FcRn receptor including whole IgG, the Fc fragment of IgG, and other fragments that include the complete binding region of the FcRn receptor. The region of the Fc portion of IgG that binds to the FcRn receptor has been described based on X-ray crystallography (Burmeister et al. 1994, Nature 372:379). The major contact area of the Fc with the FcRn is near the junction of the CH2 and CH3 domains. Fc-FcRn contacts are all within a single Ig heavy chain. The FcRn binding partners include whole IgG, the Fc fragment of IgG, and other fragments of IgG that include the complete binding region of FcRn. The major contact sites include amino acid residues 248, 250-257, 272, 285, 288, 290-291, 308-311, and 314 of the CH2 domain and amino acid residues 385-387, 428, and 433-436 of the CH3 domain. References made to amino acid numbering of Igs or Ig fragments, or regions, are all based on Kabat et al. 1991, Sequences of Proteins of Immunological Interest, U.S. Department of Public Health, Bethesda, Md.

[0205] Fc regions or FcRn binding partners bound to FcRn can be effectively shuttled across epithelial barriers by FcRn, thus providing a non-invasive means to systemically administer a desired therapeutic molecule. Additionally, fusion proteins comprising an Fc region or an FcRn binding partner are endocytosed by cells expressing the FcRn. But instead of being marked for degradation, these fusion proteins are recycled out into circulation again, thus increasing the *in vivo* half-life of these proteins. In certain embodiments, the portions of Ig constant regions are an Fc region or an FcRn binding partner that typically associates, via disulfide bonds and other non-specific interactions, with another Fc region or another FcRn binding partner to form dimers and higher order multimers.

[0206] Two FcRn receptors can bind a single Fc molecule. Crystallographic data suggest that each FcRn molecule binds a single polypeptide of the Fc homodimer. In one embodiment, linking the FcRn binding partner, *e.g.,* an Fc fragment of an IgG, to a biologically active molecule provides a means of delivering the biologically active molecule orally, buccally, sublingually, rectally, vaginally, as an aerosol administered nasally or via a

pulmonary route, or via an ocular route. In another embodiment, the chimeric protein can be administered invasively, *e.g.,* subcutaneously, intravenously.

[0207] An FcRn binding partner region is a molecule or a portion thereof that can be specifically bound by the FcRn receptor with consequent active transport by the FcRn receptor of the Fc region. Specifically bound refers to two molecules forming a complex that is relatively stable under physiologic conditions. Specific binding is characterized by a high affinity and a low to moderate capacity as distinguished from nonspecific binding which usually has a low affinity with a moderate to high capacity. Typically, binding is considered specific when the affinity constant KA is higher than 10^6 M^{-1}, or higher than 10^8 M^{-1}. If necessary, non-specific binding can be reduced without substantially affecting specific binding by varying the binding conditions. The appropriate binding conditions such as concentration of the molecules, ionic strength of the solution, temperature, time allowed for binding, concentration of a blocking agent (*e.g.* serum albumin, milk casein), etc., may be optimized by a skilled artisan using routine techniques.

[0208] In certain embodiments, a chimeric protein of the invention comprises one or more truncated Fc regions that are nonetheless sufficient to confer Fc receptor (FcR) binding properties to the Fc region. For example, the portion of an Fc region that binds to FcRn (*i.e.,* the FcRn binding portion) comprises from about amino acids 282-438 of IgG1, EU numbering (with the primary contact sites being amino acids 248, 250-257, 272, 285, 288, 290-291, 308-311, and 314 of the CH2 domain and amino acid residues 385-387, 428, and 433-436 of the CH3 domain. Thus, an Fc region of the invention may comprise or consist of an FcRn binding portion. FcRn binding portions may be derived from heavy chains of any isotype, including IgG1, IgG2, IgG3 and IgG4. In one embodiment, an FcRn binding portion from an antibody of the human isotype IgG1 is used. In another embodiment, an FcRn binding portion from an antibody of the human isotype IgG4 is used.

[0209] In another embodiment, the "Fc region" includes an amino acid sequence of an Fc domain or derived from an Fc domain. In certain embodiments, an Fc region comprises at least one of: a hinge (*e.g.,* upper, middle, and/or lower hinge region) domain (about amino acids 216-230 of an antibody Fc region according to EU numbering), a CH2 domain (about amino acids 231-340 of an antibody Fc region according to EU numbering), a CH3 domain (about amino acids 341-438 of an antibody Fc region according to EU numbering), a CH4 domain, or a variant, portion, or fragment thereof. In other embodiments, an Fc region comprises a complete Fc domain (*i.e.,* a hinge domain, a CH2 domain, and a CH3 domain). In some embodiments, an Fc region comprises, consists essentially of, or consists of a hinge domain (or a portion thereof) fused to a CH3 domain (or a portion thereof), a hinge domain (or a portion thereof) fused to a CH2 domain (or a portion thereof), a CH2 domain (or a portion thereof) fused to a CH3 domain (or a portion thereof), a CH2 domain (or a portion thereof) fused to both a hinge domain (or a portion thereof) and a CH3 domain (or a portion thereof). In still other embodiments, an Fc region lacks at least a portion of a CH2 domain (*e.g.,* all or part of a CH2 domain). In a particular embodiment, an Fc region comprises or consists of amino acids corresponding to EU numbers 221 to 447.

[0210] The Fc regions denoted as F, F1, or F2 herein may be obtained from a number of different sources. In one embodiment, an Fc region of the polypeptide is derived from a human Ig. It is understood, however, that an Fc region may be derived from an Ig of another mammalian species, including for example, a rodent (*e.g.* a mouse, rat, rabbit, or guinea pig) or non-human primate (*e.g.* chimpanzee, macaque) species. Moreover, the polypeptide of the Fc domains or portions thereof may be derived from any Ig class, including IgM, IgG, IgD, IgA and IgE, and any Ig isotype, including IgG1, IgG2, IgG3 and IgG4. In another embodiment, the human isotype IgG1 is used.

[0211] In certain embodiments, the Fc variant confers a change in at least one effector function imparted by an Fc region comprising said wild-type Fc domain (*e.g.,* an improvement or reduction in the ability of the Fc region to bind to Fc receptors (*e.g.* FcγRI, FcγRII, or FcγRIII) or complement proteins (*e.g.* C1q), or to trigger antibody-dependent cytotoxicity (ADCC), phagocytosis, or complement-dependent cytotoxicity (CDCC)). In other embodiments, the Fc variant provides an engineered cysteine residue.

[0212] The Fc regions of the invention may employ art-recognized Fc variants which are known to impart a change (*e.g.,* an enhancement or reduction) in effector function and/or FcR or FcRn binding. Specifically, a

binding molecule of the invention may include, for example, a change (*e.g.,* a substitution) at one or more of the amino acid positions disclosed in International PCT Publications WO88/07089A1, WO96/14339A1, WO98/05787A1, WO98/23289A1, WO99/51642A1, WO99/58572A1, WO00/09560A2, WO00/32767A1, WO00/42072A2, WO02/44215A2, WO02/060919A2, WO03/074569A2, WO04/016750A2, WO04/029207A2, WO04/035752A2, WO04/063351A2, WO04/074455A2, WO04/099249A2, WO05/040217A2, WO04/044859, WO05/070963A1, WO05/077981A2, WO05/092925A2, WO05/123780A2, WO06/019447A1, WO06/047350A2, and WO06/085967A2; US Patent Publication Nos. US2007/0231329, US2007/0231329, US2007/0237765, US2007/0237766, US2007/0237767, US2007/0243188, US20070248603, US20070286859, US20080057056 ; or US Patents 5,648,260; 5,739,277; 5,834,250; 5,869,046; 6,096,871; 6,121,022; 6,194,551; 6,242,195; 6,277,375; 6,528,624; 6,538,124; 6,737,056; 6,821,505; 6,998,253; 7,083,784; 7,404,956, and 7,317,091. In one embodiment, the specific change (*e.g.,* the specific substitution of one or more amino acids disclosed in the art) may be made at one or more of the disclosed amino acid positions. In another embodiment, a different change at one or more of the disclosed amino acid positions (*e.g.,* the different substitution of one or more amino acid position disclosed in the art) may be made.

[0213] The Fc region or FcRn binding partner of IgG can be modified according to well recognized procedures such as site directed mutagenesis and the like to yield modified IgG or Fc fragments or portions thereof that will be bound by FcRn. Such modifications include modifications remote from the FcRn contact sites as well as modifications within the contact sites that preserve or even enhance binding to the FcRn. For example, the following single amino acid residues in human IgG1 Fc (Fc γ1) can be substituted without significant loss of Fc binding affinity for FcRn: P238A, S239A, K246A, K248A, D249A, M252A, T256A, E258A, T260A, D265A, S267A, H268A, E269A, D270A, E272A, L274A, N276A, Y278A, D280A, V282A, E283A, H285A, N286A, T289A, K290A, R292A, E293A, E294A, Q295A, Y296F, N297A, S298A, Y300F, R301A, V303A, V305A, T307A, L309A, Q311A, D312A, N315A, K317A, E318A, K320A, K322A, S324A, K326A, A327Q, P329A, A330Q, P331A, E333A, K334A, T335A, S337A, K338A, K340A, Q342A, R344A, E345A, Q347A, R355A, E356A, M358A, T359A, K360A, N361A, Q362A, Y373A, S375A, D376A, A378Q, E380A, E382A, S383A, N384A, Q386A, E388A, N389A, N390A, Y391F, K392A, L398A, S400A, D401A, D413A, K414A, R416A, Q418A, Q419A, N421A, V422A, S424A, E430A, N434A, T437A, Q438A, K439A, S440A, S444A, and K447A, where for example P238A represents wild type proline substituted by alanine at position number 238. As an example, a specific embodiment incorporates the N297A mutation, removing a highly conserved N-glycosylation site. In addition to alanine other amino acids may be substituted for the wild type amino acids at the positions specified above. Mutations may be introduced singly into Fc giving rise to more than one hundred Fc regions distinct from the native Fc. Additionally, combinations of two, three, or more of these individual mutations may be introduced together, giving rise to hundreds more Fc regions. Moreover, one of the Fc region of a construct of the invention may be mutated and the other Fc region of the construct not mutated at all, or they both may be mutated but with different mutations.

[0214] Certain of the above mutations may confer new functionality upon the Fc region or FcRn binding partner. For example, one embodiment incorporates N297A, removing a highly conserved N-glycosylation site. The effect of this mutation is to reduce immunogenicity, thereby enhancing circulating half-life of the Fc region, and to render the Fc region incapable of binding to FcγRI, FcγRIIA, FcγRIIB, and FcγRIIIA, without compromising affinity for FcRn (Routledge et al. 1995, Transplantation 60:847; Friend et al. 1999, Transplantation 68:1632; Shields et al. 1995, J. Biol. Chem. 276:6591). As a further example of new functionality arising from mutations described above affinity for FcRn may be increased beyond that of wild type in some instances. This increased affinity may reflect an increased "on" rate, a decreased "off" rate or both an increased "on" rate and a decreased "off" rate. Examples of mutations believed to impart an increased affinity for FcRn include, but not limited to, T256A, T307A, E380A, and N434A (Shields et al. 2001, J. Biol. Chem. 276:6591).

[0215] Additionally, at least three human Fc gamma receptors appear to recognize a binding site on IgG within the lower hinge region, generally amino acids 234-237. Therefore, another example of new functionality and potential decreased immunogenicity may arise from mutations of this region, as for example by replacing amino acids 233-236 of human IgG1 "ELLG" to the corresponding sequence from IgG2 "PVA" (with one amino acid deletion). It has been shown that FcγRI, FcγRII, and FcγRIII, which mediate various effector functions will not bind to IgG1 when such mutations have been introduced. Ward and Ghetie 1995, Therapeutic Immunology 2:77 and Armour et al.

1999, Eur. J. Immunol. 29:2613.

[0216] In one embodiment, the Ig constant region or a portion thereof, e.g, an Fc region, is a polypeptide including the sequence PKNSSMISNTP (SEQ ID NO: 52) and optionally further including a sequence selected from HQSLGTQ (SEQ ID NO: 53), HQNLSDGK (SEQ ID NO: 54), HQNISDGK (SEQ ID NO: 55), or VISSHLGQ (SEQ ID NO: 56) (U.S. Pat. No. 5,739,277).

[0217] In another embodiment, the immunoglobulin constant region or a portion thereof comprises an amino acid sequence in the hinge region or a portion thereof that forms one or more disulfide bonds with another immunoglobulin constant region or a portion thereof. The disulfide bond by the immunoglobulin constant region or a portion thereof places the first polypeptide comprising FVIII and the second polypeptide comprising the VWF fragment together so that endogenous VWF does not replace the VWF fragment and does not bind to the FVIII. Therefore, the disulfide bond between the first immunoglobulin constant region or a portion thereof and a second immunoglobulin constant region or a portion thereof prevents interaction between endogenous VWF and the FVIII protein. This inhibition of interaction between the VWF and the FVIII protein allows the half-life of the FVIII protein to go beyond the two fold limit. The hinge region or a portion thereof can further be linked to one or more domains of CH1, CH2, CH3, a fragment thereof, and any combinations thereof. In a particular embodiment, the immunoglobulin constant region or a portion thereof is a hinge region and CH2.

[0218] In certain embodiments, the Ig constant region or a portion thereof is hemi-glycosylated. For example, the chimeric protein comprising two Fc regions or FcRn binding partners may contain a first, glycosylated, Fc region (*e.g.,* a glycosylated CH2 region) or FcRn binding partner and a second, aglycosylated, Fc region (*e.g.,* an aglycosylated CH2 region) or FcRn binding partner. In one embodiment, a linker may be interposed between the glycosylated and aglycosylated Fc regions. In another embodiment, the Fc region or FcRn binding partner is fully glycosylated, *i.e.,* all of the Fc regions are glycosylated. In other embodiments, the Fc region may be aglycosylated, *i.e.,* none of the Fc moieties are glycosylated.

[0219] In certain embodiments, a chimeric protein of the invention comprises an amino acid substitution to an Ig constant region or a portion thereof (*e.g.,* Fc variants), which alters the antigen-independent effector functions of the Ig constant region, in particular the circulating half-life of the protein.

[0220] Such proteins exhibit either increased or decreased binding to FcRn when compared to proteins lacking these substitutions and, therefore, have an increased or decreased half-life in serum, respectively. Fc variants with improved affinity for FcRn are anticipated to have longer serum half-lives, and such molecules have useful applications in methods of treating mammals where long half-life of the administered polypeptide is desired, *e.g.,* to treat a chronic disease or disorder (*see, e.g.*, US Patents 7,348,004, 7,404,956, and 7,862,820). In contrast, Fc variants with decreased FcRn binding affinity are expected to have shorter half-lives, and such molecules are also useful, for example, for administration to a mammal where a shortened circulation time may be advantageous, *e.g.* for in vivo diagnostic imaging or in situations where the starting polypeptide has toxic side effects when present in the circulation for prolonged periods. Fc variants with decreased FcRn binding affinity are also less likely to cross the placenta and, thus, are also useful in the treatment of diseases or disorders in pregnant women. In addition, other applications in which reduced FcRn binding affinity may be desired include those applications in which localization the brain, kidney, and/or liver is desired. In one exemplary embodiment, the chimeric protein of the invention exhibit reduced transport across the epithelium of kidney glomeruli from the vasculature. In another embodiment, the chimeric protein of the invention exhibit reduced transport across the blood brain barrier (BBB) from the brain, into the vascular space. In one embodiment, a protein with altered FcRn binding comprises at least one Fc region or FcRn binding partner (e.g, one or two Fc regions or FcRn binding partners) having one or more amino acid substitutions within the "FcRn binding loop" of an Ig constant region. The FcRn binding loop is comprised of amino acid residues 280-299 (according to EU numbering) of a wild-type, full-length, Fc region. In other embodiments, an Ig constant region or a portion thereof in a chimeric protein of the invention having altered FcRn binding affinity comprises at least one Fc region or FcRn binding partner having one or more amino acid substitutions within the 15 Å FcRn "contact zone." As used herein, the term 15 Å FcRn "contact zone" includes residues at the following positions of a wild-type, full-length Fc moiety: 243-261, 275-280, 282-293, 302-319, 336-

348, 367, 369, 372-389, 391, 393, 408, 424, 425-440 (EU numbering). In other embodiments, a Ig constant region or a portion thereof of the invention having altered FcRn binding affinity comprises at least one Fc region or FcRn binding partner having one or more amino acid substitutions at an amino acid position corresponding to any one of the following EU positions: 256, 277-281, 283-288, 303-309, 313, 338, 342, 376, 381, 384, 385, 387, 434 (*e.g.,* N434A or N434K), and 438. Exemplary amino acid substitutions which altered FcRn binding activity are disclosed in International PCT Publication No. WO05/047327.

[0221] An Fc region or FcRn binding partner used in the invention may also comprise an art recognized amino acid substitution which alters the glycosylation of the chimeric protein. For example, the Fc region or FcRn binding partner of the chimeric protein linked to a VWF fragment or a FVIII protein may comprise an Fc region having a mutation leading to reduced glycosylation (*e.g.*, N- or O-linked glycosylation) or may comprise an altered glycoform of the wild-type Fc moiety (*e.g.*, a low fucose or fucose-free glycan).

[0222] In one embodiment, an unprocessed chimeric protein of the invention may comprise a genetically fused Fc region (*i.e.,* scFc region) having two or more of its constituent Ig constant region or a portion thereof independently selected from the Ig constant region or a portion thereof described herein. In one embodiment, the Fc regions of a dimeric Fc region are the same. In another embodiment, at least two of the Fc regions are different. For example, the Fc regions or FcRn binding partners of the proteins of the invention comprise the same number of amino acid residues or they may differ in length by one or more amino acid residues (*e.g.,* by about 5 amino acid residues (*e.g.,* 1, 2, 3, 4, or 5 amino acid residues), about 10 residues, about 15 residues, about 20 residues, about 30 residues, about 40 residues, or about 50 residues). In yet other embodiments, the Fc regions or FcRn binding partners of the protein of the invention may differ in sequence at one or more amino acid positions. For example, at least two of the Fc regions or FcRn binding partners may differ at about 5 amino acid positions (*e.g.,* 1, 2, 3, 4, or 5 amino acid positions), about 10 positions, about 15 positions, about 20 positions, about 30 positions, about 40 positions, or about 50 positions).

E) Linkers

[0223] The chimeric protein of the present invention further comprises one or more linkers. One type of the linkers is a cleavable linker, which can be cleaved by various proteases when administered to a subject in vivo, *e.g.,* at a site of coagulation. In one embodiment, the cleavable linker allows cleavage of moiety, *e.g.,* a VWF fragment, from the chimeric protein at the site of the coagulation cascade, thus allowing activated FVIII (FVIIIa) to have its FVIIIa activity. Another type of the linkers is a processable linker, which contains an intracellular cleavage site and thus can be cleaved by an intracellular processing enzyme in a host cell, allowing convenient expression of a polypeptide and formation of a chimeric protein.

[0224] One or more linkers can be present between any two proteins in the chimeric protein. In one instance, a chimeric protein comprises (i) a VWF fragment, (ii) an XTEN sequence, and (iii) a FVIII protein, wherein the VWF fragment is linked to the XTEN sequence by a linker, *e.g.,* a cleavable linker, and the XTEN sequence is further linked to the FVIII protein (*i.e.,* V-L-X-FVIII). In another instance, a chimeric protein comprises (i) a VWF fragment, (ii) an XTEN sequence, and (iii) a FVIII protein, wherein the VWF fragment is linked to the XTEN sequence, and the XTEN sequence is linked to the FVIII protein by a linker, *e.g.,* a cleavable linker (*i.e.,* V-X-L-FVIII).

[0225] In certain embodiments, a chimeric protein comprises (i) a VWF fragment, (ii) an XTEN sequence, (iii) a first Ig constant region or a portion thereof (*e.g.,* a first Fc region), (iv) a FVIII protein, and (v) a second Ig constant region or a portion thereof (*e.g.,* a second Fc region), wherein the VWF fragment is linked to the XTEN sequence by an optional linker, *e.g.,* a cleavable linker. The XTEN sequence can be further linked to the first Ig constant region or a portion thereof by a linker, *e.g.,* a cleavable linker. The FVIII protein (with or without an XTEN sequence) can also be linked to the second Ig constant region or a portion thereof by an optional linker, *e.g.* a cleavable linker. In certain embodiments, the chimeric protein further comprises one or more linkers, *e.g.,* processable linkers, between the first Ig constant region or a portion thereof (*e.g.,* first Fc region) and the second Ig constant region or a portion thereof (*e.g.*, second Fc region), between the VWF fragment and the second Ig

constant region or a portion thereof, or between the FVIII protein and the first Ig constant region or a portion thereof (*e.g.,* first Fc region).

[0226] In some instances, the present disclosure includes a chimeric protein comprising (i) a FVIII protein, (ii) an XTEN sequence, (iii) a first Ig constant region or a portion thereof, and (iv) a second Ig constant region or a portion thereof, wherein the first Ig constant region or a portion thereof and the second Ig constant region or a portion thereof are linked by a processable linker.

[0227] The linker useful in the present invention can comprise any organic molecule. In one embodiment, the linker comprises a polymer, *e.g.*, polyethylene glycol (PEG) or hydroxyethyl starch (HES). In another embodiment, the linker comprises an amino acids sequence. The linker can comprise at least about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 300, 400 ,500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, or 2000 amino acids. The linker can comprise 1-5 amino acids, 1-10 amino acids, 1-20 amino acids, 10-50 amino acids, 50-100 amino acids, 100-200 amino acids, 200-300 amino acids, 300-400 amino acids, 400-500 amino acids, 500-600 amino acids, 600-700 amino acids, 700-800 amino acids, 800-900 amino acids, or 900-1000 amino acids. In one embodiment, the linker comprises an XTEN sequence. Additional examples of XTEN can be used according to the present invention and are disclosed in US Patent Publication Nos. 2010/0239554 A1, 2010/0323956 A1, 2011/0046060 A1, 2011/0046061 A1, 2011/0077199 A1, or 2011/0172146 A1, or International Patent Publication Nos. WO 2010091122 A1, WO 2010144502 A2, WO 2010144508 A1, WO 2011028228 A1, WO 2011028229 A1, or WO 2011028344 A2. In another embodiment, the linker is a PAS sequence.

[0228] The linker useful in the present invention can comprise any organic molecule. In one embodiment, the linker is a polymer, *e.g.,* polyethylene glycol (PEG) or hydroxyethyl starch (HES). In another embodiment, the linker is an amino acid sequence. The linker can comprise at least about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, or 2000 amino acids. The linker can comprise 1-5 amino acids, 1-10 amino acids, 1-20 amino acids, 10-50 amino acids, 50-100 amino acids, 100-200 amino acids, 200-300 amino acids, 300-400 amino acids, 400-500 amino acids, 500-600 amino acids, 600-700 amino acids, 700-800 amino acids, 800-900 amino acids, or 900-1000 amino acids.

[0229] Examples of linkers are well known in the art. In one embodiment, the linker comprises the sequence G_n. The linker can comprise the sequence $(GA)_n$. The linker can comprise the sequence $(GGS)_n$. In other embodiments, the linker comprises $(GGGS)_n$ (SEQ ID NO: 57). In still other embodiments, the linker comprises the sequence $(GGS)_n(GGGGS)_n$ (SEQ ID NO: 58). In these instances, n may be an integer from 1-100. In other instances, n may be an integer from 1-20, *i.e.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20. Examples of linkers include, but are not limited to, GGG, SGGSGGS (SEQ ID NO: 59), GGSGGSGGSGGSGGG (SEQ ID NO: 60), GGSGGSGGGGSGGGGS (SEQ ID NO: 61), GGSGGSGGSGGSGGSGGS (SEQ ID NO: 62), or GGGGSGGGGSGGGGS (SEQ ID NO: 63). The linker does not eliminate or diminish the VWF fragment activity or the clotting activity of Factor VIII. Optionally, the linker enhances the VWF fragment activity or the clotting activity of Factor VIII protein, *e.g.*, by further diminishing the effects of steric hindrance and making the VWF fragment or Factor VIII portion more accessible to its target binding site.

[0230] In one embodiment, the linker useful for the chimeric protein is 15-25 amino acids long. In another embodiment, the linker useful for the chimeric protein is 15-20 amino acids long. In some embodiments, the linker for the chimeric protein is 10-25 amino acids long. In other embodiments, the linker for the chimeric protein is 15 amino acids long. In still other embodiments, the linker for the chimeric protein is $(GGGGS)_n$ (SEQ ID NO: 64) where G represents glycine, S represents serine and n is an integer from 1-20.

F) Cleavage Sites

[0231] The linker may also incorporate a moiety capable of being cleaved either chemically (*e.g.,* hydrolysis of an ester bond), enzymatically (*i.e.,* incorporation of a protease cleavage sequence), or photolytically (*e.g.*, a chromophore such as 3-amino-3-(2-nitrophenyl) proprionic acid (ANP)) in order to release one molecule from another.

[0232] In one embodiment, the linker is a cleavable linker. The cleavable linkers can comprise one or more cleavage sites at the N-terminus or C-terminus or both. In another embodiment, the cleavable linker consists essentially of or consists of one or more cleavable sites. In other embodiments, the cleavable linker comprises heterologous amino acid linker sequences described herein or polymers and one or more cleavable sites.

[0233] In certain embodiments, a cleavable linker comprises one or more cleavage sites that can be cleaved in a host cell (*i.e.,* intracellular processing sites). Non limiting examples of the cleavage site include RRRR (SEQ ID NO: 9), RKRRKR (SEQ ID NO: 10), and RRRRS (SEQ ID NO: 11).

[0234] In other embodiments, a cleavable linker comprises one or more cleavage sites that are cleaved by a protease after a chimeric protein comprising the cleavable linker is administered to a subject. In one embodiment, the cleavage site is cleaved by a protease selected from the group consisting of factor XIa, factor XIIa, kallikrein, factor VIIa, factor IXa, factor Xa, factor IIa (thrombin), Elastase-2, MMP-12, MMP-13, MMP-17, and MMP-20. In another embodiment, the cleavage site is selected from the group consisting of a FXIa cleavage site (*e.g.,* KLTR↓AET (SEQ ID NO: 65)), a FXIa cleavage site (e.g, DFTR↓VVG (SEQ ID NO: 66)), a FXIIa cleavage site (*e.g.*, TMTR↓IVGG (SEQ ID NO: 67)), a Kallikrein cleavage site (*e.g.*, SPFR↓STGG (SEQ ID NO: 68)), a FVIIa cleavage site (*e.g.*, LQVR↓IVGG (SEQ ID NO: 69)), a FIXa cleavage site (*e.g.,* PLGR↓IVGG (SEQ ID NO: 70)), a FXa cleavage site (*e.g.*, IEGR↓TVGG (SEQ ID NO: 71)), a FIIa (thrombin) cleavage site (e.g, LTPR↓SLLV (SEQ ID NO: 72)), a Elastase-2 cleavage site (e.g, LGPV↓SGVP (SEQ ID NO: 73)), a Granzyme-B cleavage (e.g, VAGD↓SLEE (SEQ ID NO: 74)), a MMP-12 cleavage site (*e.g.,* GPAG↓LGGA (SEQ ID NO: 75)), a MMP-13 cleavage site (*e.g.*, GPAG↓LRGA (SEQ ID NO: 76)), a MMP-17 cleavage site (*e.g.,* APLG↓LRLR (SEQ ID NO: 77)), a MMP-20 cleavage site (*e.g.*, PALP↓LVAQ (SEQ ID NO: 78)), a TEV cleavage site (*e.g.*, ENLYFQ↓G (SEQ ID NO: 79)), a Enterokinase cleavage site (*e.g.*, DDDK↓IVGG (SEQ ID NO: 80)), a Protease 3C (PRESCISSION™) cleavage site (*e.g.*, LEVLFQ↓GP (SEQ ID NO: 81)), and a Sortase A cleavage site (*e.g.*, LPKT↓GSES) (SEQ ID NO: 82). In certain embodiments, the FXIa cleavage sites include, but are not limited to, *e.g.,* TQSFNDFTR (SEQ ID NO: 83) and SVSQTSKLTR (SEQ ID NO: 84). Non-limiting exemplary thrombin cleavage sites include, *e.g.,* DFLAEGGGVR (SEQ ID NO: 85), TTKIKPR (SEQ ID NO: 86), or LVPRG (SEQ ID NO: 87), and a sequence comprising, consisting essentially of, or consisting of ALRPR (SEQ ID NO: 17) (*e.g.,* ALRPRVVGGA (SEQ ID NO: 88)).

[0235] In a specific embodiment, the cleavage site is TLDPRSFLLRNPNDKYEPFWEDEEK (SEQ ID NO: 8).

POLYNUCLEOTIDES, VECTORS, AND HOST CELLS

[0236] Also provided in the disclosure is a polynucleotide encoding (a) a VWF fragment linked to an XTEN sequence and a FVIII protein, (b) a FVIII protein linked to an XTEN sequence and Fc, or (c) a FVIII protein linked to an XTEN sequence and a VWF fragment described herein. When a chimeric protein is a single polypeptide chain (*e.g.*, F2-L2-X-V-L1-F1-FVIII, wherein FVIII comprises a FVIII protein, F1 comprises a first Ig constant region or a portion thereof, *e.g.,* a first Fc region, L1 comprises a first linker, V comprises a VWF fragment, X comprises an XTEN sequence, L2 comprises a second linker, and F2 comprises a second Ig constant region or a portion thereof, *e.g.,* a second Fc region), the invention is drawn to a single polynucleotide chain encoding the single polypeptide chain. When the chimeric protein comprises a first and a second polypeptide chains (F2-L2-X-V:FVIII-F1), the first polypeptide chain comprising a VWF fragment linked to a XTEN sequence, which is further linked to a first Ig constant region or a portion thereof (*e.g.*, a first Fc region) by a cleavable linker (*e.g.*, F2-L2-X-V) and the second polypeptide chain comprising a FVIII protein and a second Ig constant region or a portion thereof (*e.g.*, a second Fc region) (e.g, FVIII-F1), wherein the first polypeptide chain and the second polypeptide chain are associated with each other, a polynucleotide can comprise the first nucleotide sequence and the second

nucleotide sequence. In one embodiment, the first polypeptide chain and the second polypeptide chain can be encoded by a single polynucleotide chain. In another embodiment, the first polypeptide chain and the second polypeptide chain are encoded by two different polynucleotides, *i.e.,* a first nucleotide sequence and a second nucleotide sequence. In another embodiment, the first nucleotide sequence and the second nucleotide sequence are on two different polynucleotides (*e.g.*, different vectors). In certain embodiments, the present invention is directed to a set of polynucleotides comprising a first nucleotide chain and a second nucleotide chain, wherein the first nucleotide chain encodes the VWF fragment of the chimeric protein and the second nucleotide chain encodes the FVIII protein. In some embodiments, a chimeric protein comprising two polypeptide chains or three polypeptide chains can be encoded by a single polynucleotide chain, and then processed into two or three (or more) polypeptide chains. In yet other embodiments, a chimeric protein comprising these polypeptide chains can be encoded by two or three polynucleotide chains.

[0237] In other embodiments, the set of the polynucleotides further comprises an additional nucleotide chain (*e.g.,* a second nucleotide chain when the chimeric polypeptide is encoded by a single polynucleotide chain or a third nucleotide chain when the chimeric protein is encoded by two polynucleotide chains) which encodes a protein convertase. The protein convertase can be selected from the group consisting of proprotein convertase subtilisin/kexin type 5 (PCSK5 or PC5), proprotein convertase subtilisin/kexin type 7 (PCSK7 or PC5), a yeast Kex 2, proprotein convertase subtilisin/kexin type 3 (PACE or PCSK3), and two or more combinations thereof. In some embodiments, the protein convertase is PACE, PC5, or PC7. In a specific embodiment, the protein convertase is PC5 or PC7. See International Application no. PCT/US2011/043568.

[0238] As used herein, an expression vector refers to any nucleic acid construct which contains the necessary elements for the transcription and translation of an inserted coding sequence, or in the case of an RNA viral vector, the necessary elements for replication and translation, when introduced into an appropriate host cell. Expression vectors can include plasmids, phagemids, viruses, and derivatives thereof.

[0239] Expression vectors of the invention will include polynucleotides encoding the chimeric protein described herein. In one embodiment, one or more of the coding sequences for the VWF fragment and XTEN, the FVIII protein and XTEN, or both are operably linked to an expression control sequence. As used herein, two nucleic acid sequences are operably linked when they are covalently linked in such a way as to permit each component nucleic acid sequence to retain its functionality. A coding sequence and a gene expression control sequence are said to be operably linked when they are covalently linked in such a way as to place the expression or transcription and/or translation of the coding sequence under the influence or control of the gene expression control sequence. Two DNA sequences are said to be operably linked if induction of a promoter in the 5' gene expression sequence results in the transcription of the coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the coding sequence, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a gene expression sequence would be operably linked to a coding nucleic acid sequence if the gene expression sequence were capable of effecting transcription of that coding nucleic acid sequence such that the resulting transcript is translated into the desired protein or polypeptide.

[0240] A gene expression control sequence as used herein is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the coding nucleic acid to which it is operably linked. The gene expression control sequence may, for example, be a mammalian or viral promoter, such as a constitutive or inducible promoter. Constitutive mammalian promoters include, but are not limited to, the promoters for the following genes: hypoxanthine phosphoribosyl transferase (HPRT), adenosine deaminase, pyruvate kinase, beta-actin promoter, and other constitutive promoters. Exemplary viral promoters which function constitutively in eukaryotic cells include, for example, promoters from the cytomegalovirus (CMV), simian virus (*e.g.*, SV40), papilloma virus, adenovirus, human immunodeficiency virus (HIV), Rous sarcoma virus, cytomegalovirus, the long terminal repeats (LTR) of Moloney leukemia virus, and other retroviruses, and the thymidine kinase promoter of herpes simplex virus. Other constitutive promoters are known to those of ordinary skill in the art. The promoters useful as gene expression

sequences of the invention also include inducible promoters. Inducible promoters are expressed in the presence of an inducing agent. For example, the metallothionein promoter is induced to promote transcription and translation in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the art.

[0241] In general, the gene expression control sequence shall include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription and translation, respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribing sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined coding nucleic acid. The gene expression sequences optionally include enhancer sequences or upstream activator sequences as desired.

[0242] Viral vectors include, but are not limited to, nucleic acid sequences from the following viruses: retrovirus, such as Moloney murine leukemia virus, Harvey murine sarcoma virus, murine mammary tumor virus, and Rous sarcoma virus; adenovirus, adeno-associated virus; SV40-type viruses; polyomaviruses; Epstein-Barr viruses; papilloma viruses; herpes virus; vaccinia virus; polio virus; and RNA virus such as a retrovirus. One can readily employ other vectors well-known in the art. Certain viral vectors are based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the gene of interest. Non-cytopathic viruses include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA. Retroviruses have been approved for human gene therapy trials. Most useful are those retroviruses that are replication-deficient (*i.e.*, capable of directing synthesis of the desired proteins, but incapable of manufacturing an infectious particle). Such genetically altered retroviral expression vectors have general utility for the high efficiency transduction of genes *in vivo.* Standard protocols for producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell line with plasmid, production of recombinant retroviruses by the packaging cell line, collection of viral particles from tissue culture media, and infection of the target cells with viral particles) are provided in Kriegler, M., Gene Transfer and Expression, A Laboratory Manual, W.H. Freeman Co., New York (1990) and Murry, E. J., Methods in Molecular Biology, Vol. 7, Humana Press, Inc., Cliffton, N.J. (1991).

[0243] In one embodiment, the virus is an adeno-associated virus, a doublestranded DNA virus. The adeno-associated virus can be engineered to be replication-deficient and is capable of infecting a wide range of cell types and species. It further has advantages such as heat and lipid solvent stability; high transduction frequencies in cells of diverse lineages, including hematopoietic cells; and lack of superinfection inhibition thus allowing multiple series of transductions. Reportedly, the adeno-associated virus can integrate into human cellular DNA in a site-specific manner, thereby minimizing the possibility of insertional mutagenesis and variability of inserted gene expression characteristic of retroviral infection. In addition, wild-type adeno-associated virus infections have been followed in tissue culture for greater than 100 passages in the absence of selective pressure, implying that the adeno-associated virus genomic integration is a relatively stable event. The adeno-associated virus can also function in an extrachromosomal fashion.

[0244] Other vectors include plasmid vectors. Plasmid vectors have been extensively described in the art and are well-known to those of skill in the art. See, *e.g.*, Sambrook et al., Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, 1989. In the last few years, plasmid vectors have been found to be particularly advantageous for delivering genes to cells *in vivo* because of their inability to replicate within and integrate into a host genome. These plasmids, however, having a promoter compatible with the host cell, can express a peptide from a gene operably encoded within the plasmid. Some commonly used plasmids available from commercial suppliers include pBR322, pUC18, pUC19, various pcDNA plasmids, pRC/CMV, various pCMV plasmids, pSV40, and pBlueScript. Additional examples of specific plasmids include pcDNA3.1, catalog number V79020; pcDNA3.1/hygro, catalog number V87020; pcDNA4/myc-His, catalog number V86320; and pBudCE4.1, catalog number V53220, all from Invitrogen (Carlsbad, CA.). Other plasmids are well-known to those of ordinary skill in the art. Additionally, plasmids may be custom designed using standard molecular biology techniques to remove and/or add specific fragments of DNA.

[0245] In one insect expression system that may be used to produce the proteins of the invention, *Autographa californica* nuclear polyhidrosis virus (AcNPV) is used as a vector to express the foreign genes. The virus grows in *Spodoptera frugiperda* cells. A coding sequence may be cloned into non-essential regions (for example, the polyhedron gene) of the virus and placed under control of an ACNPV promoter (for example, the polyhedron promoter). Successful insertion of a coding sequence will result in inactivation of the polyhedron gene and production of non-occluded recombinant virus (*i.e.*, virus lacking the proteinaceous coat coded for by the polyhedron gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* cells in which the inserted gene is expressed. (see, *e.g.*, Smith et al. (1983) J Virol 46:584; U.S. Pat. No. 4,215,051). Further examples of this expression system may be found in Ausubel et al., eds. (1989) Current Protocols in Molecular Biology, Vol. 2, Greene Publish. Assoc. & Wiley Interscience.

[0246] Another system which can be used to express the proteins of the invention is the glutamine synthetase gene expression system, also referred to as the "GS expression system" (Lonza Biologics PLC, Berkshire UK). This expression system is described in detail in U.S. Pat. No. 5,981,216.

[0247] In mammalian host cells, a number of viral based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, a coding sequence may be ligated to an adenovirus transcription/translation control complex, *e.g.*, the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by *in vitro* or *in vivo* recombination. Insertion in a non-essential region of the viral genome (*e.g.*, region E1 or E3) will result in a recombinant virus that is viable and capable of expressing peptide in infected hosts. See, *e.g.*, Logan & Shenk (1984) Proc Natl Acad Sci USA 81:3655). Alternatively, the vaccinia 7.5 K promoter may be used. See, *e.g.*, Mackett et al. (1982) Proc Natl Acad Sci USA 79:7415; Mackett et al. (1984) J Virol 49:857; Panicali et al. (1982) Proc Natl Acad Sci USA 79:4927.

[0248] To increase efficiency of production, the polynucleotides can be designed to encode multiple units of the protein of the invention separated by enzymatic cleavage sites. The resulting polypeptide can be cleaved (*e.g.*, by treatment with the appropriate enzyme) in order to recover the polypeptide units. This can increase the yield of polypeptides driven by a single promoter. When used in appropriate viral expression systems, the translation of each polypeptide encoded by the mRNA is directed internally in the transcript; *e.g.*, by an internal ribosome entry site, IRES. Thus, the polycistronic construct directs the transcription of a single, large polycistronic mRNA which, in turn, directs the translation of multiple, individual polypeptides. This approach eliminates the production and enzymatic processing of polyproteins and may significantly increase the yield of polypeptides driven by a single promoter.

[0249] Vectors used in transformation will usually contain a selectable marker used to identify transformants. In bacterial systems, this can include an antibiotic resistance gene such as ampicillin or kanamycin. Selectable markers for use in cultured mammalian cells include genes that confer resistance to drugs, such as neomycin, hygromycin, and methotrexate. The selectable marker may be an amplifiable selectable marker. One amplifiable selectable marker is the dihydrofolate reductase (DHFR) gene. Simonsen C C et al. (1983) Proc Natl Acad Sci USA 80:2495-9. Selectable markers are reviewed by Thilly (1986) Mammalian Cell Technology, Butterworth Publishers, Stoneham, Mass., and the choice of selectable markers is well within the level of ordinary skill in the art.

[0250] Selectable markers may be introduced into the cell on a separate plasmid at the same time as the gene of interest, or they may be introduced on the same plasmid. If on the same plasmid, the selectable marker and the gene of interest may be under the control of different promoters or the same promoter, the latter arrangement producing a dicistronic message. Constructs of this type are known in the art (for example, U.S. Pat. No. 4,713,339).

[0251] The expression vectors can encode for tags that permit easy purification of the recombinantly produced protein. Examples include, but are not limited to, vector pUR278 (Ruther et al. (1983) EMBO J 2:1791), in which coding sequences for the protein to be expressed may be ligated into the vector in frame with the lac z coding region so that a tagged fusion protein is produced; pGEX vectors may be used to express proteins of the invention

with a glutathione S-transferase (GST) tag. These proteins are usually soluble and can easily be purified from cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. The vectors include cleavage sites (thrombin or Factor Xa protease or PRESCISSION PROTEASE™ (Pharmacia, Peapack, N.J.)) for easy removal of the tag after purification.

[0252] The expression vector or vectors are then transfected or co-transfected into a suitable target cell, which will express the polypeptides. Transfection techniques known in the art include, but are not limited to, calcium phosphate precipitation (Wigler et al. (1978) Cell 14:725), electroporation (Neumann et al. (1982) EMBO J 1:841), and liposome-based reagents. A variety of host-expression vector systems may be utilized to express the proteins described herein including both prokaryotic and eukaryotic cells. These include, but are not limited to, microorganisms such as bacteria (*e.g.*, *E. coli*) transformed with recombinant bacteriophage DNA or plasmid DNA expression vectors containing an appropriate coding sequence; yeast or filamentous fungi transformed with recombinant yeast or fungi expression vectors containing an appropriate coding sequence; insect cell systems infected with recombinant virus expression vectors (*e.g.*, baculovirus) containing an appropriate coding sequence; plant cell systems infected with recombinant virus expression vectors (*e.g.*, cauliflower mosaic virus or tobacco mosaic virus) or transformed with recombinant plasmid expression vectors (*e.g.*, Ti plasmid) containing an appropriate coding sequence; or animal cell systems, including mammalian cells (*e.g.*, HEK 293, CHO, Cos, HeLa, HKB11, and BHK cells).

[0253] In one embodiment, the host cell is a eukaryotic cell. As used herein, a eukaryotic cell refers to any animal or plant cell having a definitive nucleus. Eukaryotic cells of animals include cells of vertebrates, *e.g.*, mammals, and cells of invertebrates, *e.g.*, insects. Eukaryotic cells of plants specifically can include, without limitation, yeast cells. A eukaryotic cell is distinct from a prokaryotic cell, *e.g.*, bacteria.

[0254] In certain embodiments, the eukaryotic cell is a mammalian cell. A mammalian cell is any cell derived from a mammal. Mammalian cells specifically include, but are not limited to, mammalian cell lines. In one embodiment, the mammalian cell is a human cell. In another embodiment, the mammalian cell is a HEK 293 cell, which is a human embryonic kidney cell line. HEK 293 cells are available as CRL-1533 from American Type Culture Collection, Manassas, VA, and as 293-H cells, Catalog No. 11631-017 or 293-F cells, Catalog No. 11625-019 from Invitrogen (Carlsbad, Calif.). In some embodiments, the mammalian cell is a PER.C6® cell, which is a human cell line derived from retina. PER.C6® cells are available from Crucell (Leiden, The Netherlands). In other embodiments, the mammalian cell is a Chinese hamster ovary (CHO) cell. CHO cells are available from American Type Culture Collection, Manassas, VA. (*e.g.*, CHO-K1; CCL-61). In still other embodiments, the mammalian cell is a baby hamster kidney (BHK) cell. BHK cells are available from American Type Culture Collection, Manassas, Va. (*e.g.*, CRL-1632). In some embodiments, the mammalian cell is a HKB11 cell, which is a hybrid cell line of a HEK293 cell and a human B cell line. Mei et al., Mol. Biotechnol. 34(2): 165-78 (2006).

[0255] In one instance, a plasmid including a FVIII(X)-Fc fusion coding sequence, a VWF fragment-L-Fc fusion coding sequence, or both and a selectable marker, *e.g.*, zeocin resistance, are transfected into HEK 293 cells, for production of a chimeric protein.

[0256] In another embodiment, a plasmid including a FVIII-Fc fusion coding sequence, a VWF fragment-XTEN-L-Fc fusion coding sequence, or both and a selectable marker, *e.g.*, zeocin resistance, are transfected into HEK 293 cells, for production of a chimeric protein.

[0257] In other instances, a plasmid including a FVIII(X)-Fc fusion coding sequence, a Fc coding sequence, or both and a selectable marker, *e.g.*, zeocin resistance, are transfected into HEK 293 cells, for production of a chimeric protein.

[0258] In some instances, a first plasmid including a FVIII(X)-Fc fusion coding sequence and a first selectable marker, *e.g.*, a zeocin resistance gene, and a second plasmid including an Fc coding sequence or a VWF fragment-L-Fc coding sequence and a second selectable marker, *e.g.*, a neomycin resistance gene, and a third plasmid including a protein convertase coding sequence and a third selectable marker, *e.g.*, a hygromycin

resistance gene, are cotransfected into HEK 293 cells, for production of the chimeric protein. The first and second plasmids can be introduced in equal amounts (*i.e.*, 1:1 molar ratio), or they can be introduced in unequal amounts.

[0259] In still other embodiments, a first plasmid including a FVIII-Fc fusion coding sequence and a first selectable marker, *e.g.*, a zeocin resistance gene, and a second plasmid including a VWF fragment-XTEN-L-Fc coding sequence and a second selectable marker, *e.g.*, a neomycin resistance gene, and a third plasmid including a protein convertase coding sequence and a third selectable marker, *e.g.*, a hygromycin resistance gene, are cotransfected into HEK 293 cells, for production of the chimeric protein. The first and second plasmids can be introduced in equal amounts (*i.e.*, 1:1 molar ratio), or they can be introduced in unequal amounts.

[0260] In yet other embodiments, a first plasmid including a FVIII(X)-Fc fusion coding sequence and a first selectable marker, *e.g.*, a zeocin resistance gene, and a second plasmid including a VWF fragment-XTEN-L-Fc coding sequence and a second selectable marker, *e.g.*, a neomycin resistance gene, and a third plasmid including a protein convertase coding sequence and a third selectable marker, *e.g.*, a hygromycin resistance gene, are cotransfected into HEK 293 cells, for production of the chimeric protein. The first and second plasmids can be introduced in equal amounts (*i.e.*, 1:1 molar ratio), or they can be introduced in unequal amounts.

[0261] In certain embodiments, a first plasmid, including a chimeric protein encoding FVIII (with or without XTEN)-F1-L1-V-XTEN-L2-F2 coding sequence and a first selectable marker, *e.g.*, a zeocin resistance gene, and a second plasmid including a protein convertase coding sequence and a second selectable marker, *e.g.*, a hygromycin resistance gene, are cotransfected into HEK 293 cells, for production of the chimeric protein. The promoters for the FVIII(X)-Fc coding sequence and the VWF-XTEN-Fc coding sequence can be different or they can be the same.

[0262] In still other embodiments, transfected cells are stably transfected. These cells can be selected and maintained as a stable cell line, using conventional techniques known to those of skill in the art.

[0263] Host cells containing DNA constructs of the protein are grown in an appropriate growth medium. As used herein, the term "appropriate growth medium" means a medium containing nutrients required for the growth of cells. Nutrients required for cell growth may include a carbon source, a nitrogen source, essential amino acids, vitamins, minerals, and growth factors. Optionally, the media can contain one or more selection factors. Optionally the media can contain bovine calf serum or fetal calf serum (FCS). In one embodiment, the media contains substantially no IgG. The growth medium will generally select for cells containing the DNA construct by, for example, drug selection or deficiency in an essential nutrient which is complemented by the selectable marker on the DNA construct or co-transfected with the DNA construct. Cultured mammalian cells are generally grown in commercially available serum-containing or serum-free media (*e.g.*, MEM, DMEM, DMEM/F12). In one embodiment, the medium is CD293 (Invitrogen, Carlsbad, CA.). In another embodiment, the medium is CD17 (Invitrogen, Carlsbad, CA.). Selection of a medium appropriate for the particular cell line used is within the level of those ordinary skilled in the art.

[0264] In order to co-express the two polypeptide chains of the chimeric protein, the host cells are cultured under conditions that allow expression of both chains. As used herein, culturing refers to maintaining living cells *in vitro* for at least a definite time. Maintaining can, but need not include, an increase in population of living cells. For example, cells maintained in culture can be static in population, but still viable and capable of producing a desired product, *e.g.*, a recombinant protein or recombinant fusion protein. Suitable conditions for culturing eukaryotic cells are well known in the art and include appropriate selection of culture media, media supplements, temperature, pH, oxygen saturation, and the like. For commercial purposes, culturing can include the use of any of various types of scale-up systems including shaker flasks, roller bottles, hollow fiber bioreactors, stirred-tank bioreactors, airlift bioreactors, Wave bioreactors, and others.

[0265] The cell culture conditions are also selected to allow association of the VWF fragment with the FVIII protein. Conditions that allow expression of the VWF fragment and/or the FVIII protein may include the presence

of a source of vitamin K. For example, in one embodiment, stably transfected HEK 293 cells are cultured in CD293 media (Invitrogen, Carlsbad, CA) or OptiCHO media (Invitrogen, Carlsbad, CA) supplemented with **4** mM glutamine.

[0266] In one aspect, the present invention is directed to a method of expressing, making, or producing the chimeric protein of the invention comprising a) transfecting a host cell comprising a polynucleotide encoding the chimeric protein of the invention and b) culturing the host cell in a culture medium under a condition suitable for expressing the chimeric protein, wherein the chimeric protein is expressed.

[0267] In further embodiments, the protein product containing the VWF fragment linked to an XTEN sequence or the FVIII protein linked to an XTEN sequence is secreted into the media. Media is separated from the cells, concentrated, filtered, and then passed over two or three affinity columns, *e.g.*, a protein A column and one or two anion exchange columns.

[0268] In certain instances, the present disclosure relates to the chimeric protein produced by the methods described herein.

[0269] *In vitro* production allows scale-up to give large amounts of the desired altered polypeptides of the invention. Techniques for mammalian cell cultivation under tissue culture conditions are known in the art and include homogeneous suspension culture, *e.g.* in an airlift reactor or in a continuous stirrer reactor, or immobilized or entrapped cell culture, *e.g.* in hollow fibers, microcapsules, on agarose microbeads or ceramic cartridges. If necessary and/or desired, the solutions of polypeptides can be purified by the customary chromatography methods, for example gel filtration, ion-exchange chromatography, hydrophobic interaction chromatography (HIC, chromatography over DEAE-cellulose or affinity chromatography.

PHARMACEUTICAL COMPOSITION

[0270] Compositions containing the chimeric protein of the present invention may contain a suitable pharmaceutically acceptable carrier. For example, they may contain excipients and/or auxiliaries that facilitate processing of the active compounds into preparations designed for delivery to the site of action.

[0271] The pharmaceutical composition can be formulated for parenteral administration (*i.e.* intravenous, subcutaneous, or intramuscular) by bolus injection. Formulations for injection can be presented in unit dosage form, *e.g.*, in ampoules or in multidose containers with an added preservative. The compositions can take such forms as suspensions, solutions, or emulsions in oily or aqueous vehicles, and contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient can be in powder form for constitution with a suitable vehicle, *e.g.*, pyrogen free water.

[0272] Suitable formulations for parenteral administration also include aqueous solutions of the active compounds in water-soluble form, for example, water-soluble salts. In addition, suspensions of the active compounds as appropriate oily injection suspensions may be administered. Suitable lipophilic solvents or vehicles include fatty oils, for example, sesame oil, or synthetic fatty acid esters, for example, ethyl oleate or triglycerides. Aqueous injection suspensions may contain substances, which increase the viscosity of the suspension, including, for example, sodium carboxymethyl cellulose, sorbitol and dextran. Optionally, the suspension may also contain stabilizers. Liposomes also can be used to encapsulate the molecules of the invention for delivery into cells or interstitial spaces. Exemplary pharmaceutically acceptable carriers are physiologically compatible solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like. In some embodiments, the composition comprises isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride. In other embodiments, the compositions comprise pharmaceutically acceptable substances such as wetting agents or minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or effectiveness of the active ingredients.

[0273] Compositions of the invention may be in a variety of forms, including, for example, liquid (*e.g.*, injectable and infusible solutions), dispersions, suspensions, semi-solid and solid dosage forms. The preferred form depends on the mode of administration and therapeutic application.

[0274] The composition can be formulated as a solution, micro emulsion, dispersion, liposome, or other ordered structure suitable to high drug concentration. Sterile injectable solutions can be prepared by incorporating the active ingredient in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active ingredient into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution. The proper fluidity of a solution can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prolonged absorption of injectable compositions can be brought about by including in the composition an agent that delays absorption, for example, monostearate salts and gelatin.

[0275] The active ingredient can be formulated with a controlled-release formulation or device. Examples of such formulations and devices include implants, transdermal patches, and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, for example, ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for the preparation of such formulations and devices are known in the art. See *e.g.*, Sustained and Controlled Release Drug Delivery Systems, J. R. Robinson, ed., Marcel Dekker, Inc., New York, 1978.

[0276] Injectable depot formulations can be made by forming microencapsulated matrices of the drug in biodegradable polymers such as polylactide-polyglycolide. Depending on the ratio of drug to polymer, and the nature of the polymer employed, the rate of drug release can be controlled. Other exemplary biodegradable polymers are polyorthoesters and polyanhydrides. Depot injectable formulations also can be prepared by entrapping the drug in liposomes or microemulsions.

[0277] Supplementary active compounds can be incorporated into the compositions. In one embodiment, the chimeric protein of the invention is formulated with another clotting factor, or a variant, fragment, analogue, or derivative thereof. For example, the clotting factor includes, but is not limited to, factor V, factor VII, factor VIII, factor IX, factor X, factor XI, factor XII, factor XIII, prothrombin, fibrinogen, von Willebrand factor or recombinant soluble tissue factor (rsTF) or activated forms of any of the preceding. The clotting factor of hemostatic agent can also include anti-fibrinolytic drugs, *e.g.*, epsilon-aminocaproic acid, tranexamic acid.

[0278] Dosage regimens may be adjusted to provide the optimum desired response. For example, a single bolus may be administered, several divided doses may be administered over time, or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. See, *e.g.*, Remington's Pharmaceutical Sciences (Mack Pub. Co., Easton, Pa. 1980).

[0279] In addition to the active compound, the liquid dosage form may contain inert ingredients such as water, ethyl alcohol, ethyl carbonate, ethyl acetate, benzyl alcohol, benzyl benzoate, propylene glycol, 1,3-butylene glycol, dimethylformamide, oils, glycerol, tetrahydrofurfuryl alcohol, polyethylene glycols, and fatty acid esters of sorbitan.

[0280] Non-limiting examples of suitable pharmaceutical carriers are also described in Remington's Pharmaceutical Sciences by E. W. Martin. Some examples of excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol, and the like. The composition can also contain pH buffering

reagents, and wetting or emulsifying agents.

[0281] For oral administration, the pharmaceutical composition can take the form of tablets or capsules prepared by conventional means. The composition can also be prepared as a liquid for example a syrup or a suspension. The liquid can include suspending agents (*e.g.*, sorbitol syrup, cellulose derivatives or hydrogenated edible fats), emulsifying agents (lecithin or acacia), non-aqueous vehicles (*e.g.*, almond oil, oily esters, ethyl alcohol, or fractionated vegetable oils), and preservatives (*e.g.*, methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations can also include flavoring, coloring and sweetening agents. Alternatively, the composition can be presented as a dry product for constitution with water or another suitable vehicle.

[0282] For buccal administration, the composition may take the form of tablets or lozenges according to conventional protocols.

[0283] For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of a nebulized aerosol with or without excipients or in the form of an aerosol spray from a pressurized pack or nebulizer, with optionally a propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoromethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit can be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator can be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

[0284] The pharmaceutical composition can also be formulated for rectal administration as a suppository or retention enema, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides.

[0285] In one embodiment, a pharmaceutical composition comprises a chimeric protein, the polynucleotide encoding the chimeric protein, the vector comprising the polynucleotide, or the host cell comprising the vector, and a pharmaceutically acceptable carrier. The FVIII protein in a chimeric protein has extended half-life compared to wild type FVIII protein or the corresponding FVIII protein without the VWF fragment. In one embodiment, wherein the half-life of the FVIII protein is extended at least about 1.5 times, at least about 2 times, at least about 2.5 times, at least about 3 times, at least about 4 times, at least about 5 times, at least about 6 times, at least about 7 times, at least about 8 times, at least about 9 times, at least about 10 times, at least about 11 times, or at least about 12 times longer than wild type FVIII. In another embodiment, the half-life of Factor VIII is at least about 17 hours, at least about 18 hours, at least about 19 hours, at least about 20 hours, at least about 21 hours, at least about 22 hours, at least about 23 hours, at least about 24 hours, at least about 25 hours, at least about 26 hours, at least about 27 hours, at least about 28 hours, at least about 29 hours, at least about 30 hours, at least about 31 hours, at least about 32 hours, at least about 33 hours, at least about 34 hours, at least about 35 hours, at least about 36 hours, at least about 48 hours, at least about 60 hours, at least about 72 hours, at least about 84 hours, at least about 96 hours, or at least about 108 hours.

[0286] In some instances, the composition is administered by a route selected from the group consisting of topical administration, intraocular administration, parenteral administration, intrathecal administration, subdural administration and oral administration. The parenteral administration can be intravenous or subcutaneous administration.

[0287] In other instances, the composition is used to treat a bleeding disease or condition in a subject in need thereof. The bleeding disease or condition is selected from the group consisting of a bleeding coagulation disorder, hemarthrosis, muscle bleed, oral bleed, hemorrhage, hemorrhage into muscles, oral hemorrhage, trauma, trauma capitis, gastrointestinal bleeding, intracranial hemorrhage, intra-abdominal hemorrhage, intrathoracic hemorrhage, bone fracture, central nervous system bleeding, bleeding in the retropharyngeal space, bleeding in the retroperitoneal space, bleeding in the illiopsoas sheath and any combinations thereof. In still other instances, the subject is scheduled to undergo a surgery. In yet other instances, the treatment is prophylactic or on-demand.

GENE THERAPY

[0288] A chimeric protein thereof of the invention can be produced in vivo in a mammal, e.g., a human patient, using a gene therapy approach to treatment of a bleeding disease or disorder selected from the group consisting of a bleeding coagulation disorder, hemarthrosis, muscle bleed, oral bleed, hemorrhage, hemorrhage into muscles, oral hemorrhage, trauma, trauma capitis, gastrointestinal bleeding, intracranial hemorrhage, intra-abdominal hemorrhage, intrathoracic hemorrhage, bone fracture, central nervous system bleeding, bleeding in the retropharyngeal space, bleeding in the retroperitoneal space, and bleeding in the illiopsoas sheath would be therapeutically beneficial. In one instance, the bleeding disease or disorder is hemophilia. In another instance, the bleeding disease or disorder is hemophilia A. This involves administration of a suitable chimeric protein-encoding nucleic acid operably linked to suitable expression control sequences. In certain instances, these sequences are incorporated into a viral vector. Suitable viral vectors for such gene therapy include adenoviral vectors, lentiviral vectors, baculoviral vectors, Epstein Barr viral vectors, papovaviral vectors, vaccinia viral vectors, herpes simplex viral vectors, and adeno associated virus (AAV) vectors. The viral vector can be a replication-defective viral vector. In other instances, an adenoviral vector has a deletion in its E1 gene or E3 gene. When an adenoviral vector is used, the mammal may not be exposed to a nucleic acid encoding a selectable marker gene. In other instances, the sequences are incorporated into a non-viral vector known to those skilled in the art.

METHODS OF USING CHIMERIC PROTEIN

[0289] The present disclosure is directed to a method of using a chimeric protein described herein to prevent or inhibit endogenous VWF binding to a FVIII protein. The present disclosure is also directed to a method of using a chimeric protein having a FVIII protein linked to XTEN and an Ig constant region or a portion thereof.

[0290] One aspect of the present disclosure is directed to preventing or inhibiting FVIII interaction with endogenous VWF by blocking or shielding the VWF binding site on the FVIII from endogenous VWF and at the same time extending half-life of the FVIII protein using an XTEN sequence in combination with an Ig constant region or a portion thereof, which can also be a half-life extender. In one instance, the disclosure is directed to a method of constructing a FVIII protein having half-life longer than wild-type FVIII. In one instance, an XTEN sequence inhibits or prevents interaction of a FVIII protein in a chimeric protein with endogenous VWF. In another instance, an Ig constant region or a portion thereof inhibits or prevents interaction of the FVIII protein with endogenous VWF. The chimeric protein useful in the method includes any one or more chimeric protein described herein.

[0291] Another aspect of the disclosure includes a method of administering to a subject in need thereof a chimeric protein comprising a FVIII protein having half-life longer than wild-type FVIII, wherein the method comprises administering the chimeric protein described herein to the subject.

[0292] In one instance, the disclosure is directed to a method of using an XTEN sequence and an Ig constant region or a portion thereof to extend a half-life of a FVIII protein and a VWF fragment to prevent or inhibit endogenous VWF interaction with a FVIII protein. A FVIII protein linked to an XTEN sequence (*e.g.,* FVIII(X)) and then bound to or associated with a VWF fragment is shielded or protected from the clearance pathway of VWF and thus has reduced clearance compared to the FVIII protein not bound to the VWF fragment. The shielded FVIII protein thus has maximum extension of a half-life compared to a FVIII protein not bound to or associated with the XTEN sequence and the VWF fragment. In certain instances, the FVIII protein associated with or protected by a VWF fragment and linked to an XTEN sequence is not cleared by a VWF clearance receptor. In other instances, the FVIII protein associated with or protected by a VWF fragment and linked to an XTEN sequence is cleared from the system slower than the FVIII protein that is not associated with or protected by the VWF fragment and linked to the XTEN sequence.

[0293] In one aspect, the chimeric protein comprising the FVIII protein linked to an XTEN sequence or the FVIII protein bound to or associated with a VWF fragment linked to XTEN has reduced clearance from circulation as the VWF fragment does not contain a VWF clearance receptor binding site. The VWF fragment prevents or inhibits clearance of FVIII bound to or associated with the VWF fragment from the system through the VWF clearance pathway. The VWF fragments useful for the present invention can also provide at least one or more VWF-like FVIII protection properties that are provided by endogenous VWF. In certain embodiments, the VWF fragment or the XTEN sequence can also mask one or more FVIII clearance receptor binding site, thereby preventing clearance of FVIII by its own clearance pathway.

[0294] In some instances, the prevention or inhibition of a FVIII protein binding to endogenous VWF by the VWF fragment or the XTEN sequence can be *in vitro* or in vivo.

[0295] Also provided is a method of increasing the half-life of a FVIII protein comprising administering the chimeric protein described herein to a subject in need thereof. The half-life of non-activated FVIII bound to or associated with full-length VWF is about 12 to 14 hours in plasma. In VWD type 3, wherein there is almost no VWF in circulation, the half-life of FVIII is only about six hours, leading to symptoms of mild to moderate hemophilia A in such patients due to decreased concentrations of FVIII. The half-life of the FVIII protein linked to or associated with the VWF fragment or the XTEN sequence of the present invention can increase at least about 1.5 times, 1.6 times, 1.7 times, 1.8 times, 1.9 times, 2.0 times, 2.1 times, 2.2 times, 2.3 times, 2.4 times, 2.6 times, 2.7. times, 2.8 times, 2.9 times, 3.0 times, 3.1 times, 3.2 times, 3.3 times, 3.4 times, 3.5 times, 3.6 times, 3.7 times, 3.8 times, 3.9 times, or 4.0 times higher than the half-life of the non-activated FVIII bound to or associated with full-length VWF.

[0296] In one embodiment, the half-life of the FVIII protein linked to or associated with the VWF fragment or linked to an Ig constant region or a portion thereof in the chimeric protein comprising an XTEN sequence increases at least about 2 times, 2.5 times, 3.0 times, 3.5 times, 4.0 times, 4.5 times, 5.0 times, 5.5 times, 6.0 times, 7 times, 8 times, 9 times, or 10 times higher than the half-life of the non-activated FVIII bound to or associated with full-length VWF. In another embodiment, the half-life of the FVIII protein linked to or associated with the VWF fragment or an Ig constant region or a portion thereof in the chimeric protein comprising an XTEN sequence increases about 2 to about 5 times, about 3 to about 10 times, about 5 to about 15 times, about 10 to about 20 times, about 15 to about 25 times, about 20 to about 30 times, about 25 to about 35 times, about 30 to about 40 times, about 35 to about 45 times higher than the half-life of the non-activated FVIII bound to or associated with full-length VWF or wild type FVIII. In a specific embodiment, the half-life of the FVIII protein linked to or associated with the VWF fragment or linked to an Ig constant region in the chimeric protein comprising an XTEN sequence increases at least about 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 times higher than the half-life of the wild type FVIII in a FVIII and VWF double knockout mouse.

[0297] In some embodiments, the half-life of the chimeric protein comprising the VWF fragment fused to a first Ig constant region or a portion thereof, *e.g.,* a first Fc region and an XTEN sequence, and a FVIII protein linked to an XTEN sequence and a second Ig constant region or a portion thereof, *e.g.,* a second Fc region, is longer than the half-life of a FVIII associated with endogenous VWF. In other embodiments, the half-life of the chimeric protein is at least about 1.5 times, 2 times, 2.5 times, 3.5 times, 3.6 times, 3.7 times, 3.8 times, 3.9 times, 4.0 times, 4.5 times, or 5.0 times the half-life of wild type FVIII or a FVIII protein associated with endogenous VWF.

[0298] In some embodiments, as a result of the invention the half-life of the FVIII protein is extended compared to a FVIII protein without the VWF fragment or wild-type FVIII. The half-life of the chimeric protein of the invention is at least about 1.5 times, at least about 2 times, at least about 2.5 times, at least about 3 times, at least about 4 times, at least about 5 times, at least about 6 times, at least about 7 times, at least about 8 times, at least about 9 times, at least about 10 times, at least about 11 times, or at least about 12 times longer than the half-life of a FVIII protein without the VWF fragment or wild-type FVIII. In one embodiment, the half-life of FVIII is about 1.5-fold to about 20-fold, about 1.5 fold to about 15 fold, or about 1.5 fold to about 10 fold longer than the half-life of wild-type FVIII. In another embodiment, the half-life of the FVIII is extended about 2-fold to about 10-fold, about 2-fold to about 9-fold, about 2-fold to about 8-fold, about 2-fold to about 7-fold, about 2-fold to about 6-fold, about 2-fold

to about 5-fold, about 2-fold to about 4-fold, about 2-fold to about 3-fold, about 2.5-fold to about 10-fold, about 2.5-fold to about 9-fold, about 2.5-fold to about 8-fold, about 2.5-fold to about 7-fold, about 2.5-fold to about 6-fold, about 2.5-fold to about 5-fold, about 2.5-fold to about 4-fold, about 2.5-fold to about 3-fold, about 3-fold to about 10-fold, about 3-fold to about 9-fold, about 3-fold to about 8-fold, about 3-fold to about 7-fold, about 3-fold to about 6-fold, about 3-fold to about 5-fold, about 3-fold to about 4-fold, about 4-fold to about 6 fold, about 5-fold to about 7-fold, or about 6-fold to about 8 fold as compared to wild-type FVIII or a FVIII protein without the VWF fragment. In other embodiments, the half-life of the chimeric protein of the invention is at least about 17 hours, at least about 18 hours, at least about 19 hours, at least about 20 hours, at least about 21 hours, at least about 22 hours, at least about 23 hours, at least about 24 hours, at least about 25 hours, at least about 26 hours, at least about 27 hours, at least about 28 hours, at least about 29 hours, at least about 30 hours, at least about 31 hours, at least about 32 hours, at least about 33 hours, at least about 34 hours, at least about 35 hours, at least about 36 hours, at least about 48 hours, at least about 60 hours, at least about 72 hours, at least about 84 hours, at least about 96 hours, or at least about 108 hours. In still other embodiments, the half-life of the chimeric protein of the invention is about 15 hours to about two weeks, about 16 hours to about one week, about 17 hours to about one week, about 18 hours to about one week, about 19 hours to about one week, about 20 hours to about one week, about 21 hours to about one week, about 22 hours to about one week, about 23 hours to about one week, about 24 hours to about one week, about 36 hours to about one week, about 48 hours to about one week, about 60 hours to about one week, about 24 hours to about six days, about 24 hours to about five days, about 24 hours to about four days, about 24 hours to about three days, or about 24 hours to about two days.

[0299] In some instances, the average half-life of the chimeric protein of the invention per subject is about 15 hours, about 16 hours, about 17 hours, about 18 hours, about 19 hours, about 20 hours, about 21 hours, about 22 hours, about 23 hours, about 24 hours (1 day), about 25 hours, about 26 hours, about 27 hours, about 28 hours, about 29 hours, about 30 hours, about 31 hours, about 32 hours, about 33 hours, about 34 hours, about 35 hours, about 36 hours, about 40 hours, about 44 hours, about 48 hours (2 days), about 54 hours, about 60 hours, about 72 hours (3 days), about 84 hours, about 96 hours (4 days), about 108 hours, about 120 hours (5 days), about six days, about seven days (one week), about eight days, about nine days, about 10 days, about 11 days, about 12 days, about 13 days, or about 14 days.

[0300] In addition, the disclosure provides a method of treating or preventing a bleeding disease or disorder comprising administering an effective amount of a chimeric protein. In one instance, the bleeding disease or disorder is selected from the group consisting of a bleeding coagulation disorder, hemarthrosis, muscle bleed, oral bleed, hemorrhage, hemorrhage into muscles, oral hemorrhage, trauma, trauma capitis, gastrointestinal bleeding, intracranial hemorrhage, intra-abdominal hemorrhage, intrathoracic hemorrhage, bone fracture, central nervous system bleeding, bleeding in the retropharyngeal space, bleeding in the retroperitoneal space, and bleeding in the illiopsoas sheath. In a specific instance, the bleeding disease or disorder is hemophilia A.

[0301] The chimeric protein comprising an XTEN sequence and an Ig constant region or a portion thereof in combination with a VWF fragment described herein, that prevents or inhibits interaction of the FVIII protein with endogenous VWF prepared by the disclosure, has many uses as will be recognized by one skilled in the art, including, but not limited to methods of treating a subject having a hemostatic disorder and methods of treating a subject in need of a general hemostatic agent. In one instance, the disclosure relates to a method of treating a subject having a hemostatic disorder comprising administering a therapeutically effective amount of the chimeric protein.

[0302] The FVIII protein portion in the chimeric protein treats or prevents a hemostatic disorder by serving as a cofactor to Factor IX on a negatively charged phospholipid surface, thereby forming a Xase complex. The binding of activated coagulation factors to a phospholipid surface localizes this process to sites of vascular damage. On a phospholipid surface, Factor VIIIa increases the maximum velocity of Factor X activation by Factor IXa, by approximately 200,000-fold, leading to the large second burst of thrombin generation.

[0303] The chimeric protein of the disclosure can be used to treat any hemostatic disorder. The hemostatic disorders that may be treated by administration of the chimeric protein of the disclosure include, but are not

limited to, hemophilia A, as well as deficiencies or structural abnormalities relating to Factor VIII. In one instance, the hemostatic disorder is hemophilia A.

[0304] The chimeric protein of the disclosure can be used prophylactically to treat a subject with a hemostatic disorder. The chimeric protein of the disclosure can be used to treat an acute bleeding episode in a subject with a hemostatic disorder. In another instance, the hemostatic disorder can be the result of a defective clotting factor, *e.g.*, von Willebrand's factor. In one instance, the hemostatic disorder is an inherited disorder. In another instance, the hemostatic disorder is an acquired disorder. The acquired disorder can result from an underlying secondary disease or condition. The unrelated condition can be, as an example, but not as a limitation, cancer, an auto-immune disease, or pregnancy. The acquired disorder can result from old age or from medication to treat an underlying secondary disorder (*e.g.* cancer chemotherapy).

[0305] The disclosure also relates to methods of treating a subject that does not have a congenital hemostatic disorder, but has a secondary disease or condition resulting in acquisition of a hemostatic disorder, *e.g.*, due to development of an anti-FVIII antibody or a surgery. The disclosure thus relates to a method of treating a subject in need of a general hemostatic agent comprising administering a therapeutically effective amount of the chimeric protein prepared by the present methods.

[0306] The present disclosure is also related to methods of reducing immunogenicity of FVIII or inducing less immunogenicity against FVIII comprising administering an effective amount of the chimeric proteins described herein, or the polynucleotides encoding the same.

[0307] In one instance, the subject in need of a general hemostatic agent is undergoing, or is about to undergo, surgery. The chimeric protein of the disclosure can be administered prior to, during, or after surgery as a prophylactic regimen. The chimeric protein of the disclosure can be administered prior to, during, or after surgery to control an acute bleeding episode..

[0308] The chimeric protein of the disclosure can be used to treat a subject having an acute bleeding episode who does not have a hemostatic disorder. The acute bleeding episode can result from severe trauma, *e.g.,* surgery, an automobile accident, wound, laceration gun shot, or any other traumatic event resulting in uncontrolled bleeding. Non limiting examples of bleeding episodes include a bleeding coagulation disorder, hemarthrosis, muscle bleed, oral bleed, hemorrhage, hemorrhage into muscles, oral hemorrhage, trauma, trauma capitis, gastrointestinal bleeding, intracranial hemorrhage, intra-abdominal hemorrhage, intrathoracic hemorrhage, bone fracture, central nervous system bleeding, bleeding in the retropharyngeal space, bleeding in the retroperitoneal space, bleeding in the illiopsoas sheath, and any combinations thereof.

[0309] In prophylactic applications, one or more compositions containing the chimeric protein of the disclosure or a cocktail thereof are administered to a patient not already in the disease state to enhance the patient's resistance or reduce symptoms associated with a disease or disorder. Such an amount is defined to be a "prophylactic effective dose." In therapeutic applications, a relatively high dosage (*e.g.*, from about 1 to 400 mg/kg of polypeptide per dose, with dosages of from 5 to 25 mg being more commonly used for radioimmuno conjugates and higher doses for cytotoxin-drug modified polypeptides) at relatively short intervals is sometimes required until progression of the disease is reduced or terminated, and until the patient shows partial or complete amelioration of symptoms of disease. Thereafter, the patient can be administered a prophylactic regime.

[0310] In some instance, a chimeric protein or a composition of the disclosure is used for on-demand treatment, which includes treatment for a bleeding episode, hemarthrosis, muscle bleed, oral bleed, hemorrhage, hemorrhage into muscles, oral hemorrhage, trauma, trauma capitis (head trauma), gastrointestinal bleeding, intracranial hemorrhage, intra-abdominal hemorrhage, intrathoracic hemorrhage, bone fracture, central nervous system bleeding, bleeding in the retropharyngeal space, bleeding in the retroperitoneal space, or bleeding in the illiopsoas sheath. The subject may be in need of surgical prophylaxis, peri-operative management, or treatment for surgery. Such surgeries include, *e.g.,* minor surgery, major surgery, tooth extraction, tonsillectomy, inguinal herniotomy, synovectomy, total knee replacement, craniotomy, osteosynthesis, trauma surgery, intracranial

surgery, intra-abdominal surgery, intrathoracic surgery, or joint replacement surgery.

[0311] In one instance, the chimeric protein of the present disclosure is administered intravenously, subcutaneously, intramuscularly, or via any mucosal surface, *e.g.*, orally, sublingually, buccally, nasally, rectally, vaginally or via pulmonary route. The chimeric protein comprising a VWF fragment and a FVIII protein of the present disclosure can be implanted within or linked to a biopolymer solid support that allows for the slow release of the chimeric protein to the site of bleeding or implanted into bandage/dressing. The dose of the chimeric protein will vary depending on the subject and upon the particular route of administration used. Dosages can range from 0.1 to 100,000 µg/kg body weight. In one instance, the dosing range is 0.1-1,000 µg/kg. In another instance, the dosing range is 0.1-500 µg/kg. The protein can be administered continuously or at specific timed intervals. *In vitro* assays may be employed to determine optimal dose ranges and/or schedules for administration. *In vitro* assays that measure clotting factor activity are known in the art, e.g., STA-CLOT VIIa-rTF clotting assay or ROTEM clotting assay. Additionally, effective doses may be extrapolated from dose-response curves obtained from animal models, *e.g.*, a hemophiliac dog (Mount et al. 2002, Blood 99(8):2670).

[0312] Having now described the present invention in detail, the same will be more clearly understood by reference to the following examples, which are included herewith for purposes of illustration only and are not intended to be limiting of the invention.

Examples

[0313] Throughout the examples, the following materials and methods were used unless otherwise stated.

Materials and Methods

[0314] In general, the practice of the present invention employs, unless otherwise indicated, conventional techniques of chemistry, biophysics, molecular biology, recombinant DNA technology, immunology (especially, *e.g.*, antibody technology), and standard techniques in electrophoresis. See, *e.g.*, Sambrook, Fritsch and Maniatis, Molecular Cloning: Cold Spring Harbor Laboratory Press (1989); Antibody Engineering Protocols (Methods in Molecular Biology), 510, Paul, S., Humana Pr (1996); Antibody Engineering: A Practical Approach (Practical Approach Series, 169), McCafferty, Ed., Irl Pr (1996); Antibodies: A Laboratory Manual, Harlow et al., CS.H.L. Press, Pub. (1999); and Current Protocols in Molecular Biology, eds. Ausubel et al., John Wiley & Sons (1992). Example 1: Cloning different VWF domains (Figure 1)

(a) Cloning of pSYN-VWF-002

[0315] pSYN-VWF-002 contains nucleotide sequences encoding a VWF fragment, which are amino acids 1-477 of SEQ ID NO: 100. [VWF-D'D3 protein sequence] Amino acid numbering represents the mature VWF sequence without propeptide and corresponds to amino acids 764-1240 of SEQ ID NO: 2. pSYN-VWF-002 construct has the FVIII signal peptide at N-terminus, which allows proper secretion of the synthesized protein and followed by a 6xHis tag at C-terminus, which is used for protein purification. It was synthesized by using following primer combinations:

ESC48- Fwd - VWF-D'D3 with VIII signal and BsiW1 site
TCGCGACGTACGGCCGCCACCATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGT

GCCTTTTGCGATTCTGCTTTAGCCTATCCTGTCGGCCCCCCATG (SEQ ID NO: 90)

ESC51- Rev- VWF D'D3 (1-477 amino acid) with 6His and Not 1 site
TGACCTCGAGCGGCCGCTCAGTGGTGATGGTGATGATGCGGCTCCTGGCAGGCTT

CACAGGTGAGGTTGACAAC (SEQ ID NO: 91)

[0316] A 50 µl PCR reaction was carried out with ESC 48/ESC 51 primer combinations and full length VWF plasmid as the template, using the 2 step PCR amplification cycle: 94 °C 2minutes; 21 cycles of (96 °C 30 seconds, 68 °C 2 minute). The 1460bp band was gel purified with a Gel Extraction kit (Qiagen, Valencia, Calif.) and cloned into the BsiWI and Not1 restriction sites of pcDNA 4 to generate pSYN-VWF 002.

(b) Cloning of pSYN-VWF- 010 and 013

[0317] pSYN-VWF-010 was constructed using pSYN-VWF-008 and pSYN-VWF-002. pSYN-VWF-008 contains the full-length VWF sequence in pcDNA 3.1 (amino acids 1-2813 of SEQ ID NO: 2), it includes 763 amino acid propeptide (*i.e.*, D1D2 domains) followed by remaining 2050 amino acids sequence of mature VWF. The FVIII signal peptide in pSYN-VWF-002 was replaced with D1D2 domains from pSYN-VWF-008, the resulting construct is pSYN-VWF-010. pSYN-VWF- 008 has a BamH1 site at Arg907 and Not1 site at the end of coding region (after stop codon). pSYN- VWF- 008 and 002 were digested with BamH1 and Not1 restriction enzymes. Inserts from pSYN- VWF-002 (1026 bp) were ligated into bamH1/Not1 digested pSYN-VWF- 008 (8242bp) to obtain pSYN-VWF -010 (D1D2D'D3: amino acid 1-1240 of SEQ ID NO: 2), a 6xHis tag was also added at the C-terminus. In transformed cells pSYN-VWF-010 is synthesized with propeptide but due to intracellular processing the secreted products do not contain any propeptide (D1D2). Protein from VWF-010 exists as dimer.

[0318] pSYN-VWF-010 was used to generate pSYN-VWF-013 which has two point mutations at C336A and C379A corresponding to SEQ ID NO: 100 (amino acid numbering represents mature VWF sequence without D1D2 domain-VWF sequence 2). These mutations are predicted to prevent dimerization of VWF D'D3 domain.

(c) Cloning of pSYN-VWF-025 and pSYN-VWF-029

[0319] pSYN-VWF-025 contains wild type D1D2D'D3 sequences of full-length VWF in pLIVE vector, and pSYN-VWF-029 contains D1D2D'D3 sequence with C336A and C379A mutation. For cloning pSYN-VWF-025, the following primer combination was used:

ESC 89-fwd with Nhelsite= CTCACTATAGGGAGACCCAAGCTGGCTAGCCG (SEQ ID NO: 92)

ESC 91-rev with Sal1= CTGGATCCCGGGAGTCGACTCGTCAGTGGTGATGGTGATGATG (SEQ ID NO: 93)

[0320] A 50 µl PCR reaction was carried out with ESC 89/ESC91 primer combinations and either pSYN-VWF 010 (for pSYN-VWF-025) or pSYN-VWF 013 (for pSYN-VWF-029) plasmid as the template using the 3 step PCR amplification cycle: 94 °C 2minutes; 21 cycles of (96 °C -30 seconds, 55 °C-30 second, 68 °C-4 minutes). The expected sized band (~3800bp) was gel purified with a Gel Extraction kit (Qiagen, Valencia, Calif.) and cloned into the Nheland Sal1 restriction sites of pLIVE-Mirus vector (Invitrogen, Carlsbad, Calif.) to generate pSYN-VWF 025 and 029.

(d) Cloning pSYN-VWF-031

[0321] pSYN-VWF-031 is a D1D2D'D3(C336A/C379A) -Fc construct which has a 48 amino acid long thrombin cleavable linker (8x GGGGS (SEQ ID NO 94) + thrombin site) in between the VWF D1D2D'D3(C336A/C379A) and the Fc sequences. To make this construct, VWF-Fc region was amplified from construct pSYN-FVIII-064 (refer

FVIII-VWF construct below). pSYN-FVIII-VWF was digested with Xba1 and Nhe1. Resulting insert region of 4165bp, containing the VWF fragment and Fc region was used as a template for amplifying the VWF and Fc region by primer combinations LW 22/LW23.

LW 22-FWD-VWF-D'D3 with FVIII signal sequence and BsiW1 site
GCGCCGGCCGTACGATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTT
GCGATTCTGCTTTAGCCTATCCTGTCGGCCCCCCATG (SEQ ID NO: 95)

LW 23-Rev- Fc with stop codon and Not1 site
TCATCAATGTATCTTATCATGTCTGAATTCGCGGCCGCTCATTTACC (SEQ ID NO:96)

[0322] The PCR product obtained from LW22/LW23 amplification (~2300bp) was cloned in BsiW1/Not1 digested pSYN-VWF-002 to obtain pSYN-VWF-014 intermediate. pSYN-VWF-014 contains FVIII signal peptide-D'D3-20 amino acid thrombin cleavable linker followed by the Fc region.

[0323] To generate the D1D2D'D3-Fc construct, the D1D2D'D3 region was amplified from pSYN-VWF-013 using primer combination LW24/LW27 by standard PCR method.

LW24- Fwd- VWF D1D2D'D3 cloning oligo with BsiW1 site
GCGCCGGCCGTACGATGATTCCTGCCAGATTTGCCGGGGTG (SEQ ID NO:97)

LW27-Rev-VWF D'D3 oligo with EcoRV CCACCGCCAGATATCGGCTCCTGGCAGGCTTCACAGGTGAG (SEQ ID NO:98)

[0324] The PCR product obtained from LW22/LW23 amplification (~3750bp) was cloned in BsiW1/EcoRV digested pSYN-VWF-014 to obtain pSYN-VWF-015 intermediate. The linker length between the VWF fragment and Fc region was changed to obtain pSYN-VWF-031.

[0325] VWF-D1D2D'D3 protein sequence 1 (SEQ ID NO: 99)

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      1  MIPARFAGVL LALALILPGT LCAEGTRGRS STARCSLFGS
DFVNTFDGSM
     51  YSFAGYCSYL LAGGCQKRSF SIIGDFQNGK RVSLSVYLGE
      FFDIHLFVNG
    101  TVTQGDQRVS MPYASKGLYL ETEAGYYKLS GEAYGFVARI
      DGSGNFQVLL
    151  SDRYFNKTCG LCGNFNIFAE DDFMTQEGTL TSDPYDFANS
      WALSSGEQWC
    201  ERASPPSSSC NISSGEMQKG LWEQCQLLKS TSVFARCHPL
      VDPEPFVALC
    251  EKTLCECAGG LECACPALLE YARTCAQEGM VLYGWTDHSA
      CSPVCPAGME
    301  YRQCVSPCAR TCQSLHINEM CQERCVDGCS CPEGQLLDEG
      LCVESTECPC
    351  VHSGKRYPPG TSLSRDCNTC ICRNSQWICS NEECPGECLV
      TGQSHFKSFD
    401  NRYFTFSGIC QYLLARDCQD HSFSIVIETV QCADDRDAVC
      TRSVTVRLPG
    451  LHNSLVKLKH GAGVAMDGQD IQLPLLKGDL RIQHTVTASV
      RLSYGEDLQM
    501  DWDGRGRLLV KLSPVYAGKT CGLCGNYNGN QGDDFLTPSG
      LAEPRVEDFG
    551  NAWKLHGDCQ DLQKQHSDPC ALNPRMTRFS EEACAVLTSP
      TFEACHRAVS
    601  PLPYLRNCRY DVCSCSDGRE CLCGALASYA AACAGRGVRV
      AWREPGRCEL
    651  NCPKGQVYLQ CGTPCNLTCR SLSYPDEECN EACLEGCFCP
      PGLYMDERGD
    701  CVPKAQCPCY YDGEIFQPED IFSDHHTMCY CEDGFMHCTM
      SGVPGSLLPD
    751  AVLSSPLSHR SKRSLSCRPP MVKLVCPADN LRAEGLECTK
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      TCQNYDLECM
      801  SMGCVSGCLC PPGMVRHENR CVALERCPCF HQGKEYAPGE
      TVKIGCNTCV
      851  CRDRKWNCTD HVCDATCSTI GMAHYLTFDG LKYLFPGECQ
      YVLVQDYCGS
      901  NPGTFRILVG NKGCSHPSVK CKKRVTILVE GGEIELFDGE
      VNVKRPMKDE

  951  THFEVVESGR YIILLLGKAL SVVWDRHLSI SVVLKQTYQE
    KVCGLCGNFD
 1001  GIQNNDLTSS NLQVEEDPVD FGNSWKVSSQ CADTRKVPLD
    SSPATCHNNI
 1051  MKQTMVDSSC RILTSDVFQD CNKLVDPEPY LDVCIYDTCS
    CESIGDCACF
 1101  CDTIAAYAHV CAQHGKVVTW RTATLCPQSC EERNLRENGY
    ECEWRYNSCA
 1151  PACQVTCQHP EPLACPVQCV EGCHAHCPPG KILDELLQTC
    VDPEDCPVCE
 1201  VAGRRFASGK KVTLNPSDPE HCQICHCDVV NLTCEACQEP*
    VWF-D'D3 protein sequence 2  (SEQ ID NO: 100)
    1  SLSCRPPMVK LVCPADNLRA EGLECTKTCQ NYDLECMSMG
    CVSGCLCPPG
   51  MVRHENRCVA LERCPCFHQG KEYAPGETVK IGCNTCVCRD
    RKWNCTDHVC
  101  DATCSTIGMA HYLTFDGLKY LFPGECQYVL VQDYCGSNPG
    TFRILVGNKG
  151  CSHPSVKCKK RVTILVEGGE IELFDGEVNV KRPMKDETHF
    EVVESGRYII
  201  LLLGKALSVV WDRHLSISVV LKQTYQEKVC GLCGNFDGIQ
    NNDLTSSNLQ
  251  VEEDPVDFGN SWKVSSQCAD TRKVPLDSSP ATCHNNIMKQ
    TMVDSSCRIL
  301  TSDVFQDCNK LVDPEPYLDV CIYDTCSCES IGDCACFCDT
    IAAYAHVCAQ
  351  HGKVVTWRTA TLCPQSCEER NLRENGYECE WRYNSCAPAC
    QVTCQHPEPL
  401  ACPVQCVEGC HAHCPPGKIL DELLQTCVDP EDCPVCEVAG
    RRFASGKKVT
  451  LNPSDPEHCQ ICHCDVVNLT CEACQEP
```

Example 2: Effects of D'D3 and XTEN fusion on FVIII half-life extension

[0326] To evaluate D'D3 FVIII half-life extension potential on rFVIII-XTEN fusion protein, a VWF D'D3 dimer was introduced into FVIII-VWF DKO mice by hydrodynamic injection of its corresponding DNA construct VWF-025 (Example 1). After D'D3 has reached the steady state expression (day5 post injection), a single dose of rFVIII-XTEN was administered by IV injection at 200 IU/kg dose. Blood samples were collected up to 120hrs post rFVIII-XTEN dosing. Plasma FVIII activity was analyzed by a FVIII chromogenic assay. The D'D3 expression level was measured by VWF ELISA, and rFVIIIFc PK profile was analyzed using WinNonlin program.

[0327] The study results were shown in Figure 2, and the PK parameter of rFVIII-XTEN with/without D'D3 in circulation was listed in Table 16. The D'D3 dimer further extended rFIII-XTEN $t_{1/2}$ from 3.4hr to 17.8hr, a 5 fold increase. In addition to half-life, 5 fold of increase on MRT, 3.6 fold increases on AUC, 3.8 fold decreases on clearance were also observed.

[0328] We have observed a synergistic effect of D'D3 fragment and XTEN technology, a serial of FVIII/VWF/XTEN constructs will be evaluated for their FVIII half-life extension potential in Hemophilic animals.

TABLE 16: rFVIII-XTEN PK parameter with/without D'D3 in blood circulation

Treatment	5min Recovery (%)	$t_{1/2}$ (hr)	MRT (hr)	Cl (mL/hr/kg)	Vss (mL/kg)	AUC_D (hr*kg*mIU /mL/mIU)
rFVIIIXTE N VWF-025	80	17.8	19.3	3.5	67.4	0.29
rFVIIIXTE N	74	3.4	3.8	13.1	63.68	0.08
Improveme nt fold	1.1	5.2	5.1	3.8	0.9	3.6

Protein purification of FVIII-XTEN

[0329] An AE288 XTEN was inserted at the C-terminus of BDD-FVIII for this study. To purify this protein, a tangential flow filtration (TFF) step was used first to buffer exchange the conditioned media. Products in the filtrate were then captured using a strong anion exchange chromatography, and then further purified using affinity chromatography. Purity of the molecule was acceptable by HPLC-SEC and was further confirmed by western blotting. The specific activity of the molecule was comparable to B-domain deleted FVIII, as measured by aPTT assay and ELISA.

FVIII chromogenic assay

[0330] The FVIII activity was measured using the COATEST SP FVIII kit from DiaPharma (lot# N089019) and all incubations were performed on a 37°C plate heater with shaking.

[0331] The range of rFVIII standard was from 100 mIU/mL to 0.78 mIU/mL. A pooled normal human plasma assay control and plasma samples (diluted with IX Coatest buffer) were added into Immulon 2HB 96-well plates in duplicate (25 µL/well). Freshly prepared IXa/FX/Phospholipid mix (50 µL), 25 µL of 25mM CaCl2, and 50 µL of FXa substrate were added sequentially into each well with 5 minutes incubation between each addition. After incubating with the substrate, 25 µL of 20% Acetic Acid was added to terminate the color reaction, and the absorbance of OD405 was measured with a SpectraMAX plus (Molecular Devices) instrument. Data were analyzed with SoftMax Pro software (version 5.2). The Lowest Level of Quantification (LLOQ) is 7.8 mIU/mL. VWF ELISA:

[0332] Goat anti-human VWF antibody (Affinity purified, affinity biological, GAVWF-AP) was used as the capture antibody at 0.5ug/well and VWF-EIA-D (Affinity Biologicals, VWF-EIA-D, 1:100 dilution) was used as the detecting antibody for the VWF ELISA. ELISA assay was performed following the standard ELISA procedure, TMB was used as the HRP substrate, PBST/1.5% BSA/0.5M NaCl buffer was used as blocking and binding buffer. The assay standard range is 100ng to 0.78ng, and assay's lowest limit of quantification (LLOQ) is 7.8ng/mL.

Example 3: Plasmid construction of XTEN containing FVIII/VWF constructs

(a) Cloning of pSYN-FVIII-161 (Figure 3)

[0333] The FVIII-161 plasmid comprises a single chain Fc (scFc) scaffold with enzyme cleavage sites which are processed during synthesis in a cell. The construct has a FVIII binding domain of full-length VWF (D'D3).

[0334] Plasmid (pSYN-FVIII-161) was designed for the expression FVIII-Fc and VWF-Fc heterodimer, where the D'D3 domains to bind FVIII and prevents FVIII interaction with phospholipids and activated protein C. Protein from pSYN-FVIII-161 is expressed in the cell as a single polypeptide where the C-terminus of the FVIII-Fc subunit is

linked to the N-terminus of the VWF D'D3-Fc subunit by a 6x (GGGGS) polypeptide linker (SEQ ID NO: 64). In addition, RRRRS (SEQ ID NO: 11) and RKRRKR (SEQ ID NO: 10) sequences were inserted at the 5' and 3' end of the polypeptide linker, respectively, for intracellular cleavage by proprotein convertases following the last Arg at each sequence. Hence, the cells can express a double chain FVIII-Fc/D'D3-Fc heterodimer where the FVIII-Fc chain has a RRRRS sequence (SEQ ID NO: 11) at the C-terminus, but the remainder of the linker sequence has been removed. An AE288 XTEN fragment immediately followed by IS{5X(GGGGS)}LVPRGSGG (SEQ ID NO: 122) polypeptide (contains thrombin cleavage site) is introduced in between the VWF domains and the Fc region to facilitate release of the VWF fragment from FVIII once the FVIII-VWF hetero-dimeric protein is activated by thrombin allowing interaction of FVIII with other clotting factors.

[0335] pSYN-FVIII-161 (SEQ ID NO: 101).protein sequence (FVIII sequence amino acid position 1-1457; underlined region represents Fc region; curvy underline represents cleavable linker in between first Fc and VWF fragment; double underlined region represents VWF fragment; bold region represents cleavable linker in between VWF fragment and Fc.

```
  1  MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQSDL
 GELPVDARFP
 51  PRVPKSFPFN TSVVYKKTLF VEFTDHLFNI AKPRPPWMGL
 LGPTIQAEVY
101  DTVVITLKNM ASHPVSLHAV GVSYWKASEG AEYDDQTSQR
 EKEDDKVFPG
151  GSHTYVWQVL KENGPMASDP LCLTYSYLSH VDLVKDLNSG
 LIGALLVCRE
201  GSLAKEKTQT LHKFILLFAV FDEGKSWHSE TKNSLMQDRD
 AASARAWPKM
251  HTVNGYVNRS LPGLIGCHRK SVYWHVIGMG TTPEVHSIFL
 EGHTFLVRNH
301  RQASLEISPI TFLTAQTLLM DLGQFLLFCH ISSHQHDGME
 AYVKVDSCPE
351  EPQLRMKNNE EAEDYDDDLT DSEMDVVRFD DDNSPSFIQI
 RSVAKKHPKT
401  WVHYIAAEEE DWDYAPLVLA PDDRSYKSQY LNNGPQRIGR
 KYKKVRFMAY
451  TDETFKTREA IQHESGILGP LLYGEVGDTL LIIFKNQASR
 PYNIYPHGIT
501  DVRPLYSRRL PKGVKHLKDF PILPGEIFKY KWTVTVEDGP
 TKSDPRCLTR
551  YYSSFVNMER DLASGLIGPL LICYKESVDQ RGNQIMSDKR
 NVILFSVFDE
601  NRSWYLTENI QRFLPNPAGV QLEDPEFQAS NIMHSINGYV
 FDSLQLSVCL
651  HEVAYWYILS IGAQTDFLSV FFSGYTFKHK MVYEDTLTLF
 PFSGETVFMS
701  MENPGLWILG CHNSDFRNRG MTALLKVSSC DKNTGDYYED
 SYEDISAYLL
751  SKNNAIEPRS FSQNPPVLKR HQREITRTTL QSDQEEIDYD
 DTISVEMKKE
801  DFDIYDEDEN QSPRSFQKKT RHYFIAAVER LWDYGMSSSP
 HVLRNRAQSG
851  SVPQFKKVVF QEFTDGSFTQ PLYRGELNEH LGLLGPYIRA
 EVEDNIMVTF
901  RNQASRPYSF YSSLISYEED QRQGAEPRKN FVKPNETKTY
 FWKVQHHMAP

951  TKDEFDCKAW AYFSDVDLEK DVHSGLIGPL LVCHTNTLNP
  AHGRQVTVQE
1001  FALFFTIFDE TKSWYFTENM ERNCRAPCNI QMEDPTFKEN
  YRFHAINGYI
1051  MDTLPGLVMA QDQRIRWYLL SMGSNENIHS IHFSGHVFTV
  RKKEEYKMAL
1101  YNLYPGVFET VEMLPSKAGI WRVECLIGEH LHAGMSTLFL
  VYSNKCQTPL
1151  GMASGHIRDF QITASGQYGQ WAPKLARLHY SGSINAWSTK
  EPFSWIKVDL
1201  LAPMIIHGIK TQGARQKFSS LYISQFIIMY SLDGKKWQTY
  RGNSTGTLMV
1251  FFGNVDSSGI KHNIFNPPII ARYIRLHPTH YSIRSTLRME
  LMGCDLNSCS
```

1301 MPLGMESKAI SDAQITASSY FTNMFATWSP SKARLHLQGR
SNAWRPQVNN
1351 PKEWLQVDFQ KTMKVTGVTT QGVKSLLTSM YVKEFLISSS
QDGHQWTLFF
1401 QNGKVKVFQG NQDSFTPVVN SLDPPLLTRY LRIHPQSWVH
QIALRMEVLG
1451 CEAQDLYDKT HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI
SRTPEVTCVV
1501 VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV
SVLTVLHQDW
1551 LNGKEYKCKV SNKALPAPIE KTISKAKGQP REPQVYTLPP
SRDELTKNQV
1601 SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS
FFLYSKLTVD
1651 KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGKRRRRSG
GGGSGGGGSG
1701 GGGSGGGGSG GGGSGGGGSR KRRKRSLSCR PPMVKLVCPA
DNLRAEGLEC
1751 TKTCQNYDLE CMSMGCVSGC LCPPGMVRHE NRCVALERCP
CFHQGKEYAP
1801 GETVKIGCNT CVCRDRKWNC TDHVCDATCS TIGMAHYLTF
DGLKYLFPGE
1851 CQYVLVQDYC GSNPGTFRIL VGNKGCSHPS VKCKKRVTIL
VEGGEIELFD
1901 GEVNVKRPMK DETHFEVVES GRYIILLLGK ALSVVWDRHL
SISVVLKQTY
1951 QEKVCGLCGN FDGIQNNDLT SSNLQVEEDP VDFGNSWKVS
SQCADTRKVP
2001 LDSSPATCHN NIMKQTMVDS SCRILTSDVF QDCNKLVDPE
PYLDVCIYDT
2051 CSCESIGDCA AFCDTIAAYA HVCAQHGKVV TWRTATLCPQ
SCEERNLREN
2101 GYEAEWRYNS CAPACQVTCQ HPEPLACPVQ CVEGCHAHCP
PGKILDELLQ
2151 TCVDPEDCPV CEVAGRRFAS GKKVTLNPSD PEHCQICHCD
VVNLTCEACQ

2201 **EPISGTSESA TPESGPGSEP ATSGSETPGT SESATPESGP GSEPATSGSE**
2251 **TPGTSESATP ESGPGTSTEP SEGSAPGSPA GSPTSTEEGT SESATPESGP**
2301 **GSEPATSGSE TPGTSESATP ESGPGSPAGS PTSTEEGSPA GSPTSTEEGT**
2351 **STEPSEGSAP GTSESATPES GPGTSESATP ESGPGTSESA TPESGPGSEP**
2401 **ATSGSETPGS EPATSGSETP GSPAGSPTST EEGTSTEPSE GSAPGTSTEP**
2451 **SEGSAPGSEP ATSGSETPGT SESATPESGP GTSTEPSEGS APDSGGGGSG**
2501 **GGGSGGGGSG GGGSGGGGSL VPRGSGG**DKT HTCPPCPAPE LLGGPSVFLF
2551 PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE
2601 EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP
2651 REPQVYTLPP SRDELTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT
2701 TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL
2751 SPGK

(b) Cloning of_pSYN-FVIII-168, 175, 172 and 174 (Figure 4A-4D)

[0336] pSYN-FVIII-168, 172, 174 and 175 are derivatives of pSYN-FVIII-161. R1645A/R1648A mutations were introduced into pSYN-FVIII-161 to form pSYN-FVIII-168, which produces a SC-FVIII isoform, and an AE288 XTEN was directly fused into the C-terminus of FVIII-HC for further half-life extension. To construct pSYN-FVIII-175, the

D'D3 codon sequence was remove form pSYN-FVIII-168 for evaluation of the effect of Fc and XTEN technology on FVIII half-life extension.

[0337] To construct pSYN-FVIII-172, the AE288 XTEN fragment was directly fused into the C-terminus of FVIII-HC for further half-life extension, and the D'D3 codon sequence was removed from pSYN-FVIII-172 to form pSYN-FVIII-174 for evaluation of the effect of Fc and XTEN technology on FVIII half-life extension.

(c) Cloning of pSYN-FVIII-170 (Figure 4E)

[0338] pSYN-FVIII-170 was constructed to evaluate the effect of XTEN and D'D3 fragment on FVIII half-life extension. The codon sequence VWF-D1D2D'D3 fragment and BDD-FVIII were introduced into the 5' and 3' end of expression casket, an AE288 XTEN codon sequence which followed by a 35 aa thrombin cleavable linker was used to connect the VWF and FVIII molecule. After intra cellular processing, the secreted protein comprises a polypeptide contains the D'D3 fragment of mature VWF molecule which is linked to the N-terminus of mature BDD-FVIII by an AE288 XTEN/35 aa thrombin cleavable linker.

pSYN-FVIII-170 protein sequence (SEQ ID NO: 102)

```
   1  SLSCRPPMVK LVCPADNLRA EGLECTKTCQ NYDLECMSMG
  CVSGCLCPPG
  51  MVRHENRCVA LERCPCFHQG KEYAPGETVK IGCNTCVCRD
  RKWNCTDHVC
 101  DATCSTIGMA HYLTFDGLKY LFPGECQYVL VQDYCGSNPG
  TFRILVGNKG
 151  CSHPSVKCKK RVTILVEGGE IELFDGEVNV KRPMKDETHF
  EVVESGRYII
 201  LLLGKALSVV WDRHLSISVV LKQTYQEKVC GLCGNFDGIQ
  NNDLTSSNLQ
 251  VEEDPVDFGN SWKVSSQCAD TRKVPLDSSP ATCHNNIMKQ
  TMVDSSCRIL
 301  TSDVFQDCNK LVDPEPYLDV CIYDTCSCES IGDCAAFCDT
  IAAYAHVCAQ
 351  HGKVVTWRTA TLCPQSCEER NLRENGYEAE WRYNSCAPAC
  QVTCQHPEPL
 401  ACPVQCVEGC HAHCPPGKIL DELLQTCVDP EDCPVCEVAG
  RRFASGKKVT
 451  LNPSDPEHCQ ICHCDVVNLT CEACQEPISG TSESATPESG
  PGSEPATSGS
 501  ETPGTSESAT PESGPGSEPA TSGSETPGTS ESATPESGPG
  TSTEPSEGSA
 551  PGSPAGSPTS TEEGTSESAT PESGPGSEPA TSGSETPGTS
  ESATPESGPG
 601  SPAGSPTSTE EGSPAGSPTS TEEGTSTEPS EGSAPGTSES
  ATPESGPGTS
 651  ESATPESGPG TSESATPESG PGSEPATSGS ETPGSEPATS
  GSETPGSPAG
 701  SPTSTEEGTS TEPSEGSAPG TSTEPSEGSA PGSEPATSGS
  ETPGTSESAT
 751  PESGPGTSTE PSEGSAPDSG GGGSGGGGSG GGGSGGGGSG
  GGGSLVPRGS
 801  GGASATRRYY LGAVELSWDY MQSDLGELPV DARFPPRVPK
  SFPFNTSVVY
 851  KKTLFVEFTD HLFNIAKPRP PWMGLLGPTI QAEVYDTVVI
  TLKNMASHPV
 901  SLHAVGVSYW KASEGAEYDD QTSQREKEDD KVFPGGSHTY
  VWQVLKENGP
 951  MASDPLCLTY SYLSHVDLVK DLNSGLIGAL LVCREGSLAK
  EKTQTLHKFI

1001  LLFAVFDEGK SWHSETKNSL MQDRDAASAR AWPKMHTVNG
   YVNRSLPGLI
1051  GCHRKSVYWH VIGMGTTPEV HSIFLEGHTF LVRNHRQASL
   EISPITFLTA
1101  QTLLMDLGQF LLFCHISSHQ HDGMEAYVKV DSCPEEPQLR
   MKNNEEAEDY
1151  DDDLTDSEMD VVRFDDDNSP SFIQIRSVAK KHPKTWVHYI
```

```
   AAEEEDWDYA
1201  PLVLAPDDRS YKSQYLNNGP QRIGRKYKKV RFMAYTDETF
   KTREAIQHES
1251  GILGPLLYGE VGDTLLIIFK NQASRPYNIY PHGITDVRPL
   YSRRLPKGVK
1301  HLKDFPILPG EIFKYKWTVT VEDGPTKSDP RCLTRYYSSF
   VNMERDLASG
1351  LIGPLLICYK ESVDQRGNQI MSDKRNVILF SVFDENRSWY
   LTENIQRFLP
1401  NPAGVQLEDP EFQASNIMHS INGYVFDSLQ LSVCLHEVAY
   WYILSIGAQT
1451  DFLSVFFSGY TFKHKMVYED TLTLFPFSGE TVFMSMENPG
   LWILGCHNSD
1501  FRNRGMTALL KVSSCDKNTG DYYEDSYEDI SAYLLSKNNA
   IEPRSFSQNP
1551  PVLKRHQREI TRTTLQSDQE EIDYDDTISV EMKKEDFDIY
   DEDENQSPRS
1601  FQKKTRHYFI AAVERLWDYG MSSSPHVLRN RAQSGSVPQF
   KKVVFQEFTD
1651  GSFTQPLYRG ELNEHLGLLG PYIRAEVEDN IMVTFRNQAS
   RPYSFYSSLI
1701  SYEEDQRQGA EPRKNFVKPN ETKTYFWKVQ HHMAPTKDEF
   DCKAWAYFSD
1751  VDLEKDVHSG LIGPLLVCHT NTLNPAHGRQ VTVQEFALFF
   TIFDETKSWY
1801  FTENMERNCR APCNIQMEDP TFKENYRFHA INGYIMDTLP
   GLVMAQDQRI
1851  RWYLLSMGSN ENIHSIHFSG HVFTVRKKEE YKMALYNLYP
   GVFETVEMLP
1901  SKAGIWRVEC LIGEHLHAGM STLFLVYSNK CQTPLGMASG
   HIRDFQITAS
1951  GQYGQWAPKL ARLHYSGSIN AWSTKEPFSW IKVDLLAPMI
   IHGIKTQGAR
2001  QKFSSLYISQ FIIMYSLDGK KWQTYRGNST GTLMVFFGNV
   DSSGIKHNIF
2051  NPPIIARYIR LHPTHYSIRS TLRMELMGCD LNSCSMPLGM
   ESKAISDAQI
2101  TASSYFTNMF ATWSPSKARL HLQGRSNAWR PQVNNPKEWL
   QVDFQKTMKV
2151  TGVTTQGVKS LLTSMYVKEF LISSSQDGHQ WTLFFQNGKV
   KVFQGNQDSF
2201  TPVVNSLDPP LLTRYLRIHP QSWVHQIALR MEVLGCEAQD LY
```

Example 4: Hydrodynamic injection of XTEN containing FVIIIF/VWF constructs in FVIII and VWF deficient mice

[0339] The XTEN containing DNA constructs in Figures 3 and 4 have combined 2-3 half-life extension elements together. To evaluate their FVIII half-life extension potential, a selective group of DNA constructs in figure 3 and figure 4 were introduced into FVIII/VWF double knockout (DKO) mice by Hydrodynamic injection (HDI) at 100ug/mouse dose. Blood samples were then collected by retro orbital blood collection at 24hr post HDI. The post HDI plasma FVIII activity was analyzed by FVIII chromogenic assay, and results were listed in Table 17 and Figure 5. Compared to wild type BDD-FVIII, all XTEN containing DNA constructs yield significantly higher FVIII plasma activity at 24hr post HDI, indicating the corresponding molecules had significant longer circulating protein half-life than BDD-FVIII. The application of the combination of those half-life extending elements was further evaluated in Hemophilic animals.

TABLE 17: FVIII plasma activity 24hr post HDI in FVIII/VWF DKO mice

DNA Construct	BDD-FVIII	FVIII-161	FVIII-168	FVIII-172	BDD-FVIII	FVIII-170
DNA Dose (µg/mouse)	100	100	100	100	50	50
FVIII Activity (mU/mL)	219±72	2446±1012	2209±609	1671±223	197±21	399±30

Hydrodynamic injection:

[0340] Hydrodynamic Injection is an efficient and safe non-viral gene delivery method to the liver in small animals, such as mice and rats. It was originally described as a rapid injection of a naked plasmid DNA/saline solution free of endotoxin at a tenth volume of the animal's body weight in about 5-7 seconds. The naked plasmid DNA contains the gene of interest and the liver produced in a tenth volume of the animal's body weight. The targeted protein is produced in the liver from the injected DNA and can be detected within 24 hours post-injection. Plasma samples were then collected to study the therapeutic property of the expressed protein.

[0341] For all the hydrodynamic injections that were performed herein, 2 ml of plasmid DNA in 0.9% sterile saline solution was delivered via intravenous tail vein injection within about 4-7 seconds to mice weighing 20-35 grams. The mice were closely monitored for the first couple of hours until the normal activity resumed. After the blood samples were collected via retro orbital blood collection, plasma samples were then obtained and stored at -80 °C for further analysis.

Example 5: Plasmid construction of co-transfection system for FVIIIFc-VWF Heterodimer contain XTEN insertions (Figure 6)

[0342] To increase the protein production yield, two co-transfection systems were generated for protein production, which contains three DNA constructs. The first DNA construct encoded a FVIII-Fc fusion protein in which a AE288 XTEN fragment was directly fuse to the C-terminus of the FVIII heavy chain and followed by either a wild type FVIII light chain fragment (pSYN-FVIII-173, Figure 6B) or a FVIII light chain fragment with R1645A/R1648A mutations (pSYN-FVIII-169, Figure 6A), the FVIII light chain was then directly fused to a single Fc fragment. The second DNA construct is pSYN-VWF-031 which encoding a D'D3-Fc fusion protein (Example 1). HEK293F cells were transfected with the two plasmid along with a third plasmid (PC5) at 80:15:5 ratio. The synthesized proteins were secreted as FVIII (XTEN) Fc/D'D3Fc heterodimer and D'D3Fc dimer and the FVIII (XTEN) Fc/D'D3Fc heterodimer was separated from the D'D3Fc dimer by protein purification.

pSYN-FVIII-169 mature Protein sequence (SEQ ID NO: 103):

```
   1  ATRRYYLGAV ELSWDYMQSD LGELPVDARF PPRVPKSFPF
  NTSVVYKKTL
  51  FVEFTDHLFN IAKPRPPWMG LLGPTIQAEV YDTVVITLKN
  MASHPVSLHA
 101  VGVSYWKASE GAEYDDQTSQ REKEDDKVFP GGSHTYVWQV
  LKENGPMASD
 151  PLCLTYSYLS HVDLVKDLNS GLIGALLVCR EGSLAKEKTQ
  TLHKFILLFA
 201  VFDEGKSWHS ETKNSLMQDR DAASARAWPK MHTVNGYVNR
  SLPGLIGCHR
 251  KSVYWHVIGM GTTPEVHSIF LEGHTFLVRN HRQASLEISP
  ITFLTAQTLL
 301  MDLGQFLLFC HISSHQHDGM EAYVKVDSCP EEPQLRMKNN
  EEAEDYDDDL
 351  TDSEMDVVRF DDDNSPSFIQ IRSVAKKHPK TWVHYIAAEE
  EDWDYAPLVL
 401  APDDRSYKSQ YLNNGPQRIG RKYKKVRFMA YTDETFKTRE
  AIQHESGILG
 451  PLLYGEVGDT LLIIFKNQAS RPYNIYPHGI TDVRPLYSRR
  LPKGVKHLKD

 501  FPILPGEIFK YKWTVTVEDG PTKSDPRCLT RYYSSFVNME
   RDLASGLIGP
 551  LLICYKESVD QRGNQIMSDK RNVILFSVFD ENRSWYLTEN
   IQRFLPNPAG
 601  VQLEDPEFQA SNIMHSINGY VFDSLQLSVC LHEVAYWYIL
   SIGAQTDFLS
 651  VFFSGYTFKH KMVYEDTLTL FPFSGETVFM SMENPGLWIL
   GCHNSDFRNR
 701  GMTALLKVSS CDKNTGDYYE DSYEDISAYL LSKNNAIEPR
   SFSQNGAPGT
 751  SESATPESGP GSEPATSGSE TPGTSESATP ESGPGSEPAT
   SGSETPGTSE
 801  SATPESGPGT STEPSEGSAP GSPAGSPTST EEGTSESATP
```

ESGPGSEPAT
851 SGSETPGTSE SATPESGPGS PAGSPTSTEE GSPAGSPTST
EEGTSTEPSE
901 GSAPGTSESA TPESGPGTSE SATPESGPGT SESATPESGP
GSEPATSGSE
951 TPGSEPATSG SETPGSPAGS PTSTEEGTST EPSEGSAPGT
STEPSEGSAP
1001 GSEPATSGSE TPGTSESATP ESGPGTSTEP SEGSAPASSP
PVLKRHQAEI
1051 TRTTLQSDQE EIDYDDTISV EMKKEDFDIY DEDENQSPRS
FQKKTRHYFI
1101 AAVERLWDYG MSSSPHVLRN RAQSGSVPQF KKVVFQEFTD
GSFTQPLYRG
1151 ELNEHLGLLG PYIRAEVEDN IMVTFRNQAS RPYSFYSSLI
SYEEDQRQGA
1201 EPRKNFVKPN ETKTYFWKVQ HHMAPTKDEF DCKAWAYFSD
VDLEKDVHSG
1251 LIGPLLVCHT NTLNPAHGRQ VTVQEFALFF TIFDETKSWY
FTENMERNCR
1301 APCNIQMEDP TFKENYRFHA INGYIMDTLP GLVMAQDQRI
RWYLLSMGSN
1351 ENIHSIHFSG HVFTVRKKEE YKMALYNLYP GVFETVEMLP
SKAGIWRVEC
1401 LIGEHLHAGM STLFLVYSNK CQTPLGMASG HIRDFQITAS
GQYGQWAPKL
1451 ARLHYSGSIN AWSTKEPFSW IKVDLLAPMI IHGIKTQGAR
QKFSSLYISQ
1501 FIIMYSLDGK KWQTYRGNST GTLMVFFGNV DSSGIKHNIF
NPPIIARYIR
1551 LHPTHYSIRS TLRMELMGCD LNSCSMPLGM ESKAISDAQI
TASSYFTNMF
1601 ATWSPSKARL HLQGRSNAWR PQVNNPKEWL QVDFQKTMKV
TGVTTQGVKS
1651 LLTSMYVKEF LISSSQDGHQ WTLFFQNGKV KVFQGNQDSF
TPVVNSLDPP
1701 LLTRYLRIHP QSWVHQIALR MEVLGCEAQD LYDKTHTCPP
CPAPELLGGP

1751 SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVKFNWY
VDGVEVHNAK
1801 TKPREEQYNS TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL
PAPIEKTISK
1851 AKGQPREPQV YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA
VEWESNGQPE
1901 NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM
HEALHNHYTQ
1951 KSLSLSPGK

pSYN-FVIII-173 mature Protein sequencing (SEQ ID NO: 104):

1 ATRRYYLGAV ELSWDYMQSD LGELPVDARF PPRVPKSFPF
NTSVVYKKTL
51 FVEFTDHLFN IAKPRPPWMG LLGPTIQAEV YDTVVITLKN
MASHPVSLHA
101 VGVSYWKASE GAEYDDQTSQ REKEDDKVFP GGSHTYVWQV
LKENGPMASD
151 PLCLTYSYLS HVDLVKDLNS GLIGALLVCR EGSLAKEKTQ
TLHKFILLFA
201 VFDEGKSWHS ETKNSLMQDR DAASARAWPK MHTVNGYVNR
SLPGLIGCHR
251 KSVYWHVIGM GTTPEVHSIF LEGHTFLVRN HRQASLEISP
ITFLTAQTLL
301 MDLGQFLLFC HISSHQHDGM EAYVKVDSCP EEPQLRMKNN
EEAEDYDDDL
351 TDSEMDVVRF DDDNSPSFIQ IRSVAKKHPK TWVHYIAAEE
EDWDYAPLVL
401 APDDRSYKSQ YLNNGPQRIG RKYKKVRFMA YTDETFKTRE
AIQHESGILG
451 PLLYGEVGDT LLIIFKNQAS RPYNIYPHGI TDVRPLYSRR
LPKGVKHLKD
501 FPILPGEIFK YKWTVTVEDG PTKSDPRCLT RYYSSFVNME
RDLASGLIGP
551 LLICYKESVD QRGNQIMSDK RNVILFSVFD ENRSWYLTEN
IQRFLPNPAG

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601  VQLEDPEFQA SNIMHSINGY VFDSLQLSVC LHEVAYWYIL
  SIGAQTDFLS
651  VFFSGYTFKH KMVYEDTLTL FPFSGETVFM SMENPGLWIL
  GCHNSDFRNR
701  GMTALLKVSS CDKNTGDYYE DSYEDISAYL LSKNNAIEPR
  SFSQNGAPGT
751  SESATPESGP GSEPATSGSE TPGTSESATP ESGPGSEPAT
  SGSETPGTSE
801  SATPESGPGT STEPSEGSAP GSPAGSPTST EEGTSESATP
  ESGPGSEPAT
851  SGSETPGTSE SATPESGPGS PAGSPTSTEE GSPAGSPTST
  EEGTSTEPSE
901  GSAPGTSESA TPESGPGTSE SATPESGPGT SESATPESGP
  GSEPATSGSE
951  TPGSEPATSG SETPGSPAGS PTSTEEGTST EPSEGSAPGT
  STEPSEGSAP

1001  GSEPATSGSE TPGTSESATP ESGPGTSTEP SEGSAPASSP
   PVLKRHQREI
1051  TRTTLQSDQE EIDYDDTISV EMKKEDFDIY DEDENQSPRS
   FQKKTRHYFI
1101  AAVERLWDYG MSSSPHVLRN RAQSGSVPQF KKVVFQEFTD
   GSFTQPLYRG
1151  ELNEHLGLLG PYIRAEVEDN IMVTFRNQAS RPYSFYSSLI
   SYEEDQRQGA
1201  EPRKNFVKPN ETKTYFWKVQ HHMAPTKDEF DCKAWAYFSD
   VDLEKDVHSG
1251  LIGPLLVCHT NTLNPAHGRQ VTVQEFALFF TIFDETKSWY
   FTENMERNCR
1301  APCNIQMEDP TFKENYRFHA INGYIMDTLP GLVMAQDQRI
   RWYLLSMGSN
1351  ENIHSIHFSG HVFTVRKKEE YKMALYNLYP GVFETVEMLP
   SKAGIWRVEC
1401  LIGEHLHAGM STLFLVYSNK CQTPLGMASG HIRDFQITAS
   GQYGQWAPKL
1451  ARLHYSGSIN AWSTKEPFSW IKVDLLAPMI IHGIKTQGAR
   QKFSSLYISQ
1501  FIIMYSLDGK KWQTYRGNST GTLMVFFGNV DSSGIKHNIF
   NPPIIARYIR
1551  LHPTHYSIRS TLRMELMGCD LNSCSMPLGM ESKAISDAQI
   TASSYFTNMF
1601  ATWSPSKARL HLQGRSNAWR PQVNNPKEWL QVDFQKTMKV
   TGVTTQGVKS
1651  LLTSMYVKEF LISSSQDGHQ WTLFFQNGKV KVFQGNQDSF
   TPVVNSLDPP
1701  LLTRYLRIHP QSWVHQIALR MEVLGCEAQD LYDKTHTCPP
   CPAPELLGGP
1751  SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVKFNWY
   VDGVEVHNAK
1801  TKPREEQYNS TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL
   PAPIEKTISK
1851  AKGQPREPQV YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA
   VEWESNGQPE
1901  NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM
   HEALHNHYTQ
1951  KSLSLSPGK
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Example 6. Protein purification for FVIII-169/VWF-031 and FVIII-173/VWF-031

[0343] A tangential flow filtration (TFF) step was used to buffer exchange the clarified conditioned media. The FVIII-169/VWF-031 or FVIII-173/VWF-031 heterodimer was then purified using a two-step chromatography process. A weak anion exchange resin was used, followed by affinity chromatography. The final purified product had acceptable purity by SEC-HPLC. The specific activity was compatible to B-domain deleted FVIII, as measured by FVIII chromogenic assay and A280 concentration. Purity and the presence of each moiety of this molecule

were confirmed by SDS-PAGE and western blotting.

Example 7. Evaluation the VWF binding ability of FVIII-169/VWF-031 by Octet assay

[0344] The VWF binding ability of FVIII-169/VWF-031 was obtained by BioLayer Interferometry (BLI) based measurements (Octet assay) at 25 °C with a ForteBio Octet 384 instrument, using Tris binding buffer (50 mM Tris, pH 7.2, 150 mM NaCl, 5 mM $CaCl_2$). The Octet assay for determining FVIII binding was based on the hydrophobic immobilization of Human von Willebrand Factor (Haematologic Technologies Catalog No. HCVWF-0191) onto the APS Biosensor, then followed by the binding of 1.0% Bovine Serum Albumin (Jackson ImmunoResearch Catalog No. 001-000-161). Briefly, hvWF (20 µg/mL) was diluted in Tris buffer and loaded across APS Biosensors for 600 sec, yielding approximately 3.0 - 3.5 nm binding on the reaction probes. Control APS probes were loaded with 1.0% BSA in the absence of hvWF for reference subtraction. After loading, all probes were incubated in Tris buffer for 300 sec to establish a new baseline. Subsequently, biosensor probes were incubated in solutions of FVIII-XTEN 169 or FVIIIFc Drug Substance (0, 0.6, 2, 6, 20, 60, 200, 600 IU/mL) for 5 min at room temperature, followed by a 5 min dissociation step. Using the Octet data analysis software, the binding response (nm) was derived from the subtracted data (Reaction probe minus Reference probe). No binding to immobilized VWF was detected for FVIII-169/VWF-031 (Figure 7), indicating a complete shielding of FVIII from full length VWF molecule by the D'D3 fragment.

Example 8. FVIII-169/VWF-031 PK in HemA and FVIII/VWF DKO mice

[0345] The PK profile of FVIII-169/VWF-031 was tested in HemA and FVIII/VWF DKO mice to evaluate the ability of the D'D3 fragment to shield the FVIII moiety from the endogenous VWF. HemA or FVIII/VWF DKO mice were treated with a single intravenous dose of FVIII-169/VWF-031 at 200 IU/kg, plasma samples were then collected at 5min, 8hr, 24hr, 48hr and 72 hours post dosing. The FVIII activity of plasma sample was tested by FVIII chromogenic assay, and half-life of FVIII-169/VWF-031 was calculated using WinNonlin program.

[0346] Complete inhibition of the constructs' binding to immobilized VWF was demonstrated by biolayer interferometry (Figure 7) for FVIII-169/VWF-031. This indicates the D'D3 fragment in the molecule had successfully blocked the FVIII binding to native VWF molecules, therefor similar half-life of FVIII-169/VWF-031 was predicted in the two different mouse strains. As shown in Figure 8A and Table 18, as expected, FVIII-169/VWF-031 had similar PK profile in both HemA and FVIII/VWF DKO mice, which has demonstrated that the half-life of FVIIIFc/VWF heterodimer is independent from the half-life of endogenous VWF. The separation of the FVIIIFc/VWF heterodimer half-life from the endogenous VWF half-life , eliminated the FVIII extension ceiling and opened the possibility of further extending FVIII half-life beyond the 2 fold half-life limit imposed by endogenous VWF.

TABLE 18: FVIII-169/VWF-031 PK in HemA and FVIII/VWF DKO mice

Mouse Strain	Recovery (%)	$t_{1/2}$ (hr)	MRT (hr)	Cl (mL/hr/kg)	Vss (mL/kg)	AUC (hr*kg*mIU/mL /mIU)
FVIII/VWF DKO	69	17.94	20.1	4.06	81.69	0.2461
HemA	83	16.65	18.44	3.57	85.72	0.28

[0347] The FVIII protecting ability of the XTEN insertion and D'D3 fragment was evaluated by comparing the half-life of FVIII-169/VWF-031 with FVIII-169/Fc and FVIIIFc in FVIII/VWF DKO mice. After a single IV administration, blood samples were collected at 5min, 8hr, 24hr, 48hr and 72hr for FVIII-169/VWF-031, 5min, 8hr, 24hr, 32hr, 48hr for FVIII-169/Fc and at 5min, 1, 2, 4, 6 and 8hrs for FVIIIFc. The FVIII activity of plasma sample was tested by FVIII chromogenic assay, and half-life of FVIII-155/VWF-031 was calculated using WinNonlin program.

[0348] The study results were summarized in Figure 8B and Table 19, rFVIIIFc has a 1.6hr half-life in DKO mice due to the loss of VWF protection. When an XTEN insertion was introduced into the FVIIIFc molecule, the resulting FVIII-169/Fc molecule has a 7hr half-life, a **4** fold half-life extension by the XTEN insertion. Finally, when D'D3 fragment was incorporated into the molecule to form FVIII-169/VWF-031, a 17hr half-life was observed, another 2.5 fold further increase by the D'D3 fragment. In addition of the half-life improvement, improved Mean residency time (MRT), Clearance (Cl) and AUC were also observed as shown in Table 19.

[0349] FVIII-169/VWF-031 has achieved 17-18hr $t_{1/2}$ in both HemA and FVIII/VWF DKO mice, which is the upper limit of the $t_{1/2}$ extension ceiling that imposed by VWF clearance. More $t_{1/2}$ extension elements can be further incorporated into this molecule, such as a second XTEN insertion within FVIII. The synergistic effect of D'D3 fragment and XTEN insertions provided the possibility of the complete protection for FVIII from its clearance pathway, a final breakthrough of the 2 fold FVIII $t_{1/2}$ extension limit might be achieved by the FVIIIFc/XTEN/VWF variants.

TABLE 19. FVIII-169/VWF-031 PK in FVIII/VWF DKO mice

Mouse Strain	Treatment	Recovery (%)	$t_{1/2}$ (hr)	MRT (hr)	Cl (mL/hr/kg)	Vss (mL/kg)	AUC/D (hr*kg* mIU/mL /mIU)
FVIII/VWF DKO	rFVIIIFc	35	1.6	2.1	57.7	120.2	0.0173
	rFVIII-169/Fc	77	7.0	6.2	6.4	39.2	0.1573
	rFVIII-169/VWF-031	69	17.9	20.1	4.1	81.7	0.2461

Example 9: FVIII-XTEN variants cell media concentrate PK in D'D3 expressing FVIII/VWF DKO mice

[0350] The ability of D'D3 fragment to extend the $t_{1/2}$ of FVII-XTEN was evaluated in the D'D3 expressing FVIII/VWF DKO mouse model (described in example 2). In this study, instead of using VWF-025 to introduce the D'D3 dimer into the circulation, VWF-029 construct was used to introduce the D'D3 monomer into the circulation. To prepare FVIII-XTEN variants protein, a small scale (50-100 mL) transient transfection culture media was prepared, at day **4** post transfection, cell culture was harvested and concentrated to reach 10-20 IU/mL of FVIII activity range which is suitable for PK study. The concentrated cell media were then used for standard PK study in FVIII/VWF DKO mice with or without D'D3 in the circulation.

[0351] Total of 6 FVIII-XTEN variants that contains 1-3 XTEN insertions were tested in the system, their $t_{1/2}$ were summarized in Table 20 and data from representative variants were plotted in Figure 9A.

[0352] Longer half-life was observed for all the FVIII-XTEN variants with the presents of D'D3 fragment in the circulation (Table 20), which demonstrated the D'D3 protection for FVIII-XTEN from its clearance pathways. Furthermore, when compared to its 14hr half-life in HemA mice, LSD0055.021 has a 20.4hr $t_{1/2}$ in D'D3 expressing DKO mice (Figure 9B, Table 20), indicates the final breakthrough of the 2 fold half-life extension ceiling for FVIII molecules. By further modify the FVIII(XTEN)/VWF molecule, we could potentially achieve even longer FVIII $t_{1/2}$, and provide HemA patients a FVIII protein that only requires once weekly or less frequent dosing regimen.

TABLE 20. FVIII-XTEN $t_{1/2}$ in D'D3 expressing FVIII/VWF DKO mice

FVIII-XTEN ID	# of XTEN insertions	Insertion sites	XTEN size	$t_{1/2}$ (hr) DKO mice	$t_{1/2}$ (hr) pLIVE-D'D3/ DKO mice	$t_{1/2}$ (hr) HemA mice
pSD-0013	1	CT	144	3.3	7.9	
LSD0003.009	2	B*/CT	144/288	9.7	16.4	
LSD0038.015	2	1656/26	144/144	7.8	17.2	

FVIII-XTEN ID	# of XTEN insertions	Insertion sites	XTEN size	$t_{1/2}$ (hr) DKO mice	$t_{1/2}$ (hr) pLIVE-D'D3/ DKO mice	$t_{1/2}$ (hr) HemA mice
LSD0049.002	3	18/B*/CT	144/144/288	12.6	17.5	
LSD0051.002	3	403/B*/CT	144/144/288	11.1	19.9	
LSD0055.021	3	1900/B*/CT	144/144/288	16	20.4	14
*B indicates an XTEN sequence (*e.g.*, 144) is inserted immediately downstream of amino acid residue 745 corresponding to mature FVIII sequence.						

Example 10: Stability of VWF- and XTEN-containing FVIII variants in FVIII/VWF double knockout (DKO) plasma

[0353] Plasma stability of rFVIIIFc protein variants was tested in FVIII/VWF double knockout (DKO) mouse plasma. For the stability assay, HEK293 cells were co-transfected with plasmids directing the expression of rFVIIIFc or FVIII-169 (rFVIIIFc with 288 AE XTEN inserted at the B-domain junction) and plasmids directing the expression of either IgG-Fc or VWF-031 (VWF D'D3 region fused to IgG-Fc). At day four post-transfection, cell culture media was harvested and concentrated to 30 IU/mL based on FVIII chromogenic activity. Concentrated cell culture medium was then added into DKO mouse plasma to yield a FVIII activity of 5 IU/mL and incubated at 37°C. Aliquots were collected at different time points for activity measurement by chromogenic assay. Activity at each time point was measured in duplicate, and the average activity was plotted as a function of time. The activity of FVIIIFc, a dual chain (dc) FVIII molecule in which heavy and light chains are held together by non-covalent interaction, decreases with time in DKO mouse plasma (Figure 10). The activity of FVIII-169:Fc, which contains a 288 AE XTEN insertion at the B-domain junction, decays at a reduced rate relative to rFVIIIFc, indicating that enhanced stability is conferred by the XTEN insertion. Given that VWF has been proposed to enhance the stability of FVIII in vivo, we evaluated the plasma stability of FVIII-169:VWF-031. This heterodimeric molecule, in which the FVIII element and the VWF D'D3 element are fused to respective hemi-domains of Fc, exhibited additional plasma stability relative to FVIII-169:Fc, indicating that the VWF D'D3 domain and XTEN have a synergistic effect on the plasma stability of rFVIIIFc. Example 11: The effect on FVIII half-life of Fc fusion, XTEN insertion and the D'D3 fragment of VWF.

[0354] To assess the effect of Fc fusion, XTEN insertion and D'D3 fragment of VWF on the half-life of FVIII, the pharmacokinetic properties of B domain deleted recombinant FVIII (rBDD-FVIII), rFVIIIFc, FVIII-169:Fc and FVIII-169:VWF-031 were evaluated in FVIII/VWF double knockout (DKO) mice.

[0355] DKO mice were treated with a single intra venous administration of 200 IU/kg of FVIII proteins, and plasma samples were collected at designated time points as indicated in Figure 11. FVIII activity of the plasma samples were analyzed by FVIII chromogenic assay and half-life was calculated using the WinNonlin-Phoenix program. The pharmacokinetic parameters of the tested molecules are listed in Table 21. The time regression curve of plasma FVIII activity for each FVIII variants were plotted in Figure 11.

[0356] Unmodified BDD-FVIII had a half-life of 0.23 hr in DKO mice, the FVIIIFc fusion protein has an extended half-life of 1.66 hr in DKO mice due to the recycling of FVIIIFc protein through the Fc:FcRn interaction. When a 288 residue of AEXTEN polypeptide was incorporated into the B domain region of FVIII within the FVIIIFc molecule, the half-life of the resulting FVIII169/Fc protein was further extended to 7.41 hr in DKO mice. Finally, with the addition of the D'D3 domain of VWF, the half-life of FVIII 169/VWF031 heterodimer has reached 17.9 hr in DKO mice (Figure 11, Table 21). In addition of the half-life, all of the other PK parameters also improved proportionally with the addition of each element (Table 21). FVIII can tolerate multiple half-life extension elements, and this synergistic effect of the three elements on FVIII half-life extension, enabled the further improvement of the half-life of FVIII-XTEN VWF heterodimers.

Table 21: PK parameters of FVIII variants

FVIII	FVIII Isoform	XTEN Insertions		$T_{1/2}$ 1/2 (hr)	MRT (hr)	Cl (mL/hr/kg)	Vss (mL/kg)	AUC_D kg*hr/mL
		Site	XTEN Length					
BDD-FVIII	dc			0.23	0.24	407.72	97.42	0.0025
FVIIIFc	**dc**			1.66	2.06	62.66	128.82	0.0161
FVIII169/Fc	**sc**	B*	AE288	7.41	6.67	6.24	41.61	0.1603
FVIII169/VWF031	**sc**	B*	AE288	17.94	20.1	4.06	81.69	0.2463
*B indicates an XTEN sequence (*e.g.*, 144) is inserted immediately downstream of amino acid residue 745 corresponding to mature FVIII sequence.								

Example 12: Pharmacokinetic properties of different FVIII-XTEN_VWF heterodimers

[0357] To evaluate the combined effect of the VWF-D'D3 fragment and XTEN insertions on the FVIII half-life, the pharmacokinetic properties of FVIII-XTEN-Fc:VWF-Fc heterodimers were tested in HemA mice and compared to those of the single chain isoform of BDD-FVIII (scBDD-FVIII) and FVIII-169:VWF-031 (example 10). Seven new FVIII-XTEN-Fc constructs were generated (protein sequences were listed in Table 24). Schematic diagrams of those constructs are shown in Figure 14A-H. FVIII-195 and FVIII-199, respectively, are the FVIII dual chain and single chain isoforms that each contains two XTEN insertions at positions 1900 and 1656. FVIII-196 and FVIII-201, respectively, are the FVIII dual chain and single chain isoforms that each contains three XTEN insertions at positions 26, 1656 and 1900. FVIII-203, -204 and -205 are sc-FVIIIFc molecules with two XTEN insertions at the B domain junction and at positions 1900, 403 or 18, respectively. Each FVIII-XTEN-Fc construct was co-expressed with VWF-031 in HEK293 cells to produce FVIII-XTEN-Fc/VWF heterodimeric proteins. At day four post-transfection, cell culture medium was harvested and either concentrated to 20 IU/mL based on FVIII chromogenic activity (FVIII-195 :VWF-031, FVIII-196:VWF-031, FVIII-199:VWF-031, FVIII-203:VWF-031 and FVIII-204:VWF-031) or purified (scBDD-FVIII, FVIII-169:VWF-031, FVIII-201:VWF-031 and FVIII-205:VWF-031). Having demonstrated the complete intra-molecular shielding of FVIII molecule from the endogenous VWF by the D'D3 fragment in the FVIII-XTEN-Fc:VWF-Fc heterodimer (FVIII-169:VWF-031, Example 5), HemA mice was chosen for the PK evaluations. Purified protein or concentrated cell culture medium was administered to 8-12 week-old HemA mice by intravenous administration at a dose of 200 IU/10 mL/kg. Plasma samples were collected at 5 min, 8 hr, 16 hr, 24 hr, 32 hr, 48 hr, 72 hr and 96 hr post-dosing. FVIII activity of the plasma samples were analyzed by FVIII chromogenic assay and half-life was calculated using the WinNonlin-Phoenix program. The pharmacokinetic parameters of the tested molecules are listed in Table 22. The plasma FVIII activities at selected time points for FVIII-XTEN-Fc/VWF-Fc variants were plotted in Figures 12A-C.

[0358] When XTEN was inserted into positions 1900 and 1656 (FVIII-195, FVIII-199), moderate improvement in half-life was observed for the scFVIII isoform (FVIII-199:VWF-031) compared to FVIII-169:VWF-031. However, the dcFVIII isoform exhibited a shorter half-life than did FVIII-169:VWF-031, indicating that the single chain isoform might be significantly more stable than the corresponding dual chain isoform (Table 22 and Figure 12A). When a third XTEN insertion was incorporated into FVIII-199 at position 26, the half-life of the resulting molecule FVIII-201:VWF-031 had reached 24.6 hr, which represents greater than a threefold half-life improvement relative to scBDD-FVIII (Table 22 and Figure 12C). We have also tested the half-life extension effect of the second XTEN insertion at position 403 (A2 domain), 1900 (A3 domain) and 18 (A1 domain) each in combination with the B domain XTEN insertion. While the addition of the A2 or A3 XTEN insertion did not confer an additional half-life benefit (Table 22, Figure 12b), the addition of the A1 insertion further extended the half-life of the FVIII-XTEN-Fc:VWF-Fc heterodimer to 29.4 hr (Table 22, Figure 12C), which is greater than threefold longer than that of scBDD-FVIII.

[0359] When XTENs were incorporated into the FVIIIFc/VWF heterodimer construct, degree of half-life

improvement of the resulting molecules was variable, and no obvious correlation was observed between half-lives and either the site or number of XTEN insertion, suggesting that the half-life of the FVIII-XTEN-Fc/VWF heterodimer is determined by the integrity of the whole molecule rather than by the number or placement of XTEN insertions.

[0360] The 24.6 hr and 29.4 hr half-lives observed for FVIII-XTEN-Fc:VWF-Fc heterodimers clearly exceeded the 1.6- to 2-fold limitation on FVIII half-life extension. If this finding translates for HemA patients, it will allow once-weekly or less frequent dosing for FVIII prophylaxis.

Table 22: PK parameters of FVIII-XTEN-Fc/VWF-Fc heterodimers

FVIII	FVIII Isoform	XTEN Insertions		$T_{1/2}$ (hr)	MRT (hr)	Cl (mL/hr/kg)	Vss (mL/kg)	AUC_D kg*hr/mL
		Site	XTEN Length					
scBDD-FVIII	sc			7.16	10.16	4.38	44.44	0.23
FVIII169/VWF031	sc	B*	AE288	16.65	18.44	3.57	65.79	0.28
FVIII195/VWF031	dc	1656/1900	AG144/ AE144	12.56	13.88	9.04	125.4 8	0.11
FVIII199/VWF031	sc	1656/1900	AG144/ AE144	18.57	20.09	6.24	125.2 8	0.16
FVIII201/VWF031	sc	26/1656/1900	AG144/AG144/AE144	24.63	33.67	1.9	63.97	0.53
FVIII203/VWF031	sc	403/B*	AE144/AE288	15.52	18	3.65	65.61	0.27
FVIII204/VWF031	sc	1900/B*	AE144/AE288	16.3	20.63	2.87	59.14	0.35
FVIII205/VWF031	sc	18/B*	AE144/AE288	29.4	37.06	1.82	67.39	0.55
*B indicates an XTEN sequence (*e.g.*, 144) is inserted immediately downstream of amino acid residue 745 corresponding to mature FVIII sequence.								

[0361] In addition to incorporating XTEN into the FVIII molecule, we also evaluated the potential half-life extension benefit of incorporating XTEN as a linker between the D'D3 and Fc fragment. FVIII-155 (scFVIIIFc) was co-expressed with VWF-034 (VWF-Fc with AE 288 XTEN plus a 35 residue thrombin cleavable linker) in HEK293 cells. At day 4 post-transfection, cell culture medium was harvested and concentrated to 20 IU/mL based on FVIII activity assay. FVIII/VWF DKO mice were dosed with concentrated cell culture media at 200 IU/10 mL/kg with a single intravenous injection. Plasma samples were collected at 5 min, 8 hr, 24 hr, 48 hr, 72 hr and 96 hr post-dosing. The FVIII activity of plasma samples was analyzed by FVIII chromogenic assay, and the regression curve of plasma FVIII activity as a function of time was plotted (Figure 13). FVIII-155/VWF-034 exhibited the same improvement in half-life as FVIII-169/VWF-031, which has AE 288 XTEN inserted into the B domain junction of FVIII, as illustrated by the over lapping regression curves for the two molecules (Figure 13). The demonstration that XTEN insertion into the VWF-Fc polypeptide confers half-life improvement of a magnitude similar to that conferred by XTEN insertion at the B domain junction of the FVIII polypeptide suggests that further half-life improvement may be possible in a heterodimeric molecule in which intra-molecular XTEN insertion in the FVIII polypeptide is combined with inter-domain XTEN insertion between the VWF and Fc elements of the VWF-Fc polypeptide.

Example 13A: Pharmacokinetic properties of additional FVIII-XTEN_VWF heterodimers

[0362] In addition to the FVIII-XTEN VWF heterodimers that were listed in Table 22, FVIII-XTEN VWF

heterodimers containing different composition of XTEN insertions, single chain and dual chain version of FVIII (Table 23A) are either tested or will be tested in HemA for their pharmacokinetic properties. Various FVIII constructs (Table 23B) and VWF constructs (Table 23C) are also disclosed below. HemA mice will be treated with a single dose of intravenous administration of the heterodimer proteins at 200 IU/10 mL/kg. Plasma samples will then be collected at 5 min, 24, 48, 72, 96 and 120 hrs post-dosing. FVIII activity of the plasma samples will be analyzed by FVIII chromogenic assay and half-life will be calculated using the WinNonlin-Phoenix program. The protein sequences of the listed heterodimers were listed in Table 25.

Table 23A. Plausible FVIII-XTEN-Fc:VWF-Fc heterodimer combinations for PK and activity improvement.

	pSYN VWF-015	pSYN VWF-031	pSYN VWF-034 **	pSYN VWF-036
pSYN FVIII 010	-	$t_{1/2}$ 8.7 hr DKO mice	To be tested	-
pSYN FVIII 155	$t_{1/2}$ 6.3 hr DKO mice	$t_{1/2}$ 10.8 hr HemA mice	$t_{1/2}$ 18.6 hr HemA mice	$t_{1/2}$ 13.3 hr HemA mice
pSYN FVIII 169 **	-	$t_{1/2}$ 16.7 hr HemA mice	$t_{1/2}$ 31.1 hr HemA mice	-
pSYN FVIII 173 **	-	$t_{1/2}$ 15.2 hr DKO mice	$t_{1/2}$ 28.9 hr HemA mice	To be tested
pSYN FVIII 205	-	$t_{1/2}$ 29.4 hr HemA mice	$t_{1/2}$ 32.4 hr HemA mice	$t_{1/2}$ 29.7 hr HemA mice
pSYN FVIII 266	-	$t_{1/2}$ 24.5 hr HemA mice	$t_{1/2}$ 27.4 hr HemA mice	-
pSYN FVII 267	-	$t_{1/2}$ 23.0 hr HemA mice	$t_{1/2}$ 25.7 hr HemA mice	
pSYN FVIII 268	-	To be tested	To be tested	To be tested
Dual chain isoform of pSYN FVIII 268		To be tested	To be tested	To be tested
**Length of XTEN can be changed to 72, 144, 288, 324, 333, 576, or 864.				

Table 23B. FVIII Constructs:

pSYN FVIII 010	dual chain FVIIIFc
pSYN FVIII 169	Single chain FVIIIFc with 288 AE XTEN in B-domain
pSYN FVIII 173	dual chain FVIIIFc with 288 AE XTEN in B-domain
pSYN FVIII 195	dual chain FVIIIFc with two 144 XTENs at amino acid 1656 and 1900
pSYN FVIII 196	dual chain FVIIIFc with three 144 XTENs at amino acid 26, 1656 and 1900
pSYN FVIII 199	Single chain FVIIIFc with two 144 XTENs at amino acid 1656 and 1900
pSYN FVIII 201	Single chain FVIIIFc with three 144 XTENs at amino acid 26, 1656 and 1900
pSYN FVIII 203	Single chain FVIIIFc with 144 AE XTEN at amino acid 1900 and 288 AE XTEN in B-domain
pSYN FVIII 204	Single chain FVIIIFc with 144 AE XTEN at amino acid 403 and 288 AE XTEN in B-domain
pSYN FVIII 205	Single chain FVIIIFc with 144 AE XTEN at amino acid 18 and 288 AE XTEN in B-domain
pSYN FVIII 207	Single chain FVIII (no Fc, no XTEN)
pSYN FVIII 266	Single chain FVIIIFc with 42 AE XTEN at amino acid 18 and 288 AE XTEN in B-domain
pSYN FVIII 267	Single chain FVIIIFc with 72 AE XTEN at amino acid 18 and 288 AE XTEN in B-domain
pSYN FVIII 268	Single chain FVIIIFc with 144 AE XTEN at amino acid 18

pSYN FVIII 269	Single chain FVIIIFc with 72 AE XTEN at amino acid 18
pSYN FVIII 271	Single chain FVIIIFc with 42 AE XTEN at amino acid 18
pSYN FVIII 272	Single chain FVIII with 144 AE XTEN at amino acid 18 and 288 AE XTEN in B-domain (no Fc)

Table 23C. VWF Constructs:

pSYN VWF031	VWF-D1D2D'D3-48aa long thrombin cleavable GS linker-Fc with C1099A/C1142A
pSYN VWF034	VWF-D1D2D'D3-288AE XTEN +35aa long thrombin cleavable GS linker-Fc with C1099A/C1142A
pSYN VWF035	VWF-D1D2D'D3-72aa long thrombin cleavable GS linker-Fc with C1099A/C1142A
pSYN VWF036	VWF-D1D2D'D3-98aa long thrombin cleavable GS linker-Fc with C1099A/C1142A
pSYN VWF041	VWF-D1D2D'D3 with 288 AE XTEN in D3 and 48aa long thrombin cleavable GS linker after D3-Fc with C1099A/C1142A

Example 13B: Pharmacokinetic properties of additional FVIII-XTEN_VWF heterodimers.

[0363] FVIII-XTEN_VWF heterodimers were tested in HemA mice for their pharmacokinetic properties. The heterodimers tested are FVIII169/VWF034, FVIII205/VWF034, FVIII205/VWF036 and FVIII266/VWF031. HemA mice were administered with a single intravenous dose of various heterodimer proteins at 200 IU/10 mL/kg. Plasma samples were collected at 5 min, 24, 48, 72, 96 and 120 hrs post-dosing. FVIII activity of the plasma samples were analyzed by FVIII chromogenic assay, and half-lives were calculated using the WinNonlin-Phoenix program. The PK results are shown below in Table 24.

Table 24. Additional FVIII-XTEN_VWF - PK in HemA Mice

Treatment	5min recovery (%)	HL (hr)	MRT (hr)	Cl (mL/hr/kg)	Vss (mL/kg)	AUC_D (hr*kg*m IU/mL/mIU)	Fold of $t_{1/2}$ increase vs scBDD-FVIII
ScBDD-FVIII		7.16	10.16	4.83	44.44	0.23	-
FVIII169/VWF034	76	**31.1**	34.57	1.73	59.77	0.58	4.3
FVIII205/VWF034	68	**32.41**	39.79	1.55	61.73	0.64	4.6
FVIII205/VWF036	74	29.71	36.35	1.61	58.43	0.62	4.1
FVIII266/VWF031	66	24.45	22.75	2.67	60.83	0.37	3.4

pSYNFVIII 010 nucleotide sequence-(Dual chain FVIIIFc) (SEQ ID NO: 125)

```
   1  ATGCAAATAG AGCTCTCCAC CTGCTTCTTT CTGTGCCTTT
  TGCGATTCTG
  51  CTTTAGTGCC ACCAGAAGAT ACTACCTGGG TGCAGTGGAA
  CTGTCATGGG
 101  ACTATATGCA AAGTGATCTC GGTGAGCTGC CTGTGGACGC
  AAGATTTCCT
 151  CCTAGAGTGC CAAAATCTTT TCCATTCAAC ACCTCAGTCG
  TGTACAAAAA
 201  GACTCTGTTT GTAGAATTCA CGGATCACCT TTTCAACATC
  GCTAAGCCAA
 251  GGCCACCCTG GATGGGTCTG CTAGGTCCTA CCATCCAGGC
  TGAGGTTTAT
 301  GATACAGTGG TCATTACACT TAAGAACATG GCTTCCCATC
  CTGTCAGTCT
 351  TCATGCTGTT GGTGTATCCT ACTGGAAAGC TTCTGAGGGA
  GCTGAATATG
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 401  ATGATCAGAC CAGTCAAAGG GAGAAAGAAG ATGATAAAGT
  CTTCCCTGGT
 451  GGAAGCCATA CATATGTCTG GCAGGTCCTG AAAGAGAATG
  GTCCAATGGC
 501  CTCTGACCCA CTGTGCCTTA CCTACTCATA TCTTTCTCAT
  GTGGACCTGG
 551  TAAAAGACTT GAATTCAGGC CTCATTGGAG CCCTACTAGT
  ATGTAGAGAA
 601  GGGAGTCTGG CCAAGGAAAA GACACAGACC TTGCACAAAT
  TTATACTACT
 651  TTTTGCTGTA TTTGATGAAG GGAAAAGTTG GCACTCAGAA
  ACAAAGAACT
 701  CCTTGATGCA GGATAGGGAT GCTGCATCTG CTCGGGCCTG
  GCCTAAAATG
 751  CACACAGTCA ATGGTTATGT AAACAGGTCT CTGCCAGGTC
  TGATTGGATG
 801  CCACAGGAAA TCAGTCTATT GGCATGTGAT TGGAATGGGC
  ACCACTCCTG
 851  AAGTGCACTC AATATTCCTC GAAGGTCACA CATTTCTTGT
  GAGGAACCAT
 901  CGCCAGGCGT CCTTGGAAAT CTCGCCAATA ACTTTCCTTA
  CTGCTCAAAC
 951  ACTCTTGATG GACCTTGGAC AGTTTCTACT GTTTTGTCAT
  ATCTCTTCCC
1001  ACCAACATGA TGGCATGGAA GCTTATGTCA AAGTAGACAG
  CTGTCCAGAG
1051  GAACCCCAAC TACGAATGAA AAATAATGAA GAAGCGGAAG
  ACTATGATGA
1101  TGATCTTACT GATTCTGAAA TGGATGTGGT CAGGTTTGAT
  GATGACAACT

1151  CTCCTTCCTT TATCCAAATT CGCTCAGTTG CCAAGAAGCA
  TCCTAAAACT
1201  TGGGTACATT ACATTGCTGC TGAAGAGGAG GACTGGGACT
  ATGCTCCCTT
1251  AGTCCTCGCC CCCGATGACA GAAGTTATAA AAGTCAATAT
  TTGAACAATG
1301  GCCCTCAGCG GATTGGTAGG AAGTACAAAA AAGTCCGATT
  TATGGCATAC
1351  ACAGATGAAA CCTTTAAGAC TCGTGAAGCT ATTCAGCATG
  AATCAGGAAT
1401  CTTGGGACCT TTACTTTATG GGGAAGTTGG AGACACACTG
  TTGATTATAT
1451  TTAAGAATCA AGCAAGCAGA CCATATAACA TCTACCCTCA
  CGGAATCACT
1501  GATGTCCGTC CTTTGTATTC AAGGACATTA CCAAAAGGTG
  TAAAACATTT
1551  GAAGGATTTT CCAATTCTGC CAGGAGAAAT ATTCAAATAT
  AAATGGACAG
1601  TGACTGTAGA AGATGGGCCA ACTAAATCAG ATCCTCGGTG
  CCTGACCCGC
1651  TATTACTCTA GTTTCGTTAA TATGGAGAGA GATCTAGCTT
  CAGGACTCAT
1701  TGGCCCTCTC CTCATCTGCT ACAAACAATC TGTAGATCAA
  AGAGGAAACC
1751  AGATAATGTC AGACAAGAGG AATGTCATCC TGTTTTCTGT
  ATTTGATGAG
1801  AACCGAAGCT GGTACCTCAC AGAGAATATA CAACGCTTTC
  TCCCCAATCC
1851  AGCTGGAGTG CAGCTTGAGG ATCCAGAGTT CCAAGCCTCC
  AACATCATGC
1901  ACAGCATCAA TGGCTATGTT TTTGATAGTT TGCAGTTGTC
  AGTTTGTTTG
1951  CATGAGGTGG CATACTGGTA CATTCTAAGC ATTGGAGCAC
  AGACTGACTT
2001  CCTTTCTGTC TTCTTCTCTC GATATACCTT CAAACACAAA
  ATGGTCTATG
2051  AAGACACACT CACCCTATTC CCATTCTCAG GAGAAACTGT
  CTTCATGTCG
2101  ATGGAAAACC CAGGTCTATG GATTCTGGGG TGCCACAACT
  CAGACTTTCG
2151  GAACAGAGGC ATGACCGCCT TACTGAAGGT TTCTAGTTGT
  GACAAGAACA
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2201  CTGGTGATTA TTACGAGGAC AGTTATGAAG ATATTTCAGC
   ATACTTGCTG
2251  AGTAAAAACA ATGCCATTGA ACCAAGAAGC TTCTCTCAAA
   ACCCACCAGT
2301  CTTGAAACGC CATCAACGGG AAATAACTCG TACTACTCTT
   CACTCACATC
2351  AAGAGGAAAT TGACTATGAT GATACCATAT CAGTTGAAAT
   GAAGAAGGAA

2401  GATTTTGACA TTTATGATGA GGATGAAAAT CAGAGCCCCC
   GCAGCTTTCA
2451  AAAGAAAACA CGACACTATT TTATTCCTGC AGTGGAGAGG
   CTCTGGGATT
2501  ATGGGATGAG TAGCTCCCCA CATGTTCTAA GAAACAGGGC
   TCAGAGTGGC
2551  AGTGTCCCTC AGTTCAAGAA AGTTGTTTTC CAGGAATTTA
   CTGATGGCTC
2601  CTTTACTCAG CCCTTATACC GTGGAGAACT AAATGAACAT
   TTGGGACTCC
2651  TGGGGCCATA TATAAGAGCA GAAGTTGAAG ATAATATCAT
   GGTAACTTTC
2701  AGAAATCAGG CCTCTCGTCC CTATTCCTTC TATTCTAGCC
   TTATTTCTTA
2751  TGAGGAAGAT CAGAGGCAAG GAGCAGAACC TAGAAAAAAC
   TTTGTCAAGC
2801  CTAATGAAAC CAAAACTTAC TTTTGGAAAG TGCAACATCA
   TATGGCACCC
2851  ACTAAAGATG AGTTTGACTG CAAAGCCTGG GCTTATTTCT
   CTGATGTTGA
2901  CCTGGAAAAA GATGTGCACT CAGGCCTGAT TGGACCCCTT
   CTGGTCTGCC
2951  ACACTAACAC ACTGAACCCT GCTCATGGGA GACAAGTGAC
   AGTACAGGAA
3001  TTTGCTCTGT TTTTCACCAT CTTTGATGAG ACCAAAAGCT
   GGTACTTCAC
3051  TGAAAATATG GAAAGAAACT GCAGGCCTCC CTGCAATATC
   CAGATGGAAG
3101  ATCCCACTTT TAAAGAGAAT TATCGCTTCC ATGCAATCAA
   TGGCTACATA
3151  ATGGATACAC TACCTGGCTT AGTAATGGCT CAGGATCAAA
   GGATTCGATG
3201  GTATCTGCTC AGCATGGGCA GCAATCAAAA CATCCATTCT
   ATTCATTTCA
3251  GTGGACATGT GTTCACTGTA CGAAAAAAAG AGGAGTATAA
   AATGGCACTG
3301  TACAATCTCT ATCCAGGTGT TTTTGAGACA GTGGAAATGT
   TACCATCCAA
3351  AGCTGGAATT TGGCGGGTGG AATGCCTTAT TGGCGAGCAT
   CTACATGCTG
3401  GGATGAGCAC ACTTTTTCTG GTGTACAGCA ATAAGTGTCA
   GACTCCCCTG
3451  GGAATGGCTT CTGGACACAT TAGAGATTTT CAGATTACAG
   CTTCAGGACA
3501  ATATGGACAG TGGGCCCCAA AGCTGGCCAG ACTTCATTAT
   TCCGGATCAA
3551  TCAATGCCTG GAGCACCAAG GAGCCCTTTT CTTGGATCAA
   GGTGGATCTG
3601  TTGGCACCAA TGATTATTCA CGGCATCAAG ACCCAGGGTG
   CCCGTCAGAA

3651  GTTCTCCAGC CTCTACATCT CTCAGTTTAT CATCATGTAT
   AGTCTTGATG
3701  GGAAGAAGTG GCAGACTTAT CGAGGAAATT CCACTGGAAC
   CTTAATGGTC
3751  TTCTTTGGCA ATGTGGATTC ATCTGGGATA AAACACAATA
   TTTTTAACCC
3801  TCCAATTATT GCTCGATACA TCCGTTTGCA CCCAACTCAT
   TATAGCATTC
3851  GCAGCACTCT TCGCATGGAG TTGATGGGCT GTGATTTAAA
   TAGTTGCAGC
3901  ATGCCATTGG GAATGGAGAG TAAAGCAATA TCAGATGCAC
   AGATTACTGC
3951  TTCATCCTAC TTTACCAATA TGTTTGCCAC CTGGTCTCCT
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   TCAAAAGCTC
4001  GACTTCACCT CCAAGGGAGG AGTAATGCCT GGAGACCTCA
   GGTGAATAAT
4051  CCAAAAGAGT GGCTGCAAGT GGACTTCCAG AAGACAATGA
   AAGTCACAGG
4101  AGTAACTACT CAGGGAGTAA AATCTCTGCT TACCAGCATG
   TATGTGAAGG
4151  AGTTCCTCAT CTCCAGCAGT CAAGATGGCC ATCAGTGGAC
   TCTCTTTTTT
4201  CAGAATGGCA AAGTAAAGGT TTTTCAGGGA AATCAAGACT
   CCTTCACACC
4251  TGTGGTGAAC TCTCTAGACC CACCGTTACT GACTCGCTAC
   CTTCGAATTC
4301  ACCCCCAGAG TTGGGTGCAC CAGATTGCCC TGAGGATGGA
   GGTTCTGGGC
4351  TGCGAGGCAC AGGACCTCTA CGACAAAACT CACACATGCC
   CACCGTGCCC
4401  AGCTCCAGAA CTCCTGGGCG GACCGTCAGT CTTCCTCTTC
   CCCCCAAAAC
4451  CCAAGGACAC CCTCATGATC TCCCGGACCC CTGAGGTCAC
   ATGCGTGGTG
4501  GTGGACGTGA GCCACGAAGA CCCTGAGGTC AAGTTCAACT
   GGTACGTGGA
4551  CGGCGTGGAG GTGCATAATG CCAAGACAAA GCCGCGGGAG
   GAGCAGTACA
4601  ACAGCACGTA CCGTGTGGTC AGCGTCCTCA CCGTCCTGCA
   CCAGGACTGG
4651  CTGAATGGCA AGGAGTACAA GTGCAAGGTC TCCAACAAAG
   CCCTCCCAGC
4701  CCCCATCGAG AAAACCATCT CCAAAGCCAA AGGGCAGCCC
   CGAGAACCAC
4751  AGGTGTACAC CCTGCCCCCA TCCCGGGATG AGCTGACCAA
   GAACCAGGTC
4801  AGCCTGACCT GCCTGGTCAA AGGCTTCTAT CCCAGCGACA
   TCCCCCTGCA
4851  GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC
   ACGCCTCCCG

4901  TGTTGGACTC CGACGGCTCC TTCTTCCTCT ACAGCAAGCT
   CACCGTGGAC
4951  AAGAGCAGGT GGCAGCAGGG GAACGTCTTC TCATGCTCCG
   TGATGCATGA
5001  GGCTCTGCAC AACCACTACA CGCAGAAGAG CCTCTCCCTG
   TCTCCGGGTA
5051  AATGA
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pSYNFVIII 010 protein seauence-(Dual chain FVIIIFc) (SEQ ID NO: 126)

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   1  MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQSDL
   GELPVDARFP
  51  PRVPKSFPFN TSVVYKKTLF VEFTDHLFNI AKPRPPWMGL
   LGPTIQAEVY
 101  DTVVITLKNM ASHPVSLHAV GVSYWKASEG AEYDDQTSQR
   EKEDDKVFPG
 151  GSHTYVWQVL KENGPMASDP LCLTYSYLSH VDLVKDLNSG
   LIGALLVCRE
 201  GSLAKEKTQT LHKFILLFAV FDEGKSWHSE TKNSLMQDRD
   AASARAWPKM
 251  HTVNGYVNRS LPGLIGCHRK SVYWHVIGMG TTPEVHSIFL
   EGHTFLVRNH
 301  RQASLEISPI TFLTAQTLLM DLGQFLLFCH ISSHQHDGME
   AYVKVDSCPE
 351  EPQLRMKNNE EAEDYDDDLT DSEMDVVRFD DDNSPSFIQI
   RSVAKKHPKT
 401  WVHYIAAEEE DWDYAPLVLA PDDRSYKSQY LNNGPQRIGR
   KYKKVRFMAY
 451  TDETFKTREA IQHESGILGP LLYGEVGDTL LIIFKNQASR
   PYNIYPHGIT
 501  DVRPLYSRRL PKGVKHLKDF PILPGEIFKY KWTVTVEDGP
   TKSDPRCLTR
 551  YYSSFVNMER DLASGLIGPL LICYKESVDQ RGNQIMSDKR
   NVILFSVFDE
 601  NRSWYLTENI QRFLPNPAGV QLEDPEFQAS NIMHSINGYV
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  FDSLQLSVCL
 651  HEVAYWYILS IGAQTDFLSV FFSGYTFKHK MVYEDTLTLF
  PFSGETVFMS
 701  MENPGLWILG CHNSDFRNRG MTALLKVSSC DKNTGDYYED
  SYEDISAYLL
 751  SKNNAIEPRS FSQNPPVLKR HQREITRTTL QSDQEEIDYD
  DTISVEMKKE
 801  DFDIYDEDEN QSPRSFQKKT RHYFIAAVER LWDYGMSSSP
  HVLRNRAQSG
 851  SVPQFKKVVF QEFTDGSFTQ PLYRGELNEH LGLLGPYIRA
  EVEDNIMVTF
 901  RNQASRPYSF YSSLISYEED QRQGAEPRKN FVKPNETKTY
  FWKVQHHMAP
 951  TKDEFDCKAW AYFSDVDLEK DVHSGLIGPL LVCHTNTLNP
  AHGRQVTVQE
1001  FALFFTIFDE TKSWYFTENM ERNCRAPCNI QMEDPTFKEN
  YRFHAINGYI

1051  MDTLPGLVMA QDQRIRWYLL SMGSNENIHS IHFSGHVFTV
  RKKEEYKMAL
1101  YNLYPGVFET VEMLPSKAGI WRVECLIGEH LHAGMSTLFL
  VYSNKCQTPL
1151  GMASGHIRDF QITASGQYGQ WAPKLARLHY SGSINAWSTK
  EPFSWIKVDL
1201  LAPMIIHGIK TQGARQKFSS LYISQFIIMY SLDGKKWQTY
  RGNSTGTLMV
1251  FFGNVDSSGI KHNIFNPPII ARYIRLHPTH YSIRSTLRME
  LMGCDLNSCS
1301  MPLGMESKAI SDAQITASSY FTNMFATWSP SKARLHLQGR
  SNAWRPQVNN
1351  PKEWLQVDFQ KTMKVTGVTT QGVKSLLTSM YVKEFLISSS
  QDGHQWTLFF
1401  QNGKVKVFQG NQDSFTPVVN SLDPPLLTRY LRIHPQSWVH
  QIALRMEVLG
1451  CEAQDLYDKT HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI
  SRTPEVTCVV
1501  VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV
  SVLTVLHQDW
1551  LNGKEYKCKV SNKALPAPIE KTISKAKGQP REPQVYTLPP
  SRDELTKNQV
1601  SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS
  FFLYSKLTVD
1651  KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK*
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Example 14: A new class of coagulation factor VIII molecules with greater than threefold half-life extension in hemophilia A mice

[0364] The new class of FVIII molecules was designed to contain two polypeptides; one that consists of a single chain B-domain deleted (BDD) FVIII with XTEN inserted at one or more locations within the FVIII sequence, and one that is composed of the D'D3 region of VWF. Each polypeptide was also recombinantly fused to the Fc region of IgG1 to enable the D'D3 region to be correctly aligned to bind the FVIII moiety. The resulting FVIII variants were expressed in HEK 293 cells by transient transfection, and purified from the conditioned media. FVIII activity was evaluated by FVIII chromogenic assay and the pharmacokinetic properties were assessed in both FVIII knockout (HemA) and FVIII/VWF double knock-out (DKO) mice.

[0365] Incorporating XTEN and D'D3 region of VWF into rFVIII led to the uncoupling of the clearance of the fusion proteins from endogenous VWF while extending their circulating half-life. FVIII in this fusion configuration is completely shielded from interacting with VWF, as measured by biolayer interferometry (Octet) analysis. Consistent with this, their pharmacokinetic profiles in HemA and DKO mice were found to be identical, indicating that their clearance rate in mice was effectively disconnected from VWF. Optimization of XTEN length and the locations for inserting XTEN identified a subset of the proteins that have exceeded the VWF limitation (16 hours),

reaching a circulating half-life of up to 30 hours in HemA mice representing a 4-fold improvement over BDD-FVIII. Importantly, these proteins maintained their functionality, as judged by FVIII chromogenic assay.

[0366] The VWF dependency has set a fundamental limitation for half-life of therapeutic FVIII. Uncoupling FVIII from VWF clearance pathways while extending half-life by the fusion of D'D3 region of VWF and XTEN has generated a novel FVIII molecule with a 4-fold half-life extension. This is the first report of an engineered FVIII that has exceeded the half-life limitation observed through industry-wide efforts in development of long-lasting FVIII, representing a potentially significant advancement in prophylactic treatment of hemophilia A.

Table 25: Protein sequences of FVIII-XTEN-Fc and VWF-Fc constructs FVIII 195 protein sequence (dual chain FVIIIFc with two 144 AE XTENs at amino acid 1656 and 1900) (SEQ ID NO: 105)

[0367]

```
   1       MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQSDL
  GELPVDARFP
  51  PRVPKSFPFN TSVVYKKTLF VEFTDHLFNI AKPRPPWMGL
  LGPTIQAEVY
 101  DTVVITLKNM ASHPVSLHAV GVSYWKASEG AEYDDQTSQR
  EKEDDKVFPG
 151  GSHTYVWQVL KENGPMASDP LCLTYSYLSH VDLVKDLNSG
  LIGALLVCRE
 201  GSLAKEKTQT LHKFILLFAV FDEGKSWHSE TKNSLMQDRD
  AASARAWPKM
 251  HTVNGYVNRS LPGLIGCHRK SVYWHVIGMG TTPEVHSIFL
  EGHTFLVRNH
 301  RQASLEISPI TFLTAQTLLM DLGQFLLFCH ISSHQHDGME
  AYVKVDSCPE
 351  EPQLRMKNNE EAEDYDDDLT DSEMDVVRFD DDNSPSFIQI
  RSVAKKHPKT
 401  WVHYIAAEEE DWDYAPLVLA PDDRSYKSQY LNNGPQRIGR
  KYKKVRFMAY
 451  TDETFKTREA IQHESGILGP LLYGEVGDTL LIIFKNQASR
  PYNIYPHGIT
 501  DVRPLYSRRL PKGVKHLKDF PILPGEIFKY KWTVTVEDGP
  TKSDPRCLTR
 551  YYSSFVNMER DLASGLIGPL LICYKESVDQ RGNQIMSDKR
  NVILFSVFDE

 601  NRSWYLTENI QRFLPNPAGV QLEDPEFQAS NIMHSINGYV
   FDSLQLSVCL
 651  HEVAYWYILS IGAQTDFLSV FFSGYTFKHK MVYEDTLTLF
   PFSGETVFMS
 701  MENPGLWILG CHNSDFRNRG MTALLKVSSC DKNTGDYYED
   SYEDISAYLL
 751  SKNNAIEPRS FSQNPPVLKR HQREITRTTL QGAPGTPGSG
   TASSSPGASP
 801  GTSSTGSPGA SPGTSSTGSP GASPGTSSTG SPGSSPSAST
   GTGPGTPGSG
 851  TASSSPGASP GTSSTGSPGA SPGTSSTGSP GASPGTSSTG
   SPGSSTPSGA
 901  TGSPGSSTPS GATGSPGASP GTSSTGSPAS SSDQEEIDYD
   DTISVEMKKE
 951  DFDIYDEDEN QSPRSFQKKT RHYFIAAVER LWDYGMSSSP
   HVLRNRAQSG
1001  SVPQFKKVVF QEFTDGSFTQ PLYRGELNEH LGLLGPYIRA
   EVEDNIMVTF
1051  RNQASRPYSF YSSLISYEED QRQGAEPRKN FVKPNETKTY
   FWKVQHHMAP
1101  TKDEFDCKAW AYFSDVDLEK DVHSGLIGPL LVCHTNTLNP
   AHGRQVTVQE
1151  FALFFTIFDE TKSWYFTENM ERNCRGAPTS ESATPESGPG
   SEPATSGSET
1201  PGTSESATPE SGPGSEPATS GSETPGTSES ATPESGPGTS
   TEPSEGSAPG
1251  TSESATPESG PGSPAGSPTS TEEGSPAGSP TSTEEGSPAG
   SPISTEEGTS
```

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1301  ESATPESGPG TSTEPSEGSA PGASSAPCNI QMEDPTFKEN
   YRFHAINGYI
1351  MDTLPGLVMA QDQRIRWYLL SMGSNENIHS IHFSGHVFTV
   RKKEEYKMAL
1401  YNLYPGVFET VEMLPSKAGI WRVECLIGEH LHAGMSTLFL
   VYSNKCQTPL
1451  GMASGHIRDF QITASGQYGQ WAPKLARLHY SGSINAWSTK
   EPFSWIKVDL
1501  LAPMIIHGIK TQGARQKFSS LYISQFIIMY SLDGKKWQTY
   RGNSTGTLMV
1551  FFGNVDSSGI KHNIFNPPII ARYIRLHPTH YSIRSTLRME
   LMGCDLNSCS
1601  MPLGMESKAI SDAQITASSY FTNMFATWSP SKARLHLQGR
   SNAWRPQVNN
1651  PKEWLQVDFQ KTMKVTGVTT QGVKSLLTSM YVKEFLISSS
   QDGHQWTLFF
1701  QNGKVKVFQG NQDSFTPVVN SLDPPLLTRY LRIHPQSWVH
   QIALRMEVLG
1751  CEAQDLYDKT HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI
   SRTPEVTCVV
1801  VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV
   SVLTVLHQDW

1851  LNGKEYKCKV SNKALPAPIE KTISKAKGQP REPQVYTLPP
   SRDELTKNQV
1901  SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS
   FFLYSKLTVD
1951  KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK*
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FVIII 196 protein sequence (dual chain FVIIIFc with three 144 AE XTENs at amino acid 26, 1656 and 1900) (SEQ ID NO: 106)

```
   1       MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQSDL
   GELPVGAPGS
  51  SPSASTGTGP GSSPSASTGT GPGASPGTSS TGSPGASPGT
   SSTGSPGSST
 101  PSGATGSPGS SPSASTGTGP GASPGTSSTG SPGSSPSAST
   GTGPGTPGSG
 151  TASSSPGSST PSGATGSPGS STPSGATGSP GASPGTSSTG
   SPASSDARFP
 201  PRVPKSFPFN TSVVYKKTLF VEFTDHLFNI AKPRPPWMGL
   LGPTIQAEVY
 251  DTVVITLKNM ASHPVSLHAV GVSYWKASEG AEYDDQTSQR
   EKEDDKVFPG
 301  GSHTYVWQVL KENGPMASDP LCLTYSYLSH VDLVKDLNSG
   LIGALLVCRE
 351  GSLAKEKTQT LHKFILLFAV FDEGKSWHSE TKNSLMQDRD
   AASARAWPKM
 401  HTVNGYVNRS LPGLIGCHRK SVYWHVIGMG TTPEVHSIFL
   EGHTFLVRNH
 451  RQASLEISPI TFLTAQTLLM DLGQFLLFCH ISSHQHDGME
   AYVKVDSCPE
 501  EPQLRMKNNE EAEDYDDDLT DSEMDVVRFD DDNSPSFIQI
   RSVAKKHPKT
 551  WVHYIAAEEE DWDYAPLVLA PDDRSYKSQY LNNGPQRIGR
   KYKKVRFMAY
 601  TDETFKTREA IQHESGILGP LLYGEVGDTL LIIFKNQASR
   PYNIYPHGIT
 651  DVRPLYSRRL PKGVKHLKDF PILPGEIFKY KWTVTVEDGP
   TKSDPRCLTR
 701  YYSSFVNMER DLASGLIGPL LICYKESVDQ RGNQIMSDKR
   NVILFSVFDE
 751  NRSWYLTENI QRFLPNPAGV QLEDPEFQAS NIMHSINGYV
   FDSLQLSVCL
 801  HEVAYWYILS IGAQTDFLSV FFSGYTFKHK MVYEDTLTLF
   PFSGETVFMS
 851  MENPGLWILG CHNSDFRNRG MTALLKVSSC DKNTGDYYED
   SYEDISAYLL
 901  SKNNAIEPRS FSQNPPVLKR HQREITRTTL QGAPGTPGSG
   TASSSPGASP
 951  GTSSTGSPGA SPGTSSTGSP GASPGTSSTG SPGSSPSAST
   GTGPGTPGSG
1001  TASSSPGASP GTSSTGSPGA SPGTSSTGSP GASPGTSSTG
```

```
1001  TASSSPGASP GTSSTGSPGA SPGTSSTGSP GASPGTSSTG
   SPGSSTPSGA

1051  TGSPGSSTPS GATGSPGASP GTSSTGSPAS SSDQEEIDYD
   DTISVEMKKE
1101  DFDIYDEDEN QSPRSFQKKT RHYFIAAVER LWDYGMSSSP
   HVLRNRAQSG
1151  SVPQFKKVVF QEFTDGSFTQ PLYRGELNEH LGLLGPYIRA
   EVEDNIMVTF
1201  RNQASRPYSF YSSLISYEED QRQGAEPRKN FVKPNETKTY
   FWKVQHHMAP
1251  TKDEFDCKAW AYFSDVDLEK DVHSGLIGPL LVCHTNTLNP
   AHGRQVTVQE
1301  FALFFTIFDE TKSWYFTENM ERNCRGAPTS ESATPESGPG
   SEPATSGSET
1351  PGTSESATPE SGPGSEPATS GSETPGTSES ATPESGPGTS
   TEPSEGSAPG
1401  TSESATPESG PGSPAGSPTS TEEGSPAGSP TSTEEGSPAG
   SPTSTEEGTS
1451  ESATPESGPG TSTEPSEGSA PGASSAPCNI QMEDPTFKEN
   YRFHAINGYI
1501  MDTLPGLVMA QDQRIRWYLL SMGSNENIHS IHFSGHVFTV
   RKKEEYKMAL
1551  YNLYPGVFET VEMLPSKAGI WRVECLIGEH LHAGMSTLFL
   VYSNKCQTPL
1601  GMASGHIRDF QITASGQYGQ WAPKLARLHY SGSINAWSTK
   EPFSWIKVDL
1651  LAPMIIHGIK TQGARQKFSS LYISQFIIMY SLDGKKWQTY
   RGNSTGTLMV
1701  FFGNVDSSGI KHNIFNPPII ARYIRLHPTH YSIRSTLRME
   LMGCDLNSCS
1751  MPLGMESKAI SDAQITASSY FTNMFATWSP SKARLHLQGR
   SNAWRPQVNN
1801  PKEWLQVDFQ KTMKVTGVTT QGVKSLLTSM YVKEFLISSS
   QDGHQWTLFF
1851  QNGKVKVFQG NQDSFTPVVN SLDPPLLTRY LRIHPQSWVH
   QIALRMEVLG
1901  CEAQDLYDKT HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI
   SRTPEVTCVV
1951  VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV
   SVLTVLHQDW
2001  LNGKEYKCKV SNKALPAPIE KTISKAKGQP REPQVYTLPP
   SRDELTKNQV
2051  SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS
   FFLYSKLTVD
2101  KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK*
```

FVIII 199 protein sequence (single chain FVIIIFc with three 144 AE XTENs at amino acid 1656 and 1900) (SEQ ID NO: 107)

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 1        MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQSDL
GELPVDARFP
51  PRVPKSFPFN TSVVYKKTLF VEFTDHLFNI AKPRPPWMGL
LGPTIQAEVY

101  DTVVITLKNM ASHPVSLHAV GVSYWKASEG AEYDDQTSQR
  EKEDDKVFPG
151  GSHTYVWQVL KENGPMASDP LCLTYSYLSH VDLVKDLNSG
  LIGALLVCRE
201  GSLAKEKTQT LHKFILLFAV FDEGKSWHSE TKNSLMQDRD
  AASARAWPKM
251  HTVNGYVNRS LPGLIGCHRK SVYWHVIGMG TTPEVHSIFL
  EGHTFLVRNH
301  RQASLEISPI TFLTAQTLLM DLGQFLLFCH ISSHQHDGME
  AYVKVDSCPE
351  EPQLRMKNNE EAEDYDDDLT DSEMDVVRFD DDNSPSFIQI
  RSVAKKHPKT
401  WVHYIAAEEE DWDYAPLVLA PDDRSYKSQY LNNGPQRIGR
  KYKKVRFMAY
451  TDETFKTREA IQHESGILGP LLYGEVGDTL LIIFKNQASR
  PYNIYPHGIT
501  DVRPLYSRRL PKGVKHLKDF PILPGEIFKY KWTVTVEDGP
  TKSDPRCLTR
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```
 551  YYSSFVNMER DLASGLIGPL LICYKESVDQ RGNQIMSDKR
  NVILFSVFDE
 601  NRSWYLTENI QRFLPNPAGV QLEDPEFQAS NIMHSINGYV
  FDSLQLSVCL
 651  HEVAYWYILS IGAQTDFLSV FFSGYTFKHK MVYEDTLTLF
  PFSGETVFMS
 701  MENPGLWILG CHNSDFRNRG MTALLKVSSC DKNTGDYYED
  SYEDISAYLL
 751  SKNNAIEPRS FSQNPPVLKR HQAEITRTTL QGAPGTPGSG
  TASSSPGASP
 801  GTSSTGSPGA SPGTSSTGSP GASPGTSSTG SPGSSPSAST
  GTGPGTPGSG
 851  TASSSPGASP GTSSTGSPGA SPGTSSTGSP GASPGTSSTG
  SPGSSTPSGA
 901  TGSPGSSTPS GATGSPGASP GTSSTGSPAS SSDQEEIDYD
  DTISVEMKKE
 951  DFDIYDEDEN QSPRSFQKKT RHYFIAAVER LWDYGMSSSP
  HVLRNRAQSG
1001  SVPQFKKVVF QEFTDGSFTQ PLYRGELNEH LGLLGPYIRA
  EVEDNIMVTF
1051  RNQASRPYSF YSSLISYEED QRQGAEPRKN FVKPNETKTY
  FWKVQHHMAP
1101  TKDEFDCKAW AYFSDVDLEK DVHSGLIGPL LVCHTNTLNP
  AHGRQVTVQE
1151  FALFFTIFDE TKSWYFTENM ERNCRGAPTS ESATPESGPG
  SEPATSGSET
1201  PGTSESATPE SGPGSEPATS GSETPGTSES ATPESGPGTS
  TEPSEGSAPG
1251  TSESATPESG PGSPAGSPTS TEEGSPAGSP TSTEEGSPAG
  SPISTEEGTS
1301  ESATPESGPG TSTEPSEGSA PGASSAPCNI QMEDPTFKEN
  YRFHAINGYI

1351  MDTLPGLVMA QDQRIRWYLL SMGSNENIHS IHFSGHVFTV
  RKKEEYKMAL
1401  YNLYPGVFET VEMLPSKAGI WRVECLIGEH LHAGMSTLFL
  VYSNKCQTPL
1451  GMASGHIRDF QITASGQYGQ WAPKLARLHY SGSINAWSTK
  EPFSWIKVDL
1501  LAPMIIHGIK TQGARQKFSS LYISQFIIMY SLDGKKWQTY
  RGNSTGTLMV
1551  FFGNVDSSGI KHNIFNPPII ARYIRLHPTH YSIRSTLRME
  LMGCDLNSCS
1601  MPLGMESKAI SDAQITASSY FTNMFATWSP SKARLHLQGR
  SNAWRPQVNN
1651  PKEWLQVDFQ KTMKVTGVTT QGVKSLLTSM YVKEFLISSS
  QDGHQWTLFF
1701  QNGKVKVFQG NQDSFTPVVN SLDPPLLTRY LRIHPQSWVH
  QIALRMEVLG
1751  CEAQDLYDKT HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI
  SRTPEVTCVV
1801  VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV
  SVLTVLHQDW
1851  LNGKEYKCKV SNKALPAPIE KTISKAKGQP REPQVYTLPP
  SRDELTKNQV
1901  SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS
  FFLYSKLTVD
1951  KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK*
```

FVIII 201 protein sequence (single chain FVIIIFc with three 144 AE XTENs at amino acid 26, 1656 &1900) (SEQ ID NO: 108)

```
   1  MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQSDL
  GELPVGAPGS
  51  SPSASTGTGP GSSPSASTGT GPGASPGTSS TGSPGASPGT
  SSTGSPGSST
 101  PSGATGSPGS SPSASTGTGP GASPGTSSTG SPGSSPSAST
  GTGPGTPGSG
 151  TASSSPGSST PSGATGSPGS STPSGATGSP GASPGTSSTG
  SPASSDARFP
 201  PRVPKSFPFN TSVVYKKTLF VEFTDHLFNI AKPRPPWMGL
  LGPTIQAEVY
```

```
251  DTVVITLKNM ASHPVSLHAV GVSYWKASEG AEYDDQTSQR
  EKEDDKVFPG
301  GSHTYVWQVL KENGPMASDP LCLTYSYLSH VDLVKDLNSG
  LIGALLVCRE
351  GSLAKEKTQT LHKFILLFAV FDEGKSWHSE TKNSLMQDRD
  AASARAWPKM
401  HTVNGYVNRS LPGLIGCHRK SVYWHVIGMG TTPEVHSIFL
  EGHTFLVRNH
451  RQASLEISPI TFLTAQTLLM DLGQFLLFCH ISSHQHDGME
  AYVKVDSCPE
501  EPQLRMKNNE EAEDYDDDLT DSEMDVVRFD DDNSPSFIQI
  RSVAKKHPKT

551  WVHYIAAEEE DWDYAPLVLA PDDRSYKSQY LNNGPQRIGR
  KYKKVRFMAY
601  TDETFKTREA IQHESGILGP LLYGEVGDTL LIIFKNQASR
  PYNIYPHGIT
651  DVRPLYSRRL PKGVKHLKDF PILPGEIFKY KWTVTVEDGP
  TKSDPRCLTR
701  YYSSFVNMER DLASGLIGPL LICYKESVDQ RGNQIMSDKR
  NVILFSVFDE
751  NRSWYLTENI QRFLPNPAGV QLEDPEFQAS NIMHSINGYV
  FDSLQLSVCL
801  HEVAYWYILS IGAQTDFLSV FFSGYTFKHK MVYEDTLTLF
  PFSGETVFMS
851  MENPGLWILG CHNSDFRNRG MTALLKVSSC DKNTGDYYED
  SYEDISAYLL
901  SKNNAIEPRS FSQNPPVLKR HQAEITRTTL QGAPGTPGSG
  TASSSPGASP
951  GTSSTGSPGA SPGTSSTGSP GASPGTSSTG SPGSSPSAST
  GTGPGTPGSG
1001 TASSSPGASP GTSSTGSPGA SPGTSSTGSP GASPGTSSTG
  SPGSSTPSGA
1051 TGSPGSSTPS GATGSPGASP GTSSTGSPAS SSDQEEIDYD
  DTISVEMKKE
1101 DFDIYDEDEN QSPRSFQKKT RHYFIAAVER LWDYGMSSSP
  HVLRNRAQSG
1151 SVPQFKKVVF QEFTDGSFTQ PLYRGELNEH LGLLGPYIRA
  EVEDNIMVTF
1201 RNQASRPYSF YSSLISYEED QRQGAEPRKN FVKPNETKTY
  FWKVQHHMAP
1251 TKDEFDCKAW AYFSDVDLEK DVHSGLIGPL LVCHTNTLNP
  AHGRQVTVQE
1301 FALFFTIFDE TKSWYFTENM ERNCRGAPTS ESATPESGPG
  SEPATSGSET
1351 PGTSESATPE SGPGSEPATS GSETPGTSES ATPESGPGTS
  TEPSEGSAPG
1401 TSESATPESG PGSPAGSPTS TEEGSPAGSP TSTEEGSPAG
  SPTSTEEGTS
1451 ESATPESGPG TSTEPSEGSA PGASSAPCNI QMEDPTFKEN
  YRFHAINGYI
1501 MDTLPGLVMA QDQRIRWYLL SMGSNENIHS IHFSGHVFTV
  RKKEEYKMAL
1551 YNLYPGVFET VEMLPSKAGI WRVECLIGEH LHAGMSTLFL
  VYSNKCQTPL
1601 GMASGHIRDF QITASGQYGQ WAPKLARLHY SGSINAWSTK
  EPFSWIKVDL
1651 LAPMIIHGIK TQGARQKFSS LYISQFIIMY SLDGKKWQTY
  RGNSTGTLMV
1701 FFGNVDSSGI KHNIFNPPII ARYIRLHPTH YSIRSTLRME
  LMGCDLNSCS
1751 MPLGMESKAI SDAQITASSY FTNMFATWSP SKARLHLQGR
  SNAWRPQVNN

1801 PKEWLQVDFQ KTMKVTGVTT QGVKSLLTSM YVKEFLISSS
  QDGHQWTLFF
1851 QNGKVKVFQG NQDSFTPVVN SLDPPLLTRY LRIHPQSWVH
  QIALRMEVLG
1901 CEAQDLYDKT HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI
  SRTPEVTCVV
1951 VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV
  SVLTVLHQDW
2001 LNGKEYKCKV SNKALPAPIE KTISKAKGQP REPQVYTLPP
```

SRDELTKNQV
2051 SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS
FFLYSKLTVD
2101 KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK*

FVIII 203 protein sequence (single chain FVIIIFc with two AE XTENs; one 288AE XTEN in B-domain and one 144 AE XTEN at amino acid 1900) (SEQ ID NO: 109)

1 MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQSDL
GELPVDARFP
51 PRVPKSFPFN TSVVYKKTLF VEFTDHLFNI AKPRPPWMGL
LGPTIQAEVY
101 DTVVITLKNM ASHPVSLHAV GVSYWKASEG AEYDDQTSQR
EKEDDKVFPG
151 GSHTYVWQVL KENGPMASDP LCLTYSYLSH VDLVKDLNSG
LIGALLVCRE
201 GSLAKEKTQT LHKFILLFAV FDEGKSWHSE TKNSLMQDRD
AASARAWPKM
251 HTVNGYVNRS LPGLIGCHRK SVYWHVIGMG TTPEVHSIFL
EGHTFLVRNH
301 RQASLEISPI TFLTAQTLLM DLGQFLLFCH ISSHQHDGME
AYVKVDSCPE
351 EPQLRMKNNE EAEDYDDDLT DSEMDVVRFD DDNSPSFIQI
RSVAKKHPKT
401 WVHYIAAEEE DWDYAPLVLA PDDRSYKSQY LNNGPQRIGR
KYKKVRFMAY
451 TDETFKTREA IQHESGILGP LLYGEVGDTL LIIFKNQASR
PYNIYPHGIT
501 DVRPLYSRRL PKGVKHLKDF PILPGEIFKY KWTVTVEDGP
TKSDPRCLTR
551 YYSSFVNMER DLASGLIGPL LICYKESVDQ RGNQIMSDKR
NVILFSVFDE
601 NRSWYLTENI QRFLPNPAGV QLEDPEFQAS NIMHSINGYV
FDSLQLSVCL
651 HEVAYWYILS IGAQTDFLSV FFSGYTFKHK MVYEDTLTLF
PFSGETVFMS
701 MENPGLWILG CHNSDFRNRG MTALLKVSSC DKNTGDYYED
SYEDISAYLL
751 SKNNAIEPRS FSQNGAPGTS ESATPESGPG SEPATSGSET
PGTSESATPE
801 SGPGSEPATS GSETPGTSES ATPESGPGTS TEPSEGSAPG
SPAGSPTSTE

851 EGTSESATPE SGPGSEPATS GSETPGTSES ATPESGPGSP
AGSPTSTEEG
901 SPAGSPTSTE EGTSTEPSEG SAPGTSESAT PESGPGTSES
ATPESGPGTS
951 ESATPESGPG SEPATSGSET PGSEPATSGS ETPGSPAGSP
TSTEEGTSTE
1001 PSEGSAPGTS TEPSEGSAPG SEPATSGSET PGTSESATPE
SGPGTSTEPS
1051 EGSAPASSPP VLKRHQAEIT RTTLQSDQEE IDYDDTISVE
MKKEDFDIYD
1101 EDENQSPRSF QKKTRHYFIA AVERLWDYGM SSSPHVLRNR
AQSGSVPQFK
1151 KVVFQEFTDG SFTQPLYRGE LNEHLGLLGP YIRAEVEDNI
MVTFRNQASR
1201 PYSFYSSLIS YEEDQRQGAE PRKNFVKPNE TKTYFWKVQH
HMAPTKDEFD
1251 CKAWAYFSDV DLEKDVHSGL IGPLLVCHTN TLNPAHGRQV
TVQEFALFFT
1301 IFDETKSWYF TENMERNCRG APTSESATPE SGPGSEPATS
GSETPGTSES
1351 ATPESGPGSE PATSGSETPG TSESATPESG PGTSTEPSEG
SAPGTSESAT
1401 PESGPGSPAG SPTSTEEGSP AGSPTSTEEG SPAGSPTSTE
EGTSESATPE
1451 SGPGTSTEPS EGSAPGASSA PCNIQMEDPT FKENYRFHAI
NGYIMDTLPG
1501 LVMAQDQRIR WYLLSMGSNE NIHSIHFSGH VFTVRKKEEY
KMALYNLYPG
1551 VFETVEMLPS KAGIWRVECL IGEHLHAGMS TLFLVYSNKC
QTPLGMASGH

```
1601  IRDFQITASG QYGQWAPKLA RLFYSGSINA WSTKEPFSWI
   KVDLLAPMII
1651  HGIKTQGARQ KFSSLYISQF IIMYSLDGKK WQTYRGNSTG
   TLMVFFGNVD
1701  SSGIKHNIFN PPIIARYIRL HPTHYSIRST LRMELMGCDL
   NSCSMPLGME
1751  SKAISDAQIT ASSYFTNMFA TWSPSKARLH LQGRSNAWRP
   QVNNPKEWLQ
1801  VDFQKTMKVT GVTTQGVKSL LTSMYVKEFL ISSSQDGHQW
   TLFFQNGKVK
1851  VFQGNQDSFT PVVNSLDPPL LTRYLRIHPQ SWVHQIALRM
   EVLGCEAQDL
1901  YDKTHTCPPC PAPELLGGPS VFLFPPKPKD TLMISRTPEV
   TCVVVDVSHE
1951  DPEVKFNWYV DGVEVHNAKT KPREEQYNST YRVVSVLTVL
   HQDWLNGKEY
2001  KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSRDELT
   KNQVSLTCLV
2051  KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSK
   LTVDKSRWQQ
2101  GNVFSCSVMH EALHNHYTQK SLSLSPGK*
```

FVIII 204 protein sequence (single chain FVIIIFc with two AE XTENs; one 288AE XTEN in B-domain and one 144 AE XTEN at amino acid 403) (SEQ ID NO: 110)

```
   1  MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQSDL
   GELPVDARFP
  51  PRVPKSFPFN TSVVYKKTLF VEFTDHLFNI AKPRPPWMGL
   LGPTIQAEVY
 101  DTVVITLKNM ASHPVSLHAV GVSYWKASEG AEYDDQTSQR
   EKEDDKVFPG
 151  GSHTYVWQVL KENGPMASDP LCLTYSYLSH VDLVKDLNSG
   LIGALLVCRE
 201  GSLAKEKTQT LHKFILLFAV FDEGKSWHSE TKNSLMQDRD
   AASARAWPKM
 251  HTVNGYVNRS LPGLIGCHRK SVYWHVIGMG TTPEVHSIFL
   EGHTFLVRNH
 301  RQASLEISPI TFLTAQTLLM DLGQFLLFCH ISSHQHDGME
   AYVKVDSCPE
 351  EPQLRMKNNE EAEDYDDDLT DSEMDVVRFD DDNSPSFIQI
   RSVAKKHPKT
 401  WVHYIAAEEE DWDYAPLVLA PDGAPTSTEP SEGSAPGSPA
   GSPTSTEEGT
 451  STEPSEGSAP GTSTEPSEGS APGTSESATP ESGPGTSTEP
   SEGSAPGTSE
 501  SATPESGPGS EPATSGSETP GTSTEPSEGS APGTSTEPSE
   GSAPGTSESA
 551  TPESGPGTSE SATPESGPGA SSDRSYKSQY LNNGPQRIGR
   KYKKVRFMAY
 601  TDETFKTREA IQHESGILGP LLYGEVGDTL LIIFKNQASR
   PYNIYPHGIT
 651  DVRPLYSRRL PKGVKHLKDF PILPGEIFKY KWTVTVEDGP
   TKSDPRCLTR
 701  YYSSFVNMER DLASGLIGPL LICYKESVDQ RGNQIMSDKR
   NVILFSVFDE
 751  NRSWYLTENI QRFLPNPAGV QLEDPEFQAS NIMHSINGYV
   FDSLQLSVCL
 801  HEVAYWYILS IGAQTDFLSV FFSGYTFKHK MVYEDTLTLF
   PFSGETVFMS
 851  MENPGLWILG CHNSDFRNRG MTALLKVSSC DKNTGDYYED
   SYEDISAYLL
 901  SKNNAIEPRS FSQNGAPGTS ESATPESGPG SEPATSGSET
   PGTSESATPE
 951  SGPGSEPATS GSETPGTSES ATPESGPGTS TEPSEGSAPG
   SPAGSPTSTE
1001  EGTSESATPE SGPGSEPATS GSETPGTSES ATPESGPGSP
   AGSPTSTEEG
1051  SPAGSPTSTE EGTSTEPSEG SAPGTSESAT PESGPGTSES
   ATPESGPGTS
1101  ESATPESGPG SEPATSGSET PGSEPATSGS ETPGSPAGSP
   TSTEEGTSTE

1151  PSEGSAPGTS TEPSEGSAPG SEPATSGSET PGTSESATPE
```

SGPGTSTEPS
1201 EGSAPASSPP VLKRHQAEIT RTTLQSDQEE IDYDDTISVE
MKKEDFDIYD
1251 EDENQSPRSF QKKTRHYFIA AVERLWDYGM SSSPHVLRNR
AQSGSVPQFK
1301 KVVFQEFTDG SFTQPLYRGE LNEHLGLLGP YIRAEVEDNI
MVTFRNQASR
1351 PYSFYSSLIS YEEDQRQGAE PRKNFVKPNE TKTYFWKVQH
HMAPTKDEFD
1401 CKAWAYFSDV DLEKDVHSGL IGPLLVCHTN TLNPAHGRQV
TVQEFALFFT
1451 IFDETKSWYF TENMERNCRA PCNIQMEDPT FKENYRFHAI
NGYIMDTLPG
1501 LVMAQDQRIR WYLLSMGSNE NIHSIHFSGH VFTVRKKEEY
KMALYNLYPG
1551 VFETVEMLPS KAGIWRVECL IGEHLHAGMS TLFLVYSNKC
QTPLGMASGH
1601 IRDFQITASG QYGQWAPKLA RLHYSGSINA WSTKEPFSWI
KVDLLAPMII
1651 HGIKTQGARQ KFSSLYISQF IIMYSLDGKK WQTYRGNSTG
TLMVFFGNVD
1701 SSGIKHNIFN PPIIARYIRL HPTHYSIRST LRMELMGCDL
NSCSMPLGME
1751 SKAISDAQIT ASSYFTNMFA TWSPSKARLH LQGRSNAWRP
QVNNPKEWLQ
1801 VDFQKTMKVT GVTTQGVKSL LTSMYVKEFL ISSSQDGHQW
TLFFQNGKVK
1851 VFQGNQDSFT PVVNSLDPPL LTRYLRIHPQ SWVHQIALRM
EVLGCEAQDL
1901 YDKTHTCPPC PAPELLGGPS VFLFPPKPKD TLMISRTPEV
TCVVVDVSHE
1951 DPEVKFNWYV DGVEVHNAKT KPREEQYNST YRVVSVLTVL
HQDWLNGKEY
2001 KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSRDELT
KNQVSLTCLV
2051 KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSK
LTVDKSRWQQ
2101 GNVFSCSVMH EALHNHYTQK SLSLSPGK*

FVIII 205 protein sequence (single chain FVIIIFc with two AE XTENs; one 288AE XTEN in B-domain and one 144 AE XTEN at amino acid 18) (SEQ ID NO: 111)

\- 1 MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQGAP
TSESATPESG
51 PGSEPATSGS ETPGTSESAT PESGPGSEPA TSGSETPGTS
ESATPESGPG
101 TSTEPSEGSA PGSPAGSPTS TEEGTSESAT PESGPGSEPA
TSGSETPGTS

151 ESATPESGPG SPAGSPTSTE EGSPAGSPTS TEEGASSSDL
GELPVDARFP
201 PRVPKSFPFN TSVVYKKTLF VEFTDHLFNI AKPRPPWMGL
LGPTIQAEVY
251 DTVVITLKNM ASHPVSLHAV GVSYWKASEG AEYDDQTSQR
EKEDDKVFPG
301 GSHTYVWQVL KENGPMASDP LCLTYSYLSH VDLVKDLNSG
LIGALLVCRE
351 GSLAKEKTQT LHKFILLFAV FDEGKSWHSE TKNSLMQDRD
AASARAWPKM
401 HTVNGYVNRS LPGLIGCHRK SVYWHVIGMG TTPEVHSIFL
EGHTFLVRNH
451 RQASLEISPI TFLTAQTLLM DLGQFLLFCH ISSHQHDGME
AYVKVDSCPE
501 EPQLRMKNNE EAEDYDDDLT DSEMDVVRFD DDNSPSFIQI
RSVAKKHPKT
551 WVHYIAAEEE DWDYAPLVLA PDDRSYKSQY LNNGPQRIGR
KYKKVRFMAY
601 TDETFKTREA IQHESGILGP LLYGEVGDTL LIIFKNQASR
PYNIYPHGIT
651 DVRPLYSRRL PKGVKHLKDF PILPGEIFKY KWTVTVEDGP
TKSDPRCLTR
701 YYSSFVNMER DLASGLIGPL LICYKESVDQ RGNQIMSDKR
NVILFSVFDE

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 751  NRSWYLTENI QRFLPNPAGV QLEDPEFQAS NIMHSINGYV
  FDSLQLSVCL
 801  HEVAYWYILS IGAQTDFLSV FFSGYTFKHK MVYEDTLTLF
  PFSGETVFMS
 851  MENPGLWILG CHNSDFRNRG MTALLKVSSC DKNTGDYYED
  SYEDISAYLL
 901  SKNNAIEPRS FSQNGAPGTS ESATPESGPG SEPATSGSET
  PGTSESATPE
 951  SGPGSEPATS GSETPGTSES ATPESGPGTS TEPSEGSAPG
  SPAGSPTSTE
1001  EGTSESATPE SGPGSEPATS GSETPGTSES ATPESGPGSP
  AGSPTSTEEG
1051  SPAGSPTSTE EGTSTEPSEG SAPGTSESAT PESGPGTSES
  ATPESGPGTS
1101  ESATPESGPG SEPATSGSET PGSEPATSGS ETPGSPAGSP
  TSTEEGTSTE
1151  PSEGSAPGTS TEPSEGSAPG SEPATSGSET PGTSESATPE
  SGPGTSTEPS
1201  EGSAPASSPP VLKRHQAEIT RTTLQSDQEE IDYDDTISVE
  MKKEDFDIYD
1251  EDENQSPRSF QKKTRHYFIA AVERLWDYGM SSSPHVLRNR
  AQSGSVPQFK
1301  KVVFQEFTDG SFTQPLYRGE LNEHLGLLGP YIRAEVEDNI
  MVTFRNQASR
1351  PYSFYSSLIS YEEDQRQGAE PRKNFVKPNE TKTYFWKVQH
  HMAPTKDEFD

1401  CKAWAYFSDV DLEKDVHSGL IGPLLVCHTN TLNPAHGRQV
  TVQEFALFFT
1451  IFDETKSWYF TENMERNCRA PCNIQMEDPT FKENYRFHAI
  NGYIMDTLPG
1501  LVMAQDQRIR WYLLSMGSNE NIHSIHFSGH VFTVRKKEEY
  KMALYNLYPG
1551  VFETVEMLPS KAGIWRVECL IGEHLHAGMS TLFLVYSNKC
  QTPLGMASGH
1601  IRDFQITASG QYGQWAPKLA RLHYSGSINA WSTKEPFSWI
  KVDLLAPMII
1651  HGIKTQGARQ KFSSLYISQF IIMYSLDGKK WQTYRGNSTG
  TLMVFFGNVD
1701  SSGIKHNIFN PPIIARYIRL HPTHYSIRST LRMELMGCDL
  NSCSMPLGME
1751  SKAISDAQIT ASSYFTNMFA TWSPSKARLH LQGRSNAWRP
  QVNNPKEWLQ
1801  VDFQKTMKVT GVTTQGVKSL LTSMYVKEFL ISSSQDGHQW
  TLFFQNGKVK
1851  VFQGNQDSFT PVVNSLDPPL LTRYLRIHPQ SWVHQIALRM
  EVLGCEAQDL
1901  YDKTHTCPPC PAPELLGGPS VFLFPPKPKD TLMISRTPEV
  TCVVVDVSHE
1951  DPEVKFNWYV DGVEVHNAKT KPREEQYNST YRVVSVLTVL
  HQDWLNGKEY
2001  KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSRDELT
  KNQVSLTCLV
2051  KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSK
  LTVDKSRWQQ
2101  GNVFSCSVMH EALHNHYTQK SLSLSPGK*
```

pSYN FVIII 266 protein sequence (FVIII Fc with 42 AE-XTEN at amino acid 18 and 288 AE XTEN in B-domain) SEQ ID NO: 112

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   1  MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQGAP
  GSPAGSPTST
  51  EEGTSESATP ESGPGSEPAT SGSETPASSS DLGELPVDAR
  FPPRVPKSFP
 101  FNTSVVYKKT LFVEFTDHLF NIAKPRPPWM GLLGPTIQAE
  VYDTVVITLK
 151  NMASHPVSLH AVGVSYWKAS EGAEYDDQTS QREKEDDKVF
  PGGSHTYVWQ
 201  VLKENGPMAS DPLCLTYSYL SHVDLVKDLN SGLIGALLVC
  REGSLAKEKT
 251  QTLHKFILLF AVFDEGKSWH SETKNSLMQD RDAASARAWP
  KMHTVNGYVN
```

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301  RSLPGLIGCH RKSVYWHVIG MGTTPEVHSI FLEGHTFLVR
  NHRQASLEIS
351  PITFLTAQTL LMDLGQFLLF CHISSHQHDG MEAYVKVDSC
  PEEPQLRMKN
401  NEEAEDYDDD LTDSEMDVVR FDDDNSPSFI QIRSVAKKHP
  KTWVHYIAAE

451  EEDWDYAPLV LAPDDRSYKS QYLNNGPQRI GRKYKKVRFM
  AYTDETFKTR
501  EAIQHESGIL GPLLYGEVGD TLLIIFKNQA SRPYNIYPHG
  ITDVRPLYSR
551  RLPKGVKHLK DFPILPGEIF KYKWTVTVED GPTKSDPRCL
  TRYYSSFVNM
601  ERDLASGLIG PLLICYKESV DQRGNQIMSD KRNVILFSVF
  DENRSWYLTE
651  NIQRFLPNPA GVQLEDPEFQ ASNIMHSING YVFDSLQLSV
  CLHEVAYWYI
701  LSIGAQTDFL SVFFSGYTFK HKMVYEDTLT LFPFSGETVF
  MSMENPGLWI
751  LGCHNSDFRN RGMTALLKVS SCDKNTGDYY EDSYEDISAY
  LLSKNNAIEP
801  RSFSQNGAPG TSESATPESG PGSEPATSGS ETPGTSESAT
  PESGPGSEPA
851  TSGSETPGTS ESATPESGPG TSTEPSEGSA PGSPAGSPTS
  TEEGTSESAT
901  PESGPGSEPA TSGSETPGTS ESATPESGPG SPAGSPTSTE
  EGSPAGSPTS
951  TEEGTSTEPS EGSAPGTSES ATPESGPGTS ESATPESGPG
  TSESATPESG
1001  PGSEPATSGS ETPGSEPATS GSETPGSPAG SPTSTEEGTS
  TEPSEGSAPG
1051  TSTEPSEGSA PGSEPATSGS ETPGTSESAT PESGPGTSTE
  PSEGSAPASS
1101  PPVLKRHQAE ITRTTLQSDQ EEIDYDDTIS VEMKKEDFDI
  YDEDENQSPR
1151  SFQKKTRHYF IAAVERLWDY GMSSSPHVLR NRAQSGSVPQ
  FKKVVFQEFT
1201  DGSFTQPLYR GELNEHLGLL GPYIRAEVED NIMVTFRNQA
  SRPYSFYSSL
1251  ISYEEDQRQG AEPRKNFVKP NETKTYFWKV QHHMAPTKDE
  FDCKAWAYFS
1301  DVDLEKDVHS GLIGPLLVCH TNTLNPAHGR QVTVQEFALF
  FTIFDETKSW
1351  YFTENMERNC RAPCNIQMED PTFKENYRFH AINGYIMDTL
  PGLVMAQDQR
1401  IRWYLLSMGS NENIHSIHFS GHVFTVRKKE EYKMALYNLY
  PGVFETVEML
1451  PSKAGIWRVE CLIGEHLHAG MSTLFLVYSN KCQTPLGMAS
  GHIRDFQITA
1501  SGQYGQWAPK LARLHYSGSI NAWSTKEPFS WIKVDLLAPM
  IIHGIKTQGA
1551  RQKFSSLYIS QFIIMYSLDG KKWQTYRGNS TGTLMVFFGN
  VDSSGIKHNI
1601  FNPPIIARYI RLHPTHYSIR STLRMELMGC DLNSCSMPLG
  MESKAISDAQ
1651  ITASSYFTNM FATWSPSKAR LHLQGRSNAW RPQVNNPKEW
  LQVDFQKTMK

1701  VTGVTTQGVK SLLTSMYVKE FLISSSQDGH QWTLFFQNGK
  VKVFQGNQDS
1751  FTPVVNSLDP PLLTRYLRIH PQSWVHQIAL RMEVLGCEAQ
  DLYDKTHTCP
1801  PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS
  HEDPEVKFNW
1851  YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK
  EYKCKVSNKA
1901  LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC
  LVKGFYPSDI
1951  AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW
  QQGNVFSCSV
2001  MHEALHNHYT QKSLSLSPGK *
```

pSYN FVIII 267 protein sequence (FVIII Fc with 72 AE-XTEN at amino acid 18 and 288 AE XTEN in B-domain) SEQ ID NO: 113

```
   1  MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQGAP
  TSESATPESG
  51  PGSEPATSGS ETPGTSESAT PESGPGSEPA TSGSETPGTS
  ESATPESGPG
 101  TSTEPSEGSA PGASSSDLGE LPVDARFPPR VPKSFPFNTS
  VVYKKTLFVE
 151  FTDHLFNIAK PRPPWMGLLG PTIQAEVYDT VVITLKNMAS
  HPVSLHAVGV
 201  SYWKASEGAE YDDQTSQREK EDDKVFPGGS HTYVWQVLKE
  NGPMASDPLC
 251  LTYSYLSHVD LVKDLNSGLI GALLVCREGS LAKEKTQTLH
  KFILLFAVFD
 301  EGKSWHSETK NSLMQDRDAA SARAWPKMHT VNGYVNRSLP
  GLIGCHRKSV
 351  YWHVIGMGTT PEVHSIFLEG HTFLVRNHRQ ASLEISPITF
  LTAQTLLMDL
 401  GQFLLFCHIS SHQHDGMEAY VKVDSCPEEP QLRMKNNEEA
  EDYDDDLTDS
 451  EMDVVRFDDD NSPSFIQIRS VAKKHPKTWV HYIAAEEEDW
  DYAPLVLAPD
 501  DRSYKSQYLN NGPQRIGRKY KKVRFMAYTD ETFKTREAIQ
  HESGILGPLL
 551  YGEVGDTLLI IFKNQASRPY NIYPHGITDV RPLYSRRLPK
  GVKHLKDFPI
 601  LPGEIFKYKW TVTVEDGPTK SDPRCLTRYY SSFVNMERDL
  ASGLIGPLLI
 651  CYKESVDQRG NQIMSDKRNV ILFSVFDENR SWYLTENIQR
  FLPNPAGVQL
 701  EDPEFQASNI MHSINGYVFD SLQLSVCLHE VAYWYILSIG
  AQTDFLSVFF
 751  SGYTFKHKMV YEDTLTLFPF SGETVFMSME NPGLWILGCH
  NSDFRNRGMT
 801  ALLKVSSCDK NTGDYYEDSY EDISAYLLSK NNAIEPRSFS
  QNGAPGTSES

 851  ATPESGPGSE PATSGSETPG TSESATPESG PGSEPATSGS
   ETPGTSESAT
 901  PESGPGTSTE PSEGSAPGSP AGSPTSTEEG TSESATPESG
   PGSEPATSGS
 951  ETPGTSESAT PESGPGSPAG SPTSTEEGSP AGSPTSTEEG
   TSTEPSEGSA
1001  PGTSESATPE SGPGTSESAT PESGPGTSES ATPESGPGSE
   PATSGSETPG
1051  SEPATSGSET PGSPAGSPTS TEEGTSTEPS EGSAPGTSTE
   PSEGSAPGSE
1101  PATSGSETPG TSESATPESG PGTSTEPSEG SAPASSPPVL
   KRHQAEITRT
1151  TLQSDQEEID YDDTISVEMK KEDFDIYDED ENQSPRSFQK
   KTRHYFIAAV
1201  ERLWDYGMSS SPHVLRNRAQ SGSVPQFKKV VFQEFTDGSF
   TQPLYRGELN
1251  EHLGLLGPYI RAEVEDNIMV TFRNQASRPY SFYSSLISYE
   EDQRQGAEPR
1301  KNFVKPNETK TYFWKVQHHM APTKDEFDCK AWAYFSDVDL
   EKDVHSGLIG
1351  PLLVCHTNTL NPAHGRQVTV QEFALFFTIF DETKSWYFTE
   NMERNCRAPC
1401  NIQMEDPTFK ENYRFHAING YIMDTLPGLV MAQDQRIRWY
   LLSMGSNENI
1451  HSIHFSGHVF TVRKKEEYKM ALYNLYPGVF ETVEMLPSKA
   GIWRVECLIG
1501  EHLHAGMSTL FLVYSNKCQT PLGMASGHIR DFQITASGQY
   GQWAPKLARL
1551  HYSGSINAWS TKEPFSWIKV DLLAPMIIHG IKTQGARQKF
   SSLYISQFII
1601  MYSLDGKKWQ TYRGNSTGTL MVFFGNVDSS GIKHNIFNPP
   IIARYIRLHP
1651  THYSIRSTLR MELMGCDLNS CSMPLGMESK AISDAQITAS
   SYFTNMFATW
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```
1701  SPSKARLHLQ GRSNAWRPQV NNPKEWLQVD FQKTMKVTGV
   TTQGVKSLLT
1751  SMYVKEFLIS SSQDGHQWTL FFQNGKVKVF QGNQDSFTPV
   VNSLDPPLLT
1801  RYLRIHPQSW VHQIALRMEV LGCEAQDLYD KTHTCPPCPA
   PELLGGPSVF
1851  LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVKFNWYVDG
   VEVHNAKTKP
1901  REEQYNSTYR VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP
   IEKTISKAKG
1951  QPREPQVYTL PPSRDELTKN QVSLTCLVKG FYPSDIAVEW
   ESNGQPENNY
2001  KTTPPVLDSD GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA
   LHNHYTQKSL
2051  SLSPGK*
```

pSYN FVIII 268 protein sequence (FVIII Fc with 144 AE-XTEN at amino acid 18) SEQ ID NO: 114

```
   1  MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQGAP
   TSESATPESG
  51  PGSEPATSGS ETPGTSESAT PESGPGSEPA TSGSETPGTS
   ESATPESGPG
 101  TSTEPSEGSA PGSPAGSPTS TEEGTSESAT PESGPGSEPA
   TSGSETPGTS
 151  ESATPESGPG SPAGSPTSTE EGSPAGSPTS TEEGASSSDL
   GELPVDARFP
 201  PRVPKSFPFN TSVVYKKTLF VEFTDHLFNI AKPRPPWMGL
   LGPTIQAEVY
 251  DTVVITLKNM ASHPVSLHAV GVSYWKASEG AEYDDQTSQR
   EKEDDKVFPG
 301  GSHTYVWQVL KENGPMASDP LCLTYSYLSH VDLVKDLNSG
   LIGALLVCRE
 351  GSLAKEKTQT LHKFILLFAV FDEGKSWHSE TKNSLMQDRD
   AASARAWPKM
 401  HTVNGYVNRS LPGLIGCHRK SVYWHVIGMG TTPEVHSIFL
   EGHTFLVRNH
 451  RQASLEISPI TFLTAQTLLM DLGQFLLFCH ISSHQHDGME
   AYVKVDSCPE
 501  EPQLRMKNNE EAEDYDDDLT DSEMDVVRFD DDNSPSFIQI
   RSVAKKHPKT
 551  WVHYIAAEEE DWDYAPLVLA PDDRSYKSQY LNNGPQRIGR
   KYKKVRFMAY
 601  TDETFKTREA IQHESGILGP LLYGEVGDTL LIIFKNQASR
   PYNIYPHGIT
 651  DVRPLYSRRL PKGVKHLKDF PILPGEIFKY KWTVTVEDGP
   TKSDPRCLTR
 701  YYSSFVNMER DLASGLIGPL LICYKESVDQ RGNQIMSDKR
   NVILFSVFDE
 751  NRSWYLTENI QRFLPNPAGV QLEDPEFQAS NIMHSINGYV
   FDSLQLSVCL
 801  HEVAYWYILS IGAQTDFLSV FFSGYTFKHK MVYEDTLTLF
   PFSGETVFMS
 851  MENPGLWILG CHNSDFRNRG MTALLKVSSC DKNTGDYYED
   SYEDISAYLL
 901  SKNNAIEPRS FSQNPPVLKR HQAEITRTTL QSDQEEIDYD
   DTISVEMKKE
 951  DFDIYDEDEN QSPRSFQKKT RHYFIAAVER LWDYGMSSSP
   HVLRNRAQSG
1001  SVPQFKKVVF QEFTDGSFTQ PLYRGELNEH LGLLGPYIRA
   EVEDNIMVTF
1051  RNQASRPYSF YSSLISYEED QRQGAEPRKN FVKPNETKTY
   FWKVQHHMAP
1101  TKDEFDCKAW AYFSDVDLEK DVHSGLIGPL LVCHTNTLNP
   AHGRQVTVQE
1151  FALFFTIFDE TKSWYFTENM ERNCRAPCNI QMEDPTFKEN
   YRFHAINGYI

1201  MDTLPGLVMA QDQRIRWYLL SMGSNENIHS IHFSGHVFTV
   RKKEEYKMAL
1251  YNLYPGVFET VEMLPSKAGI WRVECLIGEH LHAGMSTLFL
   VYSNKCQTPL
1301  GMASGHIRDF QITASGQYGQ WAPKLARLHY SGSINAWSTK
   EPFSWIKVDL
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```
1351  LAPMIIHGIK TQGARQKFSS LYISQFIIMY SLDGKKWQTY
  RGNSTGTLMV
1401  FFGNVDSSGI KHNIFNPPII ARYIRLHPTH YSIRSTLRME
  LMGCDLNSCS
1451  MPLGMESKAI SDAQITASSY FTNMFATWSP SKARLHLQGR
  SNAWRPQVNN
1501  PKEWLQVDFQ KTMKVTGVTT QGVKSLLTSM YVKEFLISSS
  QDGHQWTLFF
1551  QNGKVKVFQG NQDSFTPVVN SLDPPLLTRY LRIHPQSWVH
  QIALRMEVLG
1601  CEAQDLYDKT HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI
  SRTPEVTCVV
1651  VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV
  SVLTVLHQDW
1701  LNGKEYKCKV SNKALPAPIE KTISKAKGQP REPQVYTLPP
  SRDELTKNQV
1751  SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS
  FFLYSKLTVD
1801  KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK*
```

pSYN FVIII 269 protein sequence (FVIII Fc with 72 AE-XTEN at amino acid 18) SEQ ID NO: 115

```
   1  MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQGAP
  TSESATPESG
  51  PGSEPATSGS ETPGTSESAT PESGPGSEPA TSGSETPGTS
  ESATPESGPG
 101  TSTEPSEGSA PGASSSDLGE LPVDARFPPR VPKSFPFNTS
  VVYKKTLFVE
 151  FTDHLFNIAK PRPPWMGLLG PTIQAEVYDT VVITLKNMAS
  HPVSLHAVGV
 201  SYWKASEGAE YDDQTSQREK EDDKVFPGGS HTYVWQVLKE
  NGPMASDPLC
 251  LTYSYLSHVD LVKDLNSGLI GALLVCREGS LAKEKTQTLH
  KFILLFAVFD
 301  EGKSWHSETK NSLMQDRDAA SARAWPKMHT VNGYVNRSLP
  GLIGCHRKSV
 351  YWHVIGMGTT PEVHSIFLEG HTFLVRNHRQ ASLEISPITF
  LTAQTLLMDL
 401  GQFLLFCHIS SHQHDGMEAY VKVDSCPEEP QLRMKNNEEA
  EDYDDDLTDS
 451  EMDVVRFDDD NSPSFIQIRS VAKKHPKTWV HYIAAEEEDW
  DYAPLVLAPD
 501  DRSYKSQYLN NGPQRIGRKY KKVRFMAYTD ETFKTREAIQ
  HESGILGPLL

 551  YGEVGDTLLI IFKNQASRPY NIYPHGITDV RPLYSRRLPK
  GVKHLKDFPI
 601  LPGEIFKYKW TVTVEDGPTK SDPRCLTRYY SSFVNMERDL
  ASGLIGPLLI
 651  CYKESVDQRG NQIMSDKRNV ILFSVFDENR SWYLTENIQR
  FLPNPAGVQL
 701  EDPEFQASNI MHSINGYVFD SLQLSVCLHE VAYWYILSIG
  AQTDFLSVFF
 751  SGYTFKHKMV YEDTLTLFPF SGETVFMSME NPGLWILGCH
  NSDFRNRGMT
 801  ALLKVSSCDK NTGDYYEDSY EDISAYLLSK NNAIEPRSFS
  QNPPVLKRHQ
 851  AEITRTTLQS DQEEIDYDDT ISVEMKKEDF DIYDEDENQS
  PRSFQKKTRH
 901  YFIAAVERLW DYGMSSSPHV LRNRAQSGSV PQFKKVVFQE
  FTDGSFTQPL
 951  YRGELNEHLG LLGPYIRAEV EDNIMVTFRN QASRPYSFYS
  SLISYEEDQR
1001  QGAEPRKNFV KPNETKTYFW KVQHHMAPTK DEFDCKAWAY
  FSDVDLEKDV
1051  HSGLIGPLLV CHTNTLNPAH GRQVTVQEFA LFFTIFDETK
  SWYFTENMER
1101  NCRAPCNIQM EDPTFKENYR FHAINGYIMD TLPGLVMAQD
  QRIRWYLLSM
1151  GSNENIHSIH FSGHVFTVRK KEEYKMALYN LYPGVFETVE
  MLPSKAGIWR
1201  VECLIGEHLH AGMSTLFLVY SNKCQTPLGM ASGHIRDFQI
```

TASGQYGQWA
1251 PKLARLHYSG SINAWSTKEP FSWIKVDLLA PMIIHGIKTQ
GARQKFSSLY
1301 ISQFIIMYSL DGKKWQTYRG NSTGTLMVFF GNVDSSGIKH
NIFNPPIIAR
1351 YIRLHPTHYS IRSTLRMELM GCDLNSCSMP LGMESKAISD
AQITASSYFT
1401 NMFATWSPSK ARLHLQGRSN AWRPQVNNPK EWLQVDFQKT
MKVTGVTTQG
1451 VKSLLTSMYV KEFLISSSQD GHQWTLFFQN GKVKVFQGNQ
DSFTPVVNSL
1501 DPPLLTRYLR IHPQSWVHQI ALRMEVLGCE AQDLYDKTHT
CPPCPAPELL
1551 GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF
NWYVDGVEVH
1601 NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN
KALPAPIEKT
1651 ISKAKGQPRE PQVYTLPPSR DELTKNQVSL TCLVKGFYPS
DIAVEWESNG
1701 QPENNYKTTP PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC
SVMHEALHNH
1751 YTQKSLSLSP GK*

pSYNFVIII 271 protein sequence (FVIII Fc with 42 AE-XTEN at amino acid 18) SEQ ID NO: 116

1 MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQGAP
GSPAGSPTST
51 EEGTSESATP ESGPGSEPAT SGSETPASSS DLGELPVDAR
FPPRVPKSFP
101 FNTSVVYKKT LFVEFTDHLF NIAKPRPPWM GLLGPTIQAE
VYDTVVITLK
151 NMASHPVSLH AVGVSYWKAS EGAEYDDQTS QREKEDDKVF
PGGSHTYVWQ
201 VLKENGPMAS DPLCLTYSYL SHVDLVKDLN SGLIGALLVC
REGSLAKEKT
251 QTLHKFILLF AVFDEGKSWH SETKNSLMQD RDAASARAWP
KMHTVNGYVN
301 RSLPGLIGCH RKSVYWHVIG MGTTPEVHSI FLEGHTFLVR
NHRQASLEIS
351 PITFLTAQTL LMDLGQFLLF CHISSHQHDG MEAYVKVDSC
PEEPQLRMKN
401 NEEAEDYDDD LTDSEMDVVR FDDDNSPSFI QIRSVAKKHP
KTWVHYIAAE
451 EEDWDYAPLV LAPDDRSYKS QYLNNGPQRI GRKYKKVRFM
AYTDETFKTR
501 EAIQHESGIL GPLLYGEVGD TLLIIFKNQA SRPYNIYPHG
ITDVRPLYSR
551 RLPKGVKHLK DFPILPGEIF KYKWTVTVED GPTKSDPRCL
TRYYSSFVNM
601 ERDLASGLIG PLLICYKESV DQRGNQIMSD KRNVILFSVF
DENRSWYLTE
651 NIQRFLPNPA GVQLEDPEFQ ASNIMHSING YVFDSLQLSV
CLHEVAYWYI
701 LSIGAQTDFL SVFFSGYTFK HKMVYEDTLT LFPFSGETVF
MSMENPGLWI
751 LGCHNSDFRN RGMTALLKVS SCDKNTGDYY EDSYEDISAY
LLSKNNAIEP
801 RSFSQNPPVL KRHQAEITRT TLQSDQEEID YDDTISVEMK
KEDFDIYDED
851 ENQSPRSFQK KTRHYFIAAV ERLWDYGMSS SPHVLRNRAQ
SGSVPQFKKV
901 VFQEFTDGSF TQPLYRGELN EHLGLLGPYI RAEVEDNIMV
TFRNQASRPY
951 SFYSSLISYE EDQRQGAEPR KNFVKPNETK TYFWKVQHHM
APTKDEFDCK
1001 AWAYFSDVDL EKDVHSGLIG PLLVCHTNTL NPAHGRQVTV
QEFALFFTIF
1051 DETKSWYFTE NMERNCRAPC NIQMEDPTFK ENYRFHAING
YIMDTLPGLV
1101 MAQDQRIRWY LLSMGSNENI HSIHFSGHVF TVRKKEEYKM
ALYNLYPGVF
1151 ETVEMLPSKA GIWRVECLIG EHLHAGMSTL FLVYSNKCQT
PLGMASGHIR

```
1201  DFQITASGQY GQWAPKLARL HYSGSINAWS TKEPFSWIKV
   DLLAPMIIHG
1251  IKTQGARQKF SSLYISQFII MYSLDGKKWQ TYRGNSTGTL
   MVFFGNVDSS
1301  GIKHNIFNPP IIARYIRLHP THYSIRSTLR MELMGCDLNS
   CSMPLGMESK
1351  AISDAQITAS SYFTNMFATW SPSKARLHLQ GRSNAWRPQV
   NNPKEWLQVD
1401  FQKTMKVTGV TTQGVKSLLT SMYVKEFLIS SSQDGHQWTL
   FFQNGKVKVF
1451  QGNQDSFTPV VNSLDPPLLT RYLRIHPQSW VHQIALRMEV
   LGCEAQDLYD
1501  KTHTCPPCPA PELLGGPSVF LFPPKPKDTL MISRTPEVTC
   VVVDVSHEDP
1551  EVKFNWYVDG VEVHNAKTKP REEQYNSTYR VVSVLTVLHQ
   DWLNGKEYKC
1601  KVSNKALPAP IEKTISKAKG QPREPQVYTL PPSRDELTKN
   QVSLTCLVKG
1651  FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSKLT
   VDKSRWQQGN
1701  VFSCSVMHEA LHNHYTQKSL SLSPGK*
```

pSYN FVIII protein sequence 272 (FVIII with 144 AE XTEN at amino acid 18 and 244 AE XTEN in B-domain-no Fc) SEQ ID NO: 117

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  1  MQIELSTCFF LCLLRFCFSA TRRYYLGAVE LSWDYMQGAP
  TSESATPESG
 51  PGSEPATSGS ETPGTSESAT PESGPGSEPA TSGSETPGTS
  ESATPESGPG
101  TSTEPSEGSA PGSPAGSPTS TEEGTSESAT PESGPGSEPA
  TSGSETPGTS
151  ESATPESGPG SPAGSPTSTE EGSPAGSPTS TEEGASSSDL
  GELPVDARFP
201  PRVPKSFPFN TSVVYKKTLF VEFTDHLFNI AKPRPPWMGL
  LGPTIQAEVY
251  DTVVITLKNM ASHPVSLHAV GVSYWKASEG AEYDDQTSQR
  EKEDDKVFPG
301  GSHTYVWQVL KENGPMASDP LCLTYSYLSH VDLVKDLNSG
  LIGALLVCRE
351  GSLAKEKTQT LHKFILLFAV FDEGKSWHSE TKNSLMQDRD
  AASARAWPKM
401  HTVNGYVNRS LPGLIGCHRK SVYWHVIGMG TTPEVHSIFL
  EGHTFLVRNH
451  RQASLEISPI TFLTAQTLLM DLGQFLLFCH ISSHQHDGME
  AYVKVDSCPE
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Example 15: FVIII-XTEN-Fc:VWF-Fc heterodimers have maintained normal FVIII specific activity as compared to wild type BDD-FVIII.

[0368] The FVIII specific activity of FVIII-XTEN-Fc:VWF-Fc heterodimers were determined. Heterodimers were purified using a two-step chromatography process. A weak anion exchange resin was used, followed by affinity chromatography. The final purified product had acceptable purity by SEC-HPLC. The specific activity was compared to B-domain deleted FVIII (BDD-FVIII), as measured by FVIII chromogenic assay and A280 concentration. The data are presented in Table 26. All tested molecules had demonstrated comparable FVIII specific activities to BDD-FVIII. Purity and the presence of each moiety of the molecules were confirmed by SDS-PAGE and western blotting.

Table 26: FVIII specific activity of FVIII-XTEN-Fc:VWF-Fc heterodimers

Construct	FVIII 207 scBDDFVIII	FVIII-66 dcBDD FVIII)	FVIII 155 / vWF31	FVIII 155 / vWF39	FVIII 169 / vWF31	FVIII 205 / vWF31	FVIII 169 / vWF34
Measured Specific Activity (IU/nmol)	1473	1592	1534	1796	1511	1345	1505

[0369] The half-lives of rFVIII-XTEN/D'D3 and BDD-FVIII were compared in HemA Mice (Figure 15; Table 27). As Figure 15 shows, rFVIII-XTEN/D'D3 achieved a half-life that was four fold longer than the half-life achieved by

BDD-FVIII.

Table 27: rFVIII-XTEN/D'D3 and BDD-FVIII in HemA mice

Treatment	5 minutes Recovery (%)	HL (hr)	MRT (hr)	Cl (mL/hr/kg)	Vss (mL/kg)	AUC_D (hr*kg*mIU/mL/mIU)
BDD-FVIII	89	7.6	11	4.5	49.2	0.22
rFVIIIFc	78	16	20	2.9	57.8	0.35
rFVIII-XTEN/D'D3	86	30	36	1.8	63.4	0.57

Example 16: FVIII-XTEN-Fc:VWF-Fc heterodimer's potency (FVIII activity) in hemostasis as measured by one stage aPTT assay

[0370] The potency of FVIII-XTEN-Fc:VWF-Fc heterodimers in hemostasis was evaluated by their FVIII specific aPTT activity as summarized in Table 28. As demonstrated by Table 28, while the addition of the VWF D'D3 fragment and the insertion of XTEN into the intra-domains of FVIII reduce the FVIII specific aPTT activity of the heterodimers (as indicated by the FVIII155/VWF031 data and the FVIII205/VWF031 data), XTEN insertions in the FVIII B domain region or C-terminus of the VWF D'D3 fragment have no negative effect on the FVIII specific aPTT activity (as indicated by the FVIII169/VWF031 data and the FVIII169/VWF034 data). Compared to dual-chain BDD-FVIII (dcBDD-FVIII), FVIII155/VWF031, FVIII169/VWF031, FVIII169/VWF034 and VWF205/VWF031 showed reduction of specific aPTT activity by 2.5-fold, 2.8-fold, 2.6-fold and 5.5-fold, respectively.

Table 28: FVIII specific aPTT activity of FVIII-XTEN-Fc:VWF-Fc heterodimers

Construct	FVIII 207 scBDD-FVIII	FVIII-66 dcBDD-FVIII	FVIII 155 / VWF31	FVIII 169 / VWF31	FVIII 205 / VWF31	FVIII 169 / VWF34
Measured Specific aPTT Activity (IU/nmol)	818 ± 153	1188 ± 213	448 ± 111	416 ± 70	214 ± 38	436 ± 189

FVIII specific aPTT assay

[0371] FVIII variants were diluted with aPTT buffer (0.15 M NaCl, 0.05 M Tris-HCl, 1% BSA, pH 7.4) to the linear assay range (200- 1.6 mU/mL). 50 µL of diluted samples or standards were sequentially mixed with 50 µL of 37°C naïve human HemA pooled plasma, 50 µL of 37°C aPTT reagent (ACTIN® FSL activated cephaloplastin reagent - Dade Behring, reference # B4219-2) and incubated at 37 °C for 4 minutes. 50 µl of 20 mM $CaCl_2$ (Dade Behring [reference # ORFO37]) was then added to the reaction mixture to start the clotting reactions. Using the clotting time of each sample (the length of time from the addition of $CaCl_2$ until the onset of clot formation), the aPTT activity was calculated against the standard that was generated with the 8^{th} international standard FVIII concentrate. Specific aPTT activity was calculated against the protein concentration of each molecule that measured by OD280.

Example 17: *In vivo* efficacy of FVIII-XTEN-Fc:VWF-Fc heterodimer in HemA mice Tail Clip bleeding model

[0372] To further access the hemostasis potency of the heterodimers, the acute efficacy of FVIII 169/VWF034 and FVIII205/VWF031 was evaluated in comparison with BDD-FVIII in the HemA mice Tail clip bleeding model. HemA mice were treated with a single IV injection of BDD-FVIII at 200, 65 and 20 IU/kg to generate the post tail clip

injury blood loss control level. Blood loss from mice treated with 200 IU/kg of FVIII 169/VWF034 or FVIII205/VWF031 was compared to that of the BDD-FVIII treated control group mice to estimate their potency on hemostasis. Vehicle treated animals were used to generate blood loss baseline for the model. As shown in Figure 16, significant reduction in blood loss was observed from all FVIII treatment groups compared to that of the vehicle treated animals ($p<0.05$). Both FVIII169/VWF034 and FVIII205/VWF031 are efficacious in the HemA mice Tail Clip model. Compared to BDD-FVIII, about 3 fold lower potency was observed for FVIII169/VWF034, as demonstrated by the similar blood loss reduction achieved by 65 IU/kg BDD-FVIII and 200 IU/kg FVIII169/VWF034. As for FVIII205/VWF034, a 10 fold potency reduction has been observed, as demonstrated by the similar blood loss reduction achieved by 20 IU/kg BDD-FVIII and 200 IU/kg FVIII205/VWF031.

[0373] Even though FVIII69/VWF034 and FVIII205/VWF031 had similar specific FVIII chromogenic activity compared to rBDD-FVIII, their FVIII aPTT activity and *in vivo* potency were both reduced due to the modifications of the molecules. Those data indicate that the aPTT activity of a FVIII molecule is a more accurate measurement on predicating its *in vivo* potency on hemostasis than the FVIII chromogenic activity.

HemA mice Tail clip bleeding model

[0374] 8-10 weeks old male HemA mice were used for the study. Prior to tail clip injury, mice were anesthetized with a 50 mg/kg Ketamine/0.5 mg/kg Dexmedetomidine cocktail and placed on a 37°C heating pad to help maintain the body temperature. The tails of the mice were then be immersed in 37°C water for 10 minutes to dilate the lateral vein. After vein dilation, rFVIII or vehicle solution were injected via the tail vein and 5 min later, the distal 1 cm of the tail was cut off using a #11 scalpel with straight edge. The shed blood was collected into 13 ml of 37°C warm saline for 30 minutes and the mice were then euthanized while still under anesthesia by bilateral thoracotomy. Blood loss was quantified gravimetrically by weight change of the blood collection tubes before and after blood was collected in gram, which translated into milliliter (mL) of blood loss volume (1g weight change = 1 mL blood loss).

[0375] The foregoing description of the specific embodiments will so fully reveal the general nature of the invention that others can, by applying knowledge within the skill of the art, readily modify and/or adapt for various applications such specific embodiments, without undue experimentation, without departing from the general concept of the present invention. Therefore, such adaptations and modifications are intended to be within the meaning and range of equivalents of the disclosed embodiments, based on the teaching and guidance presented herein. It is to be understood that the phraseology or terminology herein is for the purpose of description and not of limitation, such that the terminology or phraseology of the present specification is to be interpreted by the skilled artisan in light of the teachings and guidance.

[0376] Other embodiments of the invention will be apparent to those skilled in the art from consideration of the specification and practice of the invention disclosed herein.

SEQUENCE LISTING

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<110> Biogen Idec MA Inc.
Chhabra, Ekta Seth
Liu, Tongyao

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Ala Arg Cys Ser Leu Phe Gly Ser Asp Phe Val Asn Thr Phe Asp Gly
        35                  40                  45

Ser Met Tyr Ser Phe Ala Gly Tyr Cys Ser Tyr Leu Leu Ala Gly Gly
    50                  55                  60

Cys Gln Lys Arg Ser Phe Ser Ile Ile Gly Asp Phe Gln Asn Gly Lys
65                  70                  75                  80

Arg Val Ser Leu Ser Val Tyr Leu Gly Glu Phe Phe Asp Ile His Leu
                85                  90                  95

Phe Val Asn Gly Thr Val Thr Gln Gly Asp Gln Arg Val Ser Met Pro
            100                 105                 110

Tyr Ala Ser Lys Gly Leu Tyr Leu Glu Thr Glu Ala Gly Tyr Tyr Lys
        115                 120                 125

Leu Ser Gly Glu Ala Tyr Gly Phe Val Ala Arg Ile Asp Gly Ser Gly
    130                 135                 140

Asn Phe Gln Val Leu Leu Ser Asp Arg Tyr Phe Asn Lys Thr Cys Gly
145                 150                 155                 160

Leu Cys Gly Asn Phe Asn Ile Phe Ala Glu Asp Asp Phe Met Thr Gln
                165                 170                 175

Glu Gly Thr Leu Thr Ser Asp Pro Tyr Asp Phe Ala Asn Ser Trp Ala
            180                 185                 190

Leu Ser Ser Gly Glu Gln Trp Cys Glu Arg Ala Ser Pro Pro Ser Ser
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Ser Cys Asn Ile Ser Ser Gly Glu Met Gln Lys Gly Leu Trp Glu Gln
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Cys Gln Leu Leu Lys Ser Thr Ser Val Phe Ala Arg Cys His Pro Leu
225                 230                 235                 240

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

Cys Gln Glu Arg Cys Val Asp Gly Cys Ser Cys Pro Glu Gly Gln Leu
                325                 330                 335

Leu Asp Glu Gly Leu Cys Val Glu Ser Thr Glu Cys Pro Cys Val His
            340                 345                 350

Ser Gly Lys Arg Tyr Pro Pro Gly Thr Ser Leu Ser Arg Asp Cys Asn
        355                 360                 365

Thr Cys Ile Cys Arg Asn Ser Gln Trp Ile Cys Ser Asn Glu Glu Cys
    370                 375                 380

Pro Gly Glu Cys Leu Val Thr Gly Gln Ser His Phe Lys Ser Phe Asp
385                 390                 395                 400

Asn Arg Tyr Phe Thr Phe Ser Gly Ile Cys Gln Tyr Leu Leu Ala Arg
                405                 410                 415

Asp Cys Gln Asp His Ser Phe Ser Ile Val Ile Glu Thr Val Gln Cys
            420                 425                 430

Ala Asp Asp Arg Asp Ala Val Cys Thr Arg Ser Val Thr Val Arg Leu
        435                 440                 445

Pro Gly Leu His Asn Ser Leu Val Lys Leu Lys His Gly Ala Gly Val
    450                 455                 460

Ala Met Asp Gly Gln Asp Ile Gln Leu Pro Leu Leu Lys Gly Asp Leu
465                 470                 475                 480

Arg Ile Gln His Thr Val Thr Ala Ser Val Arg Leu Ser Tyr Gly Glu
                485                 490                 495

Asp Leu Gln Met Asp Trp Asp Gly Arg Gly Arg Leu Leu Val Lys Leu
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Ser Pro Val Tyr Ala Gly Lys Thr Cys Gly Leu Cys Gly Asn Tyr Asn
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Gly Asn Gln Gly Asp Asp Phe Leu Thr Pro Ser Gly Leu Ala Glu Pro
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Arg Val Glu Asp Phe Gly Asn Ala Trp Lys Leu His Gly Asp Cys Gln
545                 550                 555                 560

Asp Leu Gln Lys Gln His Ser Asp Pro Cys Ala Leu Asn Pro Arg Met

                565                 570                 575

Thr Arg Phe Ser Glu Glu Ala Cys Ala Val Leu Thr Ser Pro Thr Phe
            580                 585                 590

Glu Ala Cys His Arg Ala Val Ser Pro Leu Pro Tyr Leu Arg Asn Cys
        595                 600                 605

Arg Tyr Asp Val Cys Ser Cys Ser Asp Gly Arg Glu Cys Leu Cys Gly
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Ala Leu Ala Ser Tyr Ala Ala Ala Cys Ala Gly Arg Gly Val Arg Val
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Val Tyr Leu Gln Cys Gly Thr Pro Cys Asn Leu Thr Cys Arg Ser Leu
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Ser Tyr Pro Asp Glu Glu Cys Asn Glu Ala Cys Leu Glu Gly Cys Phe
        675                 680                 685

Cys Pro Pro Gly Leu Tyr Met Asp Glu Arg Gly Asp Cys Val Pro Lys
    690                 695                 700

Ala Gln Cys Pro Cys Tyr Tyr Asp Gly Glu Ile Phe Gln Pro Glu Asp
705                 710                 715                 720

Ile Phe Ser Asp His His Thr Met Cys Tyr Cys Glu Asp Gly Phe Met
                725                 730                 735

His Cys Thr Met Ser Gly Val Pro Gly Ser Leu Leu Pro Asp Ala Val
            740                 745                 750

Leu Ser Ser Pro Leu Ser His Arg Ser Lys Arg Ser Leu Ser Cys Arg
        755                 760                 765

Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp Asn Leu Arg Ala Glu
    770                 775                 780

Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr Asp Leu Glu Cys Met
785                 790                 795                 800

Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro Pro Gly Met Val Arg
                805                 810                 815

His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys Pro Cys Phe His Gln
            820                 825                 830

Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys Ile Gly Cys Asn Thr
        835                 840                 845

Cys Val Cys Arg Asp Arg Lys Trp Asn Cys Thr Asp His Val Cys Asp
    850                 855                 860

Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr Leu Thr Phe Asp Gly
865                 870                 875                 880

Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr Val Leu Val Gln Asp
                885                 890                 895

Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile Leu Val Gly Asn Lys
            900                 905                 910

Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys Arg Val Thr Ile Leu
        915                 920                 925

Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly Glu Val Asn Val Lys
    930                 935                 940

Arg Pro Met Lys Asp Glu Thr His Phe Glu Val Val Glu Ser Gly Arg
945                 950                 955                 960

Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser Val Val Trp Asp Arg
                965                 970                 975

His Leu Ser Ile Ser Val Val Leu Lys Gln Thr Tyr Gln Glu Lys Val
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            980                 985                 990

Cys Gly Leu Cys Gly Asn Phe Asp  Gly Ile Gln Asn Asn  Asp Leu Thr
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Ser Ser  Asn Leu Gln Val Glu  Glu Asp Pro Val Asp  Phe Gly Asn
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Ser Trp  Lys Val Ser Ser Gln  Cys Ala Asp Thr Arg  Lys Val Pro
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Leu Asp  Ser Ser Pro Ala Thr  Cys His Asn Asn Ile  Met Lys Gln
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Thr Met  Val Asp Ser Ser Cys  Arg Ile Leu Thr Ser  Asp Val Phe
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Gln Asp  Cys Asn Lys Leu Val  Asp Pro Glu Pro Tyr  Leu Asp Val
    1070                1075                1080

Cys Ile  Tyr Asp Thr Cys Ser  Cys Glu Ser Ile Gly  Asp Cys Ala
    1085                1090                1095

Cys Phe  Cys Asp Thr Ile Ala  Ala Tyr Ala His Val  Cys Ala Gln
    1100                1105                1110

His Gly  Lys Val Val Thr Trp  Arg Thr Ala Thr Leu  Cys Pro Gln
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Ser Cys  Glu Glu Arg Asn Leu  Arg Glu Asn Gly Tyr  Glu Cys Glu
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Trp Arg  Tyr Asn Ser Cys Ala  Pro Ala Cys Gln Val  Thr Cys Gln
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His Pro  Glu Pro Leu Ala Cys  Pro Val Gln Cys Val  Glu Gly Cys
    1160                1165                1170

His Ala  His Cys Pro Pro Gly  Lys Ile Leu Asp Glu  Leu Leu Gln
    1175                1180                1185

Thr Cys  Val Asp Pro Glu Asp  Cys Pro Val Cys Glu  Val Ala Gly
    1190                1195                1200

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

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Glu Tyr  Pro Phe Ser Glu Ala  Gln Ser Lys Gly Asp  Ile Leu Gln
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Gly Leu  Ala Leu Arg Tyr Leu  Ser Asp His Ser Phe  Leu Val Ser
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Gly Asn  Pro Ala Ser Asp Glu  Ile Lys Arg Leu Pro  Gly Asp Ile
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Phe Glu  Thr Leu Pro Arg Glu  Ala Pro Asp Leu Val  Leu Gln Arg
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Cys Cys  Ser Gly Glu Gly Leu  Gln Ile Pro Thr Leu  Ser Pro Ala
    1670                1675                1680

Pro Asp  Cys Ser Gln Pro Leu  Asp Val Ile Leu Leu  Leu Asp Gly
    1685                1690                1695

Ser Ser  Ser Phe Pro Ala Ser  Tyr Phe Asp Glu Met  Lys Ser Phe
    1700                1705                1710

Ala Lys  Ala Phe Ile Ser Lys  Ala Asn Ile Gly Pro  Arg Leu Thr
    1715                1720                1725

Gln Val  Ser Val Leu Gln Tyr  Gly Ser Ile Thr Thr  Ile Asp Val
    1730                1735                1740

Pro Trp  Asn Val Val Pro Glu  Lys Ala His Leu Leu  Ser Leu Val
    1745                1750                1755

Asp Val  Met Gln Arg Glu Gly  Gly Pro Ser Gln Ile  Gly Asp Ala
    1760                1765                1770

Leu Gly  Phe Ala Val Arg Tyr  Leu Thr Ser Glu Met  His Gly Ala
    1775                1780                1785

Arg Pro  Gly Ala Ser Lys Ala  Val Val Ile Leu Val  Thr Asp Val
    1790                1795                1800

Ser Val  Asp Ser Val Asp Ala  Ala Ala Asp Ala Ala  Arg Ser Asn
    1805                1810                1815

Arg Val  Thr Val Phe Pro Ile  Gly Ile Gly Asp Arg  Tyr Asp Ala
    1820                1825                1830

Ala Gln  Leu Arg Ile Leu Ala  Gly Pro Ala Gly Asp  Ser Asn Val
    1835                1840                1845

Val Lys  Leu Gln Arg Ile Glu  Asp Leu Pro Thr Met  Val Thr Leu
    1850                1855                1860

Gly Asn  Ser Phe Leu His Lys  Leu Cys Ser Gly Phe  Val Arg Ile
    1865                1870                1875

Cys Met  Asp Glu Asp Gly Asn  Glu Lys Arg Pro Gly  Asp Val Trp
    1880                1885                1890

Thr Leu  Pro Asp Gln Cys His  Thr Val Thr Cys Gln  Pro Asp Gly
    1895                1900                1905

Gln Thr  Leu Leu Lys Ser His  Arg Val Asn Cys Asp  Arg Gly Leu
    1910                1915                1920

Arg Pro  Ser Cys Pro Asn Ser  Gln Ser Pro Val Lys  Val Glu Glu
    1925                1930                1935

Thr Cys  Gly Cys Arg Trp Thr  Cys Pro Cys Val Cys  Thr Gly Ser
    1940                1945                1950

Ser Thr  Arg His Ile Val Thr  Phe Asp Gly Gln Asn  Phe Lys Leu
    1955                1960                1965

Thr Gly  Ser Cys Ser Tyr Val  Leu Phe Gln Asn Lys  Glu Gln Asp
    1970                1975                1980

Leu Glu  Val Ile Leu His Asn  Gly Ala Cys Ser Pro  Gly Ala Arg
    1985                1990                1995

Gln Gly  Cys Met Lys Ser Ile  Glu Val Lys His Ser  Ala Leu Ser
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    2000                2005                2010

Val Glu  Xaa His Ser Asp Met  Glu Val Thr Val Asn  Gly Arg Leu
    2015                2020                2025

Val Ser  Val Pro Tyr Val Gly  Gly Asn Met Glu Val  Asn Val Tyr
    2030                2035                2040

Gly Ala  Ile Met His Glu Val  Arg Phe Asn His Leu  Gly His Ile
    2045                2050                2055

Phe Thr  Phe Thr Pro Gln Asn  Asn Glu Phe Gln Leu  Gln Leu Ser
    2060                2065                2070

Pro Lys  Thr Phe Ala Ser Lys  Thr Tyr Gly Leu Cys  Gly Ile Cys
    2075                2080                2085

Asp Glu  Asn Gly Ala Asn Asp  Phe Met Leu Arg Asp  Gly Thr Val
    2090                2095                2100

Thr Thr  Asp Trp Lys Thr Leu  Val Gln Glu Trp Thr  Val Gln Arg
    2105                2110                2115

Pro Gly  Gln Thr Cys Gln Pro  Ile Leu Glu Glu Gln  Cys Leu Val
    2120                2125                2130

Pro Asp  Ser Ser His Cys Gln  Val Leu Leu Leu Pro  Leu Phe Ala
    2135                2140                2145

Glu Cys  His Lys Val Leu Ala  Pro Ala Thr Phe Tyr  Ala Ile Cys
    2150                2155                2160

Gln Gln  Asp Ser Cys His Gln  Glu Gln Val Cys Glu  Val Ile Ala
    2165                2170                2175

Ser Tyr  Ala His Leu Cys Arg  Thr Asn Gly Val Cys  Val Asp Trp
    2180                2185                2190

Arg Thr  Pro Asp Phe Cys Ala  Met Ser Cys Pro Pro  Ser Leu Val
    2195                2200                2205

Tyr Asn  His Cys Glu His Gly  Cys Pro Arg His Cys  Asp Gly Asn
    2210                2215                2220

Val Ser  Ser Cys Gly Asp His  Pro Ser Glu Gly Cys  Phe Cys Pro
    2225                2230                2235

Pro Asp  Lys Val Met Leu Glu  Gly Ser Cys Val Pro  Glu Glu Ala
    2240                2245                2250

Cys Thr  Gln Cys Ile Gly Glu  Asp Gly Val Gln His  Gln Phe Leu
    2255                2260                2265

Glu Ala  Trp Val Pro Asp His  Gln Pro Cys Gln Ile  Cys Thr Cys
    2270                2275                2280

Leu Ser  Gly Arg Lys Val Asn  Cys Thr Thr Gln Pro  Cys Pro Thr
    2285                2290                2295

Ala Lys  Ala Pro Thr Cys Gly  Leu Cys Glu Val Ala  Arg Leu Arg
    2300                2305                2310

Gln Asn  Ala Asp Gln Cys Cys  Pro Glu Tyr Glu Cys  Val Cys Asp
    2315                2320                2325

Pro Val  Ser Cys Asp Leu Pro  Pro Val Pro His Cys  Glu Arg Gly
    2330                2335                2340

Leu Gln  Pro Thr Leu Thr Asn  Pro Gly Glu Cys Arg  Pro Asn Phe
```

2345 2350 2355

Thr Cys Ala Cys Arg Lys Glu Glu Cys Lys Arg Val Ser Pro Pro
2360 2365 2370

Ser Cys Pro Pro His Arg Leu Pro Thr Leu Arg Lys Thr Gln Cys
2375 2380 2385

Cys Asp Glu Tyr Glu Cys Ala Cys Asn Cys Val Asn Ser Thr Val
2390 2395 2400

Ser Cys Pro Leu Gly Tyr Leu Ala Ser Thr Ala Thr Asn Asp Cys
2405 2410 2415

Gly Cys Thr Thr Thr Thr Cys Leu Pro Asp Lys Val Cys Val His
2420 2425 2430

Arg Ser Thr Ile Tyr Pro Val Gly Gln Phe Trp Glu Glu Gly Cys
2435 2440 2445

Asp Val Cys Thr Cys Thr Asp Met Glu Asp Ala Val Met Gly Leu
2450 2455 2460

Arg Val Ala Gln Cys Ser Gln Lys Pro Cys Glu Asp Ser Cys Arg
2465 2470 2475

Ser Gly Phe Thr Tyr Val Leu His Glu Gly Glu Cys Cys Gly Arg

2480 2485 2490

Cys Leu Pro Ser Ala Cys Glu Val Val Thr Gly Ser Pro Arg Gly
2495 2500 2505

Asp Ser Gln Ser Ser Trp Lys Ser Val Gly Ser Gln Trp Ala Ser
2510 2515 2520

Pro Glu Asn Pro Cys Leu Ile Asn Glu Cys Val Arg Val Lys Glu
2525 2530 2535

Glu Val Phe Ile Gln Gln Arg Asn Val Ser Cys Pro Gln Leu Glu
2540 2545 2550

Val Pro Val Cys Pro Ser Gly Phe Gln Leu Ser Cys Lys Thr Ser
2555 2560 2565

Ala Cys Cys Pro Ser Cys Arg Cys Glu Arg Met Glu Ala Cys Met
2570 2575 2580

Leu Asn Gly Thr Val Ile Gly Pro Gly Lys Thr Val Met Ile Asp
2585 2590 2595

Val Cys Thr Thr Cys Arg Cys Met Val Gln Val Gly Val Ile Ser
2600 2605 2610

Gly Phe Lys Leu Glu Cys Arg Lys Thr Thr Cys Asn Pro Cys Pro
2615 2620 2625

Leu Gly Tyr Lys Glu Glu Asn Asn Thr Gly Glu Cys Cys Gly Arg
2630 2635 2640

Cys Leu Pro Thr Ala Cys Thr Ile Gln Leu Arg Gly Gly Gln Ile
2645 2650 2655

Met Thr Leu Lys Arg Asp Glu Thr Leu Gln Asp Gly Cys Asp Thr
2660 2665 2670

His Phe Cys Lys Val Asn Glu Arg Gly Glu Tyr Phe Trp Glu Lys

```
    2675                2680                2685

Arg Val  Thr Gly Cys Pro Pro  Phe Asp Glu His Lys  Cys Leu Ala
    2690                2695                2700

Glu Gly  Gly Lys Ile Met Lys  Ile Pro Gly Thr Cys  Cys Asp Thr
    2705                2710                2715

Cys Glu  Glu Pro Glu Cys Asn  Asp Ile Thr Ala Arg  Leu Gln Tyr
    2720                2725                2730

Val Lys  Val Gly Ser Cys Lys  Ser Glu Val Glu Val  Asp Ile His
    2735                2740                2745

Tyr Cys  Gln Gly Lys Cys Ala  Ser Lys Ala Met Tyr  Ser Ile Asp
    2750                2755                2760

Ile Asn  Asp Val Gln Asp Gln  Cys Ser Cys Cys Ser  Pro Thr Arg
    2765                2770                2775

Thr Glu  Pro Met Gln Val Ala  Leu His Cys Thr Asn  Gly Ser Val
    2780                2785                2790

Val Tyr  His Glu Val Leu Asn  Ala Met Glu Cys Lys  Cys Ser Pro
    2795                2800                2805

Arg Lys  Cys Ser Lys
    2810
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<210> 3

<211> 19

<212> PRT

<213> Homo sapiens

<400> 3

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

Cys Phe Ser
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<210> 4

<211> 2332

<212> PRT

<213> Homo sapiens

<400> 4

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Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr
1               5                  10                  15

Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro
            20                  25                  30

Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
        35                  40                  45

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro

    50                  55                  60

Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
65                  70                  75                  80

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
                85                  90                  95
```

```
Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
            100                 105                 110

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
        115                 120                 125

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
    130                 135                 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145                 150                 155                 160

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
                165                 170                 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
            180                 185                 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
        195                 200                 205

His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
    210                 215                 220

Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
225                 230                 235                 240

Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His
                245                 250                 255

Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu
            260                 265                 270

Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile
        275                 280                 285

Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
    290                 295                 300

Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met
305                 310                 315                 320

Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg
                325                 330                 335

Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp
            340                 345                 350

Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe
        355                 360                 365

Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His
    370                 375                 380

Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
385                 390                 395                 400

Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
                405                 410                 415

Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
            420                 425                 430

Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile
        435                 440                 445

Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile
    450                 455                 460
```

```
Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile
465                 470                 475                 480

Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys
                485                 490                 495

His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys
            500                 505                 510

Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys
        515                 520                 525

Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala
    530                 535                 540

Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp
545                 550                 555                 560

Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe
                565                 570                 575

Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln
            580                 585                 590

Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe
        595                 600                 605

Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser
    610                 615                 620

Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
625                 630                 635                 640

Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr
                645                 650                 655

Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro
            660                 665                 670

Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp
        675                 680                 685

Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala
    690                 695                 700

Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu
705                 710                 715                 720

Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala
                725                 730                 735

Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr Arg
            740                 745                 750

Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys
        755                 760                 765

Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn
    770                 775                 780

Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser Pro Thr Pro
785                 790                 795                 800

His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr Glu Thr Phe
                805                 810                 815

Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn Ser Leu Ser
            820                 825                 830
```

```
Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val
        835                 840                 845

Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly
    850                 855                 860

Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser
865                 870                 875                 880

Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala
                885                 890                 895

Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met Pro Val His
            900                 905                 910

Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys Ser Ser Pro
        915                 920                 925

Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn Asn Asp
    930                 935                 940

Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp
945                 950                 955                 960

Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys
                965                 970                 975

Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys
            980                 985                 990

Val Ser Ile Ser Leu Leu Lys Thr  Asn Lys Thr Ser Asn  Asn Ser Ala
        995                 1000                1005

Thr Asn  Arg Lys Thr His Ile  Asp Gly Pro Ser Leu  Leu Ile Glu
    1010                1015                1020

Asn Ser  Pro Ser Val Trp Gln  Asn Ile Leu Glu Ser  Asp Thr Glu
    1025                1030                1035

Phe Lys  Lys Val Thr Pro Leu  Ile His Asp Arg Met  Leu Met Asp
    1040                1045                1050

Lys Asn  Ala Thr Ala Leu Arg  Leu Asn His Met Ser  Asn Lys Thr

    1055                1060                1065

Thr Ser  Ser Lys Asn Met Glu  Met Val Gln Gln Lys  Lys Glu Gly
    1070                1075                1080

Pro Ile  Pro Pro Asp Ala Gln  Asn Pro Asp Met Ser  Phe Phe Lys
    1085                1090                1095

Met Leu  Phe Leu Pro Glu Ser  Ala Arg Trp Ile Gln  Arg Thr His
    1100                1105                1110

Gly Lys  Asn Ser Leu Asn Ser  Gly Gln Gly Pro Ser  Pro Lys Gln
    1115                1120                1125

Leu Val  Ser Leu Gly Pro Glu  Lys Ser Val Glu Gly  Gln Asn Phe
    1130                1135                1140

Leu Ser  Glu Lys Asn Lys Val  Val Val Gly Lys Gly  Glu Phe Thr
    1145                1150                1155

Lys Asp  Val Gly Leu Lys Glu  Met Val Phe Pro Ser  Ser Arg Asn
    1160                1165                1170
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```
Leu Phe  Leu Thr Asn Leu Asp  Asn Leu His Glu Asn  Asn Thr His
    1175                 1180                 1185

Asn Gln  Glu Lys Lys Ile Gln  Glu Glu Ile Glu Lys  Lys Glu Thr
    1190                 1195                 1200

Leu Ile  Gln Glu Asn Val Val  Leu Pro Gln Ile His  Thr Val Thr
    1205                 1210                 1215

Gly Thr  Lys Asn Phe Met Lys  Asn Leu Phe Leu Leu  Ser Thr Arg
    1220                 1225                 1230

Gln Asn  Val Glu Gly Ser Tyr  Asp Gly Ala Tyr Ala  Pro Val Leu
    1235                 1240                 1245

Gln Asp  Phe Arg Ser Leu Asn  Asp Ser Thr Asn Arg  Thr Lys Lys
    1250                 1255                 1260

His Thr  Ala His Phe Ser Lys  Lys Gly Glu Glu Glu  Asn Leu Glu
    1265                 1270                 1275

Gly Leu  Gly Asn Gln Thr Lys  Gln Ile Val Glu Lys  Tyr Ala Cys
    1280                 1285                 1290

Thr Thr  Arg Ile Ser Pro Asn  Thr Ser Gln Gln Asn  Phe Val Thr
    1295                 1300                 1305

Gln Arg  Ser Lys Arg Ala Leu  Lys Gln Phe Arg Leu  Pro Leu Glu
    1310                 1315                 1320

Glu Thr  Glu Leu Glu Lys Arg  Ile Ile Val Asp Asp  Thr Ser Thr
    1325                 1330                 1335

Gln Trp  Ser Lys Asn Met Lys  His Leu Thr Pro Ser  Thr Leu Thr
    1340                 1345                 1350

Gln Ile  Asp Tyr Asn Glu Lys  Glu Lys Gly Ala Ile  Thr Gln Ser
    1355                 1360                 1365

Pro Leu  Ser Asp Cys Leu Thr  Arg Ser His Ser Ile  Pro Gln Ala
    1370                 1375                 1380

Asn Arg  Ser Pro Leu Pro Ile  Ala Lys Val Ser Ser  Phe Pro Ser
    1385                 1390                 1395

Ile Arg  Pro Ile Tyr Leu Thr  Arg Val Leu Phe Gln  Asp Asn Ser
    1400                 1405                 1410

Ser His  Leu Pro Ala Ala Ser  Tyr Arg Lys Lys Asp  Ser Gly Val
    1415                 1420                 1425

Gln Glu  Ser Ser His Phe Leu  Gln Gly Ala Lys Lys  Asn Asn Leu
    1430                 1435                 1440

Ser Leu  Ala Ile Leu Thr Leu  Glu Met Thr Gly Asp  Gln Arg Glu
    1445                 1450                 1455

Val Gly  Ser Leu Gly Thr Ser  Ala Thr Asn Ser Val  Thr Tyr Lys
    1460                 1465                 1470

Lys Val  Glu Asn Thr Val Leu  Pro Lys Pro Asp Leu  Pro Lys Thr
    1475                 1480                 1485

Ser Gly  Lys Val Glu Leu Leu  Pro Lys Val His Ile  Tyr Gln Lys
    1490                 1495                 1500

Asp Leu  Phe Pro Thr Glu Thr  Ser Asn Gly Ser Pro  Gly His Leu
    1505                 1510                 1515
```

```
Asp Leu  Val Glu Gly Ser Leu  Leu Gln Gly Thr Glu  Gly Ala Ile
    1520                 1525                 1530

Lys Trp  Asn Glu Ala Asn Arg  Pro Gly Lys Val Pro  Phe Leu Arg
    1535                 1540                 1545

Val Ala  Thr Glu Ser Ser Ala  Lys Thr Pro Ser Lys  Leu Leu Asp
    1550                 1555                 1560

Pro Leu  Ala Trp Asp Asn His  Tyr Gly Thr Gln Ile  Pro Lys Glu
    1565                 1570                 1575

Glu Trp  Lys Ser Gln Glu Lys  Ser Pro Glu Lys Thr  Ala Phe Lys
    1580                 1585                 1590

Lys Lys  Asp Thr Ile Leu Ser  Leu Asn Ala Cys Glu  Ser Asn His
    1595                 1600                 1605

Ala Ile  Ala Ala Ile Asn Glu  Gly Gln Asn Lys Pro  Glu Ile Glu
    1610                 1615                 1620

Val Thr  Trp Ala Lys Gln Gly  Arg Thr Glu Arg Leu  Cys Ser Gln
    1625                 1630                 1635

Asn Pro  Pro Val Leu Lys Arg  His Gln Arg Glu Ile  Thr Arg Thr
    1640                 1645                 1650

Thr Leu  Gln Ser Asp Gln Glu  Glu Ile Asp Tyr Asp  Asp Thr Ile
    1655                 1660                 1665

Ser Val  Glu Met Lys Lys Glu  Asp Phe Asp Ile Tyr  Asp Glu Asp
    1670                 1675                 1680

Glu Asn  Gln Ser Pro Arg Ser  Phe Gln Lys Lys Thr  Arg His Tyr
    1685                 1690                 1695

Phe Ile  Ala Ala Val Glu Arg  Leu Trp Asp Tyr Gly  Met Ser Ser
    1700                 1705                 1710

Ser Pro  His Val Leu Arg Asn  Arg Ala Gln Ser Gly  Ser Val Pro
    1715                 1720                 1725

Gln Phe  Lys Lys Val Val Phe  Gln Glu Phe Thr Asp  Gly Ser Phe
    1730                 1735                 1740

Thr Gln  Pro Leu Tyr Arg Gly  Glu Leu Asn Glu His  Leu Gly Leu
    1745                 1750                 1755

Leu Gly  Pro Tyr Ile Arg Ala  Glu Val Glu Asp Asn  Ile Met Val
    1760                 1765                 1770

Thr Phe  Arg Asn Gln Ala Ser  Arg Pro Tyr Ser Phe  Tyr Ser Ser
    1775                 1780                 1785

Leu Ile  Ser Tyr Glu Glu Asp  Gln Arg Gln Gly Ala  Glu Pro Arg
    1790                 1795                 1800

Lys Asn  Phe Val Lys Pro Asn  Glu Thr Lys Thr Tyr  Phe Trp Lys
    1805                 1810                 1815

Val Gln  His His Met Ala Pro  Thr Lys Asp Glu Phe  Asp Cys Lys
    1820                 1825                 1830

Ala Trp  Ala Tyr Phe Ser Asp  Val Asp Leu Glu Lys  Asp Val His
    1835                 1840                 1845

Ser Gly  Leu Ile Gly Pro Leu  Leu Val Cys His Thr  Asn Thr Leu
    1850                 1855                 1860
```

```
Asn Pro  Ala His Gly Arg Gln  Val Thr Val Gln Glu  Phe Ala Leu
    1865                 1870                 1875

Phe Phe  Thr Ile Phe Asp Glu  Thr Lys Ser Trp Tyr  Phe Thr Glu
    1880                 1885                 1890

Asn Met  Glu Arg Asn Cys Arg  Ala Pro Cys Asn Ile  Gln Met Glu
    1895                 1900                 1905

Asp Pro  Thr Phe Lys Glu Asn  Tyr Arg Phe His Ala  Ile Asn Gly
    1910                 1915                 1920

Tyr Ile  Met Asp Thr Leu Pro  Gly Leu Val Met Ala  Gln Asp Gln
    1925                 1930                 1935

Arg Ile  Arg Trp Tyr Leu Leu  Ser Met Gly Ser Asn  Glu Asn Ile
    1940                 1945                 1950

His Ser  Ile His Phe Ser Gly  His Val Phe Thr Val  Arg Lys Lys
    1955                 1960                 1965

Glu Glu  Tyr Lys Met Ala Leu  Tyr Asn Leu Tyr Pro  Gly Val Phe
    1970                 1975                 1980

Glu Thr  Val Glu Met Leu Pro  Ser Lys Ala Gly Ile  Trp Arg Val
    1985                 1990                 1995

Glu Cys  Leu Ile Gly Glu His  Leu His Ala Gly Met  Ser Thr Leu

    2000                 2005                 2010

Phe Leu  Val Tyr Ser Asn Lys  Cys Gln Thr Pro Leu  Gly Met Ala
    2015                 2020                 2025

Ser Gly  His Ile Arg Asp Phe  Gln Ile Thr Ala Ser  Gly Gln Tyr
    2030                 2035                 2040

Gly Gln  Trp Ala Pro Lys Leu  Ala Arg Leu His Tyr  Ser Gly Ser
    2045                 2050                 2055

Ile Asn  Ala Trp Ser Thr Lys  Glu Pro Phe Ser Trp  Ile Lys Val
    2060                 2065                 2070

Asp Leu  Leu Ala Pro Met Ile  Ile His Gly Ile Lys  Thr Gln Gly
    2075                 2080                 2085

Ala Arg  Gln Lys Phe Ser Ser  Leu Tyr Ile Ser Gln  Phe Ile Ile
    2090                 2095                 2100

Met Tyr  Ser Leu Asp Gly Lys  Lys Trp Gln Thr Tyr  Arg Gly Asn
    2105                 2110                 2115

Ser Thr  Gly Thr Leu Met Val  Phe Phe Gly Asn Val  Asp Ser Ser
    2120                 2125                 2130

Gly Ile  Lys His Asn Ile Phe  Asn Pro Pro Ile Ile  Ala Arg Tyr
    2135                 2140                 2145

Ile Arg  Leu His Pro Thr His  Tyr Ser Ile Arg Ser  Thr Leu Arg
    2150                 2155                 2160

Met Glu  Leu Met Gly Cys Asp  Leu Asn Ser Cys Ser  Met Pro Leu
    2165                 2170                 2175

Gly Met  Glu Ser Lys Ala Ile  Ser Asp Ala Gln Ile  Thr Ala Ser
    2180                 2185                 2190
```

```
Ser Tyr  Phe Thr Asn Met Phe  Ala Thr Trp Ser Pro  Ser Lys Ala
    2195                 2200                 2205

Arg Leu  His Leu Gln Gly Arg  Ser Asn Ala Trp Arg  Pro Gln Val
    2210                 2215                 2220

Asn Asn  Pro Lys Glu Trp Leu  Gln Val Asp Phe Gln  Lys Thr Met
    2225                 2230                 2235

Lys Val  Thr Gly Val Thr Thr  Gln Gly Val Lys Ser  Leu Leu Thr
    2240                 2245                 2250

Ser Met  Tyr Val Lys Glu Phe  Leu Ile Ser Ser Ser  Gln Asp Gly
    2255                 2260                 2265

His Gln  Trp Thr Leu Phe Phe  Gln Asn Gly Lys Val  Lys Val Phe
    2270                 2275                 2280

Gln Gly  Asn Gln Asp Ser Phe  Thr Pro Val Val Asn  Ser Leu Asp
    2285                 2290                 2295

Pro Pro  Leu Leu Thr Arg Tyr  Leu Arg Ile His Pro  Gln Ser Trp
    2300                 2305                 2310

Val His  Gln Ile Ala Leu Arg  Met Glu Val Leu Gly  Cys Glu Ala
    2315                 2320                 2325

Gln Asp  Leu Tyr
    2330
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<210> 5

<211> 7053

<212> DNA

<213> Homo sapiens

<400> 5

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atgcaaatag agctctccac ctgcttcttt ctgtgccttt tgcgattctg ctttagtgcc       60

accagaagat actacctggg tgcagtggaa ctgtcatggg actatatgca aagtgatctc      120

ggtgagctgc ctgtggacgc aagatttcct cctagagtgc caaaatcttt tccattcaac      180

acctcagtcg tgtacaaaaa gactctgttt gtagaattca cggatcacct tttcaacatc      240

gctaagccaa ggccaccctg gatgggtctg ctaggtccta ccatccaggc tgaggtttat      300

gatacagtgg tcattacact taagaacatg gcttcccatc ctgtcagtct tcatgctgtt      360

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<223> BDDD FVIII

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Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
        35                  40                  45

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
    50                  55                  60

Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
65                  70                  75                  80

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
                85                  90                  95

Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
            100                 105                 110

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
        115                 120                 125

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
    130                 135                 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145                 150                 155                 160

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
                165                 170                 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
            180                 185                 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
        195                 200                 205

His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
    210                 215                 220

Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
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Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His
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Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu
            260                 265                 270

Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile
        275                 280                 285

Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
    290                 295                 300

Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met
305                 310                 315                 320

Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg
                325                 330                 335

Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp
            340                 345                 350

Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe
        355                 360                 365

Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His
    370                 375                 380

Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu

385                 390                 395                 400

Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
                405                 410                 415

Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
            420                 425                 430

Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile
        435                 440                 445

Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile
    450                 455                 460

Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile
465                 470                 475                 480

Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys
                485                 490                 495

His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys
            500                 505                 510

Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys
        515                 520                 525

Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala
    530                 535                 540

Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp
545                 550                 555                 560

Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe
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Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln
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Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe
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Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser
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Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
625                 630                 635                 640

Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr
                645                 650                 655

Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro
            660                 665                 670

Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp
        675                 680                 685

Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala
    690                 695                 700

Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu
705                 710                 715                 720

Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala
                725                 730                 735

Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu Lys Arg His
            740                 745                 750

Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile
        755                 760                 765

Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp
    770                 775                 780

Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys
785                 790                 795                 800

Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly
                805                 810                 815

Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser
            820                 825                 830

Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser
        835                 840                 845

Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu
    850                 855                 860

Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr
865                 870                 875                 880

Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile
                885                 890                 895

Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe
            900                 905                 910

Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His
        915                 920                 925

Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe
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Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro
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Lys Ser Trp Tyr Phe Thr Glu Asn  Met Glu Arg Asn Cys  Arg Ala Pro
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Cys Asn  Ile Gln Met Glu Asp  Pro Thr Phe Lys Glu  Asn Tyr Arg
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Phe His  Ala Ile Asn Gly Tyr  Ile Met Asp Thr Leu  Pro Gly Leu
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Val Met  Ala Gln Asp Gln Arg  Ile Arg Trp Tyr Leu  Leu Ser Met
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Gly Ser  Asn Glu Asn Ile His  Ser Ile His Phe Ser  Gly His Val
    1055                1060                1065

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

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Gly Lys  Val Lys Val Phe Gln  Gly Asn Gln Asp Ser  Phe Thr Pro
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Val Val  Asn Ser Leu Asp Pro  Pro Leu Leu Thr Arg  Tyr Leu Arg
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Ile His  Pro Gln Ser Trp Val  His Gln Ile Ala Leu  Arg Met Glu
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cagcttgagg atccagagtt ccaagcctcc aacatcatgc acagcatcaa tggctatgtt 1920

tttgatagtt tgcagttgtc agtttgtttg catgaggtgg catactggta cattctaagc 1980

attggagcac agactgactt cctttctgtc ttcttctctg gatatacctt caaacacaaa 2040

atggtctatg aagacacact caccctattc ccattctcag gagaaactgt cttcatgtcg 2100

atggaaaacc caggtctatg gattctgggg tgccacaact cagactttcg gaacagaggc 2160

atgaccgcct tactgaaggt ttctagttgt gacaagaaca ctggtgatta ttacgaggac 2220

agttatgaag atatttcagc atacttgctg agtaaaaaca atgccattga accaagaagc 2280

ttctctcaaa acccaccagt cttgaaacgc catcaacggg aaataactcg tactactctt 2340

cagtcagatc aagaggaaat tgactatgat gataccatat cagttgaaat gaagaaggaa 2400

gattttgaca tttatgatga ggatgaaaat cagagccccc gcagctttca aaagaaaaca 2460

cgacactatt ttattgctgc agtggagagg ctctgggatt atgggatgag tagctcccca 2520

catgttctaa gaaacagggc tcagagtggc agtgtccctc agttcaagaa agttgttttc 2580

caggaattta ctgatggctc ctttactcag cccttatacc gtggagaact aaatgaacat 2640

ttgggactcc tggggccata tataagagca gaagttgaag ataatatcat ggtaactttc 2700

agaaatcagg cctctcgtcc ctattccttc tattctagcc ttatttctta tgaggaagat 2760

cagaggcaag gagcagaacc tagaaaaaac tttgtcaagc ctaatgaaac caaaacttac 2820

ttttggaaag tgcaacatca tatggcaccc actaaagatg agtttgactg caaagcctgg 2880

gcttatttct ctgatgttga cctggaaaaa gatgtgcact caggcctgat tggacccctt 2940

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tttgctctgt ttttcaccat ctttgatgag accaaaagct ggtacttcac tgaaaatatg 3060

gaaagaaact gcagggctcc ctgcaatatc cagatggaag atcccacttt taaagagaat 3120

tatcgcttcc atgcaatcaa tggctacata atggatacac tacctggctt agtaatggct 3180

caggatcaaa ggattcgatg gtatctgctc agcatgggca gcaatgaaaa catccattct 3240

attcatttca gtggacatgt gttcactgta cgaaaaaaag aggagtataa aatggcactg 3300

tacaatctct atccaggtgt ttttgagaca gtggaaatgt taccatccaa agctggaatt 3360

tggcgggtgg aatgccttat tggcgagcat ctacatgctg ggatgagcac acttttctg 3420

gtgtacagca ataagtgtca gactcccctg ggaatggctt ctggacacat tagagatttt 3480

cagattacag cttcaggaca atatggacag tgggccccaa agctggccag acttcattat 3540

tccggatcaa tcaatgcctg gagcaccaag gagccctttt cttggatcaa ggtggatctg 3600

ttggcaccaa tgattattca cggcatcaag acccagggtg cccgtcagaa gttctccagc 3660

ctctacatct ctcagtttat catcatgtat agtcttgatg ggaagaagtg gcagacttat 3720

```
cgaggaaatt ccactggaac cttaatggtc ttctttggca atgtggattc atctgggata     3780

aaacacaata tttttaaccc tccaattatt gctcgataca tccgtttgca cccaactcat     3840

tatagcattc gcagcactct tcgcatggag ttgatgggct gtgatttaaa tagttgcagc     3900

atgccattgg gaatggagag taaagcaata tcagatgcac agattactgc ttcatcctac     3960

tttaccaata tgtttgccac ctggtctcct tcaaaagctc gacttcacct ccaagggagg     4020

agtaatgcct ggagacctca ggtgaataat ccaaaagagt ggctgcaagt ggacttccag     4080

aagacaatga aagtcacagg agtaactact cagggagtaa aatctctgct taccagcatg     4140

tatgtgaagg agttcctcat ctccagcagt caagatggcc atcagtggac tctcttttct     4200

cagaatggca aagtaaaggt ttttcaggga aatcaagact ccttcacacc tgtggtgaac     4260

tctctagacc caccgttact gactcgctac cttcgaattc acccccagag ttgggtgcac     4320

cagattgccc tgaggatgga ggttctgggc tgcgaggcac aggacctcta c              4371
```

<210> 8
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 8

```
Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr
1               5                   10                  15

Glu Pro Phe Trp Glu Asp Glu Glu Lys
            20                  25
```

<210> 9
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 9

```
Arg Arg Arg Arg
1
```

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

<220>
<223> cleavage site

<400> 10

```
Arg Lys Arg Arg Lys Arg
1               5
```

<210> 11
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 11
Arg Arg Arg Arg Ser
1 5

<210> 12
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 12
Thr Gln Ser Phe Asn Asp Phe Thr Arg
1 5

<210> 13
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 13
Ser Val Ser Gln Thr Ser Lys Leu Thr Arg
1 5 10

<210> 14
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 14
Asp Phe Leu Ala Glu Gly Gly Gly Val Arg
1 5 10

<210> 15
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 15
Thr Thr Lys Ile Lys Pro Arg
1 5

<210> 16
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 16
Leu Val Pro Arg Glu

Leu Val Pro Arg Gly
1 5

<210> 17
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 17
Ala Leu Arg Pro Arg
1 5

<210> 18
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 18
Lys Leu Thr Arg Ala Glu Thr
1 5

<210> 19
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 19
Asp Phe Thr Arg Val Val Gly
1 5

<210> 20
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 20
Thr Met Thr Arg Ile Val Gly Gly
1 5

<210> 21
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 21
Ser Pro Phe Arg Ser Thr Gly Gly
1 5

<210> 22
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 22
Leu Gln Val Arg Ile Val Gly Gly
1 5

<210> 23
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 23
Pro Leu Gly Arg Ile Val Gly Gly
1 5

<210> 24
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 24
Ile Glu Gly Arg Thr Val Gly Gly
1 5

<210> 25
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 25
Leu Thr Pro Arg Ser Leu Leu Val
1 5

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 26
Leu Gly Pro Val Ser Gly Val Pro
1 5

<210> 27
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 27
Val Ala Gly Asp Ser Leu Glu Glu
1 5

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 28
Gly Pro Ala Gly Leu Gly Gly Ala
1 5

<210> 29
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 29
Gly Pro Ala Gly Leu Arg Gly Ala
1 5

<210> 30
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 30
Ala Pro Leu Gly Leu Arg Leu Arg
1 5

<210> 31
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 31
Pro Ala Leu Pro Leu Val Ala Gln
1 5

<210> 32
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 32
Glu Asn Leu Tyr Phe Gln Gly
1 5

<210> 33
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 33
Asp Asp Asp Lys Ile Val Gly Gly
1 5

<210> 34
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 34
Leu Glu Val Leu Phe Gln Gly Pro
1 5

<210> 35
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 35
Leu Pro Lys Thr Gly Ser Glu Ser
1 5

<210> 36
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> AE42

<400> 36
Gly Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
1 5 10 15

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
20 25 30

Thr Ser Gly Ser Glu Thr Pro Ala Ser Ser
35 40

<210> 37

<211> 143

<212> PRT

<213> Artificial Sequence

<220>

<223> AE144

<400> 37

```
Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu
1               5                  10                  15

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
            20                  25                  30

Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
        35                  40                  45

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro
    50                  55                  60

Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly
65                  70                  75                  80

Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
                85                  90                  95

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu
            100                 105                 110

Ser Ala Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
        115                 120                 125

Glu Thr Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
    130                 135                 140
```

<210> 38

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AG144

<400> 38

```
Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
1               5                  10                  15

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr
            20                  25                  30

Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
        35                  40                  45

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro
    50                  55                  60

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
65                  70                  75                  80

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
                85                  90                  95

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Pro
            100                 105                 110
```

```
Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr Ala
        115                 120                 125

Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
    130                 135                 140
```

<210> 39

<211> 288

<212> PRT

<213> Artificial Sequence

<220>

<223> AE288

<400> 39

```
Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
1               5                   10                  15

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
            20                  25                  30

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
        35                  40                  45

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
    50                  55                  60

Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr
65                  70                  75                  80

Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
                85                  90                  95

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu
            100                 105                 110

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr
        115                 120                 125

Ser Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
    130                 135                 140

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu
145                 150                 155                 160

Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro
                165                 170                 175

Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
            180                 185                 190

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro
        195                 200                 205

Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr
    210                 215                 220

Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
225                 230                 235                 240

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro

                245                 250                 255

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
            260                 265                 270
```

```
Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
        275                 280                 285
```

<210> 40

<211> 288

<212> PRT

<213> Artificial Sequence

<220>

<223> AG288

<400> 40

```
Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser
1               5                  10                  15

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr
            20                  25                  30

Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
        35                  40                  45

Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser
    50                  55                  60

Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr
65                  70                  75                  80

Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
                85                  90                  95

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser
            100                 105                 110

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser
        115                 120                 125

Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
    130                 135                 140

Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser
145                 150                 155                 160

Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser
                165                 170                 175

Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly
            180                 185                 190

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser
        195                 200                 205

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly
    210                 215                 220

Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly
225                 230                 235                 240

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser
                245                 250                 255

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr
            260                 265                 270

Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
        275                 280                 285
```

<210> 41
<211> 576
<212> PRT
<213> Artificial Sequence

<220>
<223> AE576

<400> 41

```
Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
1               5                  10                  15

Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu
            20                  25                  30

Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
        35                  40                  45

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
    50                  55                  60

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
65                  70                  75                  80

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
                85                  90                  95

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala
            100                 105                 110

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro
        115                 120                 125

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
    130                 135                 140

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala
145                 150                 155                 160

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu
                165                 170                 175

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
            180                 185                 190

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
        195                 200                 205

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
    210                 215                 220

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
225                 230                 235                 240

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
                245                 250                 255

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
            260                 265                 270

Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
        275                 280                 285

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
    290                 295                 300
```

```
Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
305                 310                 315                 320

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
                325                 330                 335

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
            340                 345                 350

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu
        355                 360                 365

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
    370                 375                 380

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
385                 390                 395                 400

Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr
                405                 410                 415

Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
            420                 425                 430

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
        435                 440                 445

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
    450                 455                 460

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
465                 470                 475                 480

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
                485                 490                 495

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
            500                 505                 510

Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
        515                 520                 525

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala
    530                 535                 540

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro
545                 550                 555                 560

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
                565                 570                 575
```

<210> 42

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> AG576

<400> 42

```
Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser
1               5                   10                  15

Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser
            20                  25                  30

Thr Glv Thr Glv Pro Glv Ser Ser Pro Ser Ala Ser Thr Glv Thr Glv
```

```
      35                  40                  45

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser
    50                  55                  60

Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser
65                  70                  75                  80

Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
                85                  90                  95

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro
            100                 105                 110

Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser
        115                 120                 125

Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
    130                 135                 140

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser
145                 150                 155                 160

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr
                165                 170                 175

Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
            180                 185                 190

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser
        195                 200                 205

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly
    210                 215                 220

Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
225                 230                 235                 240

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro
                245                 250                 255

Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly
            260                 265                 270

Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
        275                 280                 285

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser
    290                 295                 300

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser
305                 310                 315                 320

Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
                325                 330                 335

Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser
            340                 345                 350

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser
        355                 360                 365

Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
    370                 375                 380

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro
385                 390                 395                 400
```

```
Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly
                405                 410                 415

Ala Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser
            420                 425                 430

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro
        435                 440                 445

Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly
    450                 455                 460

Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
465                 470                 475                 480

Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser

                485                 490                 495

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser
            500                 505                 510

Ser Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser
        515                 520                 525

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser
    530                 535                 540

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser
545                 550                 555                 560

Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
                565                 570                 575
```

<210> 43

<211> 864

<212> PRT

<213> Artificial Sequence

<220>

<223> AE864

<400> 43

```
Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
1               5                   10                  15

Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu
            20                  25                  30

Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
        35                  40                  45

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
    50                  55                  60

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
65                  70                  75                  80

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
                85                  90                  95

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala
            100                 105                 110

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro
```

```
                115                 120                 125

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
    130                 135                 140

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala
145                 150                 155                 160

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu
                165                 170                 175

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
            180                 185                 190

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
        195                 200                 205

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
    210                 215                 220

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
225                 230                 235                 240

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
                245                 250                 255

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
            260                 265                 270

Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
        275                 280                 285

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
    290                 295                 300

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
305                 310                 315                 320

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
                325                 330                 335

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
            340                 345                 350

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu
        355                 360                 365

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro

    370                 375                 380

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
385                 390                 395                 400

Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr
                405                 410                 415

Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
            420                 425                 430

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
        435                 440                 445

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
    450                 455                 460

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
```

```
465                 470                 475                 480

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
                485                 490                 495

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
            500                 505                 510

Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
        515                 520                 525

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala
    530                 535                 540

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro
545                 550                 555                 560

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
                565                 570                 575

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
            580                 585                 590

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
        595                 600                 605

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
    610                 615                 620

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
625                 630                 635                 640

Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr
                645                 650                 655

Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
            660                 665                 670

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu
        675                 680                 685

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr
    690                 695                 700

Ser Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
705                 710                 715                 720

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu
                725                 730                 735

Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro
            740                 745                 750

Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
        755                 760                 765

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro
    770                 775                 780

Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr
785                 790                 795                 800

Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
                805                 810                 815

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro
            820                 825                 830
```

```
Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
        835                 840                 845

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
    850                 855                 860
```

<210> 44

<211> 864

<212> PRT

<213> Artificial Sequence

<220>

<223> AG864

<400> 44

```
Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Pro
1               5                   10                  15

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
            20                  25                  30

Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
        35                  40                  45

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
    50                  55                  60

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
65                  70                  75                  80

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
                85                  90                  95

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly
            100                 105                 110

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
        115                 120                 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
    130                 135                 140

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
145                 150                 155                 160

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
                165                 170                 175

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
            180                 185                 190

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
        195                 200                 205

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
    210                 215                 220

Gly Thr Gly Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
225                 230                 235                 240

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro
                245                 250                 255

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
            260                 265                 270
```

```
Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
        275                 280                 285

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro
    290                 295                 300

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
305                 310                 315                 320

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
                325                 330                 335

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly
            340                 345                 350

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
        355                 360                 365

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
    370                 375                 380

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr
385                 390                 395                 400

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
                405                 410                 415

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
            420                 425                 430

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
        435                 440                 445

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
    450                 455                 460

Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
465                 470                 475                 480

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro
                485                 490                 495

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
            500                 505                 510

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
        515                 520                 525

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro
    530                 535                 540

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
545                 550                 555                 560

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
                565                 570                 575

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
            580                 585                 590

Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala
        595                 600                 605

Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
    610                 615                 620

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
625                 630                 635                 640
```

```
Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
               645                 650                 655

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
            660                 665                 670

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro
        675                 680                 685

Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala
    690                 695                 700

Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
705                 710                 715                 720

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro
               725                 730                 735

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
            740                 745                 750

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
        755                 760                 765

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
    770                 775                 780

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
785                 790                 795                 800

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
               805                 810                 815

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
            820                 825                 830

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
        835                 840                 845

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
    850                 855                 860
```

<210> 45

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> cleavage site

<400> 45

```
Thr Gln Ser Phe Asn Asp Phe Thr Arg
1               5
```

<210> 46

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> cleavage site

<400> 46

```
Ser Val Ser Gln Thr Ser Lys Leu Thr Arg
1               5                   10
```

<210> 47
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 47
Asp Phe Leu Ala Glu Gly Gly Gly Val Arg
1 5 10

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 48
Thr Thr Lys Ile Lys Pro Arg
1 5

<210> 49
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 49
Leu Val Pro Arg Gly
1 5

<210> 50
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 50
Ala Leu Arg Pro Arg
1 5

<210> 51
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> sortase recognition motif

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<400> 51
Leu Pro Xaa Thr Gly
1 5

<210> 52
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide

<400> 52
Pro Lys Asn Ser Ser Met Ile Ser Asn Thr Pro
1 5 10

<210> 53
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide

<400> 53
His Gln Ser Leu Gly Thr Gln
1 5

<210> 54
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide

<400> 54
His Gln Asn Leu Ser Asp Gly Lys
1 5

<210> 55
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide

<400> 55
His Gln Asn Ile Ser Asp Gly Lys
1 5

<210> 56
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide

<400> 56
Val Ile Ser Ser His Leu Gly Gln
1 5

<210> 57
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<220>
<221> REPEAT
<222> (1)..(4)
<223> Repeat from 1 to 100 times

<400> 57
Gly Gly Gly Ser
1

<210> 58
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<220>
<221> REPEAT
<222> (1)..(3)
<223> May be repeated 1 to 100 times

<220>
<221> REPEAT
<222> (4)..(8)
<223> May be repeated 1 to 100 times

<400> 58
Gly Gly Ser Gly Gly Gly Gly Ser
1 5

<210> 59
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 59
Ser Gly Gly Ser Gly Gly Ser
1 5

<210> 60
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 60
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly
1 5 10 15

<210> 61
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 61
Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 62
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 62
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15

Gly Ser

<210> 63
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 63
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 64
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<220>
<221> REPEAT
<222> (1)..(5)
<223> May be repeated 1-20 times

<400> 64
Gly Gly Gly Gly Ser
1 5

<210> 65
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage site

<400> 65
Lys Leu Thr Arg Ala Glu Thr
1 5

<210> 66
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage site

<400> 66
Asp Phe Thr Arg Val Val Gly
1 5

<210> 67
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage Site

<400> 67
Thr Met Thr Arg Ile Val Gly Gly
1 5

<210> 68
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage site

<400> 68
Ser Pro Phe Arg Ser Thr Gly Gly
1 5

<210> 69
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage site

<400> 69
Leu Gln Val Arg Ile Val Gly Gly
1 5

<210> 70
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage site

<400> 70
Pro Leu Gly Arg Ile Val Gly Gly
1 5

<210> 71
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage site

<400> 71
Ile Glu Gly Arg Thr Val Gly Gly
1 5

<210> 72
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> cleavage site

<400> 72
Leu Thr Pro Arg Ser Leu Leu Val
1 5

<210> 73
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> cleavage site

<400> 73
Leu Gly Pro Val Ser Gly Val Pro
1 5

<210> 74
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage site

<400> 74
Val Ala Gly Asp Ser Leu Glu Glu
1 5

<210> 75
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage site

<400> 75
Gly Pro Ala Gly Leu Gly Gly Ala
1 5

<210> 76
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage site

<400> 76
Gly Pro Ala Gly Leu Arg Gly Ala
1 5

<210> 77
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage site

<400> 77
Ala Pro Leu Gly Leu Arg Leu Arg
1 5

<210> 78
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage site

<400> 78
Pro Ala Leu Pro Leu Val Ala Gln
1 5

<210> 79
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (6)..(7)
<223> Cleavage site

<400> 79
Glu Asn Leu Tyr Phe Gln Gly
1 5

<210> 80
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage site

<400> 80
Asp Asp Asp Lys Ile Val Gly Gly
1 5

<210> 81
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (6)..(7)
<223> Cleavage site

<400> 81
Leu Glu Val Leu Phe Gln Gly Pro
1 5

<210> 82
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Cleavage site

<400> 82
Leu Pro Lys Thr Gly Ser Glu Ser
1 5

<210> 83
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 83
Thr Gln Ser Phe Asn Asp Phe Thr Arg
1 5

<210> 84
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 84
Ser Val Ser Gln Thr Ser Lys Leu Thr Arg
1 5 10

<210> 85
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 85
Asp Phe Leu Ala Glu Gly Gly Gly Val Arg
1 5 10

<210> 86
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 86
Thr Thr Lys Ile Lys Pro Arg
1 5

<210> 87
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> cleavage site

<400> 87
Leu Val Pro Arg Gly
1 5

<210> 88

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> cleavage site

<400> 88

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Ala Leu Arg Pro Arg Val Val Gly Gly Ala
1               5                  10
```

<210> 89

<211> 1896

<212> PRT

<213> Artificial Sequence

<220>

<223> FVIII 198

<400> 89

```
Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
        35                  40                  45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
    50                  55                  60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65                  70                  75                  80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
                85                  90                  95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
            100                 105                 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
        115                 120                 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
    130                 135                 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145                 150                 155                 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
                165                 170                 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
            180                 185                 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
        195                 200                 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
    210                 215                 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225                 230                 235                 240
```

```
Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
                245                 250                 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
            260                 265                 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
        275                 280                 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
    290                 295                 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305                 310                 315                 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His

                325                 330                 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
            340                 345                 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
        355                 360                 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
    370                 375                 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385                 390                 395                 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
                405                 410                 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
            420                 425                 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
        435                 440                 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
    450                 455                 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465                 470                 475                 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
                485                 490                 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
            500                 505                 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
        515                 520                 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
    530                 535                 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545                 550                 555                 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
                565                 570                 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
            580                 585                 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
```

595 600 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
610 615 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625 630 635 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
645 650 655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
660 665 670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705 710 715 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
740 745 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Pro
755 760 765

Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp
770 775 780

Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys
785 790 795 800

Ile Gln Asn Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser
805 810 815

Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr
820 825 830

Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
835 840 845

Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly
850 855 860

Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
865 870 875 880

Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
885 890 895

Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
900 905 910

Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met
915 920 925

Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
930 935 940

Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu
945 950 955 960

Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu

```
                965                 970                 975

Ser Ser Trp Gly Lys Asn Val Ser Ser Glu Ile Thr Arg Thr Thr Leu
            980                 985                 990

Gln Ser Asp Gln Glu Glu Ile Asp  Tyr Asp Asp Thr Ile  Ser Val Glu
        995                 1000                1005

Met Lys  Lys Glu Asp Phe Asp  Ile Tyr Asp Glu Asp  Glu Asn Gln
    1010                1015                1020

Ser Pro  Arg Ser Phe Gln Lys  Lys Thr Arg His Tyr  Phe Ile Ala
    1025                1030                1035

Ala Val  Glu Arg Leu Trp Asp  Tyr Gly Met Ser Ser  Ser Pro His
    1040                1045                1050

Val Leu  Arg Asn Arg Ala Gln  Ser Gly Ser Val Pro  Gln Phe Lys
    1055                1060                1065

Lys Val  Val Phe Gln Glu Phe  Thr Asp Gly Ser Phe  Thr Gln Pro
    1070                1075                1080

Leu Tyr  Arg Gly Glu Leu Asn  Glu His Leu Gly Leu  Leu Gly Pro
    1085                1090                1095

Tyr Ile  Arg Ala Glu Val Glu  Asp Asn Ile Met Val  Thr Phe Arg
    1100                1105                1110

Asn Gln  Ala Ser Arg Pro Tyr  Ser Phe Tyr Ser Ser  Leu Ile Ser
    1115                1120                1125

Tyr Glu  Glu Asp Gln Arg Gln  Gly Ala Glu Pro Arg  Lys Asn Phe
    1130                1135                1140

Val Lys  Pro Asn Glu Thr Lys  Thr Tyr Phe Trp Lys  Val Gln His
    1145                1150                1155

His Met  Ala Pro Thr Lys Asp  Glu Phe Asp Cys Lys  Ala Trp Ala
    1160                1165                1170

Tyr Phe  Ser Asp Val Asp Leu  Glu Lys Asp Val His  Ser Gly Leu
    1175                1180                1185

Ile Gly  Pro Leu Leu Val Cys  His Thr Asn Thr Leu  Asn Pro Ala
    1190                1195                1200

His Gly  Arg Gln Val Thr Val  Gln Glu Phe Ala Leu  Phe Phe Thr
    1205                1210                1215

Ile Phe  Asp Glu Thr Lys Ser  Trp Tyr Phe Thr Glu  Asn Met Glu
    1220                1225                1230

Arg Asn  Cys Arg Ala Pro Cys  Asn Ile Gln Met Glu  Asp Pro Thr
    1235                1240                1245

Phe Lys  Glu Asn Tyr Arg Phe  His Ala Ile Asn Gly  Tyr Ile Met
    1250                1255                1260

Asp Thr  Leu Pro Gly Leu Val  Met Ala Gln Asp Gln  Arg Ile Arg
    1265                1270                1275

Trp Tyr  Leu Leu Ser Met Gly  Ser Asn Glu Asn Ile  His Ser Ile
    1280                1285                1290

His Phe  Ser Gly His Val Phe  Thr Val Arg Lys Lys  Glu Glu Tyr
    1295                1300                1305
```

```
Lys Met  Ala Leu Tyr Asn Leu  Tyr Pro Gly Val Phe  Glu Thr Val

    1310                 1315                 1320

Glu Met  Leu Pro Ser Lys Ala  Gly Ile Trp Arg Val  Glu Cys Leu
    1325                 1330                 1335

Ile Gly  Glu His Leu His Ala  Gly Met Ser Thr Leu  Phe Leu Val
    1340                 1345                 1350

Tyr Ser  Asn Lys Cys Gln Thr  Pro Leu Gly Met Ala  Ser Gly His
    1355                 1360                 1365

Ile Arg  Asp Phe Gln Ile Thr  Ala Ser Gly Gln Tyr  Gly Gln Trp
    1370                 1375                 1380

Ala Pro  Lys Leu Ala Arg Leu  His Tyr Ser Gly Ser  Ile Asn Ala
    1385                 1390                 1395

Trp Ser  Thr Lys Glu Pro Phe  Ser Trp Ile Lys Val  Asp Leu Leu
    1400                 1405                 1410

Ala Pro  Met Ile Ile His Gly  Ile Lys Thr Gln Gly  Ala Arg Gln
    1415                 1420                 1425

Lys Phe  Ser Ser Leu Tyr Ile  Ser Gln Phe Ile Ile  Met Tyr Ser
    1430                 1435                 1440

Leu Asp  Gly Lys Lys Trp Gln  Thr Tyr Arg Gly Asn  Ser Thr Gly
    1445                 1450                 1455

Thr Leu  Met Val Phe Phe Gly  Asn Val Asp Ser Ser  Gly Ile Lys
    1460                 1465                 1470

His Asn  Ile Phe Asn Pro Pro  Ile Ile Ala Arg Tyr  Ile Arg Leu
    1475                 1480                 1485

His Pro  Thr His Tyr Ser Ile  Arg Ser Thr Leu Arg  Met Glu Leu
    1490                 1495                 1500

Met Gly  Cys Asp Leu Asn Ser  Cys Ser Met Pro Leu  Gly Met Glu
    1505                 1510                 1515

Ser Lys  Ala Ile Ser Asp Ala  Gln Ile Thr Ala Ser  Ser Tyr Phe
    1520                 1525                 1530

Thr Asn  Met Phe Ala Thr Trp  Ser Pro Ser Lys Ala  Arg Leu His
    1535                 1540                 1545

Leu Gln  Gly Arg Ser Asn Ala  Trp Arg Pro Gln Val  Asn Asn Pro
    1550                 1555                 1560

Lys Glu  Trp Leu Gln Val Asp  Phe Gln Lys Thr Met  Lys Val Thr
    1565                 1570                 1575

Gly Val  Thr Thr Gln Gly Val  Lys Ser Leu Leu Thr  Ser Met Tyr
    1580                 1585                 1590

Val Lys  Glu Phe Leu Ile Ser  Ser Ser Gln Asp Gly  His Gln Trp
    1595                 1600                 1605

Thr Leu  Phe Phe Gln Asn Gly  Lys Val Lys Val Phe  Gln Gly Asn
    1610                 1615                 1620

Gln Asp  Ser Phe Thr Pro Val  Val Asn Ser Leu Asp  Pro Pro Leu
    1625                 1630                 1635

Leu Thr  Arg Tyr Leu Arg Ile  His Pro Gln Ser Trp  Val His Gln
```

```
                                                                    Gln
    1640                1645                1650

Ile Ala  Leu Arg Met Glu Val  Leu Gly Cys Glu Ala  Gln Asp Leu
    1655                1660                1665

Tyr Asp  Lys Thr His Thr Cys  Pro Pro Cys Pro Ala  Pro Glu Leu
    1670                1675                1680

Leu Gly  Gly Pro Ser Val Phe  Leu Phe Pro Pro Lys  Pro Lys Asp
    1685                1690                1695

Thr Leu  Met Ile Ser Arg Thr  Pro Glu Val Thr Cys  Val Val Val
    1700                1705                1710

Asp Val  Ser His Glu Asp Pro  Glu Val Lys Phe Asn  Trp Tyr Val
    1715                1720                1725

Asp Gly  Val Glu Val His Asn  Ala Lys Thr Lys Pro  Arg Glu Glu
    1730                1735                1740

Gln Tyr  Asn Ser Thr Tyr Arg  Val Val Ser Val Leu  Thr Val Leu
    1745                1750                1755

His Gln  Asp Trp Leu Asn Gly  Lys Glu Tyr Lys Cys  Lys Val Ser
    1760                1765                1770

Asn Lys  Ala Leu Pro Ala Pro  Ile Glu Lys Thr Ile  Ser Lys Ala
    1775                1780                1785

Lys Gly  Gln Pro Arg Glu Pro  Gln Val Tyr Thr Leu  Pro Pro Ser
    1790                1795                1800

Arg Asp  Glu Leu Thr Lys Asn  Gln Val Ser Leu Thr  Cys Leu Val
    1805                1810                1815

Lys Gly  Phe Tyr Pro Ser Asp  Ile Ala Val Glu Trp  Glu Ser Asn
    1820                1825                1830

Gly Gln  Pro Glu Asn Asn Tyr  Lys Thr Thr Pro Pro  Val Leu Asp
    1835                1840                1845

Ser Asp  Gly Ser Phe Phe Leu  Tyr Ser Lys Leu Thr  Val Asp Lys
    1850                1855                1860

Ser Arg  Trp Gln Gln Gly Asn  Val Phe Ser Cys Ser  Val Met His
    1865                1870                1875

Glu Ala  Leu His Asn His Tyr  Thr Gln Lys Ser Leu  Ser Leu Ser
    1880                1885                1890

Pro Gly  Lys
    1895
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<210> 90

<211> 99

<212> DNA

<213> Artificial Sequence

<220>

<223> ESC48- Fwd - VWF-D'D3 with VIII signal and BsiW1 site

<400> 90

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tcgcgacgta cggccgccac catgcaaata gagctctcca cctgcttctt tctgtgcctt       60

ttgcgattct gctttagcct atcctgtcgg ccccccatg                              99
```

<210> 91

<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> ESC51- Rev- VWF D'D3 (1-477 amino acid) with 6His and Not 1 site

<400> 91
tgacctcgag cggccgctca gtggtgatgg tgatgatgcg gctcctggca ggcttcacag 60

gtgaggttga caac 74

<210> 92
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> ESC 89-fwd with Nhelsite

<400> 92
ctcactatag ggagacccaa gctggctagc cg 32

<210> 93
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> ESC 91-rev with Sal1

<400> 93
ctggatcccg ggagtcgact cgtcagtggt gatggtgatg atg 43

<210> 94
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 94
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser
35 40

<210> 95
<211> 92
<212> DNA
<213> Artificial Sequence

<220>
<223> LW 22-FWD-VWF-D'D3 with FVIII signal sequence and BsiW1 site

<400> 95

gcgccggccg tacgatgcaa atagagctct ccacctgctt ctttctgtgc cttttgcgat 60

tctgctttag cctatcctgt cggcccccca tg 92

<210> 96
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> LW23-Rev- Fc with stop codon and Not1 site

<400> 96
tcatcaatgt atcttatcat gtctgaattc gcggccgctc atttacc 47

<210> 97
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> LW24- Fwd- VWF D1D2D'D3 cloning oligo with BsiW1 site

<400> 97
gcgccggccg tacgatgatt cctgccagat ttgccggggt g 41

<210> 98
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> LW27-Rev-VWF D'D3 oligo with EcoRV

<400> 98
ccaccgccag atatcggctc ctggcaggct tcacaggtga g 41

<210> 99
<211> 1240
<212> PRT
<213> Artificial Sequence

<220>
<223> VWF-D1D2D'D3 protein sequence 1

<400> 99

Met	Ile	Pro	Ala	Arg	Phe	Ala	Gly	Val	Leu	Leu	Ala	Leu	Ala	Leu	Ile
1				5				10					15		
Leu	Pro	Gly	Thr	Leu	Cys	Ala	Glu	Gly	Thr	Arg	Gly	Arg	Ser	Ser	Thr
			20					25					30		
Ala	Arg	Cys	Ser	Leu	Phe	Gly	Ser	Asp	Phe	Val	Asn	Thr	Phe	Asp	Gly
		35					40					45			
Ser	Met	Tyr	Ser	Phe	Ala	Gly	Tyr	Cys	Ser	Tyr	Leu	Leu	Ala	Gly	Gly
	50					55					60				
Cys	Gln	Lys	Arg	Ser	Phe	Ser	Ile	Ile	Gly	Asp	Phe	Gln	Asn	Gly	Lys
65					70					75					80

```
Arg Val Ser Leu Ser Val Tyr Leu Gly Glu Phe Phe Asp Ile His Leu
                85                  90                  95

Phe Val Asn Gly Thr Val Thr Gln Gly Asp Gln Arg Val Ser Met Pro
            100                 105                 110

Tyr Ala Ser Lys Gly Leu Tyr Leu Glu Thr Glu Ala Gly Tyr Tyr Lys
        115                 120                 125

Leu Ser Gly Glu Ala Tyr Gly Phe Val Ala Arg Ile Asp Gly Ser Gly
    130                 135                 140

Asn Phe Gln Val Leu Leu Ser Asp Arg Tyr Phe Asn Lys Thr Cys Gly
145                 150                 155                 160

Leu Cys Gly Asn Phe Asn Ile Phe Ala Glu Asp Asp Phe Met Thr Gln
                165                 170                 175

Glu Gly Thr Leu Thr Ser Asp Pro Tyr Asp Phe Ala Asn Ser Trp Ala
            180                 185                 190

Leu Ser Ser Gly Glu Gln Trp Cys Glu Arg Ala Ser Pro Pro Ser Ser
        195                 200                 205

Ser Cys Asn Ile Ser Ser Gly Glu Met Gln Lys Gly Leu Trp Glu Gln
    210                 215                 220

Cys Gln Leu Leu Lys Ser Thr Ser Val Phe Ala Arg Cys His Pro Leu
225                 230                 235                 240

Val Asp Pro Glu Pro Phe Val Ala Leu Cys Glu Lys Thr Leu Cys Glu
                245                 250                 255

Cys Ala Gly Gly Leu Glu Cys Ala Cys Pro Ala Leu Leu Glu Tyr Ala
            260                 265                 270

Arg Thr Cys Ala Gln Glu Gly Met Val Leu Tyr Gly Trp Thr Asp His
        275                 280                 285

Ser Ala Cys Ser Pro Val Cys Pro Ala Gly Met Glu Tyr Arg Gln Cys
    290                 295                 300

Val Ser Pro Cys Ala Arg Thr Cys Gln Ser Leu His Ile Asn Glu Met
305                 310                 315                 320

Cys Gln Glu Arg Cys Val Asp Gly Cys Ser Cys Pro Glu Gly Gln Leu
                325                 330                 335

Leu Asp Glu Gly Leu Cys Val Glu Ser Thr Glu Cys Pro Cys Val His

            340                 345                 350

Ser Gly Lys Arg Tyr Pro Pro Gly Thr Ser Leu Ser Arg Asp Cys Asn
        355                 360                 365

Thr Cys Ile Cys Arg Asn Ser Gln Trp Ile Cys Ser Asn Glu Glu Cys
    370                 375                 380

Pro Gly Glu Cys Leu Val Thr Gly Gln Ser His Phe Lys Ser Phe Asp
385                 390                 395                 400

Asn Arg Tyr Phe Thr Phe Ser Gly Ile Cys Gln Tyr Leu Leu Ala Arg
                405                 410                 415

Asp Cys Gln Asp His Ser Phe Ser Ile Val Ile Glu Thr Val Gln Cys
            420                 425                 430

Ala Asp Asp Arg Asp Ala Val Cys Thr Arg Ser Val Thr Val Arg Leu
```

```
        435                 440                 445

Pro Gly Leu His Asn Ser Leu Val Lys Leu Lys His Gly Ala Gly Val
    450                 455                 460

Ala Met Asp Gly Gln Asp Ile Gln Leu Pro Leu Leu Lys Gly Asp Leu
465                 470                 475                 480

Arg Ile Gln His Thr Val Thr Ala Ser Val Arg Leu Ser Tyr Gly Glu
                485                 490                 495

Asp Leu Gln Met Asp Trp Asp Gly Arg Gly Arg Leu Leu Val Lys Leu
            500                 505                 510

Ser Pro Val Tyr Ala Gly Lys Thr Cys Gly Leu Cys Gly Asn Tyr Asn
        515                 520                 525

Gly Asn Gln Gly Asp Asp Phe Leu Thr Pro Ser Gly Leu Ala Glu Pro
    530                 535                 540

Arg Val Glu Asp Phe Gly Asn Ala Trp Lys Leu His Gly Asp Cys Gln
545                 550                 555                 560

Asp Leu Gln Lys Gln His Ser Asp Pro Cys Ala Leu Asn Pro Arg Met
                565                 570                 575

Thr Arg Phe Ser Glu Glu Ala Cys Ala Val Leu Thr Ser Pro Thr Phe
            580                 585                 590

Glu Ala Cys His Arg Ala Val Ser Pro Leu Pro Tyr Leu Arg Asn Cys
        595                 600                 605

Arg Tyr Asp Val Cys Ser Cys Ser Asp Gly Arg Glu Cys Leu Cys Gly
    610                 615                 620

Ala Leu Ala Ser Tyr Ala Ala Ala Cys Ala Gly Arg Gly Val Arg Val
625                 630                 635                 640

Ala Trp Arg Glu Pro Gly Arg Cys Glu Leu Asn Cys Pro Lys Gly Gln
                645                 650                 655

Val Tyr Leu Gln Cys Gly Thr Pro Cys Asn Leu Thr Cys Arg Ser Leu
            660                 665                 670

Ser Tyr Pro Asp Glu Glu Cys Asn Glu Ala Cys Leu Glu Gly Cys Phe
        675                 680                 685

Cys Pro Pro Gly Leu Tyr Met Asp Glu Arg Gly Asp Cys Val Pro Lys
    690                 695                 700

Ala Gln Cys Pro Cys Tyr Tyr Asp Gly Glu Ile Phe Gln Pro Glu Asp
705                 710                 715                 720

Ile Phe Ser Asp His His Thr Met Cys Tyr Cys Glu Asp Gly Phe Met
                725                 730                 735

His Cys Thr Met Ser Gly Val Pro Gly Ser Leu Leu Pro Asp Ala Val
            740                 745                 750

Leu Ser Ser Pro Leu Ser His Arg Ser Lys Arg Ser Leu Ser Cys Arg
        755                 760                 765

Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp Asn Leu Arg Ala Glu
    770                 775                 780

Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr Asp Leu Glu Cys Met
785                 790                 795                 800
```

```
Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro Pro Gly Met Val Arg
                805                 810                 815

His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys Pro Cys Phe His Gln
            820                 825                 830

Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys Ile Gly Cys Asn Thr
        835                 840                 845

Cys Val Cys Arg Asp Arg Lys Trp Asn Cys Thr Asp His Val Cys Asp
    850                 855                 860

Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr Leu Thr Phe Asp Gly
865                 870                 875                 880

Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr Val Leu Val Gln Asp
                885                 890                 895

Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile Leu Val Gly Asn Lys
            900                 905                 910

Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys Arg Val Thr Ile Leu
        915                 920                 925

Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly Glu Val Asn Val Lys
    930                 935                 940

Arg Pro Met Lys Asp Glu Thr His Phe Glu Val Val Glu Ser Gly Arg
945                 950                 955                 960

Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser Val Val Trp Asp Arg
                965                 970                 975

His Leu Ser Ile Ser Val Val Leu Lys Gln Thr Tyr Gln Glu Lys Val
            980                 985                 990

Cys Gly Leu Cys Gly Asn Phe Asp  Gly Ile Gln Asn Asn  Asp Leu Thr
        995                 1000                1005

Ser Ser  Asn Leu Gln Val Glu  Glu Asp Pro Val Asp  Phe Gly Asn
    1010                1015                1020

Ser Trp  Lys Val Ser Ser Gln  Cys Ala Asp Thr Arg  Lys Val Pro
    1025                1030                1035

Leu Asp  Ser Ser Pro Ala Thr  Cys His Asn Asn Ile  Met Lys Gln
    1040                1045                1050

Thr Met  Val Asp Ser Ser Cys  Arg Ile Leu Thr Ser  Asp Val Phe
    1055                1060                1065

Gln Asp  Cys Asn Lys Leu Val  Asp Pro Glu Pro Tyr  Leu Asp Val
    1070                1075                1080

Cys Ile  Tyr Asp Thr Cys Ser  Cys Glu Ser Ile Gly  Asp Cys Ala
    1085                1090                1095

Cys Phe  Cys Asp Thr Ile Ala  Ala Tyr Ala His Val  Cys Ala Gln
    1100                1105                1110

His Gly  Lys Val Val Thr Trp  Arg Thr Ala Thr Leu  Cys Pro Gln
    1115                1120                1125

Ser Cys  Glu Glu Arg Asn Leu  Arg Glu Asn Gly Tyr  Glu Cys Glu
    1130                1135                1140

Trp Arg  Tyr Asn Ser Cys Ala  Pro Ala Cys Gln Val  Thr Cys Gln
    1145                1150                1155
```

```
His Pro  Glu Pro Leu Ala Cys  Pro Val Gln Cys Val  Glu Gly Cys
    1160                 1165                 1170

His Ala  His Cys Pro Pro Gly  Lys Ile Leu Asp Glu  Leu Leu Gln
    1175                 1180                 1185

Thr Cys  Val Asp Pro Glu Asp  Cys Pro Val Cys Glu  Val Ala Gly
    1190                 1195                 1200

Arg Arg  Phe Ala Ser Gly Lys  Lys Val Thr Leu Asn  Pro Ser Asp
    1205                 1210                 1215

Pro Glu  His Cys Gln Ile Cys  His Cys Asp Val Val  Asn Leu Thr
    1220                 1225                 1230

Cys Glu  Ala Cys Gln Glu Pro
    1235                 1240
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<210> 100

<211> 477

<212> PRT

<213> Artificial Sequence

<220>

<223> VWF-D'D3 protein sequence 2

<400> 100

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Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp
1               5                  10                  15

Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr
            20                  25                  30

Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro
        35                  40                  45

Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys
    50                  55                  60

Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys
65                  70                  75                  80

Ile Gly Cys Asn Thr Cys Val Cys Arg Asp Arg Lys Trp Asn Cys Thr
                85                  90                  95

Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr
            100                 105                 110

Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr
        115                 120                 125

Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile
    130                 135                 140

Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys
145                 150                 155                 160

Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly
                165                 170                 175

Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val
            180                 185                 190

Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser
        195                 200                 205

Val Val Trp Asp Arg His Leu Ser Ile Ser Val Val Leu Lys Gln Thr
```

```
    210                 215                 220

Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln
225                 230                 235                 240

Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val
                245                 250                 255

Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg
            260                 265                 270

Lys Val Pro Leu Asp Ser Ser Pro Ala Thr Cys His Asn Asn Ile Met
        275                 280                 285

Lys Gln Thr Met Val Asp Ser Ser Cys Arg Ile Leu Thr Ser Asp Val
    290                 295                 300

Phe Gln Asp Cys Asn Lys Leu Val Asp Pro Glu Pro Tyr Leu Asp Val
305                 310                 315                 320

Cys Ile Tyr Asp Thr Cys Ser Cys Glu Ser Ile Gly Asp Cys Ala Cys
                325                 330                 335

Phe Cys Asp Thr Ile Ala Ala Tyr Ala His Val Cys Ala Gln His Gly
            340                 345                 350

Lys Val Val Thr Trp Arg Thr Ala Thr Leu Cys Pro Gln Ser Cys Glu
        355                 360                 365

Glu Arg Asn Leu Arg Glu Asn Gly Tyr Glu Cys Glu Trp Arg Tyr Asn
    370                 375                 380

Ser Cys Ala Pro Ala Cys Gln Val Thr Cys Gln His Pro Glu Pro Leu
385                 390                 395                 400

Ala Cys Pro Val Gln Cys Val Glu Gly Cys His Ala His Cys Pro Pro
                405                 410                 415

Gly Lys Ile Leu Asp Glu Leu Leu Gln Thr Cys Val Asp Pro Glu Asp
            420                 425                 430

Cys Pro Val Cys Glu Val Ala Gly Arg Arg Phe Ala Ser Gly Lys Lys
        435                 440                 445

Val Thr Leu Asn Pro Ser Asp Pro Glu His Cys Gln Ile Cys His Cys
    450                 455                 460

Asp Val Val Asn Leu Thr Cys Glu Ala Cys Gln Glu Pro
465                 470                 475
```

<210> 101

<211> 2754

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYN-FVIII-161

<400> 101

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1               5                   10                  15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
        35                  40                  45
```

```
Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
    50                  55                  60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65                  70                  75                  80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
                85                  90                  95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
            100                 105                 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
        115                 120                 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
    130                 135                 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145                 150                 155                 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
                165                 170                 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
            180                 185                 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
        195                 200                 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
    210                 215                 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225                 230                 235                 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
                245                 250                 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
            260                 265                 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
        275                 280                 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
    290                 295                 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305                 310                 315                 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
                325                 330                 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
            340                 345                 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
        355                 360                 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
    370                 375                 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385                 390                 395                 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
                405                 410                 415
```

```
                405                 410                 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
            420                 425                 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
        435                 440                 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
    450                 455                 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465                 470                 475                 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
                485                 490                 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
            500                 505                 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
        515                 520                 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp

    530                 535                 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545                 550                 555                 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
                565                 570                 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
            580                 585                 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
        595                 600                 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
    610                 615                 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625                 630                 635                 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
                645                 650                 655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
            660                 665                 670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
        675                 680                 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
    690                 695                 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705                 710                 715                 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
                725                 730                 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
            740                 745                 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu
        755                 760                 765
```

```
Lys Arg His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln
    770                 775                 780

Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu
785                 790                 795                 800

Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe
                805                 810                 815

Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp
            820                 825                 830

Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln
        835                 840                 845

Ser Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr
    850                 855                 860

Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His
865                 870                 875                 880

Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile
                885                 890                 895

Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser
            900                 905                 910

Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg
        915                 920                 925

Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
    930                 935                 940

Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp
945                 950                 955                 960

Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu
                965                 970                 975

Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His
            980                 985                 990

Gly Arg Gln Val Thr Val Gln Glu  Phe Ala Leu Phe Phe  Thr Ile Phe
        995                 1000                1005

Asp Glu  Thr Lys Ser Trp Tyr  Phe Thr Glu Asn Met  Glu Arg Asn
    1010                1015                1020

Cys Arg  Ala Pro Cys Asn Ile  Gln Met Glu Asp Pro  Thr Phe Lys
    1025                1030                1035

Glu Asn  Tyr Arg Phe His Ala  Ile Asn Gly Tyr Ile  Met Asp Thr
    1040                1045                1050

Leu Pro  Gly Leu Val Met Ala  Gln Asp Gln Arg Ile  Arg Trp Tyr
    1055                1060                1065

Leu Leu  Ser Met Gly Ser Asn  Glu Asn Ile His Ser  Ile His Phe
    1070                1075                1080

Ser Gly  His Val Phe Thr Val  Arg Lys Lys Glu Glu  Tyr Lys Met
    1085                1090                1095

Ala Leu  Tyr Asn Leu Tyr Pro  Gly Val Phe Glu Thr  Val Glu Met
    1100                1105                1110

Leu Pro  Ser Lys Ala Gly Ile  Trp Arg Val Glu Cys  Leu Ile Gly
    1115                1120                1125
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    ----                ----                ----

Glu His  Leu His Ala Gly Met  Ser Thr Leu Phe Leu  Val Tyr Ser
    1130                1135                1140

Asn Lys  Cys Gln Thr Pro Leu  Gly Met Ala Ser Gly  His Ile Arg
    1145                1150                1155

Asp Phe  Gln Ile Thr Ala Ser  Gly Gln Tyr Gly Gln  Trp Ala Pro
    1160                1165                1170

Lys Leu  Ala Arg Leu His Tyr  Ser Gly Ser Ile Asn  Ala Trp Ser
    1175                1180                1185

Thr Lys  Glu Pro Phe Ser Trp  Ile Lys Val Asp Leu  Leu Ala Pro
    1190                1195                1200

Met Ile  Ile His Gly Ile Lys  Thr Gln Gly Ala Arg  Gln Lys Phe
    1205                1210                1215

Ser Ser  Leu Tyr Ile Ser Gln  Phe Ile Ile Met Tyr  Ser Leu Asp
    1220                1225                1230

Gly Lys  Lys Trp Gln Thr Tyr  Arg Gly Asn Ser Thr  Gly Thr Leu
    1235                1240                1245

Met Val  Phe Phe Gly Asn Val  Asp Ser Ser Gly Ile  Lys His Asn
    1250                1255                1260

Ile Phe  Asn Pro Pro Ile Ile  Ala Arg Tyr Ile Arg  Leu His Pro
    1265                1270                1275

Thr His  Tyr Ser Ile Arg Ser  Thr Leu Arg Met Glu  Leu Met Gly
    1280                1285                1290

Cys Asp  Leu Asn Ser Cys Ser  Met Pro Leu Gly Met  Glu Ser Lys
    1295                1300                1305

Ala Ile  Ser Asp Ala Gln Ile  Thr Ala Ser Ser Tyr  Phe Thr Asn
    1310                1315                1320

Met Phe  Ala Thr Trp Ser Pro  Ser Lys Ala Arg Leu  His Leu Gln
    1325                1330                1335

Gly Arg  Ser Asn Ala Trp Arg  Pro Gln Val Asn Asn  Pro Lys Glu
    1340                1345                1350

Trp Leu  Gln Val Asp Phe Gln  Lys Thr Met Lys Val  Thr Gly Val
    1355                1360                1365

Thr Thr  Gln Gly Val Lys Ser  Leu Leu Thr Ser Met  Tyr Val Lys
    1370                1375                1380

Glu Phe  Leu Ile Ser Ser Ser  Gln Asp Gly His Gln  Trp Thr Leu
    1385                1390                1395

Phe Phe  Gln Asn Gly Lys Val  Lys Val Phe Gln Gly  Asn Gln Asp
    1400                1405                1410

Ser Phe  Thr Pro Val Val Asn  Ser Leu Asp Pro Pro  Leu Leu Thr
    1415                1420                1425

Arg Tyr  Leu Arg Ile His Pro  Gln Ser Trp Val His  Gln Ile Ala
    1430                1435                1440

Leu Arg  Met Glu Val Leu Gly  Cys Glu Ala Gln Asp  Leu Tyr Asp
    1445                1450                1455

Lys Thr  His Thr Cys Pro Pro  Cys Pro Ala Pro Glu  Leu Leu Gly
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                    1460                1465                1470

Gly Pro  Ser Val Phe Leu Phe  Pro Pro Lys Pro Lys  Asp Thr Leu
    1475                1480                1485

Met Ile  Ser Arg Thr Pro Glu  Val Thr Cys Val Val  Val Asp Val
    1490                1495                1500

Ser His  Glu Asp Pro Glu Val  Lys Phe Asn Trp Tyr  Val Asp Gly

    1505                1510                1515

Val Glu  Val His Asn Ala Lys  Thr Lys Pro Arg Glu  Glu Gln Tyr
    1520                1525                1530

Asn Ser  Thr Tyr Arg Val Val  Ser Val Leu Thr Val  Leu His Gln
    1535                1540                1545

Asp Trp  Leu Asn Gly Lys Glu  Tyr Lys Cys Lys Val  Ser Asn Lys
    1550                1555                1560

Ala Leu  Pro Ala Pro Ile Glu  Lys Thr Ile Ser Lys  Ala Lys Gly
    1565                1570                1575

Gln Pro  Arg Glu Pro Gln Val  Tyr Thr Leu Pro Pro  Ser Arg Asp
    1580                1585                1590

Glu Leu  Thr Lys Asn Gln Val  Ser Leu Thr Cys Leu  Val Lys Gly
    1595                1600                1605

Phe Tyr  Pro Ser Asp Ile Ala  Val Glu Trp Glu Ser  Asn Gly Gln
    1610                1615                1620

Pro Glu  Asn Asn Tyr Lys Thr  Thr Pro Pro Val Leu  Asp Ser Asp
    1625                1630                1635

Gly Ser  Phe Phe Leu Tyr Ser  Lys Leu Thr Val Asp  Lys Ser Arg
    1640                1645                1650

Trp Gln  Gln Gly Asn Val Phe  Ser Cys Ser Val Met  His Glu Ala
    1655                1660                1665

Leu His  Asn His Tyr Thr Gln  Lys Ser Leu Ser Leu  Ser Pro Gly
    1670                1675                1680

Lys Arg  Arg Arg Arg Ser Gly  Gly Gly Gly Ser Gly  Gly Gly Gly
    1685                1690                1695

Ser Gly  Gly Gly Gly Ser Gly  Gly Gly Gly Ser Gly  Gly Gly Gly
    1700                1705                1710

Ser Gly  Gly Gly Gly Ser Arg  Lys Arg Arg Lys Arg  Ser Leu Ser
    1715                1720                1725

Cys Arg  Pro Pro Met Val Lys  Leu Val Cys Pro Ala  Asp Asn Leu
    1730                1735                1740

Arg Ala  Glu Gly Leu Glu Cys  Thr Lys Thr Cys Gln  Asn Tyr Asp
    1745                1750                1755

Leu Glu  Cys Met Ser Met Gly  Cys Val Ser Gly Cys  Leu Cys Pro
    1760                1765                1770

Pro Gly  Met Val Arg His Glu  Asn Arg Cys Val Ala  Leu Glu Arg
    1775                1780                1785

Cys Pro  Cys Phe His Gln Gly  Lys Glu Tyr Ala Pro  Gly Glu Thr
    1790                1795                1800
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1790 1795 1800

Val Lys Ile Gly Cys Asn Thr Cys Val Cys Arg Asp Arg Lys Trp
1805 1810 1815

Asn Cys Thr Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly
1820 1825 1830

Met Ala His Tyr Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro
1835 1840 1845

Gly Glu Cys Gln Tyr Val Leu Val Gln Asp Tyr Cys Gly Ser Asn
1850 1855 1860

Pro Gly Thr Phe Arg Ile Leu Val Gly Asn Lys Gly Cys Ser His
1865 1870 1875

Pro Ser Val Lys Cys Lys Lys Arg Val Thr Ile Leu Val Glu Gly
1880 1885 1890

Gly Glu Ile Glu Leu Phe Asp Gly Glu Val Asn Val Lys Arg Pro
1895 1900 1905

Met Lys Asp Glu Thr His Phe Glu Val Val Glu Ser Gly Arg Tyr
1910 1915 1920

Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser Val Val Trp Asp Arg
1925 1930 1935

His Leu Ser Ile Ser Val Val Leu Lys Gln Thr Tyr Gln Glu Lys
1940 1945 1950

Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln Asn Asn Asp
1955 1960 1965

Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val Asp Phe
1970 1975 1980

Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg Lys
1985 1990 1995

Val Pro Leu Asp Ser Ser Pro Ala Thr Cys His Asn Asn Ile Met
2000 2005 2010

Lys Gln Thr Met Val Asp Ser Ser Cys Arg Ile Leu Thr Ser Asp
2015 2020 2025

Val Phe Gln Asp Cys Asn Lys Leu Val Asp Pro Glu Pro Tyr Leu
2030 2035 2040

Asp Val Cys Ile Tyr Asp Thr Cys Ser Cys Glu Ser Ile Gly Asp
2045 2050 2055

Cys Ala Ala Phe Cys Asp Thr Ile Ala Ala Tyr Ala His Val Cys
2060 2065 2070

Ala Gln His Gly Lys Val Val Thr Trp Arg Thr Ala Thr Leu Cys
2075 2080 2085

Pro Gln Ser Cys Glu Glu Arg Asn Leu Arg Glu Asn Gly Tyr Glu
2090 2095 2100

Ala Glu Trp Arg Tyr Asn Ser Cys Ala Pro Ala Cys Gln Val Thr
2105 2110 2115

Cys Gln His Pro Glu Pro Leu Ala Cys Pro Val Gln Cys Val Glu
2120 2125 2130

Gly Cys His Ala His Cys Pro Pro Gly Lys Ile Leu Asp Glu Leu

```
    2135                2140                2145

Leu Gln  Thr Cys Val Asp Pro  Glu Asp Cys Pro Val  Cys Glu Val
    2150                2155                2160

Ala Gly  Arg Arg Phe Ala Ser  Gly Lys Lys Val Thr  Leu Asn Pro
    2165                2170                2175

Ser Asp  Pro Glu His Cys Gln  Ile Cys His Cys Asp  Val Val Asn
    2180                2185                2190

Leu Thr  Cys Glu Ala Cys Gln  Glu Pro Ile Ser Gly  Thr Ser Glu
    2195                2200                2205

Ser Ala  Thr Pro Glu Ser Gly  Pro Gly Ser Glu Pro  Ala Thr Ser
    2210                2215                2220

Gly Ser  Glu Thr Pro Gly Thr  Ser Glu Ser Ala Thr  Pro Glu Ser
    2225                2230                2235

Gly Pro  Gly Ser Glu Pro Ala  Thr Ser Gly Ser Glu  Thr Pro Gly
    2240                2245                2250

Thr Ser  Glu Ser Ala Thr Pro  Glu Ser Gly Pro Gly  Thr Ser Thr
    2255                2260                2265

Glu Pro  Ser Glu Gly Ser Ala  Pro Gly Ser Pro Ala  Gly Ser Pro
    2270                2275                2280

Thr Ser  Thr Glu Glu Gly Thr  Ser Glu Ser Ala Thr  Pro Glu Ser
    2285                2290                2295

Gly Pro  Gly Ser Glu Pro Ala  Thr Ser Gly Ser Glu  Thr Pro Gly
    2300                2305                2310

Thr Ser  Glu Ser Ala Thr Pro  Glu Ser Gly Pro Gly  Ser Pro Ala
    2315                2320                2325

Gly Ser  Pro Thr Ser Thr Glu  Glu Gly Ser Pro Ala  Gly Ser Pro
    2330                2335                2340

Thr Ser  Thr Glu Glu Gly Thr  Ser Thr Glu Pro Ser  Glu Gly Ser
    2345                2350                2355

Ala Pro  Gly Thr Ser Glu Ser  Ala Thr Pro Glu Ser  Gly Pro Gly
    2360                2365                2370

Thr Ser  Glu Ser Ala Thr Pro  Glu Ser Gly Pro Gly  Thr Ser Glu
    2375                2380                2385

Ser Ala  Thr Pro Glu Ser Gly  Pro Gly Ser Glu Pro  Ala Thr Ser
    2390                2395                2400

Gly Ser  Glu Thr Pro Gly Ser  Glu Pro Ala Thr Ser  Gly Ser Glu
    2405                2410                2415

Thr Pro  Gly Ser Pro Ala Gly  Ser Pro Thr Ser Thr  Glu Glu Gly
    2420                2425                2430

Thr Ser  Thr Glu Pro Ser Glu  Gly Ser Ala Pro Gly  Thr Ser Thr
    2435                2440                2445

Glu Pro  Ser Glu Gly Ser Ala  Pro Gly Ser Glu Pro  Ala Thr Ser

    2450                2455                2460

Gly Ser  Glu Thr Pro Gly Thr  Ser Glu Ser Ala Thr  Pro Glu Ser
    2465                2470                2475
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Gly Pro  Gly Thr Ser Thr Glu  Pro Ser Glu Gly Ser  Ala Pro Asp
    2480                 2485                 2490

Ser Gly  Gly Gly Gly Ser Gly  Gly Gly Gly Ser Gly  Gly Gly Gly
    2495                 2500                 2505

Ser Gly  Gly Gly Gly Ser Gly  Gly Gly Gly Ser Leu  Val Pro Arg
    2510                 2515                 2520

Gly Ser  Gly Gly Asp Lys Thr  His Thr Cys Pro Pro  Cys Pro Ala
    2525                 2530                 2535

Pro Glu  Leu Leu Gly Gly Pro  Ser Val Phe Leu Phe  Pro Pro Lys
    2540                 2545                 2550

Pro Lys  Asp Thr Leu Met Ile  Ser Arg Thr Pro Glu  Val Thr Cys
    2555                 2560                 2565

Val Val  Val Asp Val Ser His  Glu Asp Pro Glu Val  Lys Phe Asn
    2570                 2575                 2580

Trp Tyr  Val Asp Gly Val Glu  Val His Asn Ala Lys  Thr Lys Pro
    2585                 2590                 2595

Arg Glu  Glu Gln Tyr Asn Ser  Thr Tyr Arg Val Val  Ser Val Leu
    2600                 2605                 2610

Thr Val  Leu His Gln Asp Trp  Leu Asn Gly Lys Glu  Tyr Lys Cys
    2615                 2620                 2625

Lys Val  Ser Asn Lys Ala Leu  Pro Ala Pro Ile Glu  Lys Thr Ile
    2630                 2635                 2640

Ser Lys  Ala Lys Gly Gln Pro  Arg Glu Pro Gln Val  Tyr Thr Leu
    2645                 2650                 2655

Pro Pro  Ser Arg Asp Glu Leu  Thr Lys Asn Gln Val  Ser Leu Thr
    2660                 2665                 2670

Cys Leu  Val Lys Gly Phe Tyr  Pro Ser Asp Ile Ala  Val Glu Trp
    2675                 2680                 2685

Glu Ser  Asn Gly Gln Pro Glu  Asn Asn Tyr Lys Thr  Thr Pro Pro
    2690                 2695                 2700

Val Leu  Asp Ser Asp Gly Ser  Phe Phe Leu Tyr Ser  Lys Leu Thr
    2705                 2710                 2715

Val Asp  Lys Ser Arg Trp Gln  Gln Gly Asn Val Phe  Ser Cys Ser
    2720                 2725                 2730

Val Met  His Glu Ala Leu His  Asn His Tyr Thr Gln  Lys Ser Leu
    2735                 2740                 2745

Ser Leu  Ser Pro Gly Lys
    2750
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<211> 2242

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYN-FVIII-170 protein sequence

<400> 102

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Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr
            20                  25                  30

Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro
        35                  40                  45

Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys
    50                  55                  60

Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys
65                  70                  75                  80

Ile Gly Cys Asn Thr Cys Val Cys Arg Asp Arg Lys Trp Asn Cys Thr
                85                  90                  95

Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr
            100                 105                 110

Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr
        115                 120                 125

Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile

    130                 135                 140

Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys
145                 150                 155                 160

Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly
                165                 170                 175

Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val
            180                 185                 190

Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser
        195                 200                 205

Val Val Trp Asp Arg His Leu Ser Ile Ser Val Val Leu Lys Gln Thr
    210                 215                 220

Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln
225                 230                 235                 240

Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val
                245                 250                 255

Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg
            260                 265                 270

Lys Val Pro Leu Asp Ser Ser Pro Ala Thr Cys His Asn Asn Ile Met
        275                 280                 285

Lys Gln Thr Met Val Asp Ser Ser Cys Arg Ile Leu Thr Ser Asp Val
    290                 295                 300

Phe Gln Asp Cys Asn Lys Leu Val Asp Pro Glu Pro Tyr Leu Asp Val
305                 310                 315                 320

Cys Ile Tyr Asp Thr Cys Ser Cys Glu Ser Ile Gly Asp Cys Ala Ala
                325                 330                 335

Phe Cys Asp Thr Ile Ala Ala Tyr Ala His Val Cys Ala Gln His Gly
            340                 345                 350
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Lys Val Val Thr Trp Arg Thr Ala Thr Leu Cys Pro Gln Ser Cys Glu
        355                 360                 365

Glu Arg Asn Leu Arg Glu Asn Gly Tyr Glu Ala Glu Trp Arg Tyr Asn
    370                 375                 380

Ser Cys Ala Pro Ala Cys Gln Val Thr Cys Gln His Pro Glu Pro Leu
385                 390                 395                 400

Ala Cys Pro Val Gln Cys Val Glu Gly Cys His Ala His Cys Pro Pro
                405                 410                 415

Gly Lys Ile Leu Asp Glu Leu Leu Gln Thr Cys Val Asp Pro Glu Asp
            420                 425                 430

Cys Pro Val Cys Glu Val Ala Gly Arg Arg Phe Ala Ser Gly Lys Lys
        435                 440                 445

Val Thr Leu Asn Pro Ser Asp Pro Glu His Cys Gln Ile Cys His Cys
    450                 455                 460

Asp Val Val Asn Leu Thr Cys Glu Ala Cys Gln Glu Pro Ile Ser Gly
465                 470                 475                 480

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
                485                 490                 495

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
            500                 505                 510

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
        515                 520                 525

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
    530                 535                 540

Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
545                 550                 555                 560

Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
                565                 570                 575

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser
            580                 585                 590

Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
        595                 600                 605

Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
    610                 615                 620

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser
625                 630                 635                 640

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
                645                 650                 655

Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
            660                 665                 670

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala
        675                 680                 685

Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
    690                 695                 700

Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
705                 710                 715                 720
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Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro Ala
                725                 730                 735

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
            740                 745                 750

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Asp
        755                 760                 765

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    770                 775                 780

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu Val Pro Arg Gly Ser
785                 790                 795                 800

Gly Gly Ala Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu
                805                 810                 815

Ser Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala
            820                 825                 830

Arg Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val
        835                 840                 845

Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn
    850                 855                 860

Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile
865                 870                 875                 880

Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala
                885                 890                 895

Ser His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala
            900                 905                 910

Ser Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu
        915                 920                 925

Asp Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val
    930                 935                 940

Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr
945                 950                 955                 960

Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu
                965                 970                 975

Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys
            980                 985                 990

Thr Gln Thr Leu His Lys Phe Ile  Leu Leu Phe Ala Val  Phe Asp Glu
        995                 1000                1005

Gly Lys  Ser Trp His Ser Glu  Thr Lys Asn Ser Leu  Met Gln Asp
    1010                1015                1020

Arg Asp  Ala Ala Ser Ala Arg  Ala Trp Pro Lys Met  His Thr Val
    1025                1030                1035

Asn Gly  Tyr Val Asn Arg Ser  Leu Pro Gly Leu Ile  Gly Cys His
    1040                1045                1050

Arg Lys  Ser Val Tyr Trp His  Val Ile Gly Met Gly  Thr Thr Pro
    1055                1060                1065

Glu Val  His Ser Ile Phe Leu  Glu Gly His Thr Phe  Leu Val Arg
```

```
    1070                1075                1080

Asn His  Arg Gln Ala Ser Leu  Glu Ile Ser Pro Ile  Thr Phe Leu
    1085                1090                1095

Thr Ala  Gln Thr Leu Leu Met  Asp Leu Gly Gln Phe  Leu Leu Phe
    1100                1105                1110

Cys His  Ile Ser Ser His Gln  His Asp Gly Met Glu  Ala Tyr Val
    1115                1120                1125

Lys Val  Asp Ser Cys Pro Glu  Glu Pro Gln Leu Arg  Met Lys Asn

    1130                1135                1140

Asn Glu  Glu Ala Glu Asp Tyr  Asp Asp Asp Leu Thr  Asp Ser Glu
    1145                1150                1155

Met Asp  Val Val Arg Phe Asp  Asp Asp Asn Ser Pro  Ser Phe Ile
    1160                1165                1170

Gln Ile  Arg Ser Val Ala Lys  Lys His Pro Lys Thr  Trp Val His
    1175                1180                1185

Tyr Ile  Ala Ala Glu Glu Glu  Asp Trp Asp Tyr Ala  Pro Leu Val
    1190                1195                1200

Leu Ala  Pro Asp Asp Arg Ser  Tyr Lys Ser Gln Tyr  Leu Asn Asn
    1205                1210                1215

Gly Pro  Gln Arg Ile Gly Arg  Lys Tyr Lys Lys Val  Arg Phe Met
    1220                1225                1230

Ala Tyr  Thr Asp Glu Thr Phe  Lys Thr Arg Glu Ala  Ile Gln His
    1235                1240                1245

Glu Ser  Gly Ile Leu Gly Pro  Leu Leu Tyr Gly Glu  Val Gly Asp
    1250                1255                1260

Thr Leu  Leu Ile Ile Phe Lys  Asn Gln Ala Ser Arg  Pro Tyr Asn
    1265                1270                1275

Ile Tyr  Pro His Gly Ile Thr  Asp Val Arg Pro Leu  Tyr Ser Arg
    1280                1285                1290

Arg Leu  Pro Lys Gly Val Lys  His Leu Lys Asp Phe  Pro Ile Leu
    1295                1300                1305

Pro Gly  Glu Ile Phe Lys Tyr  Lys Trp Thr Val Thr  Val Glu Asp
    1310                1315                1320

Gly Pro  Thr Lys Ser Asp Pro  Arg Cys Leu Thr Arg  Tyr Tyr Ser
    1325                1330                1335

Ser Phe  Val Asn Met Glu Arg  Asp Leu Ala Ser Gly  Leu Ile Gly
    1340                1345                1350

Pro Leu  Leu Ile Cys Tyr Lys  Glu Ser Val Asp Gln  Arg Gly Asn
    1355                1360                1365

Gln Ile  Met Ser Asp Lys Arg  Asn Val Ile Leu Phe  Ser Val Phe
    1370                1375                1380

Asp Glu  Asn Arg Ser Trp Tyr  Leu Thr Glu Asn Ile  Gln Arg Phe
    1385                1390                1395

Leu Pro  Asn Pro Ala Gly Val  Gln Leu Glu Asp Pro  Glu Phe Gln
    1400                1405                1410
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Ala Ser  Asn Ile Met His Ser  Ile Asn Gly Tyr Val  Phe Asp Ser
    1415                 1420                 1425

Leu Gln  Leu Ser Val Cys Leu  His Glu Val Ala Tyr  Trp Tyr Ile
    1430                 1435                 1440

Leu Ser  Ile Gly Ala Gln Thr  Asp Phe Leu Ser Val  Phe Phe Ser
    1445                 1450                 1455

Gly Tyr  Thr Phe Lys His Lys  Met Val Tyr Glu Asp  Thr Leu Thr
    1460                 1465                 1470

Leu Phe  Pro Phe Ser Gly Glu  Thr Val Phe Met Ser  Met Glu Asn
    1475                 1480                 1485

Pro Gly  Leu Trp Ile Leu Gly  Cys His Asn Ser Asp  Phe Arg Asn
    1490                 1495                 1500

Arg Gly  Met Thr Ala Leu Leu  Lys Val Ser Ser Cys  Asp Lys Asn
    1505                 1510                 1515

Thr Gly  Asp Tyr Tyr Glu Asp  Ser Tyr Glu Asp Ile  Ser Ala Tyr
    1520                 1525                 1530

Leu Leu  Ser Lys Asn Asn Ala  Ile Glu Pro Arg Ser  Phe Ser Gln
    1535                 1540                 1545

Asn Pro  Pro Val Leu Lys Arg  His Gln Arg Glu Ile  Thr Arg Thr
    1550                 1555                 1560

Thr Leu  Gln Ser Asp Gln Glu  Glu Ile Asp Tyr Asp  Asp Thr Ile
    1565                 1570                 1575

Ser Val  Glu Met Lys Lys Glu  Asp Phe Asp Ile Tyr  Asp Glu Asp
    1580                 1585                 1590

Glu Asn  Gln Ser Pro Arg Ser  Phe Gln Lys Lys Thr  Arg His Tyr
    1595                 1600                 1605

Phe Ile  Ala Ala Val Glu Arg  Leu Trp Asp Tyr Gly  Met Ser Ser
    1610                 1615                 1620

Ser Pro  His Val Leu Arg Asn  Arg Ala Gln Ser Gly  Ser Val Pro
    1625                 1630                 1635

Gln Phe  Lys Lys Val Val Phe  Gln Glu Phe Thr Asp  Gly Ser Phe
    1640                 1645                 1650

Thr Gln  Pro Leu Tyr Arg Gly  Glu Leu Asn Glu His  Leu Gly Leu
    1655                 1660                 1665

Leu Gly  Pro Tyr Ile Arg Ala  Glu Val Glu Asp Asn  Ile Met Val
    1670                 1675                 1680

Thr Phe  Arg Asn Gln Ala Ser  Arg Pro Tyr Ser Phe  Tyr Ser Ser
    1685                 1690                 1695

Leu Ile  Ser Tyr Glu Glu Asp  Gln Arg Gln Gly Ala  Glu Pro Arg
    1700                 1705                 1710

Lys Asn  Phe Val Lys Pro Asn  Glu Thr Lys Thr Tyr  Phe Trp Lys
    1715                 1720                 1725

Val Gln  His His Met Ala Pro  Thr Lys Asp Glu Phe  Asp Cys Lys
    1730                 1735                 1740

Ala Trp  Ala Tyr Phe Ser Asp  Val Asp Leu Glu Lys  Asp Val His
    1745                 1750                 1755
```

1745 1750 1755

Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu
1760 1765 1770

Asn Pro Ala His Gly Arg Gln Val Thr Val Gln Glu Phe Ala Leu
1775 1780 1785

Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu
1790 1795 1800

Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu
1805 1810 1815

Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly
1820 1825 1830

Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln Asp Gln
1835 1840 1845

Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn Ile
1850 1855 1860

His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys Lys
1865 1870 1875

Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe
1880 1885 1890

Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val
1895 1900 1905

Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu
1910 1915 1920

Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala
1925 1930 1935

Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr
1940 1945 1950

Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser
1955 1960 1965

Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val
1970 1975 1980

Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly
1985 1990 1995

Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile
2000 2005 2010

Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly Asn
2015 2020 2025

Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser
2030 2035 2040

Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr
2045 2050 2055

Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu Arg
2060 2065 2070

Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met Pro Leu

2075 2080 2085

```
Gly Met  Glu Ser Lys Ala Ile  Ser Asp Ala Gln Ile  Thr Ala Ser
    2090                 2095                 2100

Ser Tyr  Phe Thr Asn Met Phe  Ala Thr Trp Ser Pro  Ser Lys Ala
    2105                 2110                 2115

Arg Leu  His Leu Gln Gly Arg  Ser Asn Ala Trp Arg  Pro Gln Val
    2120                 2125                 2130

Asn Asn  Pro Lys Glu Trp Leu  Gln Val Asp Phe Gln  Lys Thr Met
    2135                 2140                 2145

Lys Val  Thr Gly Val Thr Thr  Gln Gly Val Lys Ser  Leu Leu Thr
    2150                 2155                 2160

Ser Met  Tyr Val Lys Glu Phe  Leu Ile Ser Ser Ser  Gln Asp Gly
    2165                 2170                 2175

His Gln  Trp Thr Leu Phe Phe  Gln Asn Gly Lys Val  Lys Val Phe
    2180                 2185                 2190

Gln Gly  Asn Gln Asp Ser Phe  Thr Pro Val Val Asn  Ser Leu Asp
    2195                 2200                 2205

Pro Pro  Leu Leu Thr Arg Tyr  Leu Arg Ile His Pro  Gln Ser Trp
    2210                 2215                 2220

Val His  Gln Ile Ala Leu Arg  Met Glu Val Leu Gly  Cys Glu Ala
    2225                 2230                 2235

Gln Asp  Leu Tyr
    2240
```

<210> 103

<211> 1959

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYN-FVIII-169 mature Protein sequence

<400> 103

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Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr
1               5                   10                  15

Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro
            20                  25                  30

Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
        35                  40                  45

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
    50                  55                  60

Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
65                  70                  75                  80

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
                85                  90                  95

Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
            100                 105                 110

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
        115                 120                 125
```

```
Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
    130                 135                 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145                 150                 155                 160

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
                165                 170                 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
            180                 185                 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
        195                 200                 205

His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
    210                 215                 220

Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
225                 230                 235                 240

Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His
                245                 250                 255

Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu
            260                 265                 270

Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile

        275                 280                 285

Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
    290                 295                 300

Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met
305                 310                 315                 320

Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg
                325                 330                 335

Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp
            340                 345                 350

Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe
        355                 360                 365

Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His
    370                 375                 380

Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
385                 390                 395                 400

Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
                405                 410                 415

Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
            420                 425                 430

Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile
        435                 440                 445

Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile
    450                 455                 460

Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile
465                 470                 475                 480
```

```
Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys
                485                 490                 495

His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys
            500                 505                 510

Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys
        515                 520                 525

Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala
    530                 535                 540

Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp
545                 550                 555                 560

Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe
                565                 570                 575

Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln
            580                 585                 590

Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe
        595                 600                 605

Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser
    610                 615                 620

Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
625                 630                 635                 640

Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr
                645                 650                 655

Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro
            660                 665                 670

Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp
        675                 680                 685

Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala
    690                 695                 700

Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu
705                 710                 715                 720

Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala
                725                 730                 735

Ile Glu Pro Arg Ser Phe Ser Gln Asn Gly Ala Pro Gly Thr Ser Glu
            740                 745                 750

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
        755                 760                 765

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
    770                 775                 780

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu
785                 790                 795                 800

Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu
                805                 810                 815

Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
            820                 825                 830

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
        835                 840                 845
```

```
Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
    850                 855                 860

Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
865                 870                 875                 880

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr
                885                 890                 895

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
            900                 905                 910

Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
        915                 920                 925

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
    930                 935                 940

Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly
945                 950                 955                 960

Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
                965                 970                 975

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
            980                 985                 990

Glu Pro Ser Glu Gly Ser Ala Pro  Gly Ser Glu Pro Ala  Thr Ser Gly
        995                 1000                1005

Ser Glu  Thr Pro Gly Thr Ser  Glu Ser Ala Thr Pro  Glu Ser Gly
    1010                1015                1020

Pro Gly  Thr Ser Thr Glu Pro  Ser Glu Gly Ser Ala  Pro Ala Ser
    1025                1030                1035

Ser Pro  Pro Val Leu Lys Arg  His Gln Ala Glu Ile  Thr Arg Thr
    1040                1045                1050

Thr Leu  Gln Ser Asp Gln Glu  Glu Ile Asp Tyr Asp  Asp Thr Ile
    1055                1060                1065

Ser Val  Glu Met Lys Lys Glu  Asp Phe Asp Ile Tyr  Asp Glu Asp
    1070                1075                1080

Glu Asn  Gln Ser Pro Arg Ser  Phe Gln Lys Lys Thr  Arg His Tyr
    1085                1090                1095

Phe Ile  Ala Ala Val Glu Arg  Leu Trp Asp Tyr Gly  Met Ser Ser
    1100                1105                1110

Ser Pro  His Val Leu Arg Asn  Arg Ala Gln Ser Gly  Ser Val Pro
    1115                1120                1125

Gln Phe  Lys Lys Val Val Phe  Gln Glu Phe Thr Asp  Gly Ser Phe
    1130                1135                1140

Thr Gln  Pro Leu Tyr Arg Gly  Glu Leu Asn Glu His  Leu Gly Leu
    1145                1150                1155

Leu Gly  Pro Tyr Ile Arg Ala  Glu Val Glu Asp Asn  Ile Met Val
    1160                1165                1170

Thr Phe  Arg Asn Gln Ala Ser  Arg Pro Tyr Ser Phe  Tyr Ser Ser
    1175                1180                1185

Leu Ile  Ser Tyr Glu Glu Asp  Gln Arg Gln Gly Ala  Glu Pro Arg
    1190                1195                1200
```

```
Lys Asn  Phe Val Lys Pro Asn  Glu Thr Lys Thr Tyr  Phe Trp Lys
    1205                 1210                 1215

Val Gln  His His Met Ala Pro  Thr Lys Asp Glu Phe  Asp Cys Lys
    1220                 1225                 1230

Ala Trp  Ala Tyr Phe Ser Asp  Val Asp Leu Glu Lys  Asp Val His
    1235                 1240                 1245

Ser Gly  Leu Ile Gly Pro Leu  Leu Val Cys His Thr  Asn Thr Leu
    1250                 1255                 1260

Asn Pro  Ala His Gly Arg Gln  Val Thr Val Gln Glu  Phe Ala Leu

    1265                 1270                 1275

Phe Phe  Thr Ile Phe Asp Glu  Thr Lys Ser Trp Tyr  Phe Thr Glu
    1280                 1285                 1290

Asn Met  Glu Arg Asn Cys Arg  Ala Pro Cys Asn Ile  Gln Met Glu
    1295                 1300                 1305

Asp Pro  Thr Phe Lys Glu Asn  Tyr Arg Phe His Ala  Ile Asn Gly
    1310                 1315                 1320

Tyr Ile  Met Asp Thr Leu Pro  Gly Leu Val Met Ala  Gln Asp Gln
    1325                 1330                 1335

Arg Ile  Arg Trp Tyr Leu Leu  Ser Met Gly Ser Asn  Glu Asn Ile
    1340                 1345                 1350

His Ser  Ile His Phe Ser Gly  His Val Phe Thr Val  Arg Lys Lys
    1355                 1360                 1365

Glu Glu  Tyr Lys Met Ala Leu  Tyr Asn Leu Tyr Pro  Gly Val Phe
    1370                 1375                 1380

Glu Thr  Val Glu Met Leu Pro  Ser Lys Ala Gly Ile  Trp Arg Val
    1385                 1390                 1395

Glu Cys  Leu Ile Gly Glu His  Leu His Ala Gly Met  Ser Thr Leu
    1400                 1405                 1410

Phe Leu  Val Tyr Ser Asn Lys  Cys Gln Thr Pro Leu  Gly Met Ala
    1415                 1420                 1425

Ser Gly  His Ile Arg Asp Phe  Gln Ile Thr Ala Ser  Gly Gln Tyr
    1430                 1435                 1440

Gly Gln  Trp Ala Pro Lys Leu  Ala Arg Leu His Tyr  Ser Gly Ser
    1445                 1450                 1455

Ile Asn  Ala Trp Ser Thr Lys  Glu Pro Phe Ser Trp  Ile Lys Val
    1460                 1465                 1470

Asp Leu  Leu Ala Pro Met Ile  Ile His Gly Ile Lys  Thr Gln Gly
    1475                 1480                 1485

Ala Arg  Gln Lys Phe Ser Ser  Leu Tyr Ile Ser Gln  Phe Ile Ile
    1490                 1495                 1500

Met Tyr  Ser Leu Asp Gly Lys  Lys Trp Gln Thr Tyr  Arg Gly Asn
    1505                 1510                 1515

Ser Thr  Gly Thr Leu Met Val  Phe Phe Gly Asn Val  Asp Ser Ser
    1520                 1525                 1530
```

```
Gly Ile  Lys His Asn Ile Phe  Asn Pro Pro Ile Ile  Ala Arg Tyr
    1535                 1540                 1545

Ile Arg  Leu His Pro Thr His  Tyr Ser Ile Arg Ser  Thr Leu Arg
    1550                 1555                 1560

Met Glu  Leu Met Gly Cys Asp  Leu Asn Ser Cys Ser  Met Pro Leu
    1565                 1570                 1575

Gly Met  Glu Ser Lys Ala Ile  Ser Asp Ala Gln Ile  Thr Ala Ser
    1580                 1585                 1590

Ser Tyr  Phe Thr Asn Met Phe  Ala Thr Trp Ser Pro  Ser Lys Ala
    1595                 1600                 1605

Arg Leu  His Leu Gln Gly Arg  Ser Asn Ala Trp Arg  Pro Gln Val
    1610                 1615                 1620

Asn Asn  Pro Lys Glu Trp Leu  Gln Val Asp Phe Gln  Lys Thr Met
    1625                 1630                 1635

Lys Val  Thr Gly Val Thr Thr  Gln Gly Val Lys Ser  Leu Leu Thr
    1640                 1645                 1650

Ser Met  Tyr Val Lys Glu Phe  Leu Ile Ser Ser Ser  Gln Asp Gly
    1655                 1660                 1665

His Gln  Trp Thr Leu Phe Phe  Gln Asn Gly Lys Val  Lys Val Phe
    1670                 1675                 1680

Gln Gly  Asn Gln Asp Ser Phe  Thr Pro Val Val Asn  Ser Leu Asp
    1685                 1690                 1695

Pro Pro  Leu Leu Thr Arg Tyr  Leu Arg Ile His Pro  Gln Ser Trp
    1700                 1705                 1710

Val His  Gln Ile Ala Leu Arg  Met Glu Val Leu Gly  Cys Glu Ala
    1715                 1720                 1725

Gln Asp  Leu Tyr Asp Lys Thr  His Thr Cys Pro Pro  Cys Pro Ala
    1730                 1735                 1740

Pro Glu  Leu Leu Gly Gly Pro  Ser Val Phe Leu Phe  Pro Pro Lys
    1745                 1750                 1755

Pro Lys  Asp Thr Leu Met Ile  Ser Arg Thr Pro Glu  Val Thr Cys
    1760                 1765                 1770

Val Val  Val Asp Val Ser His  Glu Asp Pro Glu Val  Lys Phe Asn
    1775                 1780                 1785

Trp Tyr  Val Asp Gly Val Glu  Val His Asn Ala Lys  Thr Lys Pro
    1790                 1795                 1800

Arg Glu  Glu Gln Tyr Asn Ser  Thr Tyr Arg Val Val  Ser Val Leu
    1805                 1810                 1815

Thr Val  Leu His Gln Asp Trp  Leu Asn Gly Lys Glu  Tyr Lys Cys
    1820                 1825                 1830

Lys Val  Ser Asn Lys Ala Leu  Pro Ala Pro Ile Glu  Lys Thr Ile
    1835                 1840                 1845

Ser Lys  Ala Lys Gly Gln Pro  Arg Glu Pro Gln Val  Tyr Thr Leu
    1850                 1855                 1860

Pro Pro  Ser Arg Asp Glu Leu  Thr Lys Asn Gln Val  Ser Leu Thr
    1865                 1870                 1875
```

```
Cys Leu  Val Lys Gly Phe Tyr  Pro Ser Asp Ile Ala  Val Glu Trp
    1880                 1885                 1890

Glu Ser  Asn Gly Gln Pro Glu  Asn Asn Tyr Lys Thr  Thr Pro Pro
    1895                 1900                 1905

Val Leu  Asp Ser Asp Gly Ser  Phe Phe Leu Tyr Ser  Lys Leu Thr
    1910                 1915                 1920

Val Asp  Lys Ser Arg Trp Gln  Gln Gly Asn Val Phe  Ser Cys Ser
    1925                 1930                 1935

Val Met  His Glu Ala Leu His  Asn His Tyr Thr Gln  Lys Ser Leu
    1940                 1945                 1950

Ser Leu  Ser Pro Gly Lys
    1955
```

<210> 104

<211> 1959

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYN-FVIII-173 mature Protein

<400> 104

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Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr
1               5                  10                  15

Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro
            20                  25                  30

Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
        35                  40                  45

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
    50                  55                  60

Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
65                  70                  75                  80

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
                85                  90                  95

Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
            100                 105                 110

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
        115                 120                 125

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
    130                 135                 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145                 150                 155                 160

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
                165                 170                 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
            180                 185                 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
```

```
        195                 200                 205

His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
    210                 215                 220

Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
225                 230                 235                 240

Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His
                245                 250                 255

Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu
            260                 265                 270

Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile
        275                 280                 285

Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
    290                 295                 300

Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met
305                 310                 315                 320

Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg
                325                 330                 335

Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp
            340                 345                 350

Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe
        355                 360                 365

Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His
    370                 375                 380

Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
385                 390                 395                 400

Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
                405                 410                 415

Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
            420                 425                 430

Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile
        435                 440                 445

Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile
    450                 455                 460

Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile
465                 470                 475                 480

Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys
                485                 490                 495

His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys
            500                 505                 510

Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys
        515                 520                 525

Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala
    530                 535                 540

Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp
545                 550                 555                 560

Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe
```

```
               565                 570                 575

Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln
            580                 585                 590

Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe
        595                 600                 605

Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser
    610                 615                 620

Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
625                 630                 635                 640

Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr
                645                 650                 655

Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro
            660                 665                 670

Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp
        675                 680                 685

Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala
    690                 695                 700

Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu
705                 710                 715                 720

Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala

               725                 730                 735

Ile Glu Pro Arg Ser Phe Ser Gln Asn Gly Ala Pro Gly Thr Ser Glu
            740                 745                 750

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
        755                 760                 765

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
    770                 775                 780

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu
785                 790                 795                 800

Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu
                805                 810                 815

Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
            820                 825                 830

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
        835                 840                 845

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
    850                 855                 860

Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
865                 870                 875                 880

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr
                885                 890                 895

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
            900                 905                 910

Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
```

```
        915                 920                 925

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
    930                 935                 940

Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly
945                 950                 955                 960

Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
                965                 970                 975

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
            980                 985                 990

Glu Pro Ser Glu Gly Ser Ala Pro  Gly Ser Glu Pro Ala  Thr Ser Gly
        995                 1000                1005

Ser Glu  Thr Pro Gly Thr Ser  Glu Ser Ala Thr Pro  Glu Ser Gly
    1010                1015                1020

Pro Gly  Thr Ser Thr Glu Pro  Ser Glu Gly Ser Ala  Pro Ala Ser
    1025                1030                1035

Ser Pro  Pro Val Leu Lys Arg  His Gln Arg Glu Ile  Thr Arg Thr
    1040                1045                1050

Thr Leu  Gln Ser Asp Gln Glu  Glu Ile Asp Tyr Asp  Asp Thr Ile
    1055                1060                1065

Ser Val  Glu Met Lys Lys Glu  Asp Phe Asp Ile Tyr  Asp Glu Asp
    1070                1075                1080

Glu Asn  Gln Ser Pro Arg Ser  Phe Gln Lys Lys Thr  Arg His Tyr
    1085                1090                1095

Phe Ile  Ala Ala Val Glu Arg  Leu Trp Asp Tyr Gly  Met Ser Ser
    1100                1105                1110

Ser Pro  His Val Leu Arg Asn  Arg Ala Gln Ser Gly  Ser Val Pro
    1115                1120                1125

Gln Phe  Lys Lys Val Val Phe  Gln Glu Phe Thr Asp  Gly Ser Phe
    1130                1135                1140

Thr Gln  Pro Leu Tyr Arg Gly  Glu Leu Asn Glu His  Leu Gly Leu
    1145                1150                1155

Leu Gly  Pro Tyr Ile Arg Ala  Glu Val Glu Asp Asn  Ile Met Val
    1160                1165                1170

Thr Phe  Arg Asn Gln Ala Ser  Arg Pro Tyr Ser Phe  Tyr Ser Ser
    1175                1180                1185

Leu Ile  Ser Tyr Glu Glu Asp  Gln Arg Gln Gly Ala  Glu Pro Arg
    1190                1195                1200

Lys Asn  Phe Val Lys Pro Asn  Glu Thr Lys Thr Tyr  Phe Trp Lys
    1205                1210                1215

Val Gln  His His Met Ala Pro  Thr Lys Asp Glu Phe  Asp Cys Lys
    1220                1225                1230

Ala Trp  Ala Tyr Phe Ser Asp  Val Asp Leu Glu Lys  Asp Val His
    1235                1240                1245

Ser Gly  Leu Ile Gly Pro Leu  Leu Val Cys His Thr  Asn Thr Leu
    1250                1255                1260

Asn Pro  Ala His Gly Arg Gln  Val Thr Val Gln Glu  Phe Ala Leu
```

```
    1265                1270                1275

Phe Phe  Thr Ile Phe Asp Glu  Thr Lys Ser Trp Tyr  Phe Thr Glu
    1280                1285                1290

Asn Met  Glu Arg Asn Cys Arg  Ala Pro Cys Asn Ile  Gln Met Glu
    1295                1300                1305

Asp Pro  Thr Phe Lys Glu Asn  Tyr Arg Phe His Ala  Ile Asn Gly
    1310                1315                1320

Tyr Ile  Met Asp Thr Leu Pro  Gly Leu Val Met Ala  Gln Asp Gln
    1325                1330                1335

Arg Ile  Arg Trp Tyr Leu Leu  Ser Met Gly Ser Asn  Glu Asn Ile
    1340                1345                1350

His Ser  Ile His Phe Ser Gly  His Val Phe Thr Val  Arg Lys Lys
    1355                1360                1365

Glu Glu  Tyr Lys Met Ala Leu  Tyr Asn Leu Tyr Pro  Gly Val Phe
    1370                1375                1380

Glu Thr  Val Glu Met Leu Pro  Ser Lys Ala Gly Ile  Trp Arg Val
    1385                1390                1395

Glu Cys  Leu Ile Gly Glu His  Leu His Ala Gly Met  Ser Thr Leu
    1400                1405                1410

Phe Leu  Val Tyr Ser Asn Lys  Cys Gln Thr Pro Leu  Gly Met Ala
    1415                1420                1425

Ser Gly  His Ile Arg Asp Phe  Gln Ile Thr Ala Ser  Gly Gln Tyr
    1430                1435                1440

Gly Gln  Trp Ala Pro Lys Leu  Ala Arg Leu His Tyr  Ser Gly Ser
    1445                1450                1455

Ile Asn  Ala Trp Ser Thr Lys  Glu Pro Phe Ser Trp  Ile Lys Val
    1460                1465                1470

Asp Leu  Leu Ala Pro Met Ile  Ile His Gly Ile Lys  Thr Gln Gly
    1475                1480                1485

Ala Arg  Gln Lys Phe Ser Ser  Leu Tyr Ile Ser Gln  Phe Ile Ile
    1490                1495                1500

Met Tyr  Ser Leu Asp Gly Lys  Lys Trp Gln Thr Tyr  Arg Gly Asn
    1505                1510                1515

Ser Thr  Gly Thr Leu Met Val  Phe Phe Gly Asn Val  Asp Ser Ser
    1520                1525                1530

Gly Ile  Lys His Asn Ile Phe  Asn Pro Pro Ile Ile  Ala Arg Tyr
    1535                1540                1545

Ile Arg  Leu His Pro Thr His  Tyr Ser Ile Arg Ser  Thr Leu Arg
    1550                1555                1560

Met Glu  Leu Met Gly Cys Asp  Leu Asn Ser Cys Ser  Met Pro Leu
    1565                1570                1575

Gly Met  Glu Ser Lys Ala Ile  Ser Asp Ala Gln Ile  Thr Ala Ser
    1580                1585                1590

Ser Tyr  Phe Thr Asn Met Phe  Ala Thr Trp Ser Pro  Ser Lys Ala
    1595                1600                1605
```

```
Arg Leu  His Leu Gln Gly Arg  Ser Asn Ala Trp Arg  Pro Gln Val
    1610                 1615                 1620

Asn Asn  Pro Lys Glu Trp Leu  Gln Val Asp Phe Gln  Lys Thr Met
    1625                 1630                 1635

Lys Val  Thr Gly Val Thr Thr  Gln Gly Val Lys Ser  Leu Leu Thr
    1640                 1645                 1650

Ser Met  Tyr Val Lys Glu Phe  Leu Ile Ser Ser Ser  Gln Asp Gly
    1655                 1660                 1665

His Gln  Trp Thr Leu Phe Phe  Gln Asn Gly Lys Val  Lys Val Phe
    1670                 1675                 1680

Gln Gly  Asn Gln Asp Ser Phe  Thr Pro Val Val Asn  Ser Leu Asp

    1685                 1690                 1695

Pro Pro  Leu Leu Thr Arg Tyr  Leu Arg Ile His Pro  Gln Ser Trp
    1700                 1705                 1710

Val His  Gln Ile Ala Leu Arg  Met Glu Val Leu Gly  Cys Glu Ala
    1715                 1720                 1725

Gln Asp  Leu Tyr Asp Lys Thr  His Thr Cys Pro Pro  Cys Pro Ala
    1730                 1735                 1740

Pro Glu  Leu Leu Gly Gly Pro  Ser Val Phe Leu Phe  Pro Pro Lys
    1745                 1750                 1755

Pro Lys  Asp Thr Leu Met Ile  Ser Arg Thr Pro Glu  Val Thr Cys
    1760                 1765                 1770

Val Val  Val Asp Val Ser His  Glu Asp Pro Glu Val  Lys Phe Asn
    1775                 1780                 1785

Trp Tyr  Val Asp Gly Val Glu  Val His Asn Ala Lys  Thr Lys Pro
    1790                 1795                 1800

Arg Glu  Glu Gln Tyr Asn Ser  Thr Tyr Arg Val Val  Ser Val Leu
    1805                 1810                 1815

Thr Val  Leu His Gln Asp Trp  Leu Asn Gly Lys Glu  Tyr Lys Cys
    1820                 1825                 1830

Lys Val  Ser Asn Lys Ala Leu  Pro Ala Pro Ile Glu  Lys Thr Ile
    1835                 1840                 1845

Ser Lys  Ala Lys Gly Gln Pro  Arg Glu Pro Gln Val  Tyr Thr Leu
    1850                 1855                 1860

Pro Pro  Ser Arg Asp Glu Leu  Thr Lys Asn Gln Val  Ser Leu Thr
    1865                 1870                 1875

Cys Leu  Val Lys Gly Phe Tyr  Pro Ser Asp Ile Ala  Val Glu Trp
    1880                 1885                 1890

Glu Ser  Asn Gly Gln Pro Glu  Asn Asn Tyr Lys Thr  Thr Pro Pro
    1895                 1900                 1905

Val Leu  Asp Ser Asp Gly Ser  Phe Phe Leu Tyr Ser  Lys Leu Thr
    1910                 1915                 1920

Val Asp  Lys Ser Arg Trp Gln  Gln Gly Asn Val Phe  Ser Cys Ser
    1925                 1930                 1935

Val Met  His Glu Ala Leu His  Asn His Tyr Thr Gln  Lys Ser Leu
```

```
                                                                    
    1940                1945                1950

Ser Leu  Ser Pro Gly Lys
    1955
```

<210> 105

<211> 1984

<212> PRT

<213> Artificial Sequence

<220>

<223> FVIII 195 protein sequence

<400> 105

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
        35                  40                  45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
    50                  55                  60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65                  70                  75                  80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
                85                  90                  95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
            100                 105                 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
        115                 120                 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
    130                 135                 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145                 150                 155                 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser

                165                 170                 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
            180                 185                 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
        195                 200                 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
    210                 215                 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225                 230                 235                 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
                245                 250                 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
            260                 265                 270
```

```
Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
        275                 280                 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
    290                 295                 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305                 310                 315                 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
                325                 330                 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
            340                 345                 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
        355                 360                 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
    370                 375                 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385                 390                 395                 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
                405                 410                 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
            420                 425                 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
        435                 440                 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
    450                 455                 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465                 470                 475                 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
                485                 490                 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
            500                 505                 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
        515                 520                 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
    530                 535                 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545                 550                 555                 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
                565                 570                 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
            580                 585                 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
        595                 600                 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
    610                 615                 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625                 630                 635                 640
```

```
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
                645                 650                 655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
            660                 665                 670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
        675                 680                 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
    690                 695                 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705                 710                 715                 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
                725                 730                 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
            740                 745                 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu
        755                 760                 765

Lys Arg His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Gly Ala Pro
    770                 775                 780

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro
785                 790                 795                 800

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
                805                 810                 815

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
            820                 825                 830

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly
        835                 840                 845

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
    850                 855                 860

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
865                 870                 875                 880

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr
                885                 890                 895

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
            900                 905                 910

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
        915                 920                 925

Ala Ser Ser Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser
    930                 935                 940

Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn
945                 950                 955                 960

Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala
                965                 970                 975

Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser Ser Ser Pro His Val
            980                 985                 990

Leu Arg Asn Arg Ala Gln Ser Gly  Ser Val Pro Gln Phe  Lys Lys Val
        995                 1000                1005
```

Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro Leu Tyr
1010 1015 1020

Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile
1025 1030 1035

Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln
1040 1045 1050

Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu
1055 1060 1065

Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys
1070 1075 1080

Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His Met
1085 1090 1095

Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe
1100 1105 1110

Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly
1115 1120 1125

Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly
1130 1135 1140

Arg Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe
1145 1150 1155

Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn

1160 1165 1170

Cys Arg Gly Ala Pro Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly
1175 1180 1185

Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr
1190 1195 1200

Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
1205 1210 1215

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
1220 1225 1230

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala
1235 1240 1245

Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser
1250 1255 1260

Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly
1265 1270 1275

Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr
1280 1285 1290

Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly
1295 1300 1305

Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ala
1310 1315 1320

Ser Ser Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys
1325 1330 1335

```
Glu Asn  Tyr Arg Phe His Ala  Ile Asn Gly Tyr Ile  Met Asp Thr
    1340                 1345                 1350

Leu Pro  Gly Leu Val Met Ala  Gln Asp Gln Arg Ile  Arg Trp Tyr
    1355                 1360                 1365

Leu Leu  Ser Met Gly Ser Asn  Glu Asn Ile His Ser  Ile His Phe
    1370                 1375                 1380

Ser Gly  His Val Phe Thr Val  Arg Lys Lys Glu Glu  Tyr Lys Met
    1385                 1390                 1395

Ala Leu  Tyr Asn Leu Tyr Pro  Gly Val Phe Glu Thr  Val Glu Met
    1400                 1405                 1410

Leu Pro  Ser Lys Ala Gly Ile  Trp Arg Val Glu Cys  Leu Ile Gly
    1415                 1420                 1425

Glu His  Leu His Ala Gly Met  Ser Thr Leu Phe Leu  Val Tyr Ser
    1430                 1435                 1440

Asn Lys  Cys Gln Thr Pro Leu  Gly Met Ala Ser Gly  His Ile Arg
    1445                 1450                 1455

Asp Phe  Gln Ile Thr Ala Ser  Gly Gln Tyr Gly Gln  Trp Ala Pro
    1460                 1465                 1470

Lys Leu  Ala Arg Leu His Tyr  Ser Gly Ser Ile Asn  Ala Trp Ser
    1475                 1480                 1485

Thr Lys  Glu Pro Phe Ser Trp  Ile Lys Val Asp Leu  Leu Ala Pro
    1490                 1495                 1500

Met Ile  Ile His Gly Ile Lys  Thr Gln Gly Ala Arg  Gln Lys Phe
    1505                 1510                 1515

Ser Ser  Leu Tyr Ile Ser Gln  Phe Ile Ile Met Tyr  Ser Leu Asp
    1520                 1525                 1530

Gly Lys  Lys Trp Gln Thr Tyr  Arg Gly Asn Ser Thr  Gly Thr Leu
    1535                 1540                 1545

Met Val  Phe Phe Gly Asn Val  Asp Ser Ser Gly Ile  Lys His Asn
    1550                 1555                 1560

Ile Phe  Asn Pro Pro Ile Ile  Ala Arg Tyr Ile Arg  Leu His Pro
    1565                 1570                 1575

Thr His  Tyr Ser Ile Arg Ser  Thr Leu Arg Met Glu  Leu Met Gly
    1580                 1585                 1590

Cys Asp  Leu Asn Ser Cys Ser  Met Pro Leu Gly Met  Glu Ser Lys
    1595                 1600                 1605

Ala Ile  Ser Asp Ala Gln Ile  Thr Ala Ser Ser Tyr  Phe Thr Asn
    1610                 1615                 1620

Met Phe  Ala Thr Trp Ser Pro  Ser Lys Ala Arg Leu  His Leu Gln
    1625                 1630                 1635

Gly Arg  Ser Asn Ala Trp Arg  Pro Gln Val Asn Asn  Pro Lys Glu
    1640                 1645                 1650

Trp Leu  Gln Val Asp Phe Gln  Lys Thr Met Lys Val  Thr Gly Val
    1655                 1660                 1665

Thr Thr  Gln Gly Val Lys Ser  Leu Leu Thr Ser Met  Tyr Val Lys
    1670                 1675                 1680
```

```
Glu Phe  Leu Ile Ser Ser Ser  Gln Asp Gly His Gln  Trp Thr Leu
    1685                 1690                 1695

Phe Phe  Gln Asn Gly Lys Val  Lys Val Phe Gln Gly  Asn Gln Asp
    1700                 1705                 1710

Ser Phe  Thr Pro Val Val Asn  Ser Leu Asp Pro Pro  Leu Leu Thr
    1715                 1720                 1725

Arg Tyr  Leu Arg Ile His Pro  Gln Ser Trp Val His  Gln Ile Ala
    1730                 1735                 1740

Leu Arg  Met Glu Val Leu Gly  Cys Glu Ala Gln Asp  Leu Tyr Asp
    1745                 1750                 1755

Lys Thr  His Thr Cys Pro Pro  Cys Pro Ala Pro Glu  Leu Leu Gly
    1760                 1765                 1770

Gly Pro  Ser Val Phe Leu Phe  Pro Pro Lys Pro Lys  Asp Thr Leu
    1775                 1780                 1785

Met Ile  Ser Arg Thr Pro Glu  Val Thr Cys Val Val  Val Asp Val
    1790                 1795                 1800

Ser His  Glu Asp Pro Glu Val  Lys Phe Asn Trp Tyr  Val Asp Gly
    1805                 1810                 1815

Val Glu  Val His Asn Ala Lys  Thr Lys Pro Arg Glu  Glu Gln Tyr
    1820                 1825                 1830

Asn Ser  Thr Tyr Arg Val Val  Ser Val Leu Thr Val  Leu His Gln
    1835                 1840                 1845

Asp Trp  Leu Asn Gly Lys Glu  Tyr Lys Cys Lys Val  Ser Asn Lys
    1850                 1855                 1860

Ala Leu  Pro Ala Pro Ile Glu  Lys Thr Ile Ser Lys  Ala Lys Gly
    1865                 1870                 1875

Gln Pro  Arg Glu Pro Gln Val  Tyr Thr Leu Pro Pro  Ser Arg Asp
    1880                 1885                 1890

Glu Leu  Thr Lys Asn Gln Val  Ser Leu Thr Cys Leu  Val Lys Gly
    1895                 1900                 1905

Phe Tyr  Pro Ser Asp Ile Ala  Val Glu Trp Glu Ser  Asn Gly Gln
    1910                 1915                 1920

Pro Glu  Asn Asn Tyr Lys Thr  Thr Pro Pro Val Leu  Asp Ser Asp
    1925                 1930                 1935

Gly Ser  Phe Phe Leu Tyr Ser  Lys Leu Thr Val Asp  Lys Ser Arg
    1940                 1945                 1950

Trp Gln  Gln Gly Asn Val Phe  Ser Cys Ser Val Met  His Glu Ala
    1955                 1960                 1965

Leu His  Asn His Tyr Thr Gln  Lys Ser Leu Ser Leu  Ser Pro Gly
    1970                 1975                 1980

Lys
```

<210> 106

<211> 2134

<212> PRT

<213> Artificial Sequence

<220>

<223> FVIII 196 protein sequence

<400> 106

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Gly Ala Pro
        35                  40                  45

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro
    50                  55                  60

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
65                  70                  75                  80

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
                85                  90                  95

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
            100                 105                 110

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
        115                 120                 125

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
    130                 135                 140

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
145                 150                 155                 160

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
                165                 170                 175

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
            180                 185                 190

Ala Ser Ser Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe Pro
        195                 200                 205

Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr
    210                 215                 220

Asp His Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu
225                 230                 235                 240

Leu Gly Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr
                245                 250                 255

Leu Lys Asn Met Ala Ser His Pro Val Ser Leu His Ala Val Gly Val
            260                 265                 270

Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser
        275                 280                 285

Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly Ser His Thr
    290                 295                 300

Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro
305                 310                 315                 320

Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp
                325                 330                 335
```

```
Leu Asn Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser
            340                 345                 350

Leu Ala Lys Glu Lys Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe
        355                 360                 365

Ala Val Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Lys Asn Ser
    370                 375                 380

Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala Trp Pro Lys Met
385                 390                 395                 400

His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly
                405                 410                 415

Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr
            420                 425                 430

Pro Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg
        435                 440                 445

Asn His Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr
    450                 455                 460

Ala Gln Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His
465                 470                 475                 480

Ile Ser Ser His Gln His Asp Gly Met Glu Ala Tyr Val Lys Val Asp
                485                 490                 495

Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn Asn Glu Glu Ala
            500                 505                 510

Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val Val Arg
        515                 520                 525

Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala
    530                 535                 540

Lys Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu
545                 550                 555                 560

Asp Trp Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr
                565                 570                 575

Lys Ser Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr

            580                 585                 590

Lys Lys Val Arg Phe Met Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg
        595                 600                 605

Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly
    610                 615                 620

Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg
625                 630                 635                 640

Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr
                645                 650                 655

Ser Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile
            660                 665                 670

Leu Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp
        675                 680                 685
```

```
Gly Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser
    690                 695                 700

Phe Val Asn Met Glu Arg Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu
705                 710                 715                 720

Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn Gln Ile Met
                725                 730                 735

Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
            740                 745                 750

Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala
        755                 760                 765

Gly Val Gln Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His
    770                 775                 780

Ser Ile Asn Gly Tyr Val Phe Asp Ser Leu Gln Leu Ser Val Cys Leu
785                 790                 795                 800

His Glu Val Ala Tyr Trp Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp
                805                 810                 815

Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys His Lys Met Val
            820                 825                 830

Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val Phe
        835                 840                 845

Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser
    850                 855                 860

Asp Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys
865                 870                 875                 880

Asp Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser
                885                 890                 895

Ala Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser
            900                 905                 910

Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg Thr
        915                 920                 925

Thr Leu Gln Gly Ala Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser
    930                 935                 940

Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala
945                 950                 955                 960

Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr
                965                 970                 975

Ser Ser Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr
            980                 985                 990

Gly Pro Gly Thr Pro Gly Ser Gly  Thr Ala Ser Ser Ser  Pro Gly Ala
        995                 1000                1005

Ser Pro  Gly Thr Ser Ser Thr  Gly Ser Pro Gly Ala  Ser Pro Gly
    1010                1015                1020

Thr Ser  Ser Thr Gly Ser Pro  Gly Ala Ser Pro Gly  Thr Ser Ser
    1025                1030                1035

Thr Gly  Ser Pro Gly Ser Ser  Thr Pro Ser Gly Ala  Thr Gly Ser
    1040                1045                1050
```

```
Pro Gly  Ser Ser Thr Pro Ser  Gly Ala Thr Gly Ser  Pro Gly Ala
    1055                 1060                 1065

Ser Pro  Gly Thr Ser Ser Thr  Gly Ser Pro Ala Ser  Ser Ser Asp
    1070                 1075                 1080

Gln Glu  Glu Ile Asp Tyr Asp  Asp Thr Ile Ser Val  Glu Met Lys
    1085                 1090                 1095

Lys Glu  Asp Phe Asp Ile Tyr  Asp Glu Asp Glu Asn  Gln Ser Pro
    1100                 1105                 1110

Arg Ser  Phe Gln Lys Lys Thr  Arg His Tyr Phe Ile  Ala Ala Val
    1115                 1120                 1125

Glu Arg  Leu Trp Asp Tyr Gly  Met Ser Ser Ser Pro  His Val Leu
    1130                 1135                 1140

Arg Asn  Arg Ala Gln Ser Gly  Ser Val Pro Gln Phe  Lys Lys Val
    1145                 1150                 1155

Val Phe  Gln Glu Phe Thr Asp  Gly Ser Phe Thr Gln  Pro Leu Tyr
    1160                 1165                 1170

Arg Gly  Glu Leu Asn Glu His  Leu Gly Leu Leu Gly  Pro Tyr Ile
    1175                 1180                 1185

Arg Ala  Glu Val Glu Asp Asn  Ile Met Val Thr Phe  Arg Asn Gln
    1190                 1195                 1200

Ala Ser  Arg Pro Tyr Ser Phe  Tyr Ser Ser Leu Ile  Ser Tyr Glu
    1205                 1210                 1215

Glu Asp  Gln Arg Gln Gly Ala  Glu Pro Arg Lys Asn  Phe Val Lys
    1220                 1225                 1230

Pro Asn  Glu Thr Lys Thr Tyr  Phe Trp Lys Val Gln  His His Met
    1235                 1240                 1245

Ala Pro  Thr Lys Asp Glu Phe  Asp Cys Lys Ala Trp  Ala Tyr Phe
    1250                 1255                 1260

Ser Asp  Val Asp Leu Glu Lys  Asp Val His Ser Gly  Leu Ile Gly
    1265                 1270                 1275

Pro Leu  Leu Val Cys His Thr  Asn Thr Leu Asn Pro  Ala His Gly
    1280                 1285                 1290

Arg Gln  Val Thr Val Gln Glu  Phe Ala Leu Phe Phe  Thr Ile Phe
    1295                 1300                 1305

Asp Glu  Thr Lys Ser Trp Tyr  Phe Thr Glu Asn Met  Glu Arg Asn
    1310                 1315                 1320

Cys Arg  Gly Ala Pro Thr Ser  Glu Ser Ala Thr Pro  Glu Ser Gly
    1325                 1330                 1335

Pro Gly  Ser Glu Pro Ala Thr  Ser Gly Ser Glu Thr  Pro Gly Thr
    1340                 1345                 1350

Ser Glu  Ser Ala Thr Pro Glu  Ser Gly Pro Gly Ser  Glu Pro Ala
    1355                 1360                 1365

Thr Ser  Gly Ser Glu Thr Pro  Gly Thr Ser Glu Ser  Ala Thr Pro
    1370                 1375                 1380

Glu Ser  Gly Pro Gly Thr Ser  Thr Glu Pro Ser Glu  Gly Ser Ala
    1385                 1390                 1395
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    ----                ----                ----

Pro Gly  Thr Ser Glu Ser Ala  Thr Pro Glu Ser Gly  Pro Gly Ser
    1400                1405                1410

Pro Ala  Gly Ser Pro Thr Ser  Thr Glu Glu Gly Ser  Pro Ala Gly
    1415                1420                1425

Ser Pro  Thr Ser Thr Glu Glu  Gly Ser Pro Ala Gly  Ser Pro Thr
    1430                1435                1440

Ser Thr  Glu Glu Gly Thr Ser  Glu Ser Ala Thr Pro  Glu Ser Gly
    1445                1450                1455

Pro Gly  Thr Ser Thr Glu Pro  Ser Glu Gly Ser Ala  Pro Gly Ala
    1460                1465                1470

Ser Ser  Ala Pro Cys Asn Ile  Gln Met Glu Asp Pro  Thr Phe Lys
    1475                1480                1485

Glu Asn  Tyr Arg Phe His Ala  Ile Asn Gly Tyr Ile  Met Asp Thr
    1490                1495                1500

Leu Pro  Gly Leu Val Met Ala  Gln Asp Gln Arg Ile  Arg Trp Tyr
    1505                1510                1515

Leu Leu  Ser Met Gly Ser Asn  Glu Asn Ile His Ser  Ile His Phe
    1520                1525                1530

Ser Gly  His Val Phe Thr Val  Arg Lys Lys Glu Glu  Tyr Lys Met
    1535                1540                1545

Ala Leu  Tyr Asn Leu Tyr Pro  Gly Val Phe Glu Thr  Val Glu Met

    1550                1555                1560

Leu Pro  Ser Lys Ala Gly Ile  Trp Arg Val Glu Cys  Leu Ile Gly
    1565                1570                1575

Glu His  Leu His Ala Gly Met  Ser Thr Leu Phe Leu  Val Tyr Ser
    1580                1585                1590

Asn Lys  Cys Gln Thr Pro Leu  Gly Met Ala Ser Gly  His Ile Arg
    1595                1600                1605

Asp Phe  Gln Ile Thr Ala Ser  Gly Gln Tyr Gly Gln  Trp Ala Pro
    1610                1615                1620

Lys Leu  Ala Arg Leu His Tyr  Ser Gly Ser Ile Asn  Ala Trp Ser
    1625                1630                1635

Thr Lys  Glu Pro Phe Ser Trp  Ile Lys Val Asp Leu  Leu Ala Pro
    1640                1645                1650

Met Ile  Ile His Gly Ile Lys  Thr Gln Gly Ala Arg  Gln Lys Phe
    1655                1660                1665

Ser Ser  Leu Tyr Ile Ser Gln  Phe Ile Ile Met Tyr  Ser Leu Asp
    1670                1675                1680

Gly Lys  Lys Trp Gln Thr Tyr  Arg Gly Asn Ser Thr  Gly Thr Leu
    1685                1690                1695

Met Val  Phe Phe Gly Asn Val  Asp Ser Ser Gly Ile  Lys His Asn
    1700                1705                1710

Ile Phe  Asn Pro Pro Ile Ile  Ala Arg Tyr Ile Arg  Leu His Pro
    1715                1720                1725
```

```
Thr His  Tyr Ser Ile Arg Ser  Thr Leu Arg Met Glu  Leu Met Gly
    1730                1735                1740

Cys Asp  Leu Asn Ser Cys Ser  Met Pro Leu Gly Met  Glu Ser Lys
    1745                1750                1755

Ala Ile  Ser Asp Ala Gln Ile  Thr Ala Ser Ser Tyr  Phe Thr Asn
    1760                1765                1770

Met Phe  Ala Thr Trp Ser Pro  Ser Lys Ala Arg Leu  His Leu Gln
    1775                1780                1785

Gly Arg  Ser Asn Ala Trp Arg  Pro Gln Val Asn Asn  Pro Lys Glu
    1790                1795                1800

Trp Leu  Gln Val Asp Phe Gln  Lys Thr Met Lys Val  Thr Gly Val
    1805                1810                1815

Thr Thr  Gln Gly Val Lys Ser  Leu Leu Thr Ser Met  Tyr Val Lys
    1820                1825                1830

Glu Phe  Leu Ile Ser Ser Ser  Gln Asp Gly His Gln  Trp Thr Leu
    1835                1840                1845

Phe Phe  Gln Asn Gly Lys Val  Lys Val Phe Gln Gly  Asn Gln Asp
    1850                1855                1860

Ser Phe  Thr Pro Val Val Asn  Ser Leu Asp Pro Pro  Leu Leu Thr
    1865                1870                1875

Arg Tyr  Leu Arg Ile His Pro  Gln Ser Trp Val His  Gln Ile Ala
    1880                1885                1890

Leu Arg  Met Glu Val Leu Gly  Cys Glu Ala Gln Asp  Leu Tyr Asp
    1895                1900                1905

Lys Thr  His Thr Cys Pro Pro  Cys Pro Ala Pro Glu  Leu Leu Gly
    1910                1915                1920

Gly Pro  Ser Val Phe Leu Phe  Pro Pro Lys Pro Lys  Asp Thr Leu
    1925                1930                1935

Met Ile  Ser Arg Thr Pro Glu  Val Thr Cys Val Val  Val Asp Val
    1940                1945                1950

Ser His  Glu Asp Pro Glu Val  Lys Phe Asn Trp Tyr  Val Asp Gly
    1955                1960                1965

Val Glu  Val His Asn Ala Lys  Thr Lys Pro Arg Glu  Glu Gln Tyr
    1970                1975                1980

Asn Ser  Thr Tyr Arg Val Val  Ser Val Leu Thr Val  Leu His Gln
    1985                1990                1995

Asp Trp  Leu Asn Gly Lys Glu  Tyr Lys Cys Lys Val  Ser Asn Lys
    2000                2005                2010

Ala Leu  Pro Ala Pro Ile Glu  Lys Thr Ile Ser Lys  Ala Lys Gly
    2015                2020                2025

Gln Pro  Arg Glu Pro Gln Val  Tyr Thr Leu Pro Pro  Ser Arg Asp
    2030                2035                2040

Glu Leu  Thr Lys Asn Gln Val  Ser Leu Thr Cys Leu  Val Lys Gly
    2045                2050                2055

Phe Tyr  Pro Ser Asp Ile Ala  Val Glu Trp Glu Ser  Asn Gly Gln
    2060                2065                2070
```

```
    2060                2065                2070

Pro Glu  Asn Asn Tyr Lys Thr  Thr Pro Pro Val Leu  Asp Ser Asp
    2075                2080                2085

Gly Ser  Phe Phe Leu Tyr Ser  Lys Leu Thr Val Asp  Lys Ser Arg
    2090                2095                2100

Trp Gln  Gln Gly Asn Val Phe  Ser Cys Ser Val Met  His Glu Ala
    2105                2110                2115

Leu His  Asn His Tyr Thr Gln  Lys Ser Leu Ser Leu  Ser Pro Gly
    2120                2125                2130

Lys
```

<210> 107

<211> 1984

<212> PRT

<213> Artificial Sequence

<220>

<223> FVIII 199 protein sequence

<400> 107

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
        35                  40                  45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
    50                  55                  60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65                  70                  75                  80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
                85                  90                  95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
            100                 105                 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
        115                 120                 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
    130                 135                 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145                 150                 155                 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
                165                 170                 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
            180                 185                 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
        195                 200                 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
    210                 215                 220
```

```
Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225                 230                 235                 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
                245                 250                 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
            260                 265                 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
        275                 280                 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
    290                 295                 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305                 310                 315                 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
                325                 330                 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
            340                 345                 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
        355                 360                 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
    370                 375                 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385                 390                 395                 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
                405                 410                 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
            420                 425                 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
        435                 440                 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
    450                 455                 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465                 470                 475                 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
                485                 490                 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
            500                 505                 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
        515                 520                 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
    530                 535                 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545                 550                 555                 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
                565                 570                 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
            580                 585                 590
```

```
Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
        595                 600                 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
    610                 615                 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625                 630                 635                 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
                645                 650                 655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
            660                 665                 670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
        675                 680                 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
    690                 695                 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705                 710                 715                 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
                725                 730                 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
            740                 745                 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu
        755                 760                 765

Lys Arg His Gln Ala Glu Ile Thr Arg Thr Thr Leu Gln Gly Ala Pro
    770                 775                 780

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro
785                 790                 795                 800

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
                805                 810                 815

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
            820                 825                 830

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly

        835                 840                 845

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
    850                 855                 860

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
865                 870                 875                 880

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr
                885                 890                 895

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
            900                 905                 910

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
        915                 920                 925

Ala Ser Ser Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser
    930                 935                 940
```

```
Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn
945                 950                 955                 960

Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala
                965                 970                 975

Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser Ser Ser Pro His Val
            980                 985                 990

Leu Arg Asn Arg Ala Gln Ser Gly  Ser Val Pro Gln Phe  Lys Lys Val
        995                 1000                1005

Val Phe  Gln Glu Phe Thr Asp  Gly Ser Phe Thr Gln  Pro Leu Tyr
    1010                1015                1020

Arg Gly  Glu Leu Asn Glu His  Leu Gly Leu Leu Gly  Pro Tyr Ile
    1025                1030                1035

Arg Ala  Glu Val Glu Asp Asn  Ile Met Val Thr Phe  Arg Asn Gln
    1040                1045                1050

Ala Ser  Arg Pro Tyr Ser Phe  Tyr Ser Ser Leu Ile  Ser Tyr Glu
    1055                1060                1065

Glu Asp  Gln Arg Gln Gly Ala  Glu Pro Arg Lys Asn  Phe Val Lys
    1070                1075                1080

Pro Asn  Glu Thr Lys Thr Tyr  Phe Trp Lys Val Gln  His His Met
    1085                1090                1095

Ala Pro  Thr Lys Asp Glu Phe  Asp Cys Lys Ala Trp  Ala Tyr Phe
    1100                1105                1110

Ser Asp  Val Asp Leu Glu Lys  Asp Val His Ser Gly  Leu Ile Gly
    1115                1120                1125

Pro Leu  Leu Val Cys His Thr  Asn Thr Leu Asn Pro  Ala His Gly
    1130                1135                1140

Arg Gln  Val Thr Val Gln Glu  Phe Ala Leu Phe Phe  Thr Ile Phe
    1145                1150                1155

Asp Glu  Thr Lys Ser Trp Tyr  Phe Thr Glu Asn Met  Glu Arg Asn
    1160                1165                1170

Cys Arg  Gly Ala Pro Thr Ser  Glu Ser Ala Thr Pro  Glu Ser Gly
    1175                1180                1185

Pro Gly  Ser Glu Pro Ala Thr  Ser Gly Ser Glu Thr  Pro Gly Thr
    1190                1195                1200

Ser Glu  Ser Ala Thr Pro Glu  Ser Gly Pro Gly Ser  Glu Pro Ala
    1205                1210                1215

Thr Ser  Gly Ser Glu Thr Pro  Gly Thr Ser Glu Ser  Ala Thr Pro
    1220                1225                1230

Glu Ser  Gly Pro Gly Thr Ser  Thr Glu Pro Ser Glu  Gly Ser Ala
    1235                1240                1245

Pro Gly  Thr Ser Glu Ser Ala  Thr Pro Glu Ser Gly  Pro Gly Ser
    1250                1255                1260

Pro Ala  Gly Ser Pro Thr Ser  Thr Glu Glu Gly Ser  Pro Ala Gly
    1265                1270                1275

Ser Pro  Thr Ser Thr Glu Glu  Gly Ser Pro Ala Gly  Ser Pro Thr
    1280                1285                1290
```

```
Ser Thr  Glu Glu Gly Thr Ser  Glu Ser Ala Thr Pro  Glu Ser Gly
    1295                 1300                 1305

Pro Gly  Thr Ser Thr Glu Pro  Ser Glu Gly Ser Ala  Pro Gly Ala
    1310                 1315                 1320

Ser Ser  Ala Pro Cys Asn Ile  Gln Met Glu Asp Pro  Thr Phe Lys
    1325                 1330                 1335

Glu Asn  Tyr Arg Phe His Ala  Ile Asn Gly Tyr Ile  Met Asp Thr
    1340                 1345                 1350

Leu Pro  Gly Leu Val Met Ala  Gln Asp Gln Arg Ile  Arg Trp Tyr
    1355                 1360                 1365

Leu Leu  Ser Met Gly Ser Asn  Glu Asn Ile His Ser  Ile His Phe
    1370                 1375                 1380

Ser Gly  His Val Phe Thr Val  Arg Lys Lys Glu Glu  Tyr Lys Met
    1385                 1390                 1395

Ala Leu  Tyr Asn Leu Tyr Pro  Gly Val Phe Glu Thr  Val Glu Met
    1400                 1405                 1410

Leu Pro  Ser Lys Ala Gly Ile  Trp Arg Val Glu Cys  Leu Ile Gly
    1415                 1420                 1425

Glu His  Leu His Ala Gly Met  Ser Thr Leu Phe Leu  Val Tyr Ser
    1430                 1435                 1440

Asn Lys  Cys Gln Thr Pro Leu  Gly Met Ala Ser Gly  His Ile Arg
    1445                 1450                 1455

Asp Phe  Gln Ile Thr Ala Ser  Gly Gln Tyr Gly Gln  Trp Ala Pro
    1460                 1465                 1470

Lys Leu  Ala Arg Leu His Tyr  Ser Gly Ser Ile Asn  Ala Trp Ser
    1475                 1480                 1485

Thr Lys  Glu Pro Phe Ser Trp  Ile Lys Val Asp Leu  Leu Ala Pro
    1490                 1495                 1500

Met Ile  Ile His Gly Ile Lys  Thr Gln Gly Ala Arg  Gln Lys Phe
    1505                 1510                 1515

Ser Ser  Leu Tyr Ile Ser Gln  Phe Ile Ile Met Tyr  Ser Leu Asp
    1520                 1525                 1530

Gly Lys  Lys Trp Gln Thr Tyr  Arg Gly Asn Ser Thr  Gly Thr Leu
    1535                 1540                 1545

Met Val  Phe Phe Gly Asn Val  Asp Ser Ser Gly Ile  Lys His Asn
    1550                 1555                 1560

Ile Phe  Asn Pro Pro Ile Ile  Ala Arg Tyr Ile Arg  Leu His Pro
    1565                 1570                 1575

Thr His  Tyr Ser Ile Arg Ser  Thr Leu Arg Met Glu  Leu Met Gly
    1580                 1585                 1590

Cys Asp  Leu Asn Ser Cys Ser  Met Pro Leu Gly Met  Glu Ser Lys
    1595                 1600                 1605

Ala Ile  Ser Asp Ala Gln Ile  Thr Ala Ser Ser Tyr  Phe Thr Asn
    1610                 1615                 1620

Met Phe  Ala Thr Trp Ser Pro  Ser Lys Ala Arg Leu  His Leu Gln
    1625                 1630                 1635
```

```
Gly Arg  Ser Asn Ala Trp Arg  Pro Gln Val Asn Asn  Pro Lys Glu
    1640                 1645                 1650

Trp Leu  Gln Val Asp Phe Gln  Lys Thr Met Lys Val  Thr Gly Val
    1655                 1660                 1665

Thr Thr  Gln Gly Val Lys Ser  Leu Leu Thr Ser Met  Tyr Val Lys
    1670                 1675                 1680

Glu Phe  Leu Ile Ser Ser Ser  Gln Asp Gly His Gln  Trp Thr Leu
    1685                 1690                 1695

Phe Phe  Gln Asn Gly Lys Val  Lys Val Phe Gln Gly  Asn Gln Asp
    1700                 1705                 1710

Ser Phe  Thr Pro Val Val Asn  Ser Leu Asp Pro Pro  Leu Leu Thr
    1715                 1720                 1725

Arg Tyr  Leu Arg Ile His Pro  Gln Ser Trp Val His  Gln Ile Ala
    1730                 1735                 1740

Leu Arg  Met Glu Val Leu Gly  Cys Glu Ala Gln Asp  Leu Tyr Asp
    1745                 1750                 1755

Lys Thr  His Thr Cys Pro Pro  Cys Pro Ala Pro Glu  Leu Leu Gly
    1760                 1765                 1770

Gly Pro  Ser Val Phe Leu Phe  Pro Pro Lys Pro Lys  Asp Thr Leu
    1775                 1780                 1785

Met Ile  Ser Arg Thr Pro Glu  Val Thr Cys Val Val  Val Asp Val

    1790                 1795                 1800

Ser His  Glu Asp Pro Glu Val  Lys Phe Asn Trp Tyr  Val Asp Gly
    1805                 1810                 1815

Val Glu  Val His Asn Ala Lys  Thr Lys Pro Arg Glu  Glu Gln Tyr
    1820                 1825                 1830

Asn Ser  Thr Tyr Arg Val Val  Ser Val Leu Thr Val  Leu His Gln
    1835                 1840                 1845

Asp Trp  Leu Asn Gly Lys Glu  Tyr Lys Cys Lys Val  Ser Asn Lys
    1850                 1855                 1860

Ala Leu  Pro Ala Pro Ile Glu  Lys Thr Ile Ser Lys  Ala Lys Gly
    1865                 1870                 1875

Gln Pro  Arg Glu Pro Gln Val  Tyr Thr Leu Pro Pro  Ser Arg Asp
    1880                 1885                 1890

Glu Leu  Thr Lys Asn Gln Val  Ser Leu Thr Cys Leu  Val Lys Gly
    1895                 1900                 1905

Phe Tyr  Pro Ser Asp Ile Ala  Val Glu Trp Glu Ser  Asn Gly Gln
    1910                 1915                 1920

Pro Glu  Asn Asn Tyr Lys Thr  Thr Pro Pro Val Leu  Asp Ser Asp
    1925                 1930                 1935

Gly Ser  Phe Phe Leu Tyr Ser  Lys Leu Thr Val Asp  Lys Ser Arg
    1940                 1945                 1950

Trp Gln  Gln Gly Asn Val Phe  Ser Cys Ser Val Met  His Glu Ala
    1955                 1960                 1965
```

```
Leu His  Asn His Tyr Thr Gln  Lys Ser Leu Ser Leu  Ser Pro Gly
    1970                 1975                 1980

Lys
```

<210> 108

<211> 2134

<212> PRT

<213> Artificial Sequence

<220>

<223> FVIII 201 protein sequence

<400> 108

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Gly Ala Pro
        35                  40                  45

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro
    50                  55                  60

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
65                  70                  75                  80

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
                85                  90                  95

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
            100                 105                 110

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
        115                 120                 125

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
    130                 135                 140

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
145                 150                 155                 160

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
                165                 170                 175

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
            180                 185                 190

Ala Ser Ser Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe Pro
        195                 200                 205

Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr
    210                 215                 220

Asp His Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu
225                 230                 235                 240

Leu Gly Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr

                245                 250                 255

Leu Lys Asn Met Ala Ser His Pro Val Ser Leu His Ala Val Gly Val
            260                 265                 270
```

```
Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser
        275                 280                 285

Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly Ser His Thr
    290                 295                 300

Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro
305                 310                 315                 320

Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp
                325                 330                 335

Leu Asn Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser
            340                 345                 350

Leu Ala Lys Glu Lys Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe
        355                 360                 365

Ala Val Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Lys Asn Ser
    370                 375                 380

Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala Trp Pro Lys Met
385                 390                 395                 400

His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly
                405                 410                 415

Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr
            420                 425                 430

Pro Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg
        435                 440                 445

Asn His Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr
    450                 455                 460

Ala Gln Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His
465                 470                 475                 480

Ile Ser Ser His Gln His Asp Gly Met Glu Ala Tyr Val Lys Val Asp
                485                 490                 495

Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn Asn Glu Glu Ala
            500                 505                 510

Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val Val Arg
        515                 520                 525

Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala
    530                 535                 540

Lys Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu
545                 550                 555                 560

Asp Trp Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr
                565                 570                 575

Lys Ser Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr
            580                 585                 590

Lys Lys Val Arg Phe Met Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg
        595                 600                 605

Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly
    610                 615                 620

Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg
```

```
625                 630                 635                 640

Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr
                645                 650                 655

Ser Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile
            660                 665                 670

Leu Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp
        675                 680                 685

Gly Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser
    690                 695                 700

Phe Val Asn Met Glu Arg Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu
705                 710                 715                 720

Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn Gln Ile Met
                725                 730                 735

Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
            740                 745                 750

Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala
        755                 760                 765

Gly Val Gln Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His
    770                 775                 780

Ser Ile Asn Gly Tyr Val Phe Asp Ser Leu Gln Leu Ser Val Cys Leu
785                 790                 795                 800

His Glu Val Ala Tyr Trp Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp
                805                 810                 815

Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys His Lys Met Val
            820                 825                 830

Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val Phe
        835                 840                 845

Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser
    850                 855                 860

Asp Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys
865                 870                 875                 880

Asp Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser
                885                 890                 895

Ala Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser
            900                 905                 910

Gln Asn Pro Pro Val Leu Lys Arg His Gln Ala Glu Ile Thr Arg Thr
        915                 920                 925

Thr Leu Gln Gly Ala Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser
    930                 935                 940

Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala
945                 950                 955                 960

Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr
                965                 970                 975

Ser Ser Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr
            980                 985                 990

Gly Pro Gly Thr Pro Gly Ser Glu Thr Ala Ser Ser Ser Pro Gly Ala
```

```
Gly Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala
        995                 1000                1005

Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly
    1010                1015                1020

Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
    1025                1030                1035

Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
    1040                1045                1050

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala
    1055                1060                1065

Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Ala Ser Ser Ser Asp
    1070                1075                1080

Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys
    1085                1090                1095

Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro
    1100                1105                1110

Arg Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val
    1115                1120                1125

Glu Arg Leu Trp Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu
    1130                1135                1140

Arg Asn Arg Ala Gln Ser Gly Ser Val Pro Gln Phe Lys Lys Val
    1145                1150                1155

Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro Leu Tyr
    1160                1165                1170

Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile
    1175                1180                1185

Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln
    1190                1195                1200

Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu
    1205                1210                1215

Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys
    1220                1225                1230

Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His Met

    1235                1240                1245

Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe
    1250                1255                1260

Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly
    1265                1270                1275

Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly
    1280                1285                1290

Arg Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe
    1295                1300                1305

Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn
    1310                1315                1320

Cys Arg Gly Ala Pro Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly
```

1325 1330 1335

Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr
1340 1345 1350

Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
1355 1360 1365

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
1370 1375 1380

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala
1385 1390 1395

Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser
1400 1405 1410

Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly
1415 1420 1425

Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr
1430 1435 1440

Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly
1445 1450 1455

Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ala
1460 1465 1470

Ser Ser Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys
1475 1480 1485

Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr
1490 1495 1500

Leu Pro Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr
1505 1510 1515

Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His Phe
1520 1525 1530

Ser Gly His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met
1535 1540 1545

Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met
1550 1555 1560

Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly
1565 1570 1575

Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser
1580 1585 1590

Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg
1595 1600 1605

Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro
1610 1615 1620

Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser
1625 1630 1635

Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro
1640 1645 1650

Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe
1655 1660 1665

```
Ser Ser  Leu Tyr Ile Ser Gln  Phe Ile Ile Met Tyr  Ser Leu Asp
    1670                 1675                 1680

Gly Lys  Lys Trp Gln Thr Tyr  Arg Gly Asn Ser Thr  Gly Thr Leu
    1685                 1690                 1695

Met Val  Phe Phe Gly Asn Val  Asp Ser Ser Gly Ile  Lys His Asn
    1700                 1705                 1710

Ile Phe  Asn Pro Pro Ile Ile  Ala Arg Tyr Ile Arg  Leu His Pro
    1715                 1720                 1725

Thr His  Tyr Ser Ile Arg Ser  Thr Leu Arg Met Glu  Leu Met Gly
    1730                 1735                 1740

Cys Asp  Leu Asn Ser Cys Ser  Met Pro Leu Gly Met  Glu Ser Lys
    1745                 1750                 1755

Ala Ile  Ser Asp Ala Gln Ile  Thr Ala Ser Ser Tyr  Phe Thr Asn
    1760                 1765                 1770

Met Phe  Ala Thr Trp Ser Pro  Ser Lys Ala Arg Leu  His Leu Gln
    1775                 1780                 1785

Gly Arg  Ser Asn Ala Trp Arg  Pro Gln Val Asn Asn  Pro Lys Glu
    1790                 1795                 1800

Trp Leu  Gln Val Asp Phe Gln  Lys Thr Met Lys Val  Thr Gly Val
    1805                 1810                 1815

Thr Thr  Gln Gly Val Lys Ser  Leu Leu Thr Ser Met  Tyr Val Lys
    1820                 1825                 1830

Glu Phe  Leu Ile Ser Ser Ser  Gln Asp Gly His Gln  Trp Thr Leu
    1835                 1840                 1845

Phe Phe  Gln Asn Gly Lys Val  Lys Val Phe Gln Gly  Asn Gln Asp
    1850                 1855                 1860

Ser Phe  Thr Pro Val Val Asn  Ser Leu Asp Pro Pro  Leu Leu Thr
    1865                 1870                 1875

Arg Tyr  Leu Arg Ile His Pro  Gln Ser Trp Val His  Gln Ile Ala
    1880                 1885                 1890

Leu Arg  Met Glu Val Leu Gly  Cys Glu Ala Gln Asp  Leu Tyr Asp
    1895                 1900                 1905

Lys Thr  His Thr Cys Pro Pro  Cys Pro Ala Pro Glu  Leu Leu Gly
    1910                 1915                 1920

Gly Pro  Ser Val Phe Leu Phe  Pro Pro Lys Pro Lys  Asp Thr Leu
    1925                 1930                 1935

Met Ile  Ser Arg Thr Pro Glu  Val Thr Cys Val Val  Val Asp Val
    1940                 1945                 1950

Ser His  Glu Asp Pro Glu Val  Lys Phe Asn Trp Tyr  Val Asp Gly
    1955                 1960                 1965

Val Glu  Val His Asn Ala Lys  Thr Lys Pro Arg Glu  Glu Gln Tyr
    1970                 1975                 1980

Asn Ser  Thr Tyr Arg Val Val  Ser Val Leu Thr Val  Leu His Gln
    1985                 1990                 1995

Asp Trp  Leu Asn Gly Lys Glu  Tyr Lys Cys Lys Val  Ser Asn Lys
    2000                 2005                 2010
```

```
Ala Leu  Pro Ala Pro Ile Glu  Lys Thr Ile Ser Lys  Ala Lys Gly
    2015                 2020                 2025

Gln Pro  Arg Glu Pro Gln Val  Tyr Thr Leu Pro Pro  Ser Arg Asp
    2030                 2035                 2040

Glu Leu  Thr Lys Asn Gln Val  Ser Leu Thr Cys Leu  Val Lys Gly
    2045                 2050                 2055

Phe Tyr  Pro Ser Asp Ile Ala  Val Glu Trp Glu Ser  Asn Gly Gln
    2060                 2065                 2070

Pro Glu  Asn Asn Tyr Lys Thr  Thr Pro Pro Val Leu  Asp Ser Asp
    2075                 2080                 2085

Gly Ser  Phe Phe Leu Tyr Ser  Lys Leu Thr Val Asp  Lys Ser Arg
    2090                 2095                 2100

Trp Gln  Gln Gly Asn Val Phe  Ser Cys Ser Val Met  His Glu Ala
    2105                 2110                 2115

Leu His  Asn His Tyr Thr Gln  Lys Ser Leu Ser Leu  Ser Pro Gly
    2120                 2125                 2130

Lys
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<210> 109

<211> 2128

<212> PRT

<213> Artificial Sequence

<220>

<223> FVIII 203 protein sequence

<400> 109

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
        35                  40                  45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
    50                  55                  60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65                  70                  75                  80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
                85                  90                  95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
            100                 105                 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
        115                 120                 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
    130                 135                 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145                 150                 155                 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
                165                 170                 175
```

```
                165                 170                 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
            180                 185                 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
        195                 200                 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
    210                 215                 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225                 230                 235                 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
                245                 250                 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
            260                 265                 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
        275                 280                 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
    290                 295                 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305                 310                 315                 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
                325                 330                 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
            340                 345                 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
        355                 360                 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
    370                 375                 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385                 390                 395                 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
                405                 410                 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
            420                 425                 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
        435                 440                 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
    450                 455                 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465                 470                 475                 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
                485                 490                 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys

            500                 505                 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
        515                 520                 525
```

```
Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
    530                 535                 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545                 550                 555                 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
                565                 570                 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
            580                 585                 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
        595                 600                 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
    610                 615                 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625                 630                 635                 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
                645                 650                 655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
            660                 665                 670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
        675                 680                 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
    690                 695                 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705                 710                 715                 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
                725                 730                 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
            740                 745                 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Gly Ala Pro Gly
        755                 760                 765

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
    770                 775                 780

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
785                 790                 795                 800

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
                805                 810                 815

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
            820                 825                 830

Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
        835                 840                 845

Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
    850                 855                 860

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser
865                 870                 875                 880

Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
                885                 890                 895
```

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                885                 890                 895

Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
            900                 905                 910

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser
        915                 920                 925

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
    930                 935                 940

Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
945                 950                 955                 960

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala
                965                 970                 975

Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
            980                 985                 990

Thr Glu Glu Gly Thr Ser Thr Glu  Pro Ser Glu Gly Ser  Ala Pro Gly
        995                 1000                1005

Thr Ser  Thr Glu Pro Ser Glu  Gly Ser Ala Pro Gly  Ser Glu Pro
    1010                1015                1020

Ala Thr  Ser Gly Ser Glu Thr  Pro Gly Thr Ser Glu  Ser Ala Thr
    1025                1030                1035

Pro Glu  Ser Gly Pro Gly Thr  Ser Thr Glu Pro Ser  Glu Gly Ser
    1040                1045                1050

Ala Pro  Ala Ser Ser Pro Pro  Val Leu Lys Arg His  Gln Ala Glu
    1055                1060                1065

Ile Thr  Arg Thr Thr Leu Gln  Ser Asp Gln Glu Glu  Ile Asp Tyr
    1070                1075                1080

Asp Asp  Thr Ile Ser Val Glu  Met Lys Lys Glu Asp  Phe Asp Ile
    1085                1090                1095

Tyr Asp  Glu Asp Glu Asn Gln  Ser Pro Arg Ser Phe  Gln Lys Lys
    1100                1105                1110

Thr Arg  His Tyr Phe Ile Ala  Ala Val Glu Arg Leu  Trp Asp Tyr
    1115                1120                1125

Gly Met  Ser Ser Ser Pro His  Val Leu Arg Asn Arg  Ala Gln Ser
    1130                1135                1140

Gly Ser  Val Pro Gln Phe Lys  Lys Val Val Phe Gln  Glu Phe Thr
    1145                1150                1155

Asp Gly  Ser Phe Thr Gln Pro  Leu Tyr Arg Gly Glu  Leu Asn Glu
    1160                1165                1170

His Leu  Gly Leu Leu Gly Pro  Tyr Ile Arg Ala Glu  Val Glu Asp
    1175                1180                1185

Asn Ile  Met Val Thr Phe Arg  Asn Gln Ala Ser Arg  Pro Tyr Ser
    1190                1195                1200

Phe Tyr  Ser Ser Leu Ile Ser  Tyr Glu Glu Asp Gln  Arg Gln Gly
    1205                1210                1215

Ala Glu  Pro Arg Lys Asn Phe  Val Lys Pro Asn Glu  Thr Lys Thr
    1220                1225                1230

Tyr Phe  Trp Lys Val Gln His  His Met Ala Pro Thr  Lys Asp Glu
```

```
    1235                1240                1245

Phe Asp  Cys Lys Ala Trp Ala  Tyr Phe Ser Asp Val  Asp Leu Glu
    1250                1255                1260

Lys Asp  Val His Ser Gly Leu  Ile Gly Pro Leu Leu  Val Cys His
    1265                1270                1275

Thr Asn  Thr Leu Asn Pro Ala  His Gly Arg Gln Val  Thr Val Gln
    1280                1285                1290

Glu Phe  Ala Leu Phe Phe Thr  Ile Phe Asp Glu Thr  Lys Ser Trp
    1295                1300                1305

Tyr Phe  Thr Glu Asn Met Glu  Arg Asn Cys Arg Gly  Ala Pro Thr
    1310                1315                1320

Ser Glu  Ser Ala Thr Pro Glu  Ser Gly Pro Gly Ser  Glu Pro Ala
    1325                1330                1335

Thr Ser  Gly Ser Glu Thr Pro  Gly Thr Ser Glu Ser  Ala Thr Pro
    1340                1345                1350

Glu Ser  Gly Pro Gly Ser Glu  Pro Ala Thr Ser Gly  Ser Glu Thr
    1355                1360                1365

Pro Gly  Thr Ser Glu Ser Ala  Thr Pro Glu Ser Gly  Pro Gly Thr
    1370                1375                1380

Ser Thr  Glu Pro Ser Glu Gly  Ser Ala Pro Gly Thr  Ser Glu Ser
    1385                1390                1395

Ala Thr  Pro Glu Ser Gly Pro  Gly Ser Pro Ala Gly  Ser Pro Thr
    1400                1405                1410

Ser Thr  Glu Glu Gly Ser Pro  Ala Gly Ser Pro Thr  Ser Thr Glu
    1415                1420                1425

Glu Gly  Ser Pro Ala Gly Ser  Pro Thr Ser Thr Glu  Glu Gly Thr
    1430                1435                1440

Ser Glu  Ser Ala Thr Pro Glu  Ser Gly Pro Gly Thr  Ser Thr Glu
    1445                1450                1455

Pro Ser  Glu Gly Ser Ala Pro  Gly Ala Ser Ser Ala  Pro Cys Asn
    1460                1465                1470

Ile Gln  Met Glu Asp Pro Thr  Phe Lys Glu Asn Tyr  Arg Phe His

    1475                1480                1485

Ala Ile  Asn Gly Tyr Ile Met  Asp Thr Leu Pro Gly  Leu Val Met
    1490                1495                1500

Ala Gln  Asp Gln Arg Ile Arg  Trp Tyr Leu Leu Ser  Met Gly Ser
    1505                1510                1515

Asn Glu  Asn Ile His Ser Ile  His Phe Ser Gly His  Val Phe Thr
    1520                1525                1530

Val Arg  Lys Lys Glu Glu Tyr  Lys Met Ala Leu Tyr  Asn Leu Tyr
    1535                1540                1545

Pro Gly  Val Phe Glu Thr Val  Glu Met Leu Pro Ser  Lys Ala Gly
    1550                1555                1560

Ile Trp  Arg Val Glu Cys Leu  Ile Gly Glu His Leu  His Ala Gly
    1565                1570                1575
```

```
Met Ser  Thr Leu Phe Leu Val  Tyr Ser Asn Lys Cys  Gln Thr Pro
    1580                 1585                 1590

Leu Gly  Met Ala Ser Gly His  Ile Arg Asp Phe Gln  Ile Thr Ala
    1595                 1600                 1605

Ser Gly  Gln Tyr Gly Gln Trp  Ala Pro Lys Leu Ala  Arg Leu His
    1610                 1615                 1620

Tyr Ser  Gly Ser Ile Asn Ala  Trp Ser Thr Lys Glu  Pro Phe Ser
    1625                 1630                 1635

Trp Ile  Lys Val Asp Leu Leu  Ala Pro Met Ile Ile  His Gly Ile
    1640                 1645                 1650

Lys Thr  Gln Gly Ala Arg Gln  Lys Phe Ser Ser Leu  Tyr Ile Ser
    1655                 1660                 1665

Gln Phe  Ile Ile Met Tyr Ser  Leu Asp Gly Lys Lys  Trp Gln Thr
    1670                 1675                 1680

Tyr Arg  Gly Asn Ser Thr Gly  Thr Leu Met Val Phe  Phe Gly Asn
    1685                 1690                 1695

Val Asp  Ser Ser Gly Ile Lys  His Asn Ile Phe Asn  Pro Pro Ile
    1700                 1705                 1710

Ile Ala  Arg Tyr Ile Arg Leu  His Pro Thr His Tyr  Ser Ile Arg
    1715                 1720                 1725

Ser Thr  Leu Arg Met Glu Leu  Met Gly Cys Asp Leu  Asn Ser Cys
    1730                 1735                 1740

Ser Met  Pro Leu Gly Met Glu  Ser Lys Ala Ile Ser  Asp Ala Gln
    1745                 1750                 1755

Ile Thr  Ala Ser Ser Tyr Phe  Thr Asn Met Phe Ala  Thr Trp Ser
    1760                 1765                 1770

Pro Ser  Lys Ala Arg Leu His  Leu Gln Gly Arg Ser  Asn Ala Trp
    1775                 1780                 1785

Arg Pro  Gln Val Asn Asn Pro  Lys Glu Trp Leu Gln  Val Asp Phe
    1790                 1795                 1800

Gln Lys  Thr Met Lys Val Thr  Gly Val Thr Thr Gln  Gly Val Lys
    1805                 1810                 1815

Ser Leu  Leu Thr Ser Met Tyr  Val Lys Glu Phe Leu  Ile Ser Ser
    1820                 1825                 1830

Ser Gln  Asp Gly His Gln Trp  Thr Leu Phe Phe Gln  Asn Gly Lys
    1835                 1840                 1845

Val Lys  Val Phe Gln Gly Asn  Gln Asp Ser Phe Thr  Pro Val Val
    1850                 1855                 1860

Asn Ser  Leu Asp Pro Pro Leu  Leu Thr Arg Tyr Leu  Arg Ile His
    1865                 1870                 1875

Pro Gln  Ser Trp Val His Gln  Ile Ala Leu Arg Met  Glu Val Leu
    1880                 1885                 1890

Gly Cys  Glu Ala Gln Asp Leu  Tyr Asp Lys Thr His  Thr Cys Pro
    1895                 1900                 1905

Pro Cys  Pro Ala Pro Glu Leu  Leu Gly Gly Pro Ser  Val Phe Leu
```

```
    1910                1915                1920

Phe Pro  Pro Lys Pro Lys Asp  Thr Leu Met Ile Ser  Arg Thr Pro
    1925                1930                1935

Glu Val  Thr Cys Val Val Val  Asp Val Ser His Glu  Asp Pro Glu
    1940                1945                1950

Val Lys  Phe Asn Trp Tyr Val  Asp Gly Val Glu Val  His Asn Ala
    1955                1960                1965

Lys Thr  Lys Pro Arg Glu Glu  Gln Tyr Asn Ser Thr  Tyr Arg Val
    1970                1975                1980

Val Ser  Val Leu Thr Val Leu  His Gln Asp Trp Leu  Asn Gly Lys
    1985                1990                1995

Glu Tyr  Lys Cys Lys Val Ser  Asn Lys Ala Leu Pro  Ala Pro Ile
    2000                2005                2010

Glu Lys  Thr Ile Ser Lys Ala  Lys Gly Gln Pro Arg  Glu Pro Gln
    2015                2020                2025

Val Tyr  Thr Leu Pro Pro Ser  Arg Asp Glu Leu Thr  Lys Asn Gln
    2030                2035                2040

Val Ser  Leu Thr Cys Leu Val  Lys Gly Phe Tyr Pro  Ser Asp Ile
    2045                2050                2055

Ala Val  Glu Trp Glu Ser Asn  Gly Gln Pro Glu Asn  Asn Tyr Lys
    2060                2065                2070

Thr Thr  Pro Pro Val Leu Asp  Ser Asp Gly Ser Phe  Phe Leu Tyr
    2075                2080                2085

Ser Lys  Leu Thr Val Asp Lys  Ser Arg Trp Gln Gln  Gly Asn Val
    2090                2095                2100

Phe Ser  Cys Ser Val Met His  Glu Ala Leu His Asn  His Tyr Thr
    2105                2110                2115

Gln Lys  Ser Leu Ser Leu Ser  Pro Gly Lys
    2120                2125
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<210> 110

<211> 2128

<212> PRT

<213> Artificial Sequence

<220>

<223> FVIII 204 protein sequence

<400> 110

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
        35                  40                  45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
    50                  55                  60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65                  70                  75                  80
```

```
Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
                85                  90                  95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
            100                 105                 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
        115                 120                 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
    130                 135                 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145                 150                 155                 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
                165                 170                 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
            180                 185                 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
        195                 200                 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
    210                 215                 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225                 230                 235                 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
                245                 250                 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
            260                 265                 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
        275                 280                 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
    290                 295                 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305                 310                 315                 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
                325                 330                 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
            340                 345                 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
        355                 360                 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
    370                 375                 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385                 390                 395                 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
                405                 410                 415

Leu Val Leu Ala Pro Asp Gly Ala Pro Thr Ser Thr Glu Pro Ser Glu
            420                 425                 430

Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
        435                 440                 445
```

```
Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
    450                 455                 460

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
465                 470                 475                 480

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
                485                 490                 495

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
            500                 505                 510

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Thr Glu Pro Ser Glu
        515                 520                 525

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
    530                 535                 540

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu
545                 550                 555                 560

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ala Ser Ser Asp Arg Ser Tyr
                565                 570                 575

Lys Ser Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr
            580                 585                 590

Lys Lys Val Arg Phe Met Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg
        595                 600                 605

Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly
    610                 615                 620

Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg
625                 630                 635                 640

Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr
                645                 650                 655

Ser Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile
            660                 665                 670

Leu Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp
        675                 680                 685

Gly Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser
    690                 695                 700

Phe Val Asn Met Glu Arg Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu
705                 710                 715                 720

Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn Gln Ile Met
                725                 730                 735

Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
            740                 745                 750

Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala
        755                 760                 765

Gly Val Gln Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His

    770                 775                 780

Ser Ile Asn Gly Tyr Val Phe Asp Ser Leu Gln Leu Ser Val Cys Leu
785                 790                 795                 800
```

```
His Glu Val Ala Tyr Trp Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp
                805                 810                 815

Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys His Lys Met Val
            820                 825                 830

Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val Phe
        835                 840                 845

Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser
    850                 855                 860

Asp Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys
865                 870                 875                 880

Asp Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser
                885                 890                 895

Ala Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser
            900                 905                 910

Gln Asn Gly Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly
        915                 920                 925

Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser
    930                 935                 940

Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser
945                 950                 955                 960

Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly
                965                 970                 975

Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro
            980                 985                 990

Ala Gly Ser Pro Thr Ser Thr Glu  Glu Gly Thr Ser Glu  Ser Ala Thr
        995                 1000                1005

Pro Glu  Ser Gly Pro Gly Ser  Glu Pro Ala Thr Ser  Gly Ser Glu
    1010                1015                1020

Thr Pro  Gly Thr Ser Glu Ser  Ala Thr Pro Glu Ser  Gly Pro Gly
    1025                1030                1035

Ser Pro  Ala Gly Ser Pro Thr  Ser Thr Glu Glu Gly  Ser Pro Ala
    1040                1045                1050

Gly Ser  Pro Thr Ser Thr Glu  Glu Gly Thr Ser Thr  Glu Pro Ser
    1055                1060                1065

Glu Gly  Ser Ala Pro Gly Thr  Ser Glu Ser Ala Thr  Pro Glu Ser
    1070                1075                1080

Gly Pro  Gly Thr Ser Glu Ser  Ala Thr Pro Glu Ser  Gly Pro Gly
    1085                1090                1095

Thr Ser  Glu Ser Ala Thr Pro  Glu Ser Gly Pro Gly  Ser Glu Pro
    1100                1105                1110

Ala Thr  Ser Gly Ser Glu Thr  Pro Gly Ser Glu Pro  Ala Thr Ser
    1115                1120                1125

Gly Ser  Glu Thr Pro Gly Ser  Pro Ala Gly Ser Pro  Thr Ser Thr
    1130                1135                1140

Glu Glu  Gly Thr Ser Thr Glu  Pro Ser Glu Gly Ser  Ala Pro Gly
    1145                1150                1155
```

```
Thr Ser  Thr Glu Pro Ser Glu  Gly Ser Ala Pro Gly  Ser Glu Pro
    1160                 1165                 1170

Ala Thr  Ser Gly Ser Glu Thr  Pro Gly Thr Ser Glu  Ser Ala Thr
    1175                 1180                 1185

Pro Glu  Ser Gly Pro Gly Thr  Ser Thr Glu Pro Ser  Glu Gly Ser
    1190                 1195                 1200

Ala Pro  Ala Ser Ser Pro Pro  Val Leu Lys Arg His  Gln Ala Glu
    1205                 1210                 1215

Ile Thr  Arg Thr Thr Leu Gln  Ser Asp Gln Glu Glu  Ile Asp Tyr
    1220                 1225                 1230

Asp Asp  Thr Ile Ser Val Glu  Met Lys Lys Glu Asp  Phe Asp Ile
    1235                 1240                 1245

Tyr Asp  Glu Asp Glu Asn Gln  Ser Pro Arg Ser Phe  Gln Lys Lys
    1250                 1255                 1260

Thr Arg  His Tyr Phe Ile Ala  Ala Val Glu Arg Leu  Trp Asp Tyr
    1265                 1270                 1275

Gly Met  Ser Ser Ser Pro His  Val Leu Arg Asn Arg  Ala Gln Ser
    1280                 1285                 1290

Gly Ser  Val Pro Gln Phe Lys  Lys Val Val Phe Gln  Glu Phe Thr
    1295                 1300                 1305

Asp Gly  Ser Phe Thr Gln Pro  Leu Tyr Arg Gly Glu  Leu Asn Glu
    1310                 1315                 1320

His Leu  Gly Leu Leu Gly Pro  Tyr Ile Arg Ala Glu  Val Glu Asp
    1325                 1330                 1335

Asn Ile  Met Val Thr Phe Arg  Asn Gln Ala Ser Arg  Pro Tyr Ser
    1340                 1345                 1350

Phe Tyr  Ser Ser Leu Ile Ser  Tyr Glu Glu Asp Gln  Arg Gln Gly
    1355                 1360                 1365

Ala Glu  Pro Arg Lys Asn Phe  Val Lys Pro Asn Glu  Thr Lys Thr
    1370                 1375                 1380

Tyr Phe  Trp Lys Val Gln His  His Met Ala Pro Thr  Lys Asp Glu
    1385                 1390                 1395

Phe Asp  Cys Lys Ala Trp Ala  Tyr Phe Ser Asp Val  Asp Leu Glu
    1400                 1405                 1410

Lys Asp  Val His Ser Gly Leu  Ile Gly Pro Leu Leu  Val Cys His
    1415                 1420                 1425

Thr Asn  Thr Leu Asn Pro Ala  His Gly Arg Gln Val  Thr Val Gln
    1430                 1435                 1440

Glu Phe  Ala Leu Phe Phe Thr  Ile Phe Asp Glu Thr  Lys Ser Trp
    1445                 1450                 1455

Tyr Phe  Thr Glu Asn Met Glu  Arg Asn Cys Arg Ala  Pro Cys Asn
    1460                 1465                 1470

Ile Gln  Met Glu Asp Pro Thr  Phe Lys Glu Asn Tyr  Arg Phe His
    1475                 1480                 1485

Ala Ile  Asn Gly Tyr Ile Met  Asp Thr Leu Pro Gly  Leu Val Met
```

```
    1490                1495                1500

Ala Gln  Asp Gln Arg Ile Arg  Trp Tyr Leu Leu Ser  Met Gly Ser
    1505                1510                1515

Asn Glu  Asn Ile His Ser Ile  His Phe Ser Gly His  Val Phe Thr
    1520                1525                1530

Val Arg  Lys Lys Glu Glu Tyr  Lys Met Ala Leu Tyr  Asn Leu Tyr
    1535                1540                1545

Pro Gly  Val Phe Glu Thr Val  Glu Met Leu Pro Ser  Lys Ala Gly
    1550                1555                1560

Ile Trp  Arg Val Glu Cys Leu  Ile Gly Glu His Leu  His Ala Gly
    1565                1570                1575

Met Ser  Thr Leu Phe Leu Val  Tyr Ser Asn Lys Cys  Gln Thr Pro
    1580                1585                1590

Leu Gly  Met Ala Ser Gly His  Ile Arg Asp Phe Gln  Ile Thr Ala
    1595                1600                1605

Ser Gly  Gln Tyr Gly Gln Trp  Ala Pro Lys Leu Ala  Arg Leu His
    1610                1615                1620

Tyr Ser  Gly Ser Ile Asn Ala  Trp Ser Thr Lys Glu  Pro Phe Ser
    1625                1630                1635

Trp Ile  Lys Val Asp Leu Leu  Ala Pro Met Ile Ile  His Gly Ile
    1640                1645                1650

Lys Thr  Gln Gly Ala Arg Gln  Lys Phe Ser Ser Leu  Tyr Ile Ser
    1655                1660                1665

Gln Phe  Ile Ile Met Tyr Ser  Leu Asp Gly Lys Lys  Trp Gln Thr
    1670                1675                1680

Tyr Arg  Gly Asn Ser Thr Gly  Thr Leu Met Val Phe  Phe Gly Asn
    1685                1690                1695

Val Asp  Ser Ser Gly Ile Lys  His Asn Ile Phe Asn  Pro Pro Ile
    1700                1705                1710

Ile Ala  Arg Tyr Ile Arg Leu  His Pro Thr His Tyr  Ser Ile Arg
    1715                1720                1725

Ser Thr  Leu Arg Met Glu Leu  Met Gly Cys Asp Leu  Asn Ser Cys

    1730                1735                1740

Ser Met  Pro Leu Gly Met Glu  Ser Lys Ala Ile Ser  Asp Ala Gln
    1745                1750                1755

Ile Thr  Ala Ser Ser Tyr Phe  Thr Asn Met Phe Ala  Thr Trp Ser
    1760                1765                1770

Pro Ser  Lys Ala Arg Leu His  Leu Gln Gly Arg Ser  Asn Ala Trp
    1775                1780                1785

Arg Pro  Gln Val Asn Asn Pro  Lys Glu Trp Leu Gln  Val Asp Phe
    1790                1795                1800

Gln Lys  Thr Met Lys Val Thr  Gly Val Thr Thr Gln  Gly Val Lys
    1805                1810                1815

Ser Leu  Leu Thr Ser Met Tyr  Val Lys Glu Phe Leu  Ile Ser Ser
    1820                1825                1830
```

```
Ser Gln  Asp Gly His Gln Trp  Thr Leu Phe Phe Gln  Asn Gly Lys
    1835                 1840                 1845

Val Lys  Val Phe Gln Gly Asn  Gln Asp Ser Phe Thr  Pro Val Val
    1850                 1855                 1860

Asn Ser  Leu Asp Pro Pro Leu  Leu Thr Arg Tyr Leu  Arg Ile His
    1865                 1870                 1875

Pro Gln  Ser Trp Val His Gln  Ile Ala Leu Arg Met  Glu Val Leu
    1880                 1885                 1890

Gly Cys  Glu Ala Gln Asp Leu  Tyr Asp Lys Thr His  Thr Cys Pro
    1895                 1900                 1905

Pro Cys  Pro Ala Pro Glu Leu  Leu Gly Gly Pro Ser  Val Phe Leu
    1910                 1915                 1920

Phe Pro  Pro Lys Pro Lys Asp  Thr Leu Met Ile Ser  Arg Thr Pro
    1925                 1930                 1935

Glu Val  Thr Cys Val Val Val  Asp Val Ser His Glu  Asp Pro Glu
    1940                 1945                 1950

Val Lys  Phe Asn Trp Tyr Val  Asp Gly Val Glu Val  His Asn Ala
    1955                 1960                 1965

Lys Thr  Lys Pro Arg Glu Glu  Gln Tyr Asn Ser Thr  Tyr Arg Val
    1970                 1975                 1980

Val Ser  Val Leu Thr Val Leu  His Gln Asp Trp Leu  Asn Gly Lys
    1985                 1990                 1995

Glu Tyr  Lys Cys Lys Val Ser  Asn Lys Ala Leu Pro  Ala Pro Ile
    2000                 2005                 2010

Glu Lys  Thr Ile Ser Lys Ala  Lys Gly Gln Pro Arg  Glu Pro Gln
    2015                 2020                 2025

Val Tyr  Thr Leu Pro Pro Ser  Arg Asp Glu Leu Thr  Lys Asn Gln
    2030                 2035                 2040

Val Ser  Leu Thr Cys Leu Val  Lys Gly Phe Tyr Pro  Ser Asp Ile
    2045                 2050                 2055

Ala Val  Glu Trp Glu Ser Asn  Gly Gln Pro Glu Asn  Asn Tyr Lys
    2060                 2065                 2070

Thr Thr  Pro Pro Val Leu Asp  Ser Asp Gly Ser Phe  Phe Leu Tyr
    2075                 2080                 2085

Ser Lys  Leu Thr Val Asp Lys  Ser Arg Trp Gln Gln  Gly Asn Val
    2090                 2095                 2100

Phe Ser  Cys Ser Val Met His  Glu Ala Leu His Asn  His Tyr Thr
    2105                 2110                 2115

Gln Lys  Ser Leu Ser Leu Ser  Pro Gly Lys
    2120                 2125
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<210> 111

<211> 2128

<212> PRT

<213> Artificial Sequence

<220>

<223> FVIII 205 protein sequence

<400> 111

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Gly Ala Pro Thr Ser Glu Ser Ala Thr Pro Glu

        35                  40                  45

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
    50                  55                  60

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
65                  70                  75                  80

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
                85                  90                  95

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
            100                 105                 110

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
        115                 120                 125

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
    130                 135                 140

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
145                 150                 155                 160

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly
                165                 170                 175

Ser Pro Thr Ser Thr Glu Glu Gly Ala Ser Ser Ser Asp Leu Gly Glu
            180                 185                 190

Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe Pro
        195                 200                 205

Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr
    210                 215                 220

Asp His Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu
225                 230                 235                 240

Leu Gly Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr
                245                 250                 255

Leu Lys Asn Met Ala Ser His Pro Val Ser Leu His Ala Val Gly Val
            260                 265                 270

Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser
        275                 280                 285

Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly Ser His Thr
    290                 295                 300

Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro
305                 310                 315                 320

Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp
                325                 330                 335
```

```
Leu Asn Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser
            340                 345                 350

Leu Ala Lys Glu Lys Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe
        355                 360                 365

Ala Val Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Lys Asn Ser
    370                 375                 380

Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala Trp Pro Lys Met
385                 390                 395                 400

His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly
                405                 410                 415

Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr
            420                 425                 430

Pro Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg
        435                 440                 445

Asn His Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr
    450                 455                 460

Ala Gln Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His
465                 470                 475                 480

Ile Ser Ser His Gln His Asp Gly Met Glu Ala Tyr Val Lys Val Asp
                485                 490                 495

Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn Asn Glu Glu Ala
            500                 505                 510

Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val Val Arg
        515                 520                 525

Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala
    530                 535                 540

Lys Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu
545                 550                 555                 560

Asp Trp Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr
                565                 570                 575

Lys Ser Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr
            580                 585                 590

Lys Lys Val Arg Phe Met Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg
        595                 600                 605

Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly
    610                 615                 620

Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg
625                 630                 635                 640

Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr
                645                 650                 655

Ser Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile
            660                 665                 670

Leu Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp
        675                 680                 685

Gly Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser
    690                 695                 700
```

```
Phe Val Asn Met Glu Arg Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu
705                 710                 715                 720

Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn Gln Ile Met
                725                 730                 735

Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
            740                 745                 750

Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala
        755                 760                 765

Gly Val Gln Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His
    770                 775                 780

Ser Ile Asn Gly Tyr Val Phe Asp Ser Leu Gln Leu Ser Val Cys Leu
785                 790                 795                 800

His Glu Val Ala Tyr Trp Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp
                805                 810                 815

Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys His Lys Met Val
            820                 825                 830

Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val Phe
        835                 840                 845

Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser
    850                 855                 860

Asp Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys
865                 870                 875                 880

Asp Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser
                885                 890                 895

Ala Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser
            900                 905                 910

Gln Asn Gly Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly
        915                 920                 925

Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser
    930                 935                 940

Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser
945                 950                 955                 960

Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly
                965                 970                 975

Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro
            980                 985                 990

Ala Gly Ser Pro Thr Ser Thr Glu  Glu Gly Thr Ser Glu  Ser Ala Thr
        995                 1000                1005

Pro Glu  Ser Gly Pro Gly Ser  Glu Pro Ala Thr Ser  Gly Ser Glu
    1010                1015                1020

Thr Pro  Gly Thr Ser Glu Ser  Ala Thr Pro Glu Ser  Gly Pro Gly
    1025                1030                1035

Ser Pro  Ala Gly Ser Pro Thr  Ser Thr Glu Glu Gly  Ser Pro Ala

    1040                1045                1050
```

```
Gly Ser  Pro Thr Ser Thr Glu  Glu Gly Thr Ser Thr  Glu Pro Ser
    1055                 1060                 1065

Glu Gly  Ser Ala Pro Gly Thr  Ser Glu Ser Ala Thr  Pro Glu Ser
    1070                 1075                 1080

Gly Pro  Gly Thr Ser Glu Ser  Ala Thr Pro Glu Ser  Gly Pro Gly
    1085                 1090                 1095

Thr Ser  Glu Ser Ala Thr Pro  Glu Ser Gly Pro Gly  Ser Glu Pro
    1100                 1105                 1110

Ala Thr  Ser Gly Ser Glu Thr  Pro Gly Ser Glu Pro  Ala Thr Ser
    1115                 1120                 1125

Gly Ser  Glu Thr Pro Gly Ser  Pro Ala Gly Ser Pro  Thr Ser Thr
    1130                 1135                 1140

Glu Glu  Gly Thr Ser Thr Glu  Pro Ser Glu Gly Ser  Ala Pro Gly
    1145                 1150                 1155

Thr Ser  Thr Glu Pro Ser Glu  Gly Ser Ala Pro Gly  Ser Glu Pro
    1160                 1165                 1170

Ala Thr  Ser Gly Ser Glu Thr  Pro Gly Thr Ser Glu  Ser Ala Thr
    1175                 1180                 1185

Pro Glu  Ser Gly Pro Gly Thr  Ser Thr Glu Pro Ser  Glu Gly Ser
    1190                 1195                 1200

Ala Pro  Ala Ser Ser Pro Pro  Val Leu Lys Arg His  Gln Ala Glu
    1205                 1210                 1215

Ile Thr  Arg Thr Thr Leu Gln  Ser Asp Gln Glu Glu  Ile Asp Tyr
    1220                 1225                 1230

Asp Asp  Thr Ile Ser Val Glu  Met Lys Lys Glu Asp  Phe Asp Ile
    1235                 1240                 1245

Tyr Asp  Glu Asp Glu Asn Gln  Ser Pro Arg Ser Phe  Gln Lys Lys
    1250                 1255                 1260

Thr Arg  His Tyr Phe Ile Ala  Ala Val Glu Arg Leu  Trp Asp Tyr
    1265                 1270                 1275

Gly Met  Ser Ser Ser Pro His  Val Leu Arg Asn Arg  Ala Gln Ser
    1280                 1285                 1290

Gly Ser  Val Pro Gln Phe Lys  Lys Val Val Phe Gln  Glu Phe Thr
    1295                 1300                 1305

Asp Gly  Ser Phe Thr Gln Pro  Leu Tyr Arg Gly Glu  Leu Asn Glu
    1310                 1315                 1320

His Leu  Gly Leu Leu Gly Pro  Tyr Ile Arg Ala Glu  Val Glu Asp
    1325                 1330                 1335

Asn Ile  Met Val Thr Phe Arg  Asn Gln Ala Ser Arg  Pro Tyr Ser
    1340                 1345                 1350

Phe Tyr  Ser Ser Leu Ile Ser  Tyr Glu Glu Asp Gln  Arg Gln Gly
    1355                 1360                 1365

Ala Glu  Pro Arg Lys Asn Phe  Val Lys Pro Asn Glu  Thr Lys Thr
    1370                 1375                 1380

Tyr Phe  Trp Lys Val Gln His  His Met Ala Pro Thr  Lys Asp Glu
    1385                 1390                 1395
```

```
Phe Asp  Cys Lys Ala Trp Ala  Tyr Phe Ser Asp Val  Asp Leu Glu
    1400                 1405                 1410

Lys Asp  Val His Ser Gly Leu  Ile Gly Pro Leu Leu  Val Cys His
    1415                 1420                 1425

Thr Asn  Thr Leu Asn Pro Ala  His Gly Arg Gln Val  Thr Val Gln
    1430                 1435                 1440

Glu Phe  Ala Leu Phe Phe Thr  Ile Phe Asp Glu Thr  Lys Ser Trp
    1445                 1450                 1455

Tyr Phe  Thr Glu Asn Met Glu  Arg Asn Cys Arg Ala  Pro Cys Asn
    1460                 1465                 1470

Ile Gln  Met Glu Asp Pro Thr  Phe Lys Glu Asn Tyr  Arg Phe His
    1475                 1480                 1485

Ala Ile  Asn Gly Tyr Ile Met  Asp Thr Leu Pro Gly  Leu Val Met
    1490                 1495                 1500

Ala Gln  Asp Gln Arg Ile Arg  Trp Tyr Leu Leu Ser  Met Gly Ser
    1505                 1510                 1515

Asn Glu  Asn Ile His Ser Ile  His Phe Ser Gly His  Val Phe Thr
    1520                 1525                 1530

Val Arg  Lys Lys Glu Glu Tyr  Lys Met Ala Leu Tyr  Asn Leu Tyr
    1535                 1540                 1545

Pro Gly  Val Phe Glu Thr Val  Glu Met Leu Pro Ser  Lys Ala Gly
    1550                 1555                 1560

Ile Trp  Arg Val Glu Cys Leu  Ile Gly Glu His Leu  His Ala Gly
    1565                 1570                 1575

Met Ser  Thr Leu Phe Leu Val  Tyr Ser Asn Lys Cys  Gln Thr Pro
    1580                 1585                 1590

Leu Gly  Met Ala Ser Gly His  Ile Arg Asp Phe Gln  Ile Thr Ala
    1595                 1600                 1605

Ser Gly  Gln Tyr Gly Gln Trp  Ala Pro Lys Leu Ala  Arg Leu His
    1610                 1615                 1620

Tyr Ser  Gly Ser Ile Asn Ala  Trp Ser Thr Lys Glu  Pro Phe Ser
    1625                 1630                 1635

Trp Ile  Lys Val Asp Leu Leu  Ala Pro Met Ile Ile  His Gly Ile
    1640                 1645                 1650

Lys Thr  Gln Gly Ala Arg Gln  Lys Phe Ser Ser Leu  Tyr Ile Ser
    1655                 1660                 1665

Gln Phe  Ile Ile Met Tyr Ser  Leu Asp Gly Lys Lys  Trp Gln Thr
    1670                 1675                 1680

Tyr Arg  Gly Asn Ser Thr Gly  Thr Leu Met Val Phe  Phe Gly Asn
    1685                 1690                 1695

Val Asp  Ser Ser Gly Ile Lys  His Asn Ile Phe Asn  Pro Pro Ile
    1700                 1705                 1710

Ile Ala  Arg Tyr Ile Arg Leu  His Pro Thr His Tyr  Ser Ile Arg
    1715                 1720                 1725

Ser Thr  Leu Arg Met Glu Leu  Met Gly Cys Asp Leu  Asn Ser Cys
    1730                 1735                 1740
```

Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln
1745 1750 1755

Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser
1760 1765 1770

Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp
1775 1780 1785

Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe
1790 1795 1800

Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys
1805 1810 1815

Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser
1820 1825 1830

Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys
1835 1840 1845

Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val
1850 1855 1860

Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His
1865 1870 1875

Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu
1880 1885 1890

Gly Cys Glu Ala Gln Asp Leu Tyr Asp Lys Thr His Thr Cys Pro
1895 1900 1905

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
1910 1915 1920

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
1925 1930 1935

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
1940 1945 1950

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
1955 1960 1965

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
1970 1975 1980

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys

1985 1990 1995

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
2000 2005 2010

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
2015 2020 2025

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
2030 2035 2040

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
2045 2050 2055

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
2060 2065 2070

```
Thr Thr  Pro Pro Val Leu Asp  Ser Asp Gly Ser Phe  Phe Leu Tyr
    2075                 2080                 2085

Ser Lys  Leu Thr Val Asp Lys  Ser Arg Trp Gln Gln  Gly Asn Val
    2090                 2095                 2100

Phe Ser  Cys Ser Val Met His  Glu Ala Leu His Asn  His Tyr Thr
    2105                 2110                 2115

Gln Lys  Ser Leu Ser Leu Ser  Pro Gly Lys
    2120                 2125
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<210> 112

<211> 2020

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYN FVIII 266 protein sequence

<400> 112

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Gly Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr
        35                  40                  45

Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
    50                  55                  60

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Ala Ser Ser Ser
65                  70                  75                  80

Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro
                85                  90                  95

Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe
            100                 105                 110

Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro
        115                 120                 125

Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr
    130                 135                 140

Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val Ser Leu His
145                 150                 155                 160

Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr Asp
                165                 170                 175

Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly
            180                 185                 190

Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met
        195                 200                 205

Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp
    210                 215                 220

Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu Leu Val Cys
225                 230                 235                 240
```

```
Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu His Lys Phe
                245                 250                 255

Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp His Ser Glu
            260                 265                 270

Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala
        275                 280                 285

Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro
    290                 295                 300

Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly

305                 310                 315                 320

Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu Gly His Thr
                325                 330                 335

Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile
            340                 345                 350

Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly Gln Phe Leu
        355                 360                 365

Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu Ala Tyr
    370                 375                 380

Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn
385                 390                 395                 400

Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met
                405                 410                 415

Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile
            420                 425                 430

Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His Tyr Ile Ala
        435                 440                 445

Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp
    450                 455                 460

Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile
465                 470                 475                 480

Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr Asp Glu Thr
                485                 490                 495

Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro
            500                 505                 510

Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn
        515                 520                 525

Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val
    530                 535                 540

Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys
545                 550                 555                 560

Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val
                565                 570                 575

Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg
            580                 585                 590
```

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Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser Gly Leu
        595                 600                 605

Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly
    610                 615                 620

Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe
625                 630                 635                 640

Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu
                645                 650                 655

Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe Gln Ala Ser
            660                 665                 670

Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser Leu Gln Leu
        675                 680                 685

Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu Ser Ile Gly
    690                 695                 700

Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys
705                 710                 715                 720

His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly
                725                 730                 735

Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly
            740                 745                 750

Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys
        755                 760                 765

Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr
    770                 775                 780

Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu Pro
785                 790                 795                 800

Arg Ser Phe Ser Gln Asn Gly Ala Pro Gly Thr Ser Glu Ser Ala Thr
                805                 810                 815

Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr
            820                 825                 830

Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu
        835                 840                 845

Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr
    850                 855                 860

Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala
865                 870                 875                 880

Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser
                885                 890                 895

Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser
            900                 905                 910

Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly
        915                 920                 925

Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro
    930                 935                 940

Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser
945                 950                 955                 960
```

```
Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly
                965                 970                 975

Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser
            980                 985                 990

Glu Ser Ala Thr Pro Glu Ser Gly  Pro Gly Ser Glu Pro  Ala Thr Ser
        995                 1000                1005

Gly Ser  Glu Thr Pro Gly Ser  Glu Pro Ala Thr Ser  Gly Ser Glu
    1010                1015                1020

Thr Pro  Gly Ser Pro Ala Gly  Ser Pro Thr Ser Thr  Glu Glu Gly
    1025                1030                1035

Thr Ser  Thr Glu Pro Ser Glu  Gly Ser Ala Pro Gly  Thr Ser Thr
    1040                1045                1050

Glu Pro  Ser Glu Gly Ser Ala  Pro Gly Ser Glu Pro  Ala Thr Ser
    1055                1060                1065

Gly Ser  Glu Thr Pro Gly Thr  Ser Glu Ser Ala Thr  Pro Glu Ser
    1070                1075                1080

Gly Pro  Gly Thr Ser Thr Glu  Pro Ser Glu Gly Ser  Ala Pro Ala
    1085                1090                1095

Ser Ser  Pro Pro Val Leu Lys  Arg His Gln Ala Glu  Ile Thr Arg
    1100                1105                1110

Thr Thr  Leu Gln Ser Asp Gln  Glu Glu Ile Asp Tyr  Asp Asp Thr
    1115                1120                1125

Ile Ser  Val Glu Met Lys Lys  Glu Asp Phe Asp Ile  Tyr Asp Glu
    1130                1135                1140

Asp Glu  Asn Gln Ser Pro Arg  Ser Phe Gln Lys Lys  Thr Arg His
    1145                1150                1155

Tyr Phe  Ile Ala Ala Val Glu  Arg Leu Trp Asp Tyr  Gly Met Ser
    1160                1165                1170

Ser Ser  Pro His Val Leu Arg  Asn Arg Ala Gln Ser  Gly Ser Val
    1175                1180                1185

Pro Gln  Phe Lys Lys Val Val  Phe Gln Glu Phe Thr  Asp Gly Ser
    1190                1195                1200

Phe Thr  Gln Pro Leu Tyr Arg  Gly Glu Leu Asn Glu  His Leu Gly
    1205                1210                1215

Leu Leu  Gly Pro Tyr Ile Arg  Ala Glu Val Glu Asp  Asn Ile Met
    1220                1225                1230

Val Thr  Phe Arg Asn Gln Ala  Ser Arg Pro Tyr Ser  Phe Tyr Ser
    1235                1240                1245

Ser Leu  Ile Ser Tyr Glu Glu  Asp Gln Arg Gln Gly  Ala Glu Pro
    1250                1255                1260

Arg Lys  Asn Phe Val Lys Pro  Asn Glu Thr Lys Thr  Tyr Phe Trp
    1265                1270                1275

Lys Val  Gln His His Met Ala  Pro Thr Lys Asp Glu  Phe Asp Cys
    1280                1285                1290

Lys Ala  Trp Ala Tyr Phe Ser  Asp Val Asp Leu Glu  Lys Asp Val
```

```
    1295                1300                1305

His Ser  Gly Leu Ile Gly Pro  Leu Leu Val Cys His  Thr Asn Thr
    1310                1315                1320

Leu Asn  Pro Ala His Gly Arg  Gln Val Thr Val Gln  Glu Phe Ala
    1325                1330                1335

Leu Phe  Phe Thr Ile Phe Asp  Glu Thr Lys Ser Trp  Tyr Phe Thr
    1340                1345                1350

Glu Asn  Met Glu Arg Asn Cys  Arg Ala Pro Cys Asn  Ile Gln Met
    1355                1360                1365

Glu Asp  Pro Thr Phe Lys Glu  Asn Tyr Arg Phe His  Ala Ile Asn
    1370                1375                1380

Gly Tyr  Ile Met Asp Thr Leu  Pro Gly Leu Val Met  Ala Gln Asp
    1385                1390                1395

Gln Arg  Ile Arg Trp Tyr Leu  Leu Ser Met Gly Ser  Asn Glu Asn
    1400                1405                1410

Ile His  Ser Ile His Phe Ser  Gly His Val Phe Thr  Val Arg Lys
    1415                1420                1425

Lys Glu  Glu Tyr Lys Met Ala  Leu Tyr Asn Leu Tyr  Pro Gly Val
    1430                1435                1440

Phe Glu  Thr Val Glu Met Leu  Pro Ser Lys Ala Gly  Ile Trp Arg
    1445                1450                1455

Val Glu  Cys Leu Ile Gly Glu  His Leu His Ala Gly  Met Ser Thr
    1460                1465                1470

Leu Phe  Leu Val Tyr Ser Asn  Lys Cys Gln Thr Pro  Leu Gly Met
    1475                1480                1485

Ala Ser  Gly His Ile Arg Asp  Phe Gln Ile Thr Ala  Ser Gly Gln
    1490                1495                1500

Tyr Gly  Gln Trp Ala Pro Lys  Leu Ala Arg Leu His  Tyr Ser Gly
    1505                1510                1515

Ser Ile  Asn Ala Trp Ser Thr  Lys Glu Pro Phe Ser  Trp Ile Lys
    1520                1525                1530

Val Asp  Leu Leu Ala Pro Met  Ile Ile His Gly Ile  Lys Thr Gln
    1535                1540                1545

Gly Ala  Arg Gln Lys Phe Ser  Ser Leu Tyr Ile Ser  Gln Phe Ile
    1550                1555                1560

Ile Met  Tyr Ser Leu Asp Gly  Lys Lys Trp Gln Thr  Tyr Arg Gly
    1565                1570                1575

Asn Ser  Thr Gly Thr Leu Met  Val Phe Phe Gly Asn  Val Asp Ser
    1580                1585                1590

Ser Gly  Ile Lys His Asn Ile  Phe Asn Pro Pro Ile  Ile Ala Arg
    1595                1600                1605

Tyr Ile  Arg Leu His Pro Thr  His Tyr Ser Ile Arg  Ser Thr Leu
    1610                1615                1620

Arg Met  Glu Leu Met Gly Cys  Asp Leu Asn Ser Cys  Ser Met Pro
    1625                1630                1635
```

```
Leu Gly  Met Glu Ser Lys Ala  Ile Ser Asp Ala Gln  Ile Thr Ala
    1640                 1645                 1650

Ser Ser  Tyr Phe Thr Asn Met  Phe Ala Thr Trp Ser  Pro Ser Lys
    1655                 1660                 1665

Ala Arg  Leu His Leu Gln Gly  Arg Ser Asn Ala Trp  Arg Pro Gln
    1670                 1675                 1680

Val Asn  Asn Pro Lys Glu Trp  Leu Gln Val Asp Phe  Gln Lys Thr
    1685                 1690                 1695

Met Lys  Val Thr Gly Val Thr  Thr Gln Gly Val Lys  Ser Leu Leu
    1700                 1705                 1710

Thr Ser  Met Tyr Val Lys Glu  Phe Leu Ile Ser Ser  Ser Gln Asp
    1715                 1720                 1725

Gly His  Gln Trp Thr Leu Phe  Phe Gln Asn Gly Lys  Val Lys Val
    1730                 1735                 1740

Phe Gln  Gly Asn Gln Asp Ser  Phe Thr Pro Val Val  Asn Ser Leu
    1745                 1750                 1755

Asp Pro  Pro Leu Leu Thr Arg  Tyr Leu Arg Ile His  Pro Gln Ser
    1760                 1765                 1770

Trp Val  His Gln Ile Ala Leu  Arg Met Glu Val Leu  Gly Cys Glu
    1775                 1780                 1785

Ala Gln  Asp Leu Tyr Asp Lys  Thr His Thr Cys Pro  Pro Cys Pro
    1790                 1795                 1800

Ala Pro  Glu Leu Leu Gly Gly  Pro Ser Val Phe Leu  Phe Pro Pro
    1805                 1810                 1815

Lys Pro  Lys Asp Thr Leu Met  Ile Ser Arg Thr Pro  Glu Val Thr
    1820                 1825                 1830

Cys Val  Val Val Asp Val Ser  His Glu Asp Pro Glu  Val Lys Phe
    1835                 1840                 1845

Asn Trp  Tyr Val Asp Gly Val  Glu Val His Asn Ala  Lys Thr Lys
    1850                 1855                 1860

Pro Arg  Glu Glu Gln Tyr Asn  Ser Thr Tyr Arg Val  Val Ser Val
    1865                 1870                 1875

Leu Thr  Val Leu His Gln Asp  Trp Leu Asn Gly Lys  Glu Tyr Lys
    1880                 1885                 1890

Cys Lys  Val Ser Asn Lys Ala  Leu Pro Ala Pro Ile  Glu Lys Thr
    1895                 1900                 1905

Ile Ser  Lys Ala Lys Gly Gln  Pro Arg Glu Pro Gln  Val Tyr Thr
    1910                 1915                 1920

Leu Pro  Pro Ser Arg Asp Glu  Leu Thr Lys Asn Gln  Val Ser Leu
    1925                 1930                 1935

Thr Cys  Leu Val Lys Gly Phe  Tyr Pro Ser Asp Ile  Ala Val Glu
    1940                 1945                 1950

Trp Glu  Ser Asn Gly Gln Pro  Glu Asn Asn Tyr Lys  Thr Thr Pro
    1955                 1960                 1965

Pro Val  Leu Asp Ser Asp Gly  Ser Phe Phe Leu Tyr  Ser Lys Leu
    1970                 1975                 1980
```

```
Thr Val  Asp Lys Ser Arg Trp  Gln Gln Gly Asn Val  Phe Ser Cys
    1985                 1990                 1995

Ser Val  Met His Glu Ala Leu  His Asn His Tyr Thr  Gln Lys Ser
    2000                 2005                 2010

Leu Ser  Leu Ser Pro Gly Lys
    2015                 2020
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<210> 113

<211> 2056

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYN FVIII 267 protein sequence

<400> 113

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Gly Ala Pro Thr Ser Glu Ser Ala Thr Pro Glu
        35                  40                  45

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
    50                  55                  60

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
65                  70                  75                  80

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
                85                  90                  95

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
            100                 105                 110

Ala Ser Ser Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro
        115                 120                 125

Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys
    130                 135                 140

Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys
145                 150                 155                 160

Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu
                165                 170                 175

Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro
            180                 185                 190

Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly
        195                 200                 205

Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys
    210                 215                 220

Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu
225                 230                 235                 240

Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu
                245                 250                 255
```

```
Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala
            260                 265                 270

Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr
        275                 280                 285

Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser
    290                 295                 300

Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala
305                 310                 315                 320

Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn
                325                 330                 335

Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp
            340                 345                 350

His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu
        355                 360                 365

Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu
    370                 375                 380

Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu
385                 390                 395                 400

Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly
                405                 410                 415

Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu
            420                 425                 430

Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr
        435                 440                 445

Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser
    450                 455                 460

Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val
465                 470                 475                 480

His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val
                485                 490                 495

Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly
            500                 505                 510

Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr
        515                 520                 525

Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly
    530                 535                 540

Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile
545                 550                 555                 560

Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly
                565                 570                 575

Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val
            580                 585                 590

Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr
        595                 600                 605

Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg
    610                 615                 620
```

```
Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu
625                 630                 635                 640

Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val
                645                 650                 655

Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu
            660                 665                 670

Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile
        675                 680                 685

Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu

    690                 695                 700

Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp
705                 710                 715                 720

Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile
                725                 730                 735

Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly
            740                 745                 750

Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe
        755                 760                 765

Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu
    770                 775                 780

Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr
785                 790                 795                 800

Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr
                805                 810                 815

Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn
            820                 825                 830

Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Gly Ala Pro Gly Thr Ser
        835                 840                 845

Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser
    850                 855                 860

Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly
865                 870                 875                 880

Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser
                885                 890                 895

Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser
            900                 905                 910

Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu
        915                 920                 925

Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu
    930                 935                 940

Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr
945                 950                 955                 960

Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu
                965                 970                 975
```

```
Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser
            980                 985                 990

Thr Glu Pro Ser Glu Gly Ser Ala  Pro Gly Thr Ser Glu  Ser Ala Thr
        995                 1000                1005

Pro Glu  Ser Gly Pro Gly Thr  Ser Glu Ser Ala Thr  Pro Glu Ser
    1010                1015                1020

Gly Pro  Gly Thr Ser Glu Ser  Ala Thr Pro Glu Ser  Gly Pro Gly
    1025                1030                1035

Ser Glu  Pro Ala Thr Ser Gly  Ser Glu Thr Pro Gly  Ser Glu Pro
    1040                1045                1050

Ala Thr  Ser Gly Ser Glu Thr  Pro Gly Ser Pro Ala  Gly Ser Pro
    1055                1060                1065

Thr Ser  Thr Glu Glu Gly Thr  Ser Thr Glu Pro Ser  Glu Gly Ser
    1070                1075                1080

Ala Pro  Gly Thr Ser Thr Glu  Pro Ser Glu Gly Ser  Ala Pro Gly
    1085                1090                1095

Ser Glu  Pro Ala Thr Ser Gly  Ser Glu Thr Pro Gly  Thr Ser Glu
    1100                1105                1110

Ser Ala  Thr Pro Glu Ser Gly  Pro Gly Thr Ser Thr  Glu Pro Ser
    1115                1120                1125

Glu Gly  Ser Ala Pro Ala Ser  Ser Pro Pro Val Leu  Lys Arg His
    1130                1135                1140

Gln Ala  Glu Ile Thr Arg Thr  Thr Leu Gln Ser Asp  Gln Glu Glu
    1145                1150                1155

Ile Asp  Tyr Asp Asp Thr Ile  Ser Val Glu Met Lys  Lys Glu Asp
    1160                1165                1170

Phe Asp  Ile Tyr Asp Glu Asp  Glu Asn Gln Ser Pro  Arg Ser Phe
    1175                1180                1185

Gln Lys  Lys Thr Arg His Tyr  Phe Ile Ala Ala Val  Glu Arg Leu
    1190                1195                1200

Trp Asp  Tyr Gly Met Ser Ser  Ser Pro His Val Leu  Arg Asn Arg
    1205                1210                1215

Ala Gln  Ser Gly Ser Val Pro  Gln Phe Lys Lys Val  Val Phe Gln
    1220                1225                1230

Glu Phe  Thr Asp Gly Ser Phe  Thr Gln Pro Leu Tyr  Arg Gly Glu
    1235                1240                1245

Leu Asn  Glu His Leu Gly Leu  Leu Gly Pro Tyr Ile  Arg Ala Glu
    1250                1255                1260

Val Glu  Asp Asn Ile Met Val  Thr Phe Arg Asn Gln  Ala Ser Arg
    1265                1270                1275

Pro Tyr  Ser Phe Tyr Ser Ser  Leu Ile Ser Tyr Glu  Glu Asp Gln
    1280                1285                1290

Arg Gln  Gly Ala Glu Pro Arg  Lys Asn Phe Val Lys  Pro Asn Glu
    1295                1300                1305

Thr Lys  Thr Tyr Phe Trp Lys  Val Gln His His Met  Ala Pro Thr
    1310                1315                1320
```

```
Lys Asp  Glu Phe Asp Cys Lys  Ala Trp Ala Tyr Phe  Ser Asp Val
    1325                 1330                 1335

Asp Leu  Glu Lys Asp Val His  Ser Gly Leu Ile Gly  Pro Leu Leu
    1340                 1345                 1350

Val Cys  His Thr Asn Thr Leu  Asn Pro Ala His Gly  Arg Gln Val
    1355                 1360                 1365

Thr Val  Gln Glu Phe Ala Leu  Phe Phe Thr Ile Phe  Asp Glu Thr
    1370                 1375                 1380

Lys Ser  Trp Tyr Phe Thr Glu  Asn Met Glu Arg Asn  Cys Arg Ala
    1385                 1390                 1395

Pro Cys  Asn Ile Gln Met Glu  Asp Pro Thr Phe Lys  Glu Asn Tyr
    1400                 1405                 1410

Arg Phe  His Ala Ile Asn Gly  Tyr Ile Met Asp Thr  Leu Pro Gly
    1415                 1420                 1425

Leu Val  Met Ala Gln Asp Gln  Arg Ile Arg Trp Tyr  Leu Leu Ser
    1430                 1435                 1440

Met Gly  Ser Asn Glu Asn Ile  His Ser Ile His Phe  Ser Gly His
    1445                 1450                 1455

Val Phe  Thr Val Arg Lys Lys  Glu Glu Tyr Lys Met  Ala Leu Tyr
    1460                 1465                 1470

Asn Leu  Tyr Pro Gly Val Phe  Glu Thr Val Glu Met  Leu Pro Ser
    1475                 1480                 1485

Lys Ala  Gly Ile Trp Arg Val  Glu Cys Leu Ile Gly  Glu His Leu
    1490                 1495                 1500

His Ala  Gly Met Ser Thr Leu  Phe Leu Val Tyr Ser  Asn Lys Cys
    1505                 1510                 1515

Gln Thr  Pro Leu Gly Met Ala  Ser Gly His Ile Arg  Asp Phe Gln
    1520                 1525                 1530

Ile Thr  Ala Ser Gly Gln Tyr  Gly Gln Trp Ala Pro  Lys Leu Ala
    1535                 1540                 1545

Arg Leu  His Tyr Ser Gly Ser  Ile Asn Ala Trp Ser  Thr Lys Glu
    1550                 1555                 1560

Pro Phe  Ser Trp Ile Lys Val  Asp Leu Leu Ala Pro  Met Ile Ile
    1565                 1570                 1575

His Gly  Ile Lys Thr Gln Gly  Ala Arg Gln Lys Phe  Ser Ser Leu
    1580                 1585                 1590

Tyr Ile  Ser Gln Phe Ile Ile  Met Tyr Ser Leu Asp  Gly Lys Lys
    1595                 1600                 1605

Trp Gln  Thr Tyr Arg Gly Asn  Ser Thr Gly Thr Leu  Met Val Phe
    1610                 1615                 1620

Phe Gly  Asn Val Asp Ser Ser  Gly Ile Lys His Asn  Ile Phe Asn
    1625                 1630                 1635

Pro Pro  Ile Ile Ala Arg Tyr  Ile Arg Leu His Pro  Thr His Tyr
    1640                 1645                 1650

Ser Ile  Arg Ser Thr Leu Arg  Met Glu Leu Met Gly  Cys Asp Leu
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    1655                1660                1665

Asn Ser  Cys Ser Met Pro Leu  Gly Met Glu Ser Lys  Ala Ile Ser
    1670                1675                1680

Asp Ala  Gln Ile Thr Ala Ser  Ser Tyr Phe Thr Asn  Met Phe Ala
    1685                1690                1695

Thr Trp  Ser Pro Ser Lys Ala  Arg Leu His Leu Gln  Gly Arg Ser
    1700                1705                1710

Asn Ala  Trp Arg Pro Gln Val  Asn Asn Pro Lys Glu  Trp Leu Gln
    1715                1720                1725

Val Asp  Phe Gln Lys Thr Met  Lys Val Thr Gly Val  Thr Thr Gln
    1730                1735                1740

Gly Val  Lys Ser Leu Leu Thr  Ser Met Tyr Val Lys  Glu Phe Leu
    1745                1750                1755

Ile Ser  Ser Ser Gln Asp Gly  His Gln Trp Thr Leu  Phe Phe Gln
    1760                1765                1770

Asn Gly  Lys Val Lys Val Phe  Gln Gly Asn Gln Asp  Ser Phe Thr
    1775                1780                1785

Pro Val  Val Asn Ser Leu Asp  Pro Pro Leu Leu Thr  Arg Tyr Leu
    1790                1795                1800

Arg Ile  His Pro Gln Ser Trp  Val His Gln Ile Ala  Leu Arg Met
    1805                1810                1815

Glu Val  Leu Gly Cys Glu Ala  Gln Asp Leu Tyr Asp  Lys Thr His
    1820                1825                1830

Thr Cys  Pro Pro Cys Pro Ala  Pro Glu Leu Leu Gly  Gly Pro Ser
    1835                1840                1845

Val Phe  Leu Phe Pro Pro Lys  Pro Lys Asp Thr Leu  Met Ile Ser
    1850                1855                1860

Arg Thr  Pro Glu Val Thr Cys  Val Val Val Asp Val  Ser His Glu
    1865                1870                1875

Asp Pro  Glu Val Lys Phe Asn  Trp Tyr Val Asp Gly  Val Glu Val
    1880                1885                1890

His Asn  Ala Lys Thr Lys Pro  Arg Glu Glu Gln Tyr  Asn Ser Thr
    1895                1900                1905

Tyr Arg  Val Val Ser Val Leu  Thr Val Leu His Gln  Asp Trp Leu
    1910                1915                1920

Asn Gly  Lys Glu Tyr Lys Cys  Lys Val Ser Asn Lys  Ala Leu Pro
    1925                1930                1935

Ala Pro  Ile Glu Lys Thr Ile  Ser Lys Ala Lys Gly  Gln Pro Arg
    1940                1945                1950

Glu Pro  Gln Val Tyr Thr Leu  Pro Pro Ser Arg Asp  Glu Leu Thr
    1955                1960                1965

Lys Asn  Gln Val Ser Leu Thr  Cys Leu Val Lys Gly  Phe Tyr Pro
    1970                1975                1980

Ser Asp  Ile Ala Val Glu Trp  Glu Ser Asn Gly Gln  Pro Glu Asn
    1985                1990                1995
```

```
Asn Tyr  Lys Thr Thr Pro Pro  Val Leu Asp Ser Asp  Gly Ser Phe
    2000                 2005                 2010

Phe Leu  Tyr Ser Lys Leu Thr  Val Asp Lys Ser Arg  Trp Gln Gln
    2015                 2020                 2025

Gly Asn  Val Phe Ser Cys Ser  Val Met His Glu Ala  Leu His Asn
    2030                 2035                 2040

His Tyr  Thr Gln Lys Ser Leu  Ser Leu Ser Pro Gly  Lys
    2045                 2050                 2055
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<210> 114

<211> 1834

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYN FVIII 268 protein sequence

<400> 114

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Gly Ala Pro Thr Ser Glu Ser Ala Thr Pro Glu

        35                  40                  45

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
    50                  55                  60

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
65                  70                  75                  80

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
                85                  90                  95

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
            100                 105                 110

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
        115                 120                 125

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
    130                 135                 140

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
145                 150                 155                 160

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly
                165                 170                 175

Ser Pro Thr Ser Thr Glu Glu Gly Ala Ser Ser Ser Asp Leu Gly Glu
            180                 185                 190

Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe Pro
        195                 200                 205

Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr
    210                 215                 220

Asp His Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu
```

```
225                 230                 235                 240

Leu Gly Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr
                245                 250                 255

Leu Lys Asn Met Ala Ser His Pro Val Ser Leu His Ala Val Gly Val
            260                 265                 270

Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser
        275                 280                 285

Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly Ser His Thr
    290                 295                 300

Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro
305                 310                 315                 320

Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp
                325                 330                 335

Leu Asn Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser
            340                 345                 350

Leu Ala Lys Glu Lys Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe
        355                 360                 365

Ala Val Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Lys Asn Ser
    370                 375                 380

Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala Trp Pro Lys Met
385                 390                 395                 400

His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly
                405                 410                 415

Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr
            420                 425                 430

Pro Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg
        435                 440                 445

Asn His Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr
    450                 455                 460

Ala Gln Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His
465                 470                 475                 480

Ile Ser Ser His Gln His Asp Gly Met Glu Ala Tyr Val Lys Val Asp
                485                 490                 495

Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn Asn Glu Glu Ala
            500                 505                 510

Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val Val Arg
        515                 520                 525

Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala
    530                 535                 540

Lys Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu
545                 550                 555                 560

Asp Trp Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr
                565                 570                 575

Lys Ser Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr
            580                 585                 590

Lys Lys Val Arg Phe Met Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg
```

595 600 605

Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly
610 615 620

Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg
625 630 635 640

Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr
645 650 655

Ser Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile
660 665 670

Leu Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp
675 680 685

Gly Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser
690 695 700

Phe Val Asn Met Glu Arg Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu
705 710 715 720

Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn Gln Ile Met
725 730 735

Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
740 745 750

Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala
755 760 765

Gly Val Gln Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His
770 775 780

Ser Ile Asn Gly Tyr Val Phe Asp Ser Leu Gln Leu Ser Val Cys Leu
785 790 795 800

His Glu Val Ala Tyr Trp Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp
805 810 815

Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys His Lys Met Val
820 825 830

Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val Phe
835 840 845

Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser
850 855 860

Asp Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys
865 870 875 880

Asp Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser
885 890 895

Ala Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser
900 905 910

Gln Asn Pro Pro Val Leu Lys Arg His Gln Ala Glu Ile Thr Arg Thr
915 920 925

Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser
930 935 940

Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn
945 950 955 960

```
Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala
                965                 970                 975

Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser Ser Ser Pro His Val
            980                 985                 990

Leu Arg Asn Arg Ala Gln Ser Gly  Ser Val Pro Gln Phe  Lys Lys Val
        995                 1000                1005

Val Phe  Gln Glu Phe Thr Asp  Gly Ser Phe Thr Gln  Pro Leu Tyr
    1010                1015                1020

Arg Gly  Glu Leu Asn Glu His  Leu Gly Leu Leu Gly  Pro Tyr Ile
    1025                1030                1035

Arg Ala  Glu Val Glu Asp Asn  Ile Met Val Thr Phe  Arg Asn Gln

    1040                1045                1050

Ala Ser  Arg Pro Tyr Ser Phe  Tyr Ser Ser Leu Ile  Ser Tyr Glu
    1055                1060                1065

Glu Asp  Gln Arg Gln Gly Ala  Glu Pro Arg Lys Asn  Phe Val Lys
    1070                1075                1080

Pro Asn  Glu Thr Lys Thr Tyr  Phe Trp Lys Val Gln  His His Met
    1085                1090                1095

Ala Pro  Thr Lys Asp Glu Phe  Asp Cys Lys Ala Trp  Ala Tyr Phe
    1100                1105                1110

Ser Asp  Val Asp Leu Glu Lys  Asp Val His Ser Gly  Leu Ile Gly
    1115                1120                1125

Pro Leu  Leu Val Cys His Thr  Asn Thr Leu Asn Pro  Ala His Gly
    1130                1135                1140

Arg Gln  Val Thr Val Gln Glu  Phe Ala Leu Phe Phe  Thr Ile Phe
    1145                1150                1155

Asp Glu  Thr Lys Ser Trp Tyr  Phe Thr Glu Asn Met  Glu Arg Asn
    1160                1165                1170

Cys Arg  Ala Pro Cys Asn Ile  Gln Met Glu Asp Pro  Thr Phe Lys
    1175                1180                1185

Glu Asn  Tyr Arg Phe His Ala  Ile Asn Gly Tyr Ile  Met Asp Thr
    1190                1195                1200

Leu Pro  Gly Leu Val Met Ala  Gln Asp Gln Arg Ile  Arg Trp Tyr
    1205                1210                1215

Leu Leu  Ser Met Gly Ser Asn  Glu Asn Ile His Ser  Ile His Phe
    1220                1225                1230

Ser Gly  His Val Phe Thr Val  Arg Lys Lys Glu Glu  Tyr Lys Met
    1235                1240                1245

Ala Leu  Tyr Asn Leu Tyr Pro  Gly Val Phe Glu Thr  Val Glu Met
    1250                1255                1260

Leu Pro  Ser Lys Ala Gly Ile  Trp Arg Val Glu Cys  Leu Ile Gly
    1265                1270                1275

Glu His  Leu His Ala Gly Met  Ser Thr Leu Phe Leu  Val Tyr Ser
    1280                1285                1290

Asn Lys  Cys Gln Thr Pro Leu  Gly Met Ala Ser Gly  His Ile Arg
```

```
    1295                1300                1305

Asp Phe  Gln Ile Thr Ala Ser  Gly Gln Tyr Gly Gln  Trp Ala Pro
    1310                1315                1320

Lys Leu  Ala Arg Leu His Tyr  Ser Gly Ser Ile Asn  Ala Trp Ser
    1325                1330                1335

Thr Lys  Glu Pro Phe Ser Trp  Ile Lys Val Asp Leu  Leu Ala Pro
    1340                1345                1350

Met Ile  Ile His Gly Ile Lys  Thr Gln Gly Ala Arg  Gln Lys Phe
    1355                1360                1365

Ser Ser  Leu Tyr Ile Ser Gln  Phe Ile Ile Met Tyr  Ser Leu Asp
    1370                1375                1380

Gly Lys  Lys Trp Gln Thr Tyr  Arg Gly Asn Ser Thr  Gly Thr Leu
    1385                1390                1395

Met Val  Phe Phe Gly Asn Val  Asp Ser Ser Gly Ile  Lys His Asn
    1400                1405                1410

Ile Phe  Asn Pro Pro Ile Ile  Ala Arg Tyr Ile Arg  Leu His Pro
    1415                1420                1425

Thr His  Tyr Ser Ile Arg Ser  Thr Leu Arg Met Glu  Leu Met Gly
    1430                1435                1440

Cys Asp  Leu Asn Ser Cys Ser  Met Pro Leu Gly Met  Glu Ser Lys
    1445                1450                1455

Ala Ile  Ser Asp Ala Gln Ile  Thr Ala Ser Ser Tyr  Phe Thr Asn
    1460                1465                1470

Met Phe  Ala Thr Trp Ser Pro  Ser Lys Ala Arg Leu  His Leu Gln
    1475                1480                1485

Gly Arg  Ser Asn Ala Trp Arg  Pro Gln Val Asn Asn  Pro Lys Glu
    1490                1495                1500

Trp Leu  Gln Val Asp Phe Gln  Lys Thr Met Lys Val  Thr Gly Val
    1505                1510                1515

Thr Thr  Gln Gly Val Lys Ser  Leu Leu Thr Ser Met  Tyr Val Lys
    1520                1525                1530

Glu Phe  Leu Ile Ser Ser Ser  Gln Asp Gly His Gln  Trp Thr Leu
    1535                1540                1545

Phe Phe  Gln Asn Gly Lys Val  Lys Val Phe Gln Gly  Asn Gln Asp
    1550                1555                1560

Ser Phe  Thr Pro Val Val Asn  Ser Leu Asp Pro Pro  Leu Leu Thr
    1565                1570                1575

Arg Tyr  Leu Arg Ile His Pro  Gln Ser Trp Val His  Gln Ile Ala
    1580                1585                1590

Leu Arg  Met Glu Val Leu Gly  Cys Glu Ala Gln Asp  Leu Tyr Asp
    1595                1600                1605

Lys Thr  His Thr Cys Pro Pro  Cys Pro Ala Pro Glu  Leu Leu Gly
    1610                1615                1620

Gly Pro  Ser Val Phe Leu Phe  Pro Pro Lys Pro Lys  Asp Thr Leu
    1625                1630                1635

Met Ile  Ser Arg Thr Pro Glu  Val Thr Cys Val Val  Val Asp Val
```

```
                                                                  Val Asp Val
    1640                1645                1650

Ser His  Glu Asp Pro Glu Val  Lys Phe Asn Trp Tyr  Val Asp Gly
    1655                1660                1665

Val Glu  Val His Asn Ala Lys  Thr Lys Pro Arg Glu  Glu Gln Tyr
    1670                1675                1680

Asn Ser  Thr Tyr Arg Val Val  Ser Val Leu Thr Val  Leu His Gln
    1685                1690                1695

Asp Trp  Leu Asn Gly Lys Glu  Tyr Lys Cys Lys Val  Ser Asn Lys
    1700                1705                1710

Ala Leu  Pro Ala Pro Ile Glu  Lys Thr Ile Ser Lys  Ala Lys Gly
    1715                1720                1725

Gln Pro  Arg Glu Pro Gln Val  Tyr Thr Leu Pro Pro  Ser Arg Asp
    1730                1735                1740

Glu Leu  Thr Lys Asn Gln Val  Ser Leu Thr Cys Leu  Val Lys Gly
    1745                1750                1755

Phe Tyr  Pro Ser Asp Ile Ala  Val Glu Trp Glu Ser  Asn Gly Gln
    1760                1765                1770

Pro Glu  Asn Asn Tyr Lys Thr  Thr Pro Pro Val Leu  Asp Ser Asp
    1775                1780                1785

Gly Ser  Phe Phe Leu Tyr Ser  Lys Leu Thr Val Asp  Lys Ser Arg
    1790                1795                1800

Trp Gln  Gln Gly Asn Val Phe  Ser Cys Ser Val Met  His Glu Ala
    1805                1810                1815

Leu His  Asn His Tyr Thr Gln  Lys Ser Leu Ser Leu  Ser Pro Gly
    1820                1825                1830

Lys
```

<210> 115

<211> 1762

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYN FVIII 269 protein sequence

<400> 115

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Gly Ala Pro Thr Ser Glu Ser Ala Thr Pro Glu
        35                  40                  45

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
    50                  55                  60

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
65                  70                  75                  80

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
                85                  90                  95
```

```
Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
            100                 105                 110

Ala Ser Ser Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro
        115                 120                 125

Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys
    130                 135                 140

Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys
145                 150                 155                 160

Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu
                165                 170                 175

Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro
            180                 185                 190

Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly
        195                 200                 205

Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys
    210                 215                 220

Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu
225                 230                 235                 240

Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu
                245                 250                 255

Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala
            260                 265                 270

Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr
        275                 280                 285

Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser
    290                 295                 300

Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala
305                 310                 315                 320

Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn
                325                 330                 335

Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp
            340                 345                 350

His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu
        355                 360                 365

Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu
    370                 375                 380

Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu
385                 390                 395                 400

Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly
                405                 410                 415

Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu
            420                 425                 430

Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr
        435                 440                 445

Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser
    450                 455                 460
```

```
Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val
465                 470                 475                 480

His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val
                485                 490                 495

Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly
            500                 505                 510

Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr
        515                 520                 525

Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly
    530                 535                 540

Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile
545                 550                 555                 560

Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly
                565                 570                 575

Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val
            580                 585                 590

Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr
        595                 600                 605

Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg

    610                 615                 620

Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu
625                 630                 635                 640

Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val
                645                 650                 655

Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu
            660                 665                 670

Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile
        675                 680                 685

Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu
    690                 695                 700

Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp
705                 710                 715                 720

Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile
                725                 730                 735

Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly
            740                 745                 750

Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe
        755                 760                 765

Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu
    770                 775                 780

Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr
785                 790                 795                 800

Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr
                805                 810                 815
```

```
Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn
            820                 825                 830

Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu Lys Arg
        835                 840                 845

His Gln Ala Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu
    850                 855                 860

Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe
865                 870                 875                 880

Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys
                885                 890                 895

Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr
            900                 905                 910

Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly
        915                 920                 925

Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly
    930                 935                 940

Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly
945                 950                 955                 960

Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val
                965                 970                 975

Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu
            980                 985                 990

Ile Ser Tyr Glu Glu Asp Gln Arg  Gln Gly Ala Glu Pro  Arg Lys Asn
        995                 1000                1005

Phe Val  Lys Pro Asn Glu Thr  Lys Thr Tyr Phe Trp  Lys Val Gln
    1010                1015                1020

His His  Met Ala Pro Thr Lys  Asp Glu Phe Asp Cys  Lys Ala Trp
    1025                1030                1035

Ala Tyr  Phe Ser Asp Val Asp  Leu Glu Lys Asp Val  His Ser Gly
    1040                1045                1050

Leu Ile  Gly Pro Leu Leu Val  Cys His Thr Asn Thr  Leu Asn Pro
    1055                1060                1065

Ala His  Gly Arg Gln Val Thr  Val Gln Glu Phe Ala  Leu Phe Phe
    1070                1075                1080

Thr Ile  Phe Asp Glu Thr Lys  Ser Trp Tyr Phe Thr  Glu Asn Met
    1085                1090                1095

Glu Arg  Asn Cys Arg Ala Pro  Cys Asn Ile Gln Met  Glu Asp Pro
    1100                1105                1110

Thr Phe  Lys Glu Asn Tyr Arg  Phe His Ala Ile Asn  Gly Tyr Ile
    1115                1120                1125

Met Asp  Thr Leu Pro Gly Leu  Val Met Ala Gln Asp  Gln Arg Ile
    1130                1135                1140

Arg Trp  Tyr Leu Leu Ser Met  Gly Ser Asn Glu Asn  Ile His Ser
    1145                1150                1155

Ile His  Phe Ser Gly His Val  Phe Thr Val Arg Lys  Lys Glu Glu
    1160                1165                1170
```

```
Tyr Lys  Met Ala Leu Tyr Asn  Leu Tyr Pro Gly Val  Phe Glu Thr
    1175                 1180                 1185

Val Glu  Met Leu Pro Ser Lys  Ala Gly Ile Trp Arg  Val Glu Cys
    1190                 1195                 1200

Leu Ile  Gly Glu His Leu His  Ala Gly Met Ser Thr  Leu Phe Leu
    1205                 1210                 1215

Val Tyr  Ser Asn Lys Cys Gln  Thr Pro Leu Gly Met  Ala Ser Gly
    1220                 1225                 1230

His Ile  Arg Asp Phe Gln Ile  Thr Ala Ser Gly Gln  Tyr Gly Gln
    1235                 1240                 1245

Trp Ala  Pro Lys Leu Ala Arg  Leu His Tyr Ser Gly  Ser Ile Asn
    1250                 1255                 1260

Ala Trp  Ser Thr Lys Glu Pro  Phe Ser Trp Ile Lys  Val Asp Leu
    1265                 1270                 1275

Leu Ala  Pro Met Ile Ile His  Gly Ile Lys Thr Gln  Gly Ala Arg
    1280                 1285                 1290

Gln Lys  Phe Ser Ser Leu Tyr  Ile Ser Gln Phe Ile  Ile Met Tyr
    1295                 1300                 1305

Ser Leu  Asp Gly Lys Lys Trp  Gln Thr Tyr Arg Gly  Asn Ser Thr
    1310                 1315                 1320

Gly Thr  Leu Met Val Phe Phe  Gly Asn Val Asp Ser  Ser Gly Ile
    1325                 1330                 1335

Lys His  Asn Ile Phe Asn Pro  Pro Ile Ile Ala Arg  Tyr Ile Arg
    1340                 1345                 1350

Leu His  Pro Thr His Tyr Ser  Ile Arg Ser Thr Leu  Arg Met Glu
    1355                 1360                 1365

Leu Met  Gly Cys Asp Leu Asn  Ser Cys Ser Met Pro  Leu Gly Met
    1370                 1375                 1380

Glu Ser  Lys Ala Ile Ser Asp  Ala Gln Ile Thr Ala  Ser Ser Tyr
    1385                 1390                 1395

Phe Thr  Asn Met Phe Ala Thr  Trp Ser Pro Ser Lys  Ala Arg Leu
    1400                 1405                 1410

His Leu  Gln Gly Arg Ser Asn  Ala Trp Arg Pro Gln  Val Asn Asn
    1415                 1420                 1425

Pro Lys  Glu Trp Leu Gln Val  Asp Phe Gln Lys Thr  Met Lys Val
    1430                 1435                 1440

Thr Gly  Val Thr Thr Gln Gly  Val Lys Ser Leu Leu  Thr Ser Met
    1445                 1450                 1455

Tyr Val  Lys Glu Phe Leu Ile  Ser Ser Ser Gln Asp  Gly His Gln
    1460                 1465                 1470

Trp Thr  Leu Phe Phe Gln Asn  Gly Lys Val Lys Val  Phe Gln Gly
    1475                 1480                 1485

Asn Gln  Asp Ser Phe Thr Pro  Val Val Asn Ser Leu  Asp Pro Pro
    1490                 1495                 1500

Leu Leu  Thr Arg Tyr Leu Arg  Ile His Pro Gln Ser  Trp Val His
```

```
    1505                1510                1515

Gln Ile  Ala Leu Arg Met Glu  Val Leu Gly Cys Glu  Ala Gln Asp
    1520                1525                1530

Leu Tyr  Asp Lys Thr His Thr  Cys Pro Pro Cys Pro  Ala Pro Glu
    1535                1540                1545

Leu Leu  Gly Gly Pro Ser Val  Phe Leu Phe Pro Pro  Lys Pro Lys
    1550                1555                1560

Asp Thr  Leu Met Ile Ser Arg  Thr Pro Glu Val Thr  Cys Val Val
    1565                1570                1575

Val Asp  Val Ser His Glu Asp  Pro Glu Val Lys Phe  Asn Trp Tyr

    1580                1585                1590

Val Asp  Gly Val Glu Val His  Asn Ala Lys Thr Lys  Pro Arg Glu
    1595                1600                1605

Glu Gln  Tyr Asn Ser Thr Tyr  Arg Val Val Ser Val  Leu Thr Val
    1610                1615                1620

Leu His  Gln Asp Trp Leu Asn  Gly Lys Glu Tyr Lys  Cys Lys Val
    1625                1630                1635

Ser Asn  Lys Ala Leu Pro Ala  Pro Ile Glu Lys Thr  Ile Ser Lys
    1640                1645                1650

Ala Lys  Gly Gln Pro Arg Glu  Pro Gln Val Tyr Thr  Leu Pro Pro
    1655                1660                1665

Ser Arg  Asp Glu Leu Thr Lys  Asn Gln Val Ser Leu  Thr Cys Leu
    1670                1675                1680

Val Lys  Gly Phe Tyr Pro Ser  Asp Ile Ala Val Glu  Trp Glu Ser
    1685                1690                1695

Asn Gly  Gln Pro Glu Asn Asn  Tyr Lys Thr Thr Pro  Pro Val Leu
    1700                1705                1710

Asp Ser  Asp Gly Ser Phe Phe  Leu Tyr Ser Lys Leu  Thr Val Asp
    1715                1720                1725

Lys Ser  Arg Trp Gln Gln Gly  Asn Val Phe Ser Cys  Ser Val Met
    1730                1735                1740

His Glu  Ala Leu His Asn His  Tyr Thr Gln Lys Ser  Leu Ser Leu
    1745                1750                1755

Ser Pro  Gly Lys
    1760
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<210> 116

<211> 1726

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYNFVIII 271 protein sequence

<400> 116

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15
```

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

Trp Asp Tyr Met Gln Gly Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr
        35                  40                  45

Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
    50                  55                  60

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Ala Ser Ser Ser
65                  70                  75                  80

Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro
                85                  90                  95

Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe
            100                 105                 110

Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro
        115                 120                 125

Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr
    130                 135                 140

Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val Ser Leu His
145                 150                 155                 160

Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr Asp
                165                 170                 175

Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly
            180                 185                 190

Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met
        195                 200                 205

Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp
    210                 215                 220

Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu Leu Val Cys
225                 230                 235                 240

Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu His Lys Phe
                245                 250                 255

Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp His Ser Glu

            260                 265                 270

Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala
        275                 280                 285

Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro
    290                 295                 300

Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly
305                 310                 315                 320

Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu Gly His Thr
                325                 330                 335

Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile
            340                 345                 350

Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly Gln Phe Leu
        355                 360                 365
```

```
Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu Ala Tyr
    370                 375                 380

Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn
385                 390                 395                 400

Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met
                405                 410                 415

Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile
            420                 425                 430

Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His Tyr Ile Ala
        435                 440                 445

Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp
    450                 455                 460

Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile
465                 470                 475                 480

Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr Asp Glu Thr
                485                 490                 495

Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro
            500                 505                 510

Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn
        515                 520                 525

Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val
    530                 535                 540

Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys
545                 550                 555                 560

Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val
                565                 570                 575

Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg
            580                 585                 590

Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser Gly Leu
        595                 600                 605

Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly
    610                 615                 620

Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe
625                 630                 635                 640

Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu
                645                 650                 655

Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe Gln Ala Ser
            660                 665                 670

Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser Leu Gln Leu
        675                 680                 685

Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu Ser Ile Gly
    690                 695                 700

Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys
705                 710                 715                 720

His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly
                725                 730                 735
```

```
Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly
            740                 745                 750

Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys
        755                 760                 765

Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr
    770                 775                 780

Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu Pro
785                 790                 795                 800

Arg Ser Phe Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Ala Glu
                805                 810                 815

Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp
            820                 825                 830

Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp
        835                 840                 845

Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His
    850                 855                 860

Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser Ser
865                 870                 875                 880

Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro Gln
                885                 890                 895

Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln
            900                 905                 910

Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro
        915                 920                 925

Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn
    930                 935                 940

Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu
945                 950                 955                 960

Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys Pro
                965                 970                 975

Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His Met Ala Pro
            980                 985                 990

Thr Lys Asp Glu Phe Asp Cys Lys  Ala Trp Ala Tyr Phe  Ser Asp Val
        995                 1000                1005

Asp Leu  Glu Lys Asp Val His  Ser Gly Leu Ile Gly  Pro Leu Leu
    1010                1015                1020

Val Cys  His Thr Asn Thr Leu  Asn Pro Ala His Gly  Arg Gln Val
    1025                1030                1035

Thr Val  Gln Glu Phe Ala Leu  Phe Phe Thr Ile Phe  Asp Glu Thr
    1040                1045                1050

Lys Ser  Trp Tyr Phe Thr Glu  Asn Met Glu Arg Asn  Cys Arg Ala
    1055                1060                1065

Pro Cys  Asn Ile Gln Met Glu  Asp Pro Thr Phe Lys  Glu Asn Tyr
    1070                1075                1080

Arg Phe  His Ala Ile Asn Gly  Tyr Ile Met Asp Thr  Leu Pro Gly
    1085                1090                1095
```

```
Leu Val  Met Ala Gln Asp Gln  Arg Ile Arg Trp Tyr  Leu Leu Ser
    1100                 1105                 1110

Met Gly  Ser Asn Glu Asn Ile  His Ser Ile His Phe  Ser Gly His
    1115                 1120                 1125

Val Phe  Thr Val Arg Lys Lys  Glu Glu Tyr Lys Met  Ala Leu Tyr
    1130                 1135                 1140

Asn Leu  Tyr Pro Gly Val Phe  Glu Thr Val Glu Met  Leu Pro Ser
    1145                 1150                 1155

Lys Ala  Gly Ile Trp Arg Val  Glu Cys Leu Ile Gly  Glu His Leu
    1160                 1165                 1170

His Ala  Gly Met Ser Thr Leu  Phe Leu Val Tyr Ser  Asn Lys Cys
    1175                 1180                 1185

Gln Thr  Pro Leu Gly Met Ala  Ser Gly His Ile Arg  Asp Phe Gln
    1190                 1195                 1200

Ile Thr  Ala Ser Gly Gln Tyr  Gly Gln Trp Ala Pro  Lys Leu Ala
    1205                 1210                 1215

Arg Leu  His Tyr Ser Gly Ser  Ile Asn Ala Trp Ser  Thr Lys Glu
    1220                 1225                 1230

Pro Phe  Ser Trp Ile Lys Val  Asp Leu Leu Ala Pro  Met Ile Ile
    1235                 1240                 1245

His Gly  Ile Lys Thr Gln Gly  Ala Arg Gln Lys Phe  Ser Ser Leu

    1250                 1255                 1260

Tyr Ile  Ser Gln Phe Ile Ile  Met Tyr Ser Leu Asp  Gly Lys Lys
    1265                 1270                 1275

Trp Gln  Thr Tyr Arg Gly Asn  Ser Thr Gly Thr Leu  Met Val Phe
    1280                 1285                 1290

Phe Gly  Asn Val Asp Ser Ser  Gly Ile Lys His Asn  Ile Phe Asn
    1295                 1300                 1305

Pro Pro  Ile Ile Ala Arg Tyr  Ile Arg Leu His Pro  Thr His Tyr
    1310                 1315                 1320

Ser Ile  Arg Ser Thr Leu Arg  Met Glu Leu Met Gly  Cys Asp Leu
    1325                 1330                 1335

Asn Ser  Cys Ser Met Pro Leu  Gly Met Glu Ser Lys  Ala Ile Ser
    1340                 1345                 1350

Asp Ala  Gln Ile Thr Ala Ser  Ser Tyr Phe Thr Asn  Met Phe Ala
    1355                 1360                 1365

Thr Trp  Ser Pro Ser Lys Ala  Arg Leu His Leu Gln  Gly Arg Ser
    1370                 1375                 1380

Asn Ala  Trp Arg Pro Gln Val  Asn Asn Pro Lys Glu  Trp Leu Gln
    1385                 1390                 1395

Val Asp  Phe Gln Lys Thr Met  Lys Val Thr Gly Val  Thr Thr Gln
    1400                 1405                 1410

Gly Val  Lys Ser Leu Leu Thr  Ser Met Tyr Val Lys  Glu Phe Leu
    1415                 1420                 1425
```

```
Ile Ser  Ser Ser Gln Asp Gly  His Gln Trp Thr Leu  Phe Phe Gln
    1430                 1435                 1440

Asn Gly  Lys Val Lys Val Phe  Gln Gly Asn Gln Asp  Ser Phe Thr
    1445                 1450                 1455

Pro Val  Val Asn Ser Leu Asp  Pro Pro Leu Leu Thr  Arg Tyr Leu
    1460                 1465                 1470

Arg Ile  His Pro Gln Ser Trp  Val His Gln Ile Ala  Leu Arg Met
    1475                 1480                 1485

Glu Val  Leu Gly Cys Glu Ala  Gln Asp Leu Tyr Asp  Lys Thr His
    1490                 1495                 1500

Thr Cys  Pro Pro Cys Pro Ala  Pro Glu Leu Leu Gly  Gly Pro Ser
    1505                 1510                 1515

Val Phe  Leu Phe Pro Pro Lys  Pro Lys Asp Thr Leu  Met Ile Ser
    1520                 1525                 1530

Arg Thr  Pro Glu Val Thr Cys  Val Val Val Asp Val  Ser His Glu
    1535                 1540                 1545

Asp Pro  Glu Val Lys Phe Asn  Trp Tyr Val Asp Gly  Val Glu Val
    1550                 1555                 1560

His Asn  Ala Lys Thr Lys Pro  Arg Glu Glu Gln Tyr  Asn Ser Thr
    1565                 1570                 1575

Tyr Arg  Val Val Ser Val Leu  Thr Val Leu His Gln  Asp Trp Leu
    1580                 1585                 1590

Asn Gly  Lys Glu Tyr Lys Cys  Lys Val Ser Asn Lys  Ala Leu Pro
    1595                 1600                 1605

Ala Pro  Ile Glu Lys Thr Ile  Ser Lys Ala Lys Gly  Gln Pro Arg
    1610                 1615                 1620

Glu Pro  Gln Val Tyr Thr Leu  Pro Pro Ser Arg Asp  Glu Leu Thr
    1625                 1630                 1635

Lys Asn  Gln Val Ser Leu Thr  Cys Leu Val Lys Gly  Phe Tyr Pro
    1640                 1645                 1650

Ser Asp  Ile Ala Val Glu Trp  Glu Ser Asn Gly Gln  Pro Glu Asn
    1655                 1660                 1665

Asn Tyr  Lys Thr Thr Pro Pro  Val Leu Asp Ser Asp  Gly Ser Phe
    1670                 1675                 1680

Phe Leu  Tyr Ser Lys Leu Thr  Val Asp Lys Ser Arg  Trp Gln Gln
    1685                 1690                 1695

Gly Asn  Val Phe Ser Cys Ser  Val Met His Glu Ala  Leu His Asn
    1700                 1705                 1710

His Tyr  Thr Gln Lys Ser Leu  Ser Leu Ser Pro Gly  Lys
    1715                 1720                 1725
```

<210> 117

<211> 1901

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYN FVIII protein sequence 272

<400> 117

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Gly Ala Pro Thr Ser Glu Ser Ala Thr Pro Glu
        35                  40                  45

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
    50                  55                  60

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
65                  70                  75                  80

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
                85                  90                  95

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
            100                 105                 110

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
        115                 120                 125

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
    130                 135                 140

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
145                 150                 155                 160

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly
                165                 170                 175

Ser Pro Thr Ser Thr Glu Glu Gly Ala Ser Ser Ser Asp Leu Gly Glu
            180                 185                 190

Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe Pro
        195                 200                 205

Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr
    210                 215                 220

Asp His Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu
225                 230                 235                 240

Leu Gly Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr
                245                 250                 255

Leu Lys Asn Met Ala Ser His Pro Val Ser Leu His Ala Val Gly Val
            260                 265                 270

Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser
        275                 280                 285

Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly Ser His Thr
    290                 295                 300

Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro
305                 310                 315                 320

Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp
                325                 330                 335

Leu Asn Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser
            340                 345                 350
```

```
Leu Ala Lys Glu Lys Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe
        355                 360                 365

Ala Val Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Lys Asn Ser
    370                 375                 380

Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala Trp Pro Lys Met
385                 390                 395                 400

His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly
                405                 410                 415

Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr
            420                 425                 430

Pro Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg
        435                 440                 445

Asn His Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr
    450                 455                 460

Ala Gln Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His
465                 470                 475                 480

Ile Ser Ser His Gln His Asp Gly Met Glu Ala Tyr Val Lys Val Asp
                485                 490                 495

Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn Asn Glu Glu Ala
            500                 505                 510

Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val Val Arg
        515                 520                 525

Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala
    530                 535                 540

Lys Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu
545                 550                 555                 560

Asp Trp Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr
                565                 570                 575

Lys Ser Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr
            580                 585                 590

Lys Lys Val Arg Phe Met Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg
        595                 600                 605

Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly
    610                 615                 620

Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg
625                 630                 635                 640

Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr
                645                 650                 655

Ser Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile
            660                 665                 670

Leu Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp
        675                 680                 685

Gly Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser
    690                 695                 700

Phe Val Asn Met Glu Arg Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu
705                 710                 715                 720
```

```
Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn Gln Ile Met
                725                 730                 735

Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
            740                 745                 750

Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala
        755                 760                 765

Gly Val Gln Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His
    770                 775                 780

Ser Ile Asn Gly Tyr Val Phe Asp Ser Leu Gln Leu Ser Val Cys Leu
785                 790                 795                 800

His Glu Val Ala Tyr Trp Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp
                805                 810                 815

Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys His Lys Met Val
            820                 825                 830

Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val Phe
        835                 840                 845

Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser
    850                 855                 860

Asp Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys
865                 870                 875                 880

Asp Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser
                885                 890                 895

Ala Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser
            900                 905                 910

Gln Asn Gly Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly
        915                 920                 925

Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser
    930                 935                 940

Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser
945                 950                 955                 960

Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly

                965                 970                 975

Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro
            980                 985                 990

Ala Gly Ser Pro Thr Ser Thr Glu  Glu Gly Thr Ser Glu  Ser Ala Thr
        995                 1000                1005

Pro Glu  Ser Gly Pro Gly Ser  Glu Pro Ala Thr Ser  Gly Ser Glu
    1010                1015                1020

Thr Pro  Gly Thr Ser Glu Ser  Ala Thr Pro Glu Ser  Gly Pro Gly
    1025                1030                1035

Ser Pro  Ala Gly Ser Pro Thr  Ser Thr Glu Glu Gly  Ser Pro Ala
    1040                1045                1050

Gly Ser  Pro Thr Ser Thr Glu  Glu Gly Thr Ser Thr  Glu Pro Ser
    1055                1060                1065
```

```
Glu Gly  Ser Ala Pro Gly Thr  Ser Glu Ser Ala Thr  Pro Glu Ser
    1070                 1075                 1080

Gly Pro  Gly Thr Ser Glu Ser  Ala Thr Pro Glu Ser  Gly Pro Gly
    1085                 1090                 1095

Thr Ser  Glu Ser Ala Thr Pro  Glu Ser Gly Pro Gly  Ser Glu Pro
    1100                 1105                 1110

Ala Thr  Ser Gly Ser Glu Thr  Pro Gly Ser Glu Pro  Ala Thr Ser
    1115                 1120                 1125

Gly Ser  Glu Thr Pro Gly Ser  Pro Ala Gly Ser Pro  Thr Ser Thr
    1130                 1135                 1140

Glu Glu  Gly Thr Ser Thr Glu  Pro Ser Glu Gly Ser  Ala Pro Gly
    1145                 1150                 1155

Thr Ser  Thr Glu Pro Ser Glu  Gly Ser Ala Pro Gly  Ser Glu Pro
    1160                 1165                 1170

Ala Thr  Ser Gly Ser Glu Thr  Pro Gly Thr Ser Glu  Ser Ala Thr
    1175                 1180                 1185

Pro Glu  Ser Gly Pro Gly Thr  Ser Thr Glu Pro Ser  Glu Gly Ser
    1190                 1195                 1200

Ala Pro  Ala Ser Ser Pro Pro  Val Leu Lys Arg His  Gln Ala Glu
    1205                 1210                 1215

Ile Thr  Arg Thr Thr Leu Gln  Ser Asp Gln Glu Glu  Ile Asp Tyr
    1220                 1225                 1230

Asp Asp  Thr Ile Ser Val Glu  Met Lys Lys Glu Asp  Phe Asp Ile
    1235                 1240                 1245

Tyr Asp  Glu Asp Glu Asn Gln  Ser Pro Arg Ser Phe  Gln Lys Lys
    1250                 1255                 1260

Thr Arg  His Tyr Phe Ile Ala  Ala Val Glu Arg Leu  Trp Asp Tyr
    1265                 1270                 1275

Gly Met  Ser Ser Ser Pro His  Val Leu Arg Asn Arg  Ala Gln Ser
    1280                 1285                 1290

Gly Ser  Val Pro Gln Phe Lys  Lys Val Val Phe Gln  Glu Phe Thr
    1295                 1300                 1305

Asp Gly  Ser Phe Thr Gln Pro  Leu Tyr Arg Gly Glu  Leu Asn Glu
    1310                 1315                 1320

His Leu  Gly Leu Leu Gly Pro  Tyr Ile Arg Ala Glu  Val Glu Asp
    1325                 1330                 1335

Asn Ile  Met Val Thr Phe Arg  Asn Gln Ala Ser Arg  Pro Tyr Ser
    1340                 1345                 1350

Phe Tyr  Ser Ser Leu Ile Ser  Tyr Glu Glu Asp Gln  Arg Gln Gly
    1355                 1360                 1365

Ala Glu  Pro Arg Lys Asn Phe  Val Lys Pro Asn Glu  Thr Lys Thr
    1370                 1375                 1380

Tyr Phe  Trp Lys Val Gln His  His Met Ala Pro Thr  Lys Asp Glu
    1385                 1390                 1395

Phe Asp  Cys Lys Ala Trp Ala  Tyr Phe Ser Asp Val  Asp Leu Glu
    1400                 1405                 1410
```

```
Lys Asp  Val His Ser Gly Leu  Ile Gly Pro Leu Leu  Val Cys His
    1415                 1420                 1425

Thr Asn  Thr Leu Asn Pro Ala  His Gly Arg Gln Val  Thr Val Gln
    1430                 1435                 1440

Glu Phe  Ala Leu Phe Phe Thr  Ile Phe Asp Glu Thr  Lys Ser Trp
    1445                 1450                 1455

Tyr Phe  Thr Glu Asn Met Glu  Arg Asn Cys Arg Ala  Pro Cys Asn
    1460                 1465                 1470

Ile Gln  Met Glu Asp Pro Thr  Phe Lys Glu Asn Tyr  Arg Phe His
    1475                 1480                 1485

Ala Ile  Asn Gly Tyr Ile Met  Asp Thr Leu Pro Gly  Leu Val Met
    1490                 1495                 1500

Ala Gln  Asp Gln Arg Ile Arg  Trp Tyr Leu Leu Ser  Met Gly Ser
    1505                 1510                 1515

Asn Glu  Asn Ile His Ser Ile  His Phe Ser Gly His  Val Phe Thr
    1520                 1525                 1530

Val Arg  Lys Lys Glu Glu Tyr  Lys Met Ala Leu Tyr  Asn Leu Tyr
    1535                 1540                 1545

Pro Gly  Val Phe Glu Thr Val  Glu Met Leu Pro Ser  Lys Ala Gly
    1550                 1555                 1560

Ile Trp  Arg Val Glu Cys Leu  Ile Gly Glu His Leu  His Ala Gly
    1565                 1570                 1575

Met Ser  Thr Leu Phe Leu Val  Tyr Ser Asn Lys Cys  Gln Thr Pro
    1580                 1585                 1590

Leu Gly  Met Ala Ser Gly His  Ile Arg Asp Phe Gln  Ile Thr Ala
    1595                 1600                 1605

Ser Gly  Gln Tyr Gly Gln Trp  Ala Pro Lys Leu Ala  Arg Leu His
    1610                 1615                 1620

Tyr Ser  Gly Ser Ile Asn Ala  Trp Ser Thr Lys Glu  Pro Phe Ser
    1625                 1630                 1635

Trp Ile  Lys Val Asp Leu Leu  Ala Pro Met Ile Ile  His Gly Ile
    1640                 1645                 1650

Lys Thr  Gln Gly Ala Arg Gln  Lys Phe Ser Ser Leu  Tyr Ile Ser
    1655                 1660                 1665

Gln Phe  Ile Ile Met Tyr Ser  Leu Asp Gly Lys Lys  Trp Gln Thr
    1670                 1675                 1680

Tyr Arg  Gly Asn Ser Thr Gly  Thr Leu Met Val Phe  Phe Gly Asn
    1685                 1690                 1695

Val Asp  Ser Ser Gly Ile Lys  His Asn Ile Phe Asn  Pro Pro Ile
    1700                 1705                 1710

Ile Ala  Arg Tyr Ile Arg Leu  His Pro Thr His Tyr  Ser Ile Arg
    1715                 1720                 1725

Ser Thr  Leu Arg Met Glu Leu  Met Gly Cys Asp Leu  Asn Ser Cys
    1730                 1735                 1740

Ser Met  Pro Leu Gly Met Glu  Ser Lys Ala Ile Ser  Asp Ala Gln
    1745                 1750                 1755
```

```
Ile Thr  Ala Ser Ser Tyr Phe  Thr Asn Met Phe Ala  Thr Trp Ser
    1760                 1765                 1770

Pro Ser  Lys Ala Arg Leu His  Leu Gln Gly Arg Ser  Asn Ala Trp
    1775                 1780                 1785

Arg Pro  Gln Val Asn Asn Pro  Lys Glu Trp Leu Gln  Val Asp Phe
    1790                 1795                 1800

Gln Lys  Thr Met Lys Val Thr  Gly Val Thr Thr Gln  Gly Val Lys
    1805                 1810                 1815

Ser Leu  Leu Thr Ser Met Tyr  Val Lys Glu Phe Leu  Ile Ser Ser
    1820                 1825                 1830

Ser Gln  Asp Gly His Gln Trp  Thr Leu Phe Phe Gln  Asn Gly Lys
    1835                 1840                 1845

Val Lys  Val Phe Gln Gly Asn  Gln Asp Ser Phe Thr  Pro Val Val
    1850                 1855                 1860

Asn Ser  Leu Asp Pro Pro Leu  Leu Thr Arg Tyr Leu  Arg Ile His
    1865                 1870                 1875

Pro Gln  Ser Trp Val His Gln  Ile Ala Leu Arg Met  Glu Val Leu
    1880                 1885                 1890

Gly Cys  Glu Ala Gln Asp Leu  Tyr
    1895                 1900
```

<210> 118

<211> 1515

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYN VWF 031 protein sequence

<400> 118

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Met Ile Pro Ala Arg Phe Ala Gly Val Leu Leu Ala Leu Ala Leu Ile
1               5                  10                  15

Leu Pro Gly Thr Leu Cys Ala Glu Gly Thr Arg Gly Arg Ser Ser Thr
            20                  25                  30

Ala Arg Cys Ser Leu Phe Gly Ser Asp Phe Val Asn Thr Phe Asp Gly
        35                  40                  45

Ser Met Tyr Ser Phe Ala Gly Tyr Cys Ser Tyr Leu Leu Ala Gly Gly
    50                  55                  60

Cys Gln Lys Arg Ser Phe Ser Ile Ile Gly Asp Phe Gln Asn Gly Lys
65                  70                  75                  80

Arg Val Ser Leu Ser Val Tyr Leu Gly Glu Phe Phe Asp Ile His Leu
                85                  90                  95

Phe Val Asn Gly Thr Val Thr Gln Gly Asp Gln Arg Val Ser Met Pro
            100                 105                 110

Tyr Ala Ser Lys Gly Leu Tyr Leu Glu Thr Glu Ala Gly Tyr Tyr Lys
        115                 120                 125

Leu Ser Gly Glu Ala Tyr Gly Phe Val Ala Arg Ile Asp Gly Ser Gly
    130                 135                 140
```

```
Asn Phe Gln Val Leu Leu Ser Asp Arg Tyr Phe Asn Lys Thr Cys Gly
145                 150                 155                 160

Leu Cys Gly Asn Phe Asn Ile Phe Ala Glu Asp Asp Phe Met Thr Gln
                165                 170                 175

Glu Gly Thr Leu Thr Ser Asp Pro Tyr Asp Phe Ala Asn Ser Trp Ala
            180                 185                 190

Leu Ser Ser Gly Glu Gln Trp Cys Glu Arg Ala Ser Pro Pro Ser Ser
        195                 200                 205

Ser Cys Asn Ile Ser Ser Gly Glu Met Gln Lys Gly Leu Trp Glu Gln
    210                 215                 220

Cys Gln Leu Leu Lys Ser Thr Ser Val Phe Ala Arg Cys His Pro Leu
225                 230                 235                 240

Val Asp Pro Glu Pro Phe Val Ala Leu Cys Glu Lys Thr Leu Cys Glu
                245                 250                 255

Cys Ala Gly Gly Leu Glu Cys Ala Cys Pro Ala Leu Leu Glu Tyr Ala
            260                 265                 270

Arg Thr Cys Ala Gln Glu Gly Met Val Leu Tyr Gly Trp Thr Asp His
        275                 280                 285

Ser Ala Cys Ser Pro Val Cys Pro Ala Gly Met Glu Tyr Arg Gln Cys
    290                 295                 300

Val Ser Pro Cys Ala Arg Thr Cys Gln Ser Leu His Ile Asn Glu Met
305                 310                 315                 320

Cys Gln Glu Arg Cys Val Asp Gly Cys Ser Cys Pro Glu Gly Gln Leu
                325                 330                 335

Leu Asp Glu Gly Leu Cys Val Glu Ser Thr Glu Cys Pro Cys Val His
            340                 345                 350

Ser Gly Lys Arg Tyr Pro Pro Gly Thr Ser Leu Ser Arg Asp Cys Asn
        355                 360                 365

Thr Cys Ile Cys Arg Asn Ser Gln Trp Ile Cys Ser Asn Glu Glu Cys
    370                 375                 380

Pro Gly Glu Cys Leu Val Thr Gly Gln Ser His Phe Lys Ser Phe Asp
385                 390                 395                 400

Asn Arg Tyr Phe Thr Phe Ser Gly Ile Cys Gln Tyr Leu Leu Ala Arg
                405                 410                 415

Asp Cys Gln Asp His Ser Phe Ser Ile Val Ile Glu Thr Val Gln Cys
            420                 425                 430

Ala Asp Asp Arg Asp Ala Val Cys Thr Arg Ser Val Thr Val Arg Leu
        435                 440                 445

Pro Gly Leu His Asn Ser Leu Val Lys Leu Lys His Gly Ala Gly Val
    450                 455                 460

Ala Met Asp Gly Gln Asp Ile Gln Leu Pro Leu Leu Lys Gly Asp Leu

465                 470                 475                 480

Arg Ile Gln His Thr Val Thr Ala Ser Val Arg Leu Ser Tyr Gly Glu
                485                 490                 495
```

```
Asp Leu Gln Met Asp Trp Asp Gly Arg Gly Arg Leu Leu Val Lys Leu
            500                 505                 510

Ser Pro Val Tyr Ala Gly Lys Thr Cys Gly Leu Cys Gly Asn Tyr Asn
        515                 520                 525

Gly Asn Gln Gly Asp Asp Phe Leu Thr Pro Ser Gly Leu Ala Glu Pro
    530                 535                 540

Arg Val Glu Asp Phe Gly Asn Ala Trp Lys Leu His Gly Asp Cys Gln
545                 550                 555                 560

Asp Leu Gln Lys Gln His Ser Asp Pro Cys Ala Leu Asn Pro Arg Met
                565                 570                 575

Thr Arg Phe Ser Glu Glu Ala Cys Ala Val Leu Thr Ser Pro Thr Phe
            580                 585                 590

Glu Ala Cys His Arg Ala Val Ser Pro Leu Pro Tyr Leu Arg Asn Cys
        595                 600                 605

Arg Tyr Asp Val Cys Ser Cys Ser Asp Gly Arg Glu Cys Leu Cys Gly
    610                 615                 620

Ala Leu Ala Ser Tyr Ala Ala Ala Cys Ala Gly Arg Gly Val Arg Val
625                 630                 635                 640

Ala Trp Arg Glu Pro Gly Arg Cys Glu Leu Asn Cys Pro Lys Gly Gln
                645                 650                 655

Val Tyr Leu Gln Cys Gly Thr Pro Cys Asn Leu Thr Cys Arg Ser Leu
            660                 665                 670

Ser Tyr Pro Asp Glu Glu Cys Asn Glu Ala Cys Leu Glu Gly Cys Phe
        675                 680                 685

Cys Pro Pro Gly Leu Tyr Met Asp Glu Arg Gly Asp Cys Val Pro Lys
    690                 695                 700

Ala Gln Cys Pro Cys Tyr Tyr Asp Gly Glu Ile Phe Gln Pro Glu Asp
705                 710                 715                 720

Ile Phe Ser Asp His His Thr Met Cys Tyr Cys Glu Asp Gly Phe Met
                725                 730                 735

His Cys Thr Met Ser Gly Val Pro Gly Ser Leu Leu Pro Asp Ala Val
            740                 745                 750

Leu Ser Ser Pro Leu Ser His Arg Ser Lys Arg Ser Leu Ser Cys Arg
        755                 760                 765

Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp Asn Leu Arg Ala Glu
    770                 775                 780

Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr Asp Leu Glu Cys Met
785                 790                 795                 800

Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro Pro Gly Met Val Arg
                805                 810                 815

His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys Pro Cys Phe His Gln
            820                 825                 830

Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys Ile Gly Cys Asn Thr
        835                 840                 845

Cys Val Cys Arg Asp Arg Lys Trp Asn Cys Thr Asp His Val Cys Asp
```

```
    850                 855                 860

Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr Leu Thr Phe Asp Gly
865                 870                 875                 880

Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr Val Leu Val Gln Asp
                885                 890                 895

Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile Leu Val Gly Asn Lys
            900                 905                 910

Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys Arg Val Thr Ile Leu
        915                 920                 925

Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly Glu Val Asn Val Lys
    930                 935                 940

Arg Pro Met Lys Asp Glu Thr His Phe Glu Val Val Glu Ser Gly Arg
945                 950                 955                 960

Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser Val Val Trp Asp Arg
                965                 970                 975

His Leu Ser Ile Ser Val Val Leu Lys Gln Thr Tyr Gln Glu Lys Val
            980                 985                 990

Cys Gly Leu Cys Gly Asn Phe Asp  Gly Ile Gln Asn Asn  Asp Leu Thr
        995                 1000                1005

Ser Ser  Asn Leu Gln Val Glu  Glu Asp Pro Val Asp  Phe Gly Asn
    1010                1015                1020

Ser Trp  Lys Val Ser Ser Gln  Cys Ala Asp Thr Arg  Lys Val Pro
    1025                1030                1035

Leu Asp  Ser Ser Pro Ala Thr  Cys His Asn Asn Ile  Met Lys Gln
    1040                1045                1050

Thr Met  Val Asp Ser Ser Cys  Arg Ile Leu Thr Ser  Asp Val Phe
    1055                1060                1065

Gln Asp  Cys Asn Lys Leu Val  Asp Pro Glu Pro Tyr  Leu Asp Val
    1070                1075                1080

Cys Ile  Tyr Asp Thr Cys Ser  Cys Glu Ser Ile Gly  Asp Cys Ala
    1085                1090                1095

Ala Phe  Cys Asp Thr Ile Ala  Ala Tyr Ala His Val  Cys Ala Gln
    1100                1105                1110

His Gly  Lys Val Val Thr Trp  Arg Thr Ala Thr Leu  Cys Pro Gln
    1115                1120                1125

Ser Cys  Glu Glu Arg Asn Leu  Arg Glu Asn Gly Tyr  Glu Ala Glu
    1130                1135                1140

Trp Arg  Tyr Asn Ser Cys Ala  Pro Ala Cys Gln Val  Thr Cys Gln
    1145                1150                1155

His Pro  Glu Pro Leu Ala Cys  Pro Val Gln Cys Val  Glu Gly Cys
    1160                1165                1170

His Ala  His Cys Pro Pro Gly  Lys Ile Leu Asp Glu  Leu Leu Gln
    1175                1180                1185

Thr Cys  Val Asp Pro Glu Asp  Cys Pro Val Cys Glu  Val Ala Gly
    1190                1195                1200

Arg Arg  Phe Ala Ser Gly Lys  Lys Val Thr Leu Asn  Pro Ser Asp
```

```
    1205                1210                1215

Pro Glu  His Cys Gln Ile Cys  His Cys Asp Val Val  Asn Leu Thr
    1220                1225                1230

Cys Glu  Ala Cys Gln Glu Pro  Ile Ser Gly Gly Gly  Gly Ser Gly
    1235                1240                1245

Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Gly
    1250                1255                1260

Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Leu Val Pro  Arg Gly Ser
    1265                1270                1275

Gly Gly  Gly Gly Ser Gly Gly  Gly Gly Ser Asp Lys  Thr His Thr
    1280                1285                1290

Cys Pro  Pro Cys Pro Ala Pro  Glu Leu Leu Gly Gly  Pro Ser Val
    1295                1300                1305

Phe Leu  Phe Pro Pro Lys Pro  Lys Asp Thr Leu Met  Ile Ser Arg
    1310                1315                1320

Thr Pro  Glu Val Thr Cys Val  Val Val Asp Val Ser  His Glu Asp
    1325                1330                1335

Pro Glu  Val Lys Phe Asn Trp  Tyr Val Asp Gly Val  Glu Val His
    1340                1345                1350

Asn Ala  Lys Thr Lys Pro Arg  Glu Glu Gln Tyr Asn  Ser Thr Tyr
    1355                1360                1365

Arg Val  Val Ser Val Leu Thr  Val Leu His Gln Asp  Trp Leu Asn
    1370                1375                1380

Gly Lys  Glu Tyr Lys Cys Lys  Val Ser Asn Lys Ala  Leu Pro Ala
    1385                1390                1395

Pro Ile  Glu Lys Thr Ile Ser  Lys Ala Lys Gly Gln  Pro Arg Glu
    1400                1405                1410

Pro Gln  Val Tyr Thr Leu Pro  Pro Ser Arg Asp Glu  Leu Thr Lys
    1415                1420                1425

Asn Gln  Val Ser Leu Thr Cys  Leu Val Lys Gly Phe  Tyr Pro Ser
    1430                1435                1440

Asp Ile  Ala Val Glu Trp Glu  Ser Asn Gly Gln Pro  Glu Asn Asn

    1445                1450                1455

Tyr Lys  Thr Thr Pro Pro Val  Leu Asp Ser Asp Gly  Ser Phe Phe
    1460                1465                1470

Leu Tyr  Ser Lys Leu Thr Val  Asp Lys Ser Arg Trp  Gln Gln Gly
    1475                1480                1485

Asn Val  Phe Ser Cys Ser Val  Met His Glu Ala Leu  His Asn His
    1490                1495                1500

Tyr Thr  Gln Lys Ser Leu Ser  Leu Ser Pro Gly Lys
    1505                1510                1515
```

<210> 119

<211> 1778

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYN VWF 034 protein sequence

<400> 119

```
Met Ile Pro Ala Arg Phe Ala Gly Val Leu Leu Ala Leu Ala Leu Ile
1               5                  10                  15

Leu Pro Gly Thr Leu Cys Ala Glu Gly Thr Arg Gly Arg Ser Ser Thr
            20                  25                  30

Ala Arg Cys Ser Leu Phe Gly Ser Asp Phe Val Asn Thr Phe Asp Gly
        35                  40                  45

Ser Met Tyr Ser Phe Ala Gly Tyr Cys Ser Tyr Leu Leu Ala Gly Gly
    50                  55                  60

Cys Gln Lys Arg Ser Phe Ser Ile Ile Gly Asp Phe Gln Asn Gly Lys
65                  70                  75                  80

Arg Val Ser Leu Ser Val Tyr Leu Gly Glu Phe Phe Asp Ile His Leu
                85                  90                  95

Phe Val Asn Gly Thr Val Thr Gln Gly Asp Gln Arg Val Ser Met Pro
            100                 105                 110

Tyr Ala Ser Lys Gly Leu Tyr Leu Glu Thr Glu Ala Gly Tyr Tyr Lys
        115                 120                 125

Leu Ser Gly Glu Ala Tyr Gly Phe Val Ala Arg Ile Asp Gly Ser Gly
    130                 135                 140

Asn Phe Gln Val Leu Leu Ser Asp Arg Tyr Phe Asn Lys Thr Cys Gly
145                 150                 155                 160

Leu Cys Gly Asn Phe Asn Ile Phe Ala Glu Asp Asp Phe Met Thr Gln
                165                 170                 175

Glu Gly Thr Leu Thr Ser Asp Pro Tyr Asp Phe Ala Asn Ser Trp Ala
            180                 185                 190

Leu Ser Ser Gly Glu Gln Trp Cys Glu Arg Ala Ser Pro Pro Ser Ser
        195                 200                 205

Ser Cys Asn Ile Ser Ser Gly Glu Met Gln Lys Gly Leu Trp Glu Gln
    210                 215                 220

Cys Gln Leu Leu Lys Ser Thr Ser Val Phe Ala Arg Cys His Pro Leu
225                 230                 235                 240

Val Asp Pro Glu Pro Phe Val Ala Leu Cys Glu Lys Thr Leu Cys Glu
                245                 250                 255

Cys Ala Gly Gly Leu Glu Cys Ala Cys Pro Ala Leu Leu Glu Tyr Ala
            260                 265                 270

Arg Thr Cys Ala Gln Glu Gly Met Val Leu Tyr Gly Trp Thr Asp His
        275                 280                 285

Ser Ala Cys Ser Pro Val Cys Pro Ala Gly Met Glu Tyr Arg Gln Cys
    290                 295                 300

Val Ser Pro Cys Ala Arg Thr Cys Gln Ser Leu His Ile Asn Glu Met
305                 310                 315                 320

Cys Gln Glu Arg Cys Val Asp Gly Cys Ser Cys Pro Glu Gly Gln Leu
```

```
                325                 330                 335

Leu Asp Glu Gly Leu Cys Val Glu Ser Thr Glu Cys Pro Cys Val His
            340                 345                 350

Ser Gly Lys Arg Tyr Pro Pro Gly Thr Ser Leu Ser Arg Asp Cys Asn
        355                 360                 365

Thr Cys Ile Cys Arg Asn Ser Gln Trp Ile Cys Ser Asn Glu Glu Cys
    370                 375                 380

Pro Gly Glu Cys Leu Val Thr Gly Gln Ser His Phe Lys Ser Phe Asp

385                 390                 395                 400

Asn Arg Tyr Phe Thr Phe Ser Gly Ile Cys Gln Tyr Leu Leu Ala Arg
                405                 410                 415

Asp Cys Gln Asp His Ser Phe Ser Ile Val Ile Glu Thr Val Gln Cys
            420                 425                 430

Ala Asp Asp Arg Asp Ala Val Cys Thr Arg Ser Val Thr Val Arg Leu
        435                 440                 445

Pro Gly Leu His Asn Ser Leu Val Lys Leu Lys His Gly Ala Gly Val
    450                 455                 460

Ala Met Asp Gly Gln Asp Ile Gln Leu Pro Leu Leu Lys Gly Asp Leu
465                 470                 475                 480

Arg Ile Gln His Thr Val Thr Ala Ser Val Arg Leu Ser Tyr Gly Glu
                485                 490                 495

Asp Leu Gln Met Asp Trp Asp Gly Arg Gly Arg Leu Leu Val Lys Leu
            500                 505                 510

Ser Pro Val Tyr Ala Gly Lys Thr Cys Gly Leu Cys Gly Asn Tyr Asn
        515                 520                 525

Gly Asn Gln Gly Asp Asp Phe Leu Thr Pro Ser Gly Leu Ala Glu Pro
    530                 535                 540

Arg Val Glu Asp Phe Gly Asn Ala Trp Lys Leu His Gly Asp Cys Gln
545                 550                 555                 560

Asp Leu Gln Lys Gln His Ser Asp Pro Cys Ala Leu Asn Pro Arg Met
                565                 570                 575

Thr Arg Phe Ser Glu Glu Ala Cys Ala Val Leu Thr Ser Pro Thr Phe
            580                 585                 590

Glu Ala Cys His Arg Ala Val Ser Pro Leu Pro Tyr Leu Arg Asn Cys
        595                 600                 605

Arg Tyr Asp Val Cys Ser Cys Ser Asp Gly Arg Glu Cys Leu Cys Gly
    610                 615                 620

Ala Leu Ala Ser Tyr Ala Ala Ala Cys Ala Gly Arg Gly Val Arg Val
625                 630                 635                 640

Ala Trp Arg Glu Pro Gly Arg Cys Glu Leu Asn Cys Pro Lys Gly Gln
                645                 650                 655

Val Tyr Leu Gln Cys Gly Thr Pro Cys Asn Leu Thr Cys Arg Ser Leu
            660                 665                 670

Ser Tyr Pro Asp Glu Glu Cys Asn Glu Ala Cys Leu Glu Gly Cys Phe
        675                 680                 685
```

```
Cys Pro Pro Gly Leu Tyr Met Asp Glu Arg Gly Asp Cys Val Pro Lys
    690                 695                 700

Ala Gln Cys Pro Cys Tyr Tyr Asp Gly Glu Ile Phe Gln Pro Glu Asp
705                 710                 715                 720

Ile Phe Ser Asp His His Thr Met Cys Tyr Cys Glu Asp Gly Phe Met
                725                 730                 735

His Cys Thr Met Ser Gly Val Pro Gly Ser Leu Leu Pro Asp Ala Val
            740                 745                 750

Leu Ser Ser Pro Leu Ser His Arg Ser Lys Arg Ser Leu Ser Cys Arg
        755                 760                 765

Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp Asn Leu Arg Ala Glu
    770                 775                 780

Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr Asp Leu Glu Cys Met
785                 790                 795                 800

Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro Pro Gly Met Val Arg
                805                 810                 815

His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys Pro Cys Phe His Gln
            820                 825                 830

Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys Ile Gly Cys Asn Thr
        835                 840                 845

Cys Val Cys Arg Asp Arg Lys Trp Asn Cys Thr Asp His Val Cys Asp
    850                 855                 860

Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr Leu Thr Phe Asp Gly
865                 870                 875                 880

Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr Val Leu Val Gln Asp
                885                 890                 895

Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile Leu Val Gly Asn Lys
            900                 905                 910

Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys Arg Val Thr Ile Leu
        915                 920                 925

Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly Glu Val Asn Val Lys
    930                 935                 940

Arg Pro Met Lys Asp Glu Thr His Phe Glu Val Val Glu Ser Gly Arg
945                 950                 955                 960

Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser Val Val Trp Asp Arg
                965                 970                 975

His Leu Ser Ile Ser Val Val Leu Lys Gln Thr Tyr Gln Glu Lys Val
            980                 985                 990

Cys Gly Leu Cys Gly Asn Phe Asp  Gly Ile Gln Asn Asn  Asp Leu Thr
        995                 1000                1005

Ser Ser  Asn Leu Gln Val Glu  Glu Asp Pro Val Asp  Phe Gly Asn
    1010                1015                1020

Ser Trp  Lys Val Ser Ser Gln  Cys Ala Asp Thr Arg  Lys Val Pro
    1025                1030                1035

Leu Asp  Ser Ser Pro Ala Thr  Cys His Asn Asn Ile  Met Lys Gln
```

```
    1040                1045                1050

Thr Met  Val Asp Ser Ser Cys  Arg Ile Leu Thr Ser  Asp Val Phe
    1055                1060                1065

Gln Asp  Cys Asn Lys Leu Val  Asp Pro Glu Pro Tyr  Leu Asp Val
    1070                1075                1080

Cys Ile  Tyr Asp Thr Cys Ser  Cys Glu Ser Ile Gly  Asp Cys Ala
    1085                1090                1095

Ala Phe  Cys Asp Thr Ile Ala  Ala Tyr Ala His Val  Cys Ala Gln
    1100                1105                1110

His Gly  Lys Val Val Thr Trp  Arg Thr Ala Thr Leu  Cys Pro Gln
    1115                1120                1125

Ser Cys  Glu Glu Arg Asn Leu  Arg Glu Asn Gly Tyr  Glu Ala Glu
    1130                1135                1140

Trp Arg  Tyr Asn Ser Cys Ala  Pro Ala Cys Gln Val  Thr Cys Gln
    1145                1150                1155

His Pro  Glu Pro Leu Ala Cys  Pro Val Gln Cys Val  Glu Gly Cys
    1160                1165                1170

His Ala  His Cys Pro Pro Gly  Lys Ile Leu Asp Glu  Leu Leu Gln
    1175                1180                1185

Thr Cys  Val Asp Pro Glu Asp  Cys Pro Val Cys Glu  Val Ala Gly
    1190                1195                1200

Arg Arg  Phe Ala Ser Gly Lys  Lys Val Thr Leu Asn  Pro Ser Asp
    1205                1210                1215

Pro Glu  His Cys Gln Ile Cys  His Cys Asp Val Val  Asn Leu Thr
    1220                1225                1230

Cys Glu  Ala Cys Gln Glu Pro  Ile Ser Gly Thr Ser  Glu Ser Ala
    1235                1240                1245

Thr Pro  Glu Ser Gly Pro Gly  Ser Glu Pro Ala Thr  Ser Gly Ser
    1250                1255                1260

Glu Thr  Pro Gly Thr Ser Glu  Ser Ala Thr Pro Glu  Ser Gly Pro
    1265                1270                1275

Gly Ser  Glu Pro Ala Thr Ser  Gly Ser Glu Thr Pro  Gly Thr Ser
    1280                1285                1290

Glu Ser  Ala Thr Pro Glu Ser  Gly Pro Gly Thr Ser  Thr Glu Pro
    1295                1300                1305

Ser Glu  Gly Ser Ala Pro Gly  Ser Pro Ala Gly Ser  Pro Thr Ser
    1310                1315                1320

Thr Glu  Glu Gly Thr Ser Glu  Ser Ala Thr Pro Glu  Ser Gly Pro
    1325                1330                1335

Gly Ser  Glu Pro Ala Thr Ser  Gly Ser Glu Thr Pro  Gly Thr Ser
    1340                1345                1350

Glu Ser  Ala Thr Pro Glu Ser  Gly Pro Gly Ser Pro  Ala Gly Ser
    1355                1360                1365

Pro Thr  Ser Thr Glu Glu Gly  Ser Pro Ala Gly Ser  Pro Thr Ser

    1370                1375                1380
```

```
Thr Glu  Glu Gly Thr Ser Thr  Glu Pro Ser Glu Gly  Ser Ala Pro
    1385                 1390                 1395

Gly Thr  Ser Glu Ser Ala Thr  Pro Glu Ser Gly Pro  Gly Thr Ser
    1400                 1405                 1410

Glu Ser  Ala Thr Pro Glu Ser  Gly Pro Gly Thr Ser  Glu Ser Ala
    1415                 1420                 1425

Thr Pro  Glu Ser Gly Pro Gly  Ser Glu Pro Ala Thr  Ser Gly Ser
    1430                 1435                 1440

Glu Thr  Pro Gly Ser Glu Pro  Ala Thr Ser Gly Ser  Glu Thr Pro
    1445                 1450                 1455

Gly Ser  Pro Ala Gly Ser Pro  Thr Ser Thr Glu Glu  Gly Thr Ser
    1460                 1465                 1470

Thr Glu  Pro Ser Glu Gly Ser  Ala Pro Gly Thr Ser  Thr Glu Pro
    1475                 1480                 1485

Ser Glu  Gly Ser Ala Pro Gly  Ser Glu Pro Ala Thr  Ser Gly Ser
    1490                 1495                 1500

Glu Thr  Pro Gly Thr Ser Glu  Ser Ala Thr Pro Glu  Ser Gly Pro
    1505                 1510                 1515

Gly Thr  Ser Thr Glu Pro Ser  Glu Gly Ser Ala Pro  Asp Ile Gly
    1520                 1525                 1530

Gly Gly  Gly Gly Ser Gly Gly  Gly Gly Ser Leu Val  Pro Arg Gly
    1535                 1540                 1545

Ser Gly  Gly Asp Lys Thr His  Thr Cys Pro Pro Cys  Pro Ala Pro
    1550                 1555                 1560

Glu Leu  Leu Gly Gly Pro Ser  Val Phe Leu Phe Pro  Pro Lys Pro
    1565                 1570                 1575

Lys Asp  Thr Leu Met Ile Ser  Arg Thr Pro Glu Val  Thr Cys Val
    1580                 1585                 1590

Val Val  Asp Val Ser His Glu  Asp Pro Glu Val Lys  Phe Asn Trp
    1595                 1600                 1605

Tyr Val  Asp Gly Val Glu Val  His Asn Ala Lys Thr  Lys Pro Arg
    1610                 1615                 1620

Glu Glu  Gln Tyr Asn Ser Thr  Tyr Arg Val Val Ser  Val Leu Thr
    1625                 1630                 1635

Val Leu  His Gln Asp Trp Leu  Asn Gly Lys Glu Tyr  Lys Cys Lys
    1640                 1645                 1650

Val Ser  Asn Lys Ala Leu Pro  Ala Pro Ile Glu Lys  Thr Ile Ser
    1655                 1660                 1665

Lys Ala  Lys Gly Gln Pro Arg  Glu Pro Gln Val Tyr  Thr Leu Pro
    1670                 1675                 1680

Pro Ser  Arg Asp Glu Leu Thr  Lys Asn Gln Val Ser  Leu Thr Cys
    1685                 1690                 1695

Leu Val  Lys Gly Phe Tyr Pro  Ser Asp Ile Ala Val  Glu Trp Glu
    1700                 1705                 1710
```

```
Ser Asn  Gly Gln Pro Glu Asn  Asn Tyr Lys Thr Thr  Pro Pro Val
    1715                 1720                 1725

Leu Asp  Ser Asp Gly Ser Phe  Phe Leu Tyr Ser Lys  Leu Thr Val
    1730                 1735                 1740

Asp Lys  Ser Arg Trp Gln Gln  Gly Asn Val Phe Ser  Cys Ser Val
    1745                 1750                 1755

Met His  Glu Ala Leu His Asn  His Tyr Thr Gln Lys  Ser Leu Ser
    1760                 1765                 1770

Leu Ser  Pro Gly Lys
    1775
```

<210> 120

<211> 1565

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYN VWF 036 protein sequence

<400> 120

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Met Ile Pro Ala Arg Phe Ala Gly Val Leu Leu Ala Leu Ala Leu Ile
1               5                  10                  15

Leu Pro Gly Thr Leu Cys Ala Glu Gly Thr Arg Gly Arg Ser Ser Thr

            20                  25                  30

Ala Arg Cys Ser Leu Phe Gly Ser Asp Phe Val Asn Thr Phe Asp Gly
        35                  40                  45

Ser Met Tyr Ser Phe Ala Gly Tyr Cys Ser Tyr Leu Leu Ala Gly Gly
    50                  55                  60

Cys Gln Lys Arg Ser Phe Ser Ile Ile Gly Asp Phe Gln Asn Gly Lys
65                  70                  75                  80

Arg Val Ser Leu Ser Val Tyr Leu Gly Glu Phe Phe Asp Ile His Leu
                85                  90                  95

Phe Val Asn Gly Thr Val Thr Gln Gly Asp Gln Arg Val Ser Met Pro
            100                 105                 110

Tyr Ala Ser Lys Gly Leu Tyr Leu Glu Thr Glu Ala Gly Tyr Tyr Lys
        115                 120                 125

Leu Ser Gly Glu Ala Tyr Gly Phe Val Ala Arg Ile Asp Gly Ser Gly
    130                 135                 140

Asn Phe Gln Val Leu Leu Ser Asp Arg Tyr Phe Asn Lys Thr Cys Gly
145                 150                 155                 160

Leu Cys Gly Asn Phe Asn Ile Phe Ala Glu Asp Asp Phe Met Thr Gln
                165                 170                 175

Glu Gly Thr Leu Thr Ser Asp Pro Tyr Asp Phe Ala Asn Ser Trp Ala
            180                 185                 190

Leu Ser Ser Gly Glu Gln Trp Cys Glu Arg Ala Ser Pro Pro Ser Ser
        195                 200                 205

Ser Cys Asn Ile Ser Ser Gly Glu Met Gln Lys Gly Leu Trp Glu Gln
    210                 215                 220
```

```
Cys Gln Leu Leu Lys Ser Thr Ser Val Phe Ala Arg Cys His Pro Leu
225                 230                 235                 240

Val Asp Pro Glu Pro Phe Val Ala Leu Cys Glu Lys Thr Leu Cys Glu
                245                 250                 255

Cys Ala Gly Gly Leu Glu Cys Ala Cys Pro Ala Leu Leu Glu Tyr Ala
            260                 265                 270

Arg Thr Cys Ala Gln Glu Gly Met Val Leu Tyr Gly Trp Thr Asp His
        275                 280                 285

Ser Ala Cys Ser Pro Val Cys Pro Ala Gly Met Glu Tyr Arg Gln Cys
    290                 295                 300

Val Ser Pro Cys Ala Arg Thr Cys Gln Ser Leu His Ile Asn Glu Met
305                 310                 315                 320

Cys Gln Glu Arg Cys Val Asp Gly Cys Ser Cys Pro Glu Gly Gln Leu
                325                 330                 335

Leu Asp Glu Gly Leu Cys Val Glu Ser Thr Glu Cys Pro Cys Val His
            340                 345                 350

Ser Gly Lys Arg Tyr Pro Pro Gly Thr Ser Leu Ser Arg Asp Cys Asn
        355                 360                 365

Thr Cys Ile Cys Arg Asn Ser Gln Trp Ile Cys Ser Asn Glu Glu Cys
    370                 375                 380

Pro Gly Glu Cys Leu Val Thr Gly Gln Ser His Phe Lys Ser Phe Asp
385                 390                 395                 400

Asn Arg Tyr Phe Thr Phe Ser Gly Ile Cys Gln Tyr Leu Leu Ala Arg
                405                 410                 415

Asp Cys Gln Asp His Ser Phe Ser Ile Val Ile Glu Thr Val Gln Cys
            420                 425                 430

Ala Asp Asp Arg Asp Ala Val Cys Thr Arg Ser Val Thr Val Arg Leu
        435                 440                 445

Pro Gly Leu His Asn Ser Leu Val Lys Leu Lys His Gly Ala Gly Val
    450                 455                 460

Ala Met Asp Gly Gln Asp Ile Gln Leu Pro Leu Leu Lys Gly Asp Leu
465                 470                 475                 480

Arg Ile Gln His Thr Val Thr Ala Ser Val Arg Leu Ser Tyr Gly Glu
                485                 490                 495

Asp Leu Gln Met Asp Trp Asp Gly Arg Gly Arg Leu Leu Val Lys Leu
            500                 505                 510

Ser Pro Val Tyr Ala Gly Lys Thr Cys Gly Leu Cys Gly Asn Tyr Asn
        515                 520                 525

Gly Asn Gln Gly Asp Asp Phe Leu Thr Pro Ser Gly Leu Ala Glu Pro
    530                 535                 540

Arg Val Glu Asp Phe Gly Asn Ala Trp Lys Leu His Gly Asp Cys Gln
545                 550                 555                 560

Asp Leu Gln Lys Gln His Ser Asp Pro Cys Ala Leu Asn Pro Arg Met
                565                 570                 575

Thr Arg Phe Ser Glu Glu Ala Cys Ala Val Leu Thr Ser Pro Thr Phe
            580                 585                 590
```

```
Glu Ala Cys His Arg Ala Val Ser Pro Leu Pro Tyr Leu Arg Asn Cys
        595                 600                 605

Arg Tyr Asp Val Cys Ser Cys Ser Asp Gly Arg Glu Cys Leu Cys Gly
    610                 615                 620

Ala Leu Ala Ser Tyr Ala Ala Ala Cys Ala Gly Arg Gly Val Arg Val
625                 630                 635                 640

Ala Trp Arg Glu Pro Gly Arg Cys Glu Leu Asn Cys Pro Lys Gly Gln
                645                 650                 655

Val Tyr Leu Gln Cys Gly Thr Pro Cys Asn Leu Thr Cys Arg Ser Leu
            660                 665                 670

Ser Tyr Pro Asp Glu Glu Cys Asn Glu Ala Cys Leu Glu Gly Cys Phe
        675                 680                 685

Cys Pro Pro Gly Leu Tyr Met Asp Glu Arg Gly Asp Cys Val Pro Lys
    690                 695                 700

Ala Gln Cys Pro Cys Tyr Tyr Asp Gly Glu Ile Phe Gln Pro Glu Asp
705                 710                 715                 720

Ile Phe Ser Asp His His Thr Met Cys Tyr Cys Glu Asp Gly Phe Met
                725                 730                 735

His Cys Thr Met Ser Gly Val Pro Gly Ser Leu Leu Pro Asp Ala Val
            740                 745                 750

Leu Ser Ser Pro Leu Ser His Arg Ser Lys Arg Ser Leu Ser Cys Arg
        755                 760                 765

Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp Asn Leu Arg Ala Glu
    770                 775                 780

Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr Asp Leu Glu Cys Met
785                 790                 795                 800

Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro Pro Gly Met Val Arg
                805                 810                 815

His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys Pro Cys Phe His Gln
            820                 825                 830

Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys Ile Gly Cys Asn Thr
        835                 840                 845

Cys Val Cys Arg Asp Arg Lys Trp Asn Cys Thr Asp His Val Cys Asp
    850                 855                 860

Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr Leu Thr Phe Asp Gly
865                 870                 875                 880

Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr Val Leu Val Gln Asp
                885                 890                 895

Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile Leu Val Gly Asn Lys
            900                 905                 910

Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys Arg Val Thr Ile Leu
        915                 920                 925

Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly Glu Val Asn Val Lys
    930                 935                 940

Arg Pro Met Lys Asp Glu Thr His Phe Glu Val Val Glu Ser Gly Arg
945                 950                 955                 960
```

```
Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser Val Val Trp Asp Arg
                965                 970                 975

His Leu Ser Ile Ser Val Val Leu Lys Gln Thr Tyr Gln Glu Lys Val
            980                 985                 990

Cys Gly Leu Cys Gly Asn Phe Asp  Gly Ile Gln Asn Asn  Asp Leu Thr
        995                 1000                1005

Ser Ser  Asn Leu Gln Val Glu  Glu Asp Pro Val Asp  Phe Gly Asn
    1010                1015                1020

Ser Trp  Lys Val Ser Ser Gln  Cys Ala Asp Thr Arg  Lys Val Pro

    1025                1030                1035

Leu Asp  Ser Ser Pro Ala Thr  Cys His Asn Asn Ile  Met Lys Gln
    1040                1045                1050

Thr Met  Val Asp Ser Ser Cys  Arg Ile Leu Thr Ser  Asp Val Phe
    1055                1060                1065

Gln Asp  Cys Asn Lys Leu Val  Asp Pro Glu Pro Tyr  Leu Asp Val
    1070                1075                1080

Cys Ile  Tyr Asp Thr Cys Ser  Cys Glu Ser Ile Gly  Asp Cys Ala
    1085                1090                1095

Ala Phe  Cys Asp Thr Ile Ala  Ala Tyr Ala His Val  Cys Ala Gln
    1100                1105                1110

His Gly  Lys Val Val Thr Trp  Arg Thr Ala Thr Leu  Cys Pro Gln
    1115                1120                1125

Ser Cys  Glu Glu Arg Asn Leu  Arg Glu Asn Gly Tyr  Glu Ala Glu
    1130                1135                1140

Trp Arg  Tyr Asn Ser Cys Ala  Pro Ala Cys Gln Val  Thr Cys Gln
    1145                1150                1155

His Pro  Glu Pro Leu Ala Cys  Pro Val Gln Cys Val  Glu Gly Cys
    1160                1165                1170

His Ala  His Cys Pro Pro Gly  Lys Ile Leu Asp Glu  Leu Leu Gln
    1175                1180                1185

Thr Cys  Val Asp Pro Glu Asp  Cys Pro Val Cys Glu  Val Ala Gly
    1190                1195                1200

Arg Arg  Phe Ala Ser Gly Lys  Lys Val Thr Leu Asn  Pro Ser Asp
    1205                1210                1215

Pro Glu  His Cys Gln Ile Cys  His Cys Asp Val Val  Asn Leu Thr
    1220                1225                1230

Cys Glu  Ala Cys Gln Glu Pro  Ile Ser Gly Gly Gly  Gly Ser Gly
    1235                1240                1245

Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Gly
    1250                1255                1260

Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Gly
    1265                1270                1275

Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Gly
    1280                1285                1290
```

```
Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Gly
    1295                 1300                 1305

Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Leu
    1310                 1315                 1320

Val Pro  Arg Gly Ser Gly Gly  Gly Gly Ser Gly Gly  Gly Gly Ser
    1325                 1330                 1335

Asp Lys  Thr His Thr Cys Pro  Pro Cys Pro Ala Pro  Glu Leu Leu
    1340                 1345                 1350

Gly Gly  Pro Ser Val Phe Leu  Phe Pro Pro Lys Pro  Lys Asp Thr
    1355                 1360                 1365

Leu Met  Ile Ser Arg Thr Pro  Glu Val Thr Cys Val  Val Val Asp
    1370                 1375                 1380

Val Ser  His Glu Asp Pro Glu  Val Lys Phe Asn Trp  Tyr Val Asp
    1385                 1390                 1395

Gly Val  Glu Val His Asn Ala  Lys Thr Lys Pro Arg  Glu Glu Gln
    1400                 1405                 1410

Tyr Asn  Ser Thr Tyr Arg Val  Val Ser Val Leu Thr  Val Leu His
    1415                 1420                 1425

Gln Asp  Trp Leu Asn Gly Lys  Glu Tyr Lys Cys Lys  Val Ser Asn
    1430                 1435                 1440

Lys Ala  Leu Pro Ala Pro Ile  Glu Lys Thr Ile Ser  Lys Ala Lys
    1445                 1450                 1455

Gly Gln  Pro Arg Glu Pro Gln  Val Tyr Thr Leu Pro  Pro Ser Arg
    1460                 1465                 1470

Asp Glu  Leu Thr Lys Asn Gln  Val Ser Leu Thr Cys  Leu Val Lys
    1475                 1480                 1485

Gly Phe  Tyr Pro Ser Asp Ile  Ala Val Glu Trp Glu  Ser Asn Gly
    1490                 1495                 1500

Gln Pro  Glu Asn Asn Tyr Lys  Thr Thr Pro Pro Val  Leu Asp Ser
    1505                 1510                 1515

Asp Gly  Ser Phe Phe Leu Tyr  Ser Lys Leu Thr Val  Asp Lys Ser
    1520                 1525                 1530

Arg Trp  Gln Gln Gly Asn Val  Phe Ser Cys Ser Val  Met His Glu
    1535                 1540                 1545

Ala Leu  His Asn His Tyr Thr  Gln Lys Ser Leu Ser  Leu Ser Pro
    1550                 1555                 1560

Gly Lys
    1565
```

<210> 121

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYN Fc-015 protein sequence

<400> 121

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Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                  10                  15

Gly Ser Thr Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
            20                  25                  30

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        35                  40                  45

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    50                  55                  60

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
65                  70                  75                  80

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
                85                  90                  95

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            100                 105                 110

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
        115                 120                 125

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    130                 135                 140

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
145                 150                 155                 160

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                165                 170                 175

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            180                 185                 190

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        195                 200                 205

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
    210                 215                 220

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
225                 230                 235                 240

Leu Ser Leu Ser Pro Gly Lys
                245
```

<210> 122

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide

<400> 122

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1               5                  10                  15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly
            20                  25                  30

Gly
```

<210> 123

<211> 1240

<212> PRT

<213> Artificial Sequence

<220>

<223> VWF-D1D2D'D3

<400> 123

```
Met Ile Pro Ala Arg Phe Ala Gly Val Leu Leu Ala Leu Ala Leu Ile
1               5                  10                  15

Leu Pro Gly Thr Leu Cys Ala Glu Gly Thr Arg Gly Arg Ser Ser Thr
            20                  25                  30

Ala Arg Cys Ser Leu Phe Gly Ser Asp Phe Val Asn Thr Phe Asp Gly
        35                  40                  45

Ser Met Tyr Ser Phe Ala Gly Tyr Cys Ser Tyr Leu Leu Ala Gly Gly
    50                  55                  60

Cys Gln Lys Arg Ser Phe Ser Ile Ile Gly Asp Phe Gln Asn Gly Lys
65                  70                  75                  80

Arg Val Ser Leu Ser Val Tyr Leu Gly Glu Phe Phe Asp Ile His Leu
                85                  90                  95

Phe Val Asn Gly Thr Val Thr Gln Gly Asp Gln Arg Val Ser Met Pro
            100                 105                 110

Tyr Ala Ser Lys Gly Leu Tyr Leu Glu Thr Glu Ala Gly Tyr Tyr Lys
        115                 120                 125

Leu Ser Gly Glu Ala Tyr Gly Phe Val Ala Arg Ile Asp Gly Ser Gly
    130                 135                 140

Asn Phe Gln Val Leu Leu Ser Asp Arg Tyr Phe Asn Lys Thr Cys Gly
145                 150                 155                 160

Leu Cys Gly Asn Phe Asn Ile Phe Ala Glu Asp Asp Phe Met Thr Gln
                165                 170                 175

Glu Gly Thr Leu Thr Ser Asp Pro Tyr Asp Phe Ala Asn Ser Trp Ala
            180                 185                 190

Leu Ser Ser Gly Glu Gln Trp Cys Glu Arg Ala Ser Pro Pro Ser Ser
        195                 200                 205

Ser Cys Asn Ile Ser Ser Gly Glu Met Gln Lys Gly Leu Trp Glu Gln
    210                 215                 220

Cys Gln Leu Leu Lys Ser Thr Ser Val Phe Ala Arg Cys His Pro Leu
225                 230                 235                 240

Val Asp Pro Glu Pro Phe Val Ala Leu Cys Glu Lys Thr Leu Cys Glu
                245                 250                 255

Cys Ala Gly Gly Leu Glu Cys Ala Cys Pro Ala Leu Leu Glu Tyr Ala
            260                 265                 270

Arg Thr Cys Ala Gln Glu Gly Met Val Leu Tyr Gly Trp Thr Asp His
        275                 280                 285

Ser Ala Cys Ser Pro Val Cys Pro Ala Gly Met Glu Tyr Arg Gln Cys
    290                 295                 300

Val Ser Pro Cys Ala Arg Thr Cys Gln Ser Leu His Ile Asn Glu Met
305                 310                 315                 320
```

```
Cys Gln Glu Arg Cys Val Asp Gly Cys Ser Cys Pro Glu Gly Gln Leu
                325                 330                 335

Leu Asp Glu Gly Leu Cys Val Glu Ser Thr Glu Cys Pro Cys Val His
            340                 345                 350

Ser Gly Lys Arg Tyr Pro Pro Gly Thr Ser Leu Ser Arg Asp Cys Asn
        355                 360                 365

Thr Cys Ile Cys Arg Asn Ser Gln Trp Ile Cys Ser Asn Glu Glu Cys
    370                 375                 380

Pro Gly Glu Cys Leu Val Thr Gly Gln Ser His Phe Lys Ser Phe Asp
385                 390                 395                 400

Asn Arg Tyr Phe Thr Phe Ser Gly Ile Cys Gln Tyr Leu Leu Ala Arg
                405                 410                 415

Asp Cys Gln Asp His Ser Phe Ser Ile Val Ile Glu Thr Val Gln Cys
            420                 425                 430

Ala Asp Asp Arg Asp Ala Val Cys Thr Arg Ser Val Thr Val Arg Leu
        435                 440                 445

Pro Gly Leu His Asn Ser Leu Val Lys Leu Lys His Gly Ala Gly Val
    450                 455                 460

Ala Met Asp Gly Gln Asp Ile Gln Leu Pro Leu Leu Lys Gly Asp Leu
465                 470                 475                 480

Arg Ile Gln His Thr Val Thr Ala Ser Val Arg Leu Ser Tyr Gly Glu
                485                 490                 495

Asp Leu Gln Met Asp Trp Asp Gly Arg Gly Arg Leu Leu Val Lys Leu

            500                 505                 510

Ser Pro Val Tyr Ala Gly Lys Thr Cys Gly Leu Cys Gly Asn Tyr Asn
        515                 520                 525

Gly Asn Gln Gly Asp Asp Phe Leu Thr Pro Ser Gly Leu Ala Glu Pro
    530                 535                 540

Arg Val Glu Asp Phe Gly Asn Ala Trp Lys Leu His Gly Asp Cys Gln
545                 550                 555                 560

Asp Leu Gln Lys Gln His Ser Asp Pro Cys Ala Leu Asn Pro Arg Met
                565                 570                 575

Thr Arg Phe Ser Glu Glu Ala Cys Ala Val Leu Thr Ser Pro Thr Phe
            580                 585                 590

Glu Ala Cys His Arg Ala Val Ser Pro Leu Pro Tyr Leu Arg Asn Cys
        595                 600                 605

Arg Tyr Asp Val Cys Ser Cys Ser Asp Gly Arg Glu Cys Leu Cys Gly
    610                 615                 620

Ala Leu Ala Ser Tyr Ala Ala Ala Cys Ala Gly Arg Gly Val Arg Val
625                 630                 635                 640

Ala Trp Arg Glu Pro Gly Arg Cys Glu Leu Asn Cys Pro Lys Gly Gln
                645                 650                 655

Val Tyr Leu Gln Cys Gly Thr Pro Cys Asn Leu Thr Cys Arg Ser Leu
            660                 665                 670
```

```
Ser Tyr Pro Asp Glu Glu Cys Asn Glu Ala Cys Leu Glu Gly Cys Phe
        675                 680                 685

Cys Pro Pro Gly Leu Tyr Met Asp Glu Arg Gly Asp Cys Val Pro Lys
    690                 695                 700

Ala Gln Cys Pro Cys Tyr Tyr Asp Gly Glu Ile Phe Gln Pro Glu Asp
705                 710                 715                 720

Ile Phe Ser Asp His His Thr Met Cys Tyr Cys Glu Asp Gly Phe Met
                725                 730                 735

His Cys Thr Met Ser Gly Val Pro Gly Ser Leu Leu Pro Asp Ala Val
            740                 745                 750

Leu Ser Ser Pro Leu Ser His Arg Ser Lys Arg Ser Leu Ser Cys Arg
        755                 760                 765

Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp Asn Leu Arg Ala Glu
    770                 775                 780

Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr Asp Leu Glu Cys Met
785                 790                 795                 800

Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro Pro Gly Met Val Arg
                805                 810                 815

His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys Pro Cys Phe His Gln
            820                 825                 830

Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys Ile Gly Cys Asn Thr
        835                 840                 845

Cys Val Cys Arg Asp Arg Lys Trp Asn Cys Thr Asp His Val Cys Asp
    850                 855                 860

Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr Leu Thr Phe Asp Gly
865                 870                 875                 880

Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr Val Leu Val Gln Asp
                885                 890                 895

Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile Leu Val Gly Asn Lys
            900                 905                 910

Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys Arg Val Thr Ile Leu
        915                 920                 925

Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly Glu Val Asn Val Lys
    930                 935                 940

Arg Pro Met Lys Asp Glu Thr His Phe Glu Val Val Glu Ser Gly Arg
945                 950                 955                 960

Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser Val Val Trp Asp Arg
                965                 970                 975

His Leu Ser Ile Ser Val Val Leu Lys Gln Thr Tyr Gln Glu Lys Val
            980                 985                 990

Cys Gly Leu Cys Gly Asn Phe Asp  Gly Ile Gln Asn Asn  Asp Leu Thr
        995                 1000                1005

Ser Ser  Asn Leu Gln Val Glu  Glu Asp Pro Val Asp  Phe Gly Asn
    1010                1015                1020

Ser Trp  Lys Val Ser Ser Gln  Cys Ala Asp Thr Arg  Lys Val Pro
    1025                1030                1035
```

```
Leu Asp  Ser Ser Pro Ala Thr  Cys His Asn Asn Ile  Met Lys Gln
    1040                 1045                 1050

Thr Met  Val Asp Ser Ser Cys  Arg Ile Leu Thr Ser  Asp Val Phe
    1055                 1060                 1065

Gln Asp  Cys Asn Lys Leu Val  Asp Pro Glu Pro Tyr  Leu Asp Val
    1070                 1075                 1080

Cys Ile  Tyr Asp Thr Cys Ser  Cys Glu Ser Ile Gly  Asp Cys Ala
    1085                 1090                 1095

Cys Phe  Cys Asp Thr Ile Ala  Ala Tyr Ala His Val  Cys Ala Gln
    1100                 1105                 1110

His Gly  Lys Val Val Thr Trp  Arg Thr Ala Thr Leu  Cys Pro Gln
    1115                 1120                 1125

Ser Cys  Glu Glu Arg Asn Leu  Arg Glu Asn Gly Tyr  Glu Cys Glu
    1130                 1135                 1140

Trp Arg  Tyr Asn Ser Cys Ala  Pro Ala Cys Gln Val  Thr Cys Gln
    1145                 1150                 1155

His Pro  Glu Pro Leu Ala Cys  Pro Val Gln Cys Val  Glu Gly Cys
    1160                 1165                 1170

His Ala  His Cys Pro Pro Gly  Lys Ile Leu Asp Glu  Leu Leu Gln
    1175                 1180                 1185

Thr Cys  Val Asp Pro Glu Asp  Cys Pro Val Cys Glu  Val Ala Gly
    1190                 1195                 1200

Arg Arg  Phe Ala Ser Gly Lys  Lys Val Thr Leu Asn  Pro Ser Asp
    1205                 1210                 1215

Pro Glu  His Cys Gln Ile Cys  His Cys Asp Val Val  Asn Leu Thr
    1220                 1225                 1230

Cys Glu  Ala Cys Gln Glu Pro
    1235                 1240
```

<210> 124

<211> 477

<212> PRT

<213> Artificial Sequence

<220>

<223> VWF-D'D3

<400> 124

```
Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp
1               5                  10                  15

Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr
            20                  25                  30

Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro
        35                  40                  45

Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys
    50                  55                  60

Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys
65                  70                  75                  80
```

```
Ile Gly Cys Asn Thr Cys Val Cys Arg Asp Arg Lys Trp Asn Cys Thr
                85                  90                  95

Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr
            100                 105                 110

Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr
        115                 120                 125

Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile
    130                 135                 140

Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys
145                 150                 155                 160

Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly
                165                 170                 175

Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val
            180                 185                 190

Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser
        195                 200                 205

Val Val Trp Asp Arg His Leu Ser Ile Ser Val Val Leu Lys Gln Thr
    210                 215                 220

Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln
225                 230                 235                 240

Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val
                245                 250                 255

Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg
            260                 265                 270

Lys Val Pro Leu Asp Ser Ser Pro Ala Thr Cys His Asn Asn Ile Met
        275                 280                 285

Lys Gln Thr Met Val Asp Ser Ser Cys Arg Ile Leu Thr Ser Asp Val
    290                 295                 300

Phe Gln Asp Cys Asn Lys Leu Val Asp Pro Glu Pro Tyr Leu Asp Val
305                 310                 315                 320

Cys Ile Tyr Asp Thr Cys Ser Cys Glu Ser Ile Gly Asp Cys Ala Cys
                325                 330                 335

Phe Cys Asp Thr Ile Ala Ala Tyr Ala His Val Cys Ala Gln His Gly
            340                 345                 350

Lys Val Val Thr Trp Arg Thr Ala Thr Leu Cys Pro Gln Ser Cys Glu
        355                 360                 365

Glu Arg Asn Leu Arg Glu Asn Gly Tyr Glu Cys Glu Trp Arg Tyr Asn
    370                 375                 380

Ser Cys Ala Pro Ala Cys Gln Val Thr Cys Gln His Pro Glu Pro Leu
385                 390                 395                 400

Ala Cys Pro Val Gln Cys Val Glu Gly Cys His Ala His Cys Pro Pro
                405                 410                 415

Gly Lys Ile Leu Asp Glu Leu Leu Gln Thr Cys Val Asp Pro Glu Asp
            420                 425                 430

Cys Pro Val Cys Glu Val Ala Gly Arg Arg Phe Ala Ser Gly Lys Lys
        435                 440                 445
```

```
Val Thr Leu Asn Pro Ser Asp Pro Glu His Cys Gln Ile Cys His Cys
    450                 455                 460

Asp Val Val Asn Leu Thr Cys Glu Ala Cys Gln Glu Pro
465                 470                 475
```

<210> 125
<211> 5055
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYNFVIII 010

<400> 125

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atgcaaatag agctctccac ctgcttcttt ctgtgccttt tgcgattctg ctttagtgcc       60
accagaagat actacctggg tgcagtggaa ctgtcatggg actatatgca aagtgatctc      120
ggtgagctgc ctgtggacgc aagatttcct cctagagtgc caaaatcttt tccattcaac      180
acctcagtcg tgtacaaaaa gactctgttt gtagaattca cggatcacct tttcaacatc      240
gctaagccaa ggccaccctg gatgggtctg ctaggtccta ccatccaggc tgaggtttat      300
gatacagtgg tcattacact taagaacatg gcttcccatc ctgtcagtct tcatgctgtt      360
ggtgtatcct actggaaagc ttctgaggga gctgaatatg atgatcagac cagtcaaagg      420
gagaaagaag atgataaagt cttccctggt ggaagccata catatgtctg gcaggtcctg      480
aaagagaatg gtccaatggc ctctgaccca ctgtgcctta cctactcata tctttctcat      540
gtggacctgg taaaagactt gaattcaggc ctcattggag ccctactagt atgtagagaa      600
gggagtctgg ccaaggaaaa gacacagacc ttgcacaaat ttatactact ttttgctgta      660
tttgatgaag ggaaaagttg gcactcagaa acaaagaact ccttgatgca ggatagggat      720
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ctgccaggtc tgattggatg ccacaggaaa tcagtctatt ggcatgtgat tggaatgggc      840
accactcctg aagtgcactc aatattcctc gaaggtcaca catttcttgt gaggaaccat      900
cgccaggcgt ccttggaaat ctcgccaata actttcctta ctgctcaaac actcttgatg      960
gaccttggac agtttctact gttttgtcat atctcttccc accaacatga tggcatggaa     1020
gcttatgtca aagtagacag ctgtccagag gaaccccaac tacgaatgaa aaataatgaa     1080
gaagcggaag actatgatga tgatcttact gattctgaaa tggatgtggt caggtttgat     1140
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tgggtacatt acattgctgc tgaagaggag gactgggact atgctccctt agtcctcgcc     1260
cccgatgaca gaagttataa aagtcaatat ttgaacaatg gccctcagcg gattggtagg     1320
aagtacaaaa aagtccgatt tatggcatac acagatgaaa cctttaagac tcgtgaagct     1380
attcagcatg aatcaggaat cttgggacct ttactttatg gggaagttgg agacacactg     1440

ttgattatat ttaagaatca agcaagcaga ccatataaca tctaccctca cggaatcact     1500
gatgtccgtc ctttgtattc aaggagatta ccaaaaggtg taaaacattt gaaggatttt     1560
ccaattctgc caggagaaat attcaaatat aaatggacag tgactgtaga agatgggcca     1620
actaaatcag atcctcggtg cctgacccgc tattactcta gtttcgttaa tatggagaga     1680
gatctagctt caggactcat tggccctctc ctcatctgct acaaagaatc tgtagatcaa     1740
agaggaaacc agataatgtc agacaagagg aatgtcatcc tgttttctgt atttgatgag     1800
aaccgaagct ggtacctcac agagaatata caacgctttc tccccaatcc agctggagtg     1860
cagcttgagg atccagagtt ccaagcctcc aacatcatgc acagcatcaa tggctatgtt     1920
tttgatagtt tgcagttgtc agtttgtttg catgaggtgg catactggta cattctaagc     1980
attggagcac agactgactt cctttctgtc ttcttctctg gatatacctt caaacacaaa     2040
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atggtctatg aagacacact caccctattc ccattctcag gagaaactgt cttcatgtcg 2100

atggaaaacc caggtctatg gattctgggg tgccacaact cagactttcg gaacagaggc 2160

atgaccgcct tactgaaggt ttctagttgt gacaagaaca ctggtgatta ttacgaggac 2220

agttatgaag atatttcagc atacttgctg agtaaaaaca atgccattga accaagaagc 2280

ttctctcaaa acccaccagt cttgaaacgc catcaacggg aaataactcg tactactctt 2340

cagtcagatc aagaggaaat tgactatgat gataccatat cagttgaaat gaagaaggaa 2400

gattttgaca tttatgatga ggatgaaaat cagagccccc gcagctttca aaagaaaaca 2460

cgacactatt ttattgctgc agtggagagg ctctgggatt atgggatgag tagctcccca 2520

catgttctaa gaaacagggc tcagagtggc agtgtccctc agttcaagaa agttgttttc 2580

caggaattta ctgatggctc ctttactcag cccttatacc gtggagaact aaatgaacat 2640

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tttgctctgt ttttcaccat ctttgatgag accaaaagct ggtacttcac tgaaaatatg 3060

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caggatcaaa ggattcgatg gtatctgctc agcatgggca gcaatgaaaa catccattct 3240

attcatttca gtggacatgt gttcactgta cgaaaaaaag aggagtataa aatggcactg 3300

tacaatctct atccaggtgt ttttgagaca gtggaaatgt taccatccaa agctggaatt 3360

tggcgggtgg aatgccttat tggcgagcat ctacatgctg ggatgagcac acttttctg 3420

gtgtacagca ataagtgtca gactcccctg ggaatggctt ctggacacat tagagatttt 3480

cagattacag cttcaggaca atatggacag tgggccccaa agctggccag acttcattat 3540

tccggatcaa tcaatgcctg gagcaccaag gagccctttt cttggatcaa ggtggatctg 3600

ttggcaccaa tgattattca cggcatcaag acccagggtg cccgtcagaa gttctccagc 3660

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agtaatgcct ggagacctca ggtgaataat ccaaaagagt ggctgcaagt ggacttccag 4080

aagacaatga aagtcacagg agtaactact cagggagtaa aatctctgct taccagcatg 4140

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cagaatggca aagtaaaggt ttttcaggga aatcaagact ccttcacacc tgtggtgaac 4260

tctctagacc caccgttact gactcgctac cttcgaattc acccccagag ttgggtgcac 4320

cagattgccc tgaggatgga ggttctgggc tgcgaggcac aggacctcta cgacaaaact 4380

cacacatgcc caccgtgccc agctccagaa ctcctgggcg gaccgtcagt cttcctcttc 4440

cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 4500

gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 4560

gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 4620

agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 4680

tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 4740

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cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc     4800

agcctgacct gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc     4860

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgttggactc cgacggctcc     4920

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc     4980

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<210> 126

<211> 1684

<212> PRT

<213> Artificial Sequence

<220>

<223> pSYNFVIII 010

<400> 126

```
Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1               5                  10                  15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
        35                  40                  45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
    50                  55                  60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65                  70                  75                  80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
                85                  90                  95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
            100                 105                 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
        115                 120                 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
    130                 135                 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145                 150                 155                 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
                165                 170                 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
            180                 185                 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
        195                 200                 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
    210                 215                 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225                 230                 235                 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
                245                 250                 255
```

```
Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
            260                 265                 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
        275                 280                 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
    290                 295                 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305                 310                 315                 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
                325                 330                 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
            340                 345                 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
        355                 360                 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
    370                 375                 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385                 390                 395                 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
                405                 410                 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
            420                 425                 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
        435                 440                 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
    450                 455                 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465                 470                 475                 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
                485                 490                 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
            500                 505                 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
        515                 520                 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
    530                 535                 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545                 550                 555                 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
                565                 570                 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
            580                 585                 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
        595                 600                 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
    610                 615                 620
```

```
Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625                 630                 635                 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
                645                 650                 655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
            660                 665                 670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
        675                 680                 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
    690                 695                 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705                 710                 715                 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
                725                 730                 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
            740                 745                 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu
        755                 760                 765

Lys Arg His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln
    770                 775                 780

Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu
785                 790                 795                 800

Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe
                805                 810                 815

Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp
            820                 825                 830

Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln
        835                 840                 845

Ser Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr
    850                 855                 860

Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His
865                 870                 875                 880

Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile
                885                 890                 895

Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser
            900                 905                 910

Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg
        915                 920                 925

Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
    930                 935                 940

Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp
945                 950                 955                 960

Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu
                965                 970                 975

Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His
```

```
                                                
```

```
Met Phe  Ala Thr Trp Ser Pro  Ser Lys Ala Arg Leu  His Leu Gln
    1325                 1330                 1335

Gly Arg  Ser Asn Ala Trp Arg  Pro Gln Val Asn Asn  Pro Lys Glu
    1340                 1345                 1350

Trp Leu  Gln Val Asp Phe Gln  Lys Thr Met Lys Val  Thr Gly Val
    1355                 1360                 1365

Thr Thr  Gln Gly Val Lys Ser  Leu Leu Thr Ser Met  Tyr Val Lys
    1370                 1375                 1380

Glu Phe  Leu Ile Ser Ser Ser  Gln Asp Gly His Gln  Trp Thr Leu
    1385                 1390                 1395

Phe Phe  Gln Asn Gly Lys Val  Lys Val Phe Gln Gly  Asn Gln Asp
    1400                 1405                 1410

Ser Phe  Thr Pro Val Val Asn  Ser Leu Asp Pro Pro  Leu Leu Thr
    1415                 1420                 1425

Arg Tyr  Leu Arg Ile His Pro  Gln Ser Trp Val His  Gln Ile Ala
    1430                 1435                 1440

Leu Arg  Met Glu Val Leu Gly  Cys Glu Ala Gln Asp  Leu Tyr Asp
    1445                 1450                 1455

Lys Thr  His Thr Cys Pro Pro  Cys Pro Ala Pro Glu  Leu Leu Gly
    1460                 1465                 1470

Gly Pro  Ser Val Phe Leu Phe  Pro Pro Lys Pro Lys  Asp Thr Leu
    1475                 1480                 1485

Met Ile  Ser Arg Thr Pro Glu  Val Thr Cys Val Val  Val Asp Val
    1490                 1495                 1500

Ser His  Glu Asp Pro Glu Val  Lys Phe Asn Trp Tyr  Val Asp Gly
    1505                 1510                 1515

Val Glu  Val His Asn Ala Lys  Thr Lys Pro Arg Glu  Glu Gln Tyr
    1520                 1525                 1530

Asn Ser  Thr Tyr Arg Val Val  Ser Val Leu Thr Val  Leu His Gln
    1535                 1540                 1545

Asp Trp  Leu Asn Gly Lys Glu  Tyr Lys Cys Lys Val  Ser Asn Lys
    1550                 1555                 1560

Ala Leu  Pro Ala Pro Ile Glu  Lys Thr Ile Ser Lys  Ala Lys Gly
    1565                 1570                 1575

Gln Pro  Arg Glu Pro Gln Val  Tyr Thr Leu Pro Pro  Ser Arg Asp
    1580                 1585                 1590

Glu Leu  Thr Lys Asn Gln Val  Ser Leu Thr Cys Leu  Val Lys Gly
    1595                 1600                 1605

Phe Tyr  Pro Ser Asp Ile Ala  Val Glu Trp Glu Ser  Asn Gly Gln
    1610                 1615                 1620

Pro Glu  Asn Asn Tyr Lys Thr  Thr Pro Pro Val Leu  Asp Ser Asp
    1625                 1630                 1635

Gly Ser  Phe Phe Leu Tyr Ser  Lys Leu Thr Val Asp  Lys Ser Arg
    1640                 1645                 1650

Trp Gln  Gln Gly Asn Val Phe  Ser Cys Ser Val Met  His Glu Ala
```

```
    1655                1660                1665

Leu His  Asn His Tyr Thr Gln  Lys Ser Leu Ser Leu  Ser Pro Gly
    1670                1675                1680

Lys
```

<210> 127

<211> 78

<212> PRT

<213> Artificial Sequence

<220>

<223> AE72 XTEN

<400> 127

```
Gly Ala Pro Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser
1               5                   10                  15

Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala
            20                  25                  30

Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu
        35                  40                  45

Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr
    50                  55                  60

Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ala Ser Ser
65                  70                  75
```

<210> 128

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AE144_2A

<400> 128

```
Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly
1               5                   10                  15

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly
            20                  25                  30

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
        35                  40                  45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
    50                  55                  60

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
65                  70                  75                  80

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly

                85                  90                  95

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
            100                 105                 110

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
        115                 120                 125
```

```
Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
    130                 135                 140
```

<210> 129

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AE144_3B

<400> 129

```
Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
1               5                   10                  15

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
            20                  25                  30

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
        35                  40                  45

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
    50                  55                  60

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
65                  70                  75                  80

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
                85                  90                  95

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
            100                 105                 110

Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
        115                 120                 125

Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
    130                 135                 140
```

<210> 130

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AE144_4A

<400> 130

```
Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
1               5                   10                  15

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
            20                  25                  30

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
        35                  40                  45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
    50                  55                  60

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
65                  70                  75                  80

Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
```

```
                85                  90                  95

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly
            100                 105                 110

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu
        115                 120                 125

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
    130                 135                 140
```

<210> 131

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AE144_5A

<400> 131

```
Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
1               5                   10                  15

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
            20                  25                  30

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly

        35                  40                  45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
    50                  55                  60

Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
65                  70                  75                  80

Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
                85                  90                  95

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser
            100                 105                 110

Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
        115                 120                 125

Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
    130                 135                 140
```

<210> 132

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AE144_6B

<400> 132

```
Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser
1               5                   10                  15

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
            20                  25                  30

Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
        35                  40                  45
```

```
Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala
    50                  55                  60

Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
65                  70                  75                  80

Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
                85                  90                  95

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro Ala
            100                 105                 110

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
        115                 120                 125

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
    130                 135                 140
```

<210> 133

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AG144_A

<400> 133

```
Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Pro
1               5                   10                  15

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
            20                  25                  30

Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
        35                  40                  45

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
    50                  55                  60

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
65                  70                  75                  80

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
                85                  90                  95

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly
            100                 105                 110

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
        115                 120                 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
    130                 135                 140
```

<210> 134

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AG144_B

<400> 134

```
Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
```

```
1               5                   10                  15

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
            20                  25                  30

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
        35                  40                  45

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
    50                  55                  60

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
65                  70                  75                  80

Gly Thr Gly Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
                85                  90                  95

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro
            100                 105                 110

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
        115                 120                 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
    130                 135                 140
```

<210> 135

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AG144_C

<400> 135

```
Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro
1               5                   10                  15

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
            20                  25                  30

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
        35                  40                  45

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly
    50                  55                  60

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
65                  70                  75                  80

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
                85                  90                  95

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr
            100                 105                 110

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
        115                 120                 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
    130                 135                 140
```

<210> 136

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AG144_F

<400> 136

```
Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro
1               5                  10                  15

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
            20                  25                  30

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
        35                  40                  45

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
    50                  55                  60

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
65                  70                  75                  80

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
                85                  90                  95

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
            100                 105                 110

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
        115                 120                 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
    130                 135                 140
```

<210> 137

<211> 288

<212> PRT

<213> Artificial Sequence

<220>

<223> AE288_2

<400> 137

```
Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
1               5                  10                  15

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
            20                  25                  30

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
        35                  40                  45

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
    50                  55                  60

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu
65                  70                  75                  80

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
                85                  90                  95

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
            100                 105                 110

Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr
        115                 120                 125
```

```
Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
    130                 135                 140

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
145                 150                 155                 160

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
                165                 170                 175

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
            180                 185                 190

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
        195                 200                 205

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
    210                 215                 220

Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
225                 230                 235                 240

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala
                245                 250                 255

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro
            260                 265                 270

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
        275                 280                 285
```

<210> 138

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 138

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1               5                   10                  15

Gly Gly Gly Ser
            20
```

<210> 139

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<220>

<221> REPEAT

<222> (1)..(5)

<223> May be repeated 1 to 10 times

<400> 139

```
Gly Gly Gly Gly Ser
1               5
```

<210> 140

<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<220>
<221> REPEAT
<222> (2)..(6)
<223> May be repeated 1 to 10 times

<400> 140
Ser Gly Gly Gly Gly Ser
1 5

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Patentkrav

1. Kimært protein, der omfatter (i) et fragment af von Willebrand-faktor (VWF), der omfatter D'-domænet og D3-domænet af VWF, (ii) en sekvens af et ekstenderet-længde-polypeptid (XTEN), (iii) et faktor VIII (FVIII)-protein, (iv) en første konstant Ig-region eller en del deraf og (v) en anden konstant Ig-region eller en del deraf,
hvor VWF-fragmentet og XTEN-sekvensen er koblet ved hjælp af en eventuel linker, hvor XTEN-sekvensen eller VWF-fragmentet er koblet til den første konstante Ig-region eller en del deraf,
hvor FVIII-proteinet er koblet til den anden konstante Ig-region eller en del deraf,
og hvor den første konstante Ig-region eller en del deraf er forbundet med eller koblet til den anden konstante Ig-region eller en del deraf ved hjælp af en kovalent binding.

2. Kimært protein ifølge krav 1, som omfatter (i) en enkelt polypeptidkæde, der omfatter VWF-fragmentet, XTEN-sekvensen, den første konstante Ig-region eller en del deraf, den anden konstante Ig-region eller en del deraf og FVIII-proteinet, eller (ii) en første polypeptidkæde og en anden polypeptidkæde, hvor den første polypeptidkæde omfatter VWF-fragmentet, XTEN-sekvensen og den første konstante Ig-region eller en del deraf, og den anden polypeptidkæde omfatter FVIII-proteinet og den anden konstante Ig-region eller en del deraf.

3. Kimært protein ifølge krav 1, der omfatter formlen:

(a) V-L2-X-L1-F1:FVIII-L3-F2;
(b) V-L2-X-L1-F1:F2-L3-FVIII;
(c) F1-L1-X-L2-V:FVIII-L3-F2;
(d) F1-L1-X-L2-V:F2-L3-FVIII;
(e) V-L2-X-L1-F1-L4-FVIII-L3-F2;
(f) F2-L3-FVIII-L4-F1-L1-X-L2-V;
(g) FVIII-L3-F2-L4-V-L2-X-L1-F1; eller
(h) F1-L1-X-L2-V-L4-F2-L3-FVIII;

hvor V er VWF-fragmentet;
hver af L1, L2 og L3 er en eventuel linker;
L4 er en eventuel linker;
FVIII er FVIII-proteinet;
X er XTEN-sekvensen;
F1 er den første konstante immunoglobulin (Ig)-region eller en del deraf;
F2 er den anden konstante Ig-region eller en del deraf;
(-) er en peptidbinding; og
(:) er en kovalent binding.

4. Kimært protein ifølge krav 1, der omfatter formlen:
(a) FVIII(X1)-L1-F1:V-L2-X2-L3-F2;
(b) FVIII(X1)-L1-F1:F2-L3-X2-L2-V;
(c) F1-L1-FVIII(X1):V-L2-X2-L3-F2;
(d) F1-L1-FVIII(X1):F2-L3-X2-L2-V;
(e) FVIII(X1)-L1-F1-L4-V-L2-X2-L3-F2;
(f) FVIII(X1)-L1-F1-L4-F2-L3-X2-L2-V;
(g) F1-L1-FVIII(X1)-L4-V-L2-X2-L3-F2; eller
(h) F1-L1-FVIII(X1)-L4-F2-L3-X2-L2-V;
hvor FVIII(X1) omfatter FVIII-proteinet og XTEN-sekvensen, hvor XTEN-sekvensen er koblet til N-terminalen eller C-terminalen af FVIII-proteinet eller indsat umiddelbart nedstrøms for en eller flere aminosyrer ("et eller flere insertionssteder") i FVIII-proteinet;
hver af L1, L2 eller L3 er en eventuel linker;
L4 er en linker;
X2 er en anden XTEN-sekvens;
F1 er den første konstante Ig-region eller en del deraf;
F2 er den anden konstante Ig-region eller en del deraf;
V er VWF-fragmentet;
(-) er en peptidbinding; og
(:) er en kovalent binding.

5. Kimært protein ifølge et hvilket som helst af kravene 1 til 4, hvor
(a) den første konstante Ig-region eller en del deraf er en første Fc-region;

(b) den anden konstante Ig-region eller en del deraf er en anden Fc-region; eller
(c) både (a) og (b).

6. Kimært protein ifølge krav 4 eller 5, hvor det ene eller de flere insertionssteder i FVIII-proteinet er valgt fra gruppen, der består af aminosyreresterne i tabel 7, tabel 8, tabel 9 og tabel 10.

7. Kimært protein ifølge et hvilket som helst af kravene 1 til 6, hvor FVIII-proteinet omfatter B-domænet eller en del deraf eller ikke omfatter B-domænet.

8. Kimært protein ifølge et hvilket som helst af kravene 1 til 7, hvor det kimære protein omfatter mindst to XTEN, mindst tre XTEN, mindst fire XTEN, mindst fem XTEN eller mindst seks XTEN.

9. Kimært protein ifølge et hvilket som helst af kravene 1 til 8, hvor FVIII-proteinet er enkeltkædet FVIII.

10. Polynukleotid eller et sæt af polynukleotider, der koder for det kimære protein ifølge et hvilket som helst af kravene 1 til 9.

11. Vektor, der omfatter polynukleotidet eller sættet af polynukleotider ifølge krav 10 og en eller flere promotorer, der er operabelt koblet til polynukleotidet eller sættet af polynukleotider.

12. Værtscelle, der omfatter polynukleotidet eller sættet af polynukleotider ifølge krav 10 eller vektoren ifølge krav 11.

13. Farmaceutisk sammensætning, der omfatter det kimære protein ifølge et hvilket som helst af kravene 1 til 9, polynukleotidet eller sættet af polynukleotider ifølge krav 10, vektoren ifølge krav 11 eller værtscellen ifølge krav 12 og et farmaceutisk acceptabelt bæremateriale.

14. Kimært protein ifølge et hvilket som helst af kravene 1 til 9, polynukleotid ifølge krav 10, vektor ifølge krav 11, værtscelle ifølge krav 12 eller sammensætning ifølge krav 13 til anvendelse til behandling af en blødningssygdom eller -forstyrrelse hos et individ, der har brug for det.

15. Fremgangsmåde til fremstilling af et kimært protein, som omfatter transfektion af en eller flere værtsceller med polynukleotidet eller sættet af polynukleotider ifølge krav 10 eller vektoren ifølge krav 11 og ekspression af det kimære protein i værtscellen.

DRAWINGS

Figure 1: Different VWF Constructs

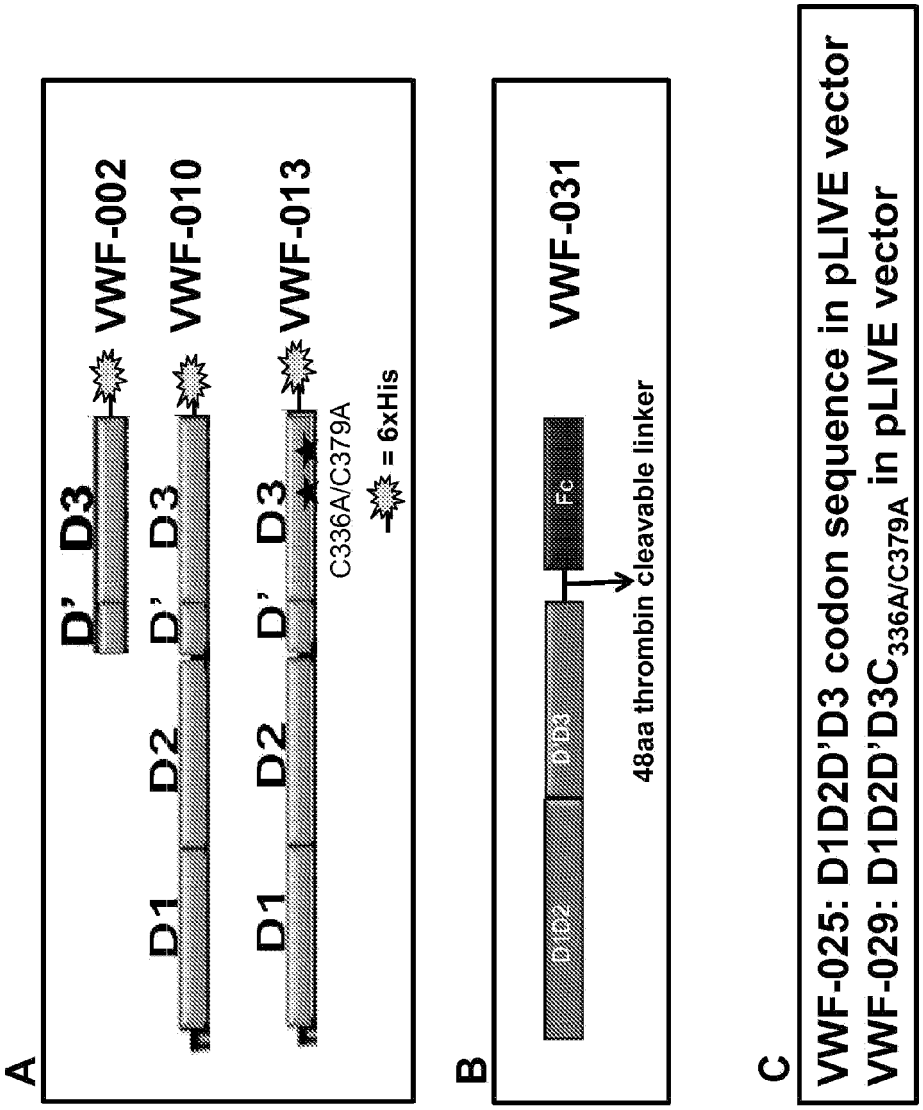
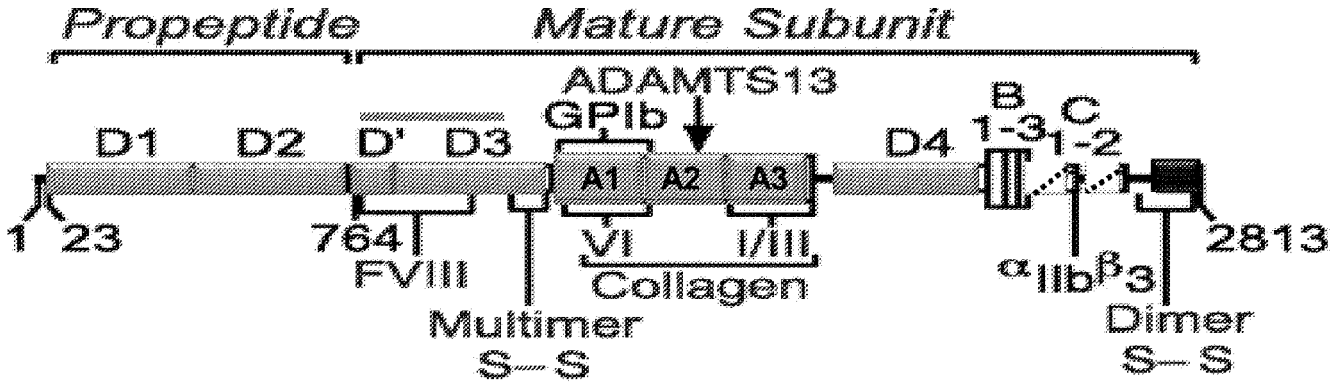


Figure 1D. Von Willebrand Factor



- ~ 250 kDa protein, forms multimers (> 20 MDa) by disulfide bonding

- Associates with FVIII (95-98%) in non-covalent complex
  - Protects FVIII from protease cleavage/activation
  - Stabilizes heavy & light chain
  - Prevents clearance of FVIII by scavenger receptors

  } **Extends half-life**

  - Clearance of FVIII-vWF complex through vWF-receptors
  - Prevents pinocytosis and recycling of rFVIIIFc?

  } **Limits half-life**

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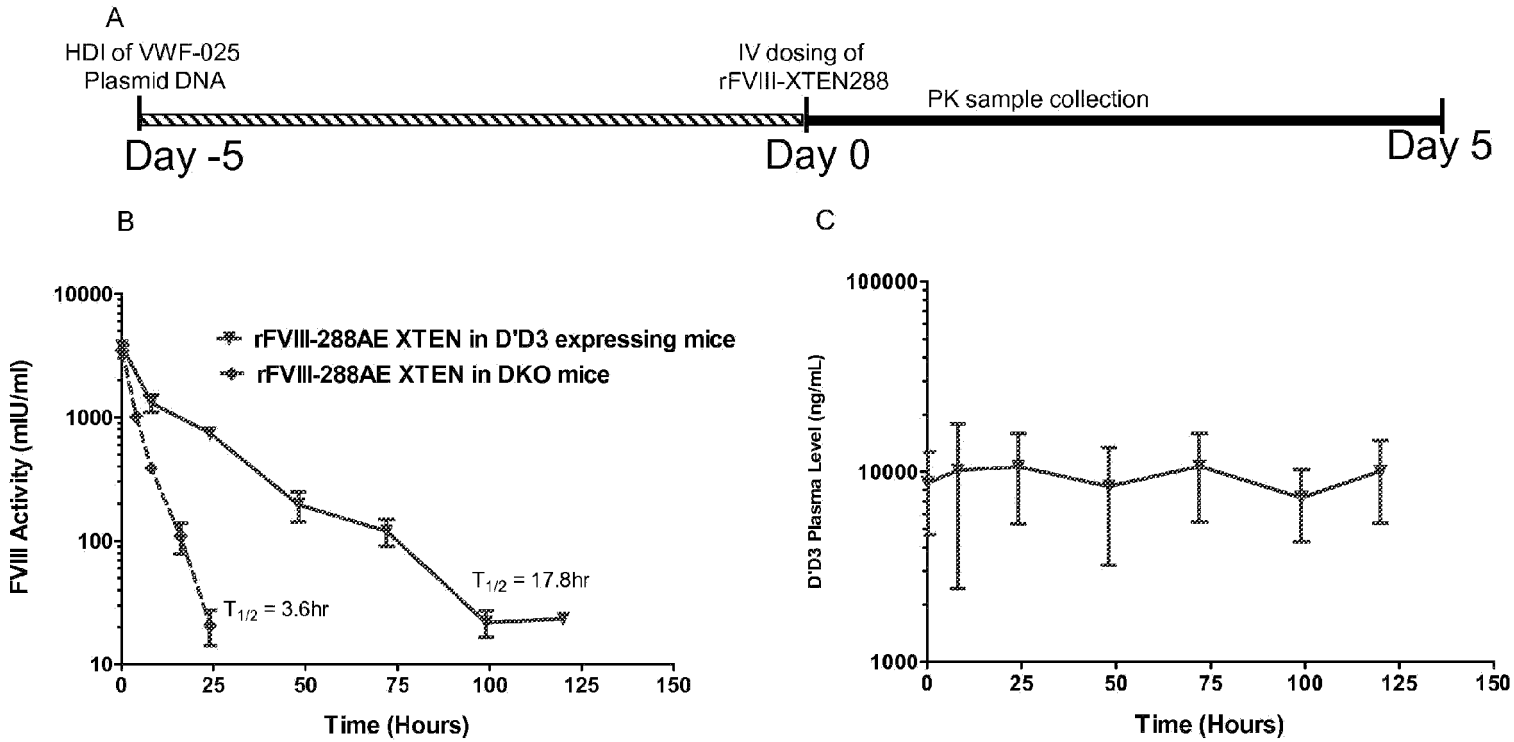
Figure 2: rFVIII-XTEN PK in VWF D'D3 Expressing Mice



5 fold additional half-life extension of FVIII-XTEN from VWF D'D3 fragment

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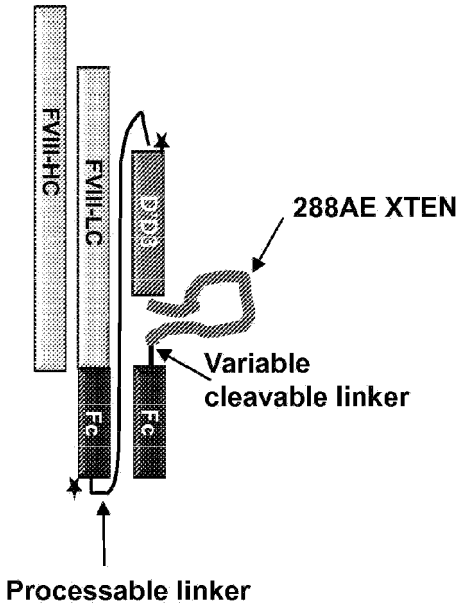
Figure 3: FVIIIFC/VWF heterodimer Constructs (variable linker)



DNA construct	Linker between VWF and Fc
FVIII-161	288AE XTEN + IS{5X(GGGGS)}LVPRGSGG
D'D3= 1-477aa with C336A/C379A)	

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Figure 4: FVIII/VWF Constructs with XTEN insertions

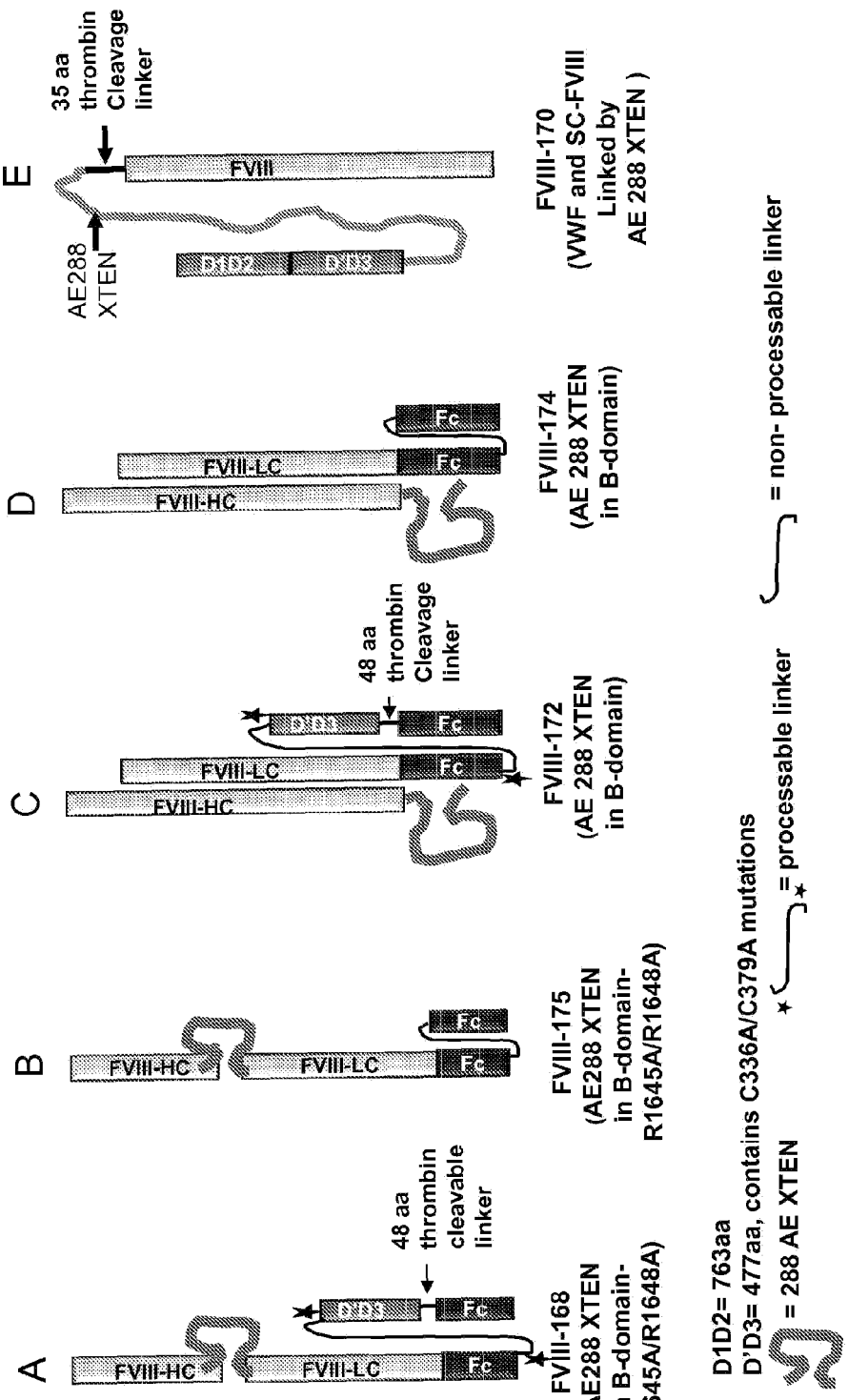

Figure 5: XTEN insertion improves the PK of FVIII/VWF heterodimers

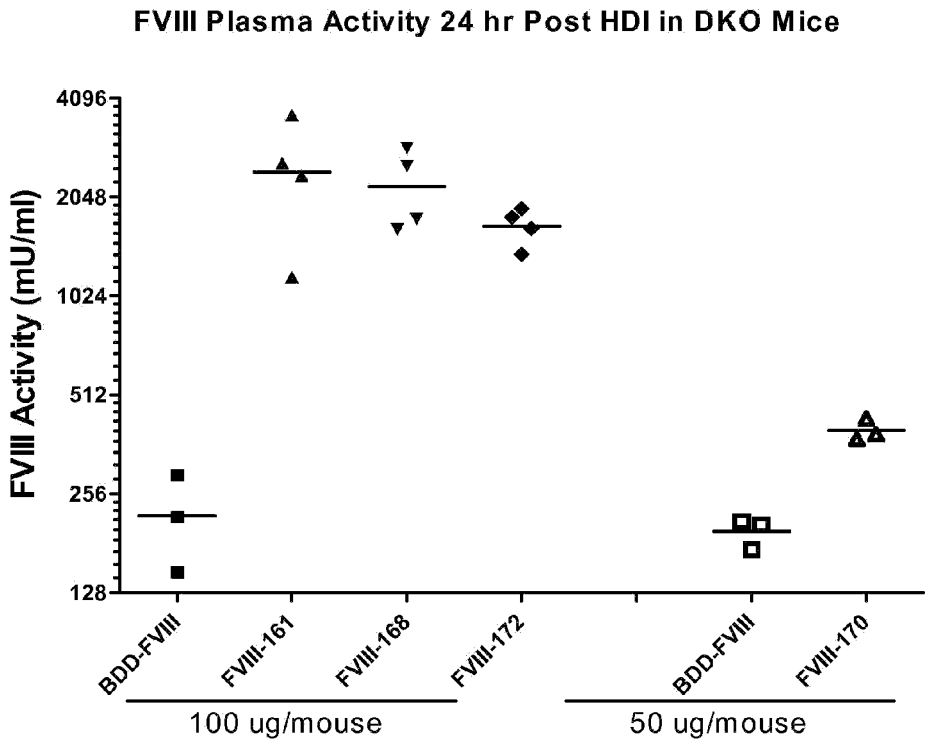

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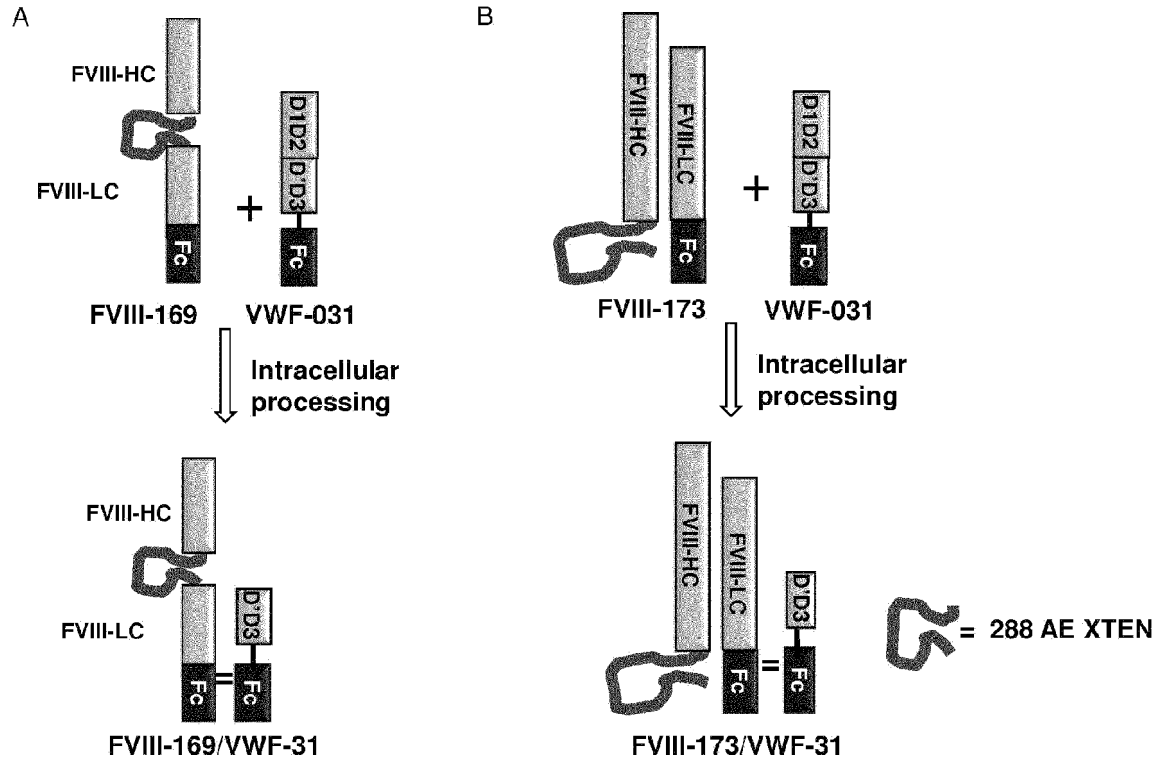
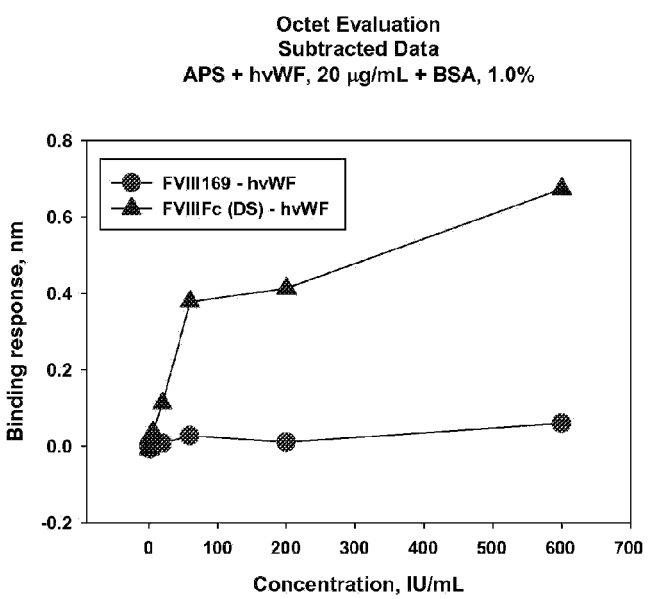
Figure 6: FVIII Constructs (Co-transfection system)



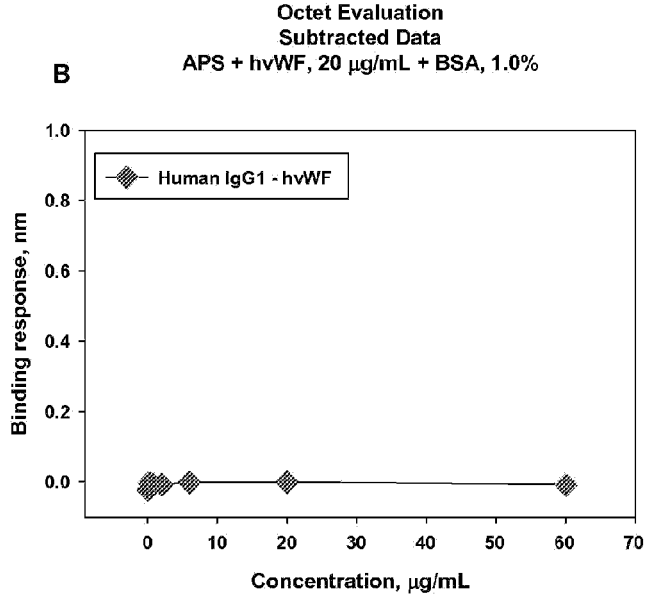
FVIII-169	SC- FVIII R1645A/R1648A with 288 AE XTEN B-domain insertion directly fused to a single Fc
FVIII-173	Dual chain - FVIIIwith288 AE XTEN B-domain insertion directly fused to a single Fc
VWF-031	D1D2D'D3 (763aa-477aa /C336A/C379A) fragment linked to a single Fc with a 48aa thrombin cleavage linker

Figure 7: FVIII-169/VWF-31 has no detectable binding toward immobilized hVWF

A



B



Analyte	APS Probe + hVWF	Protein G Probe
FVIII-169/VWF-031	-	+
rFVIIIFc	+	+
Human IgG1	-	+

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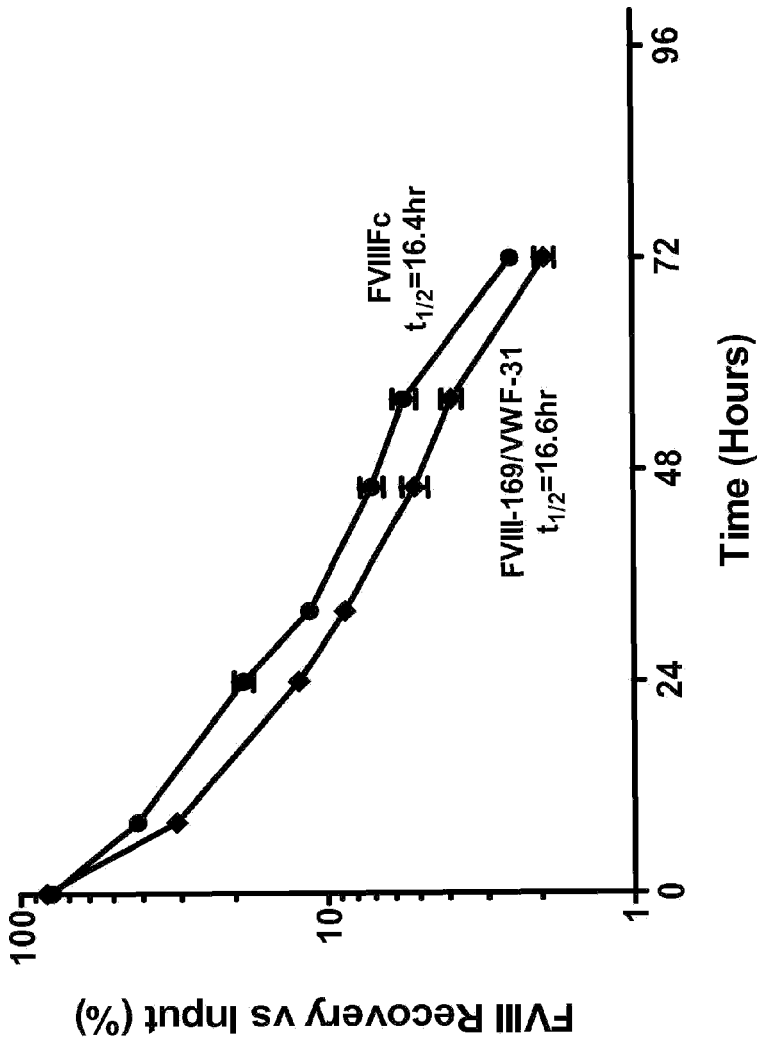

Figure 8A: FVIII-169/VWF-031 PK in HemA

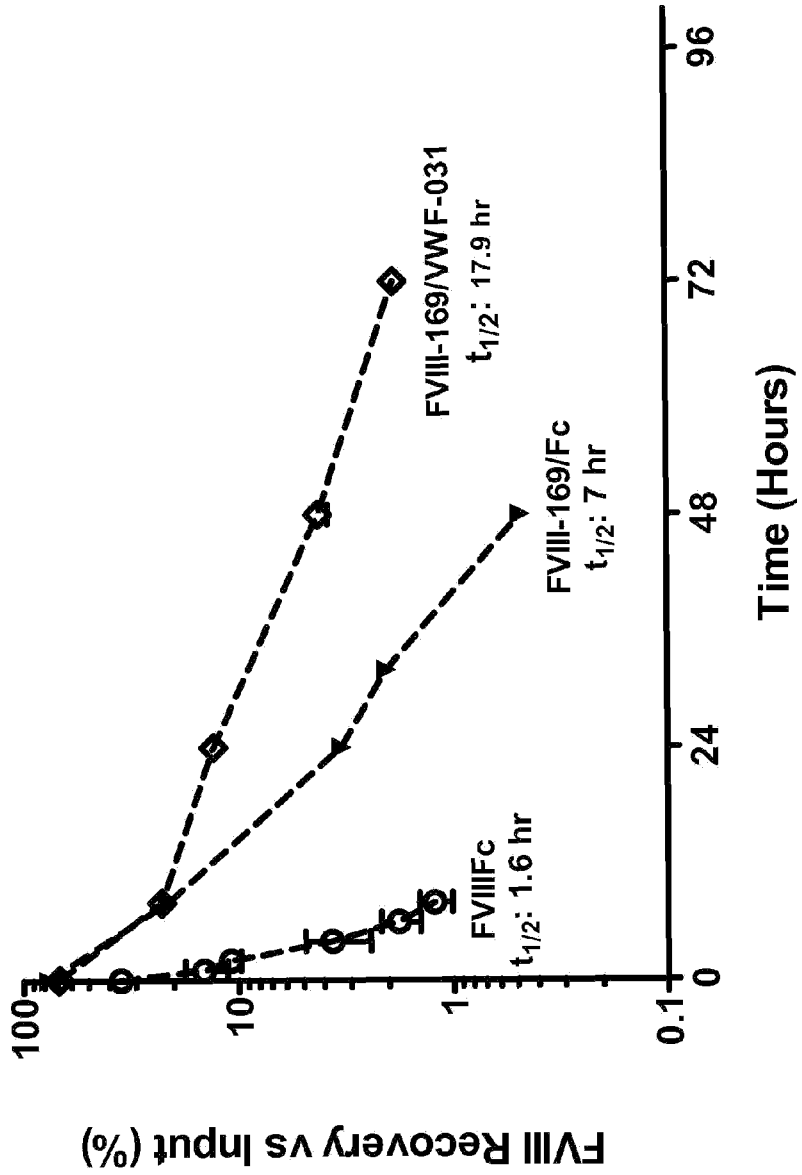

Figure 8B: FVIII-169/VWF-031 PK in FVIII/VWF DKO Mice

Figure 9A: FVIII-XTEN variants half-life in D'D3 expressing FVIII/VWF DKO mice

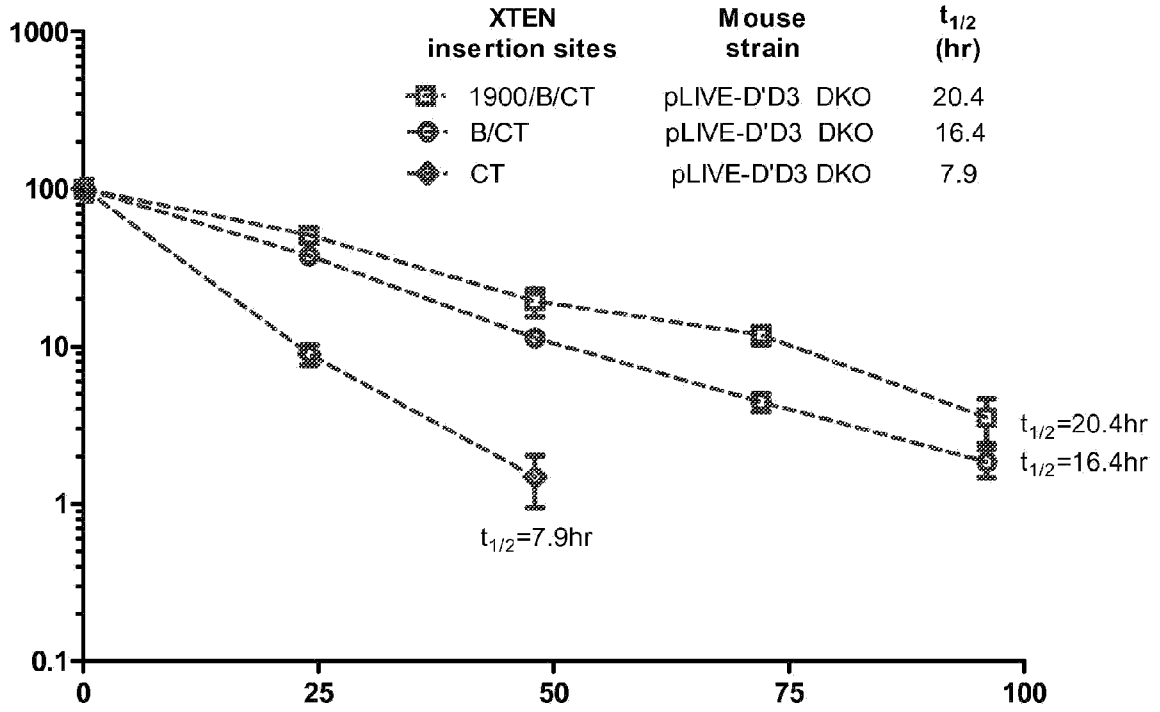

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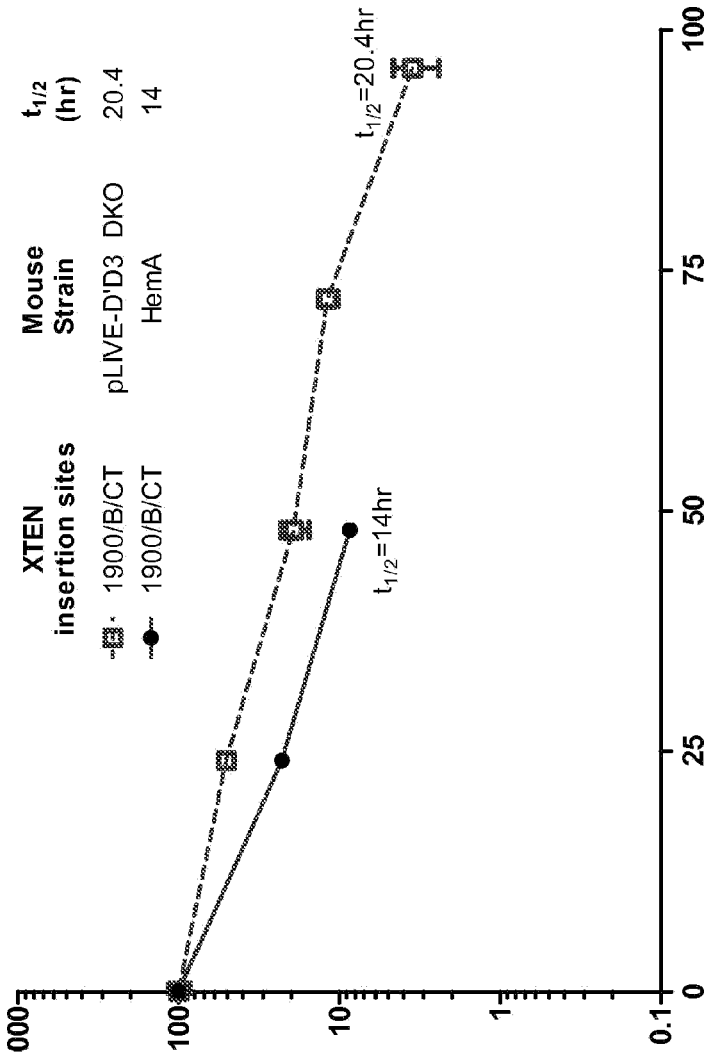
Figure 9B: PK of FVIII-XTEN with three XTEN insertions



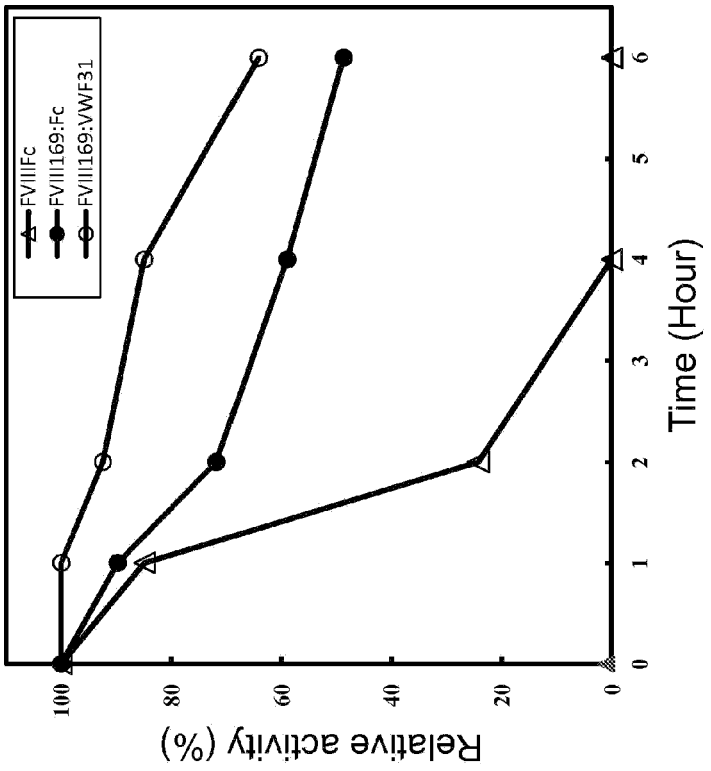


Figure 10: FVIIIFc activity in mouse DKO plasma

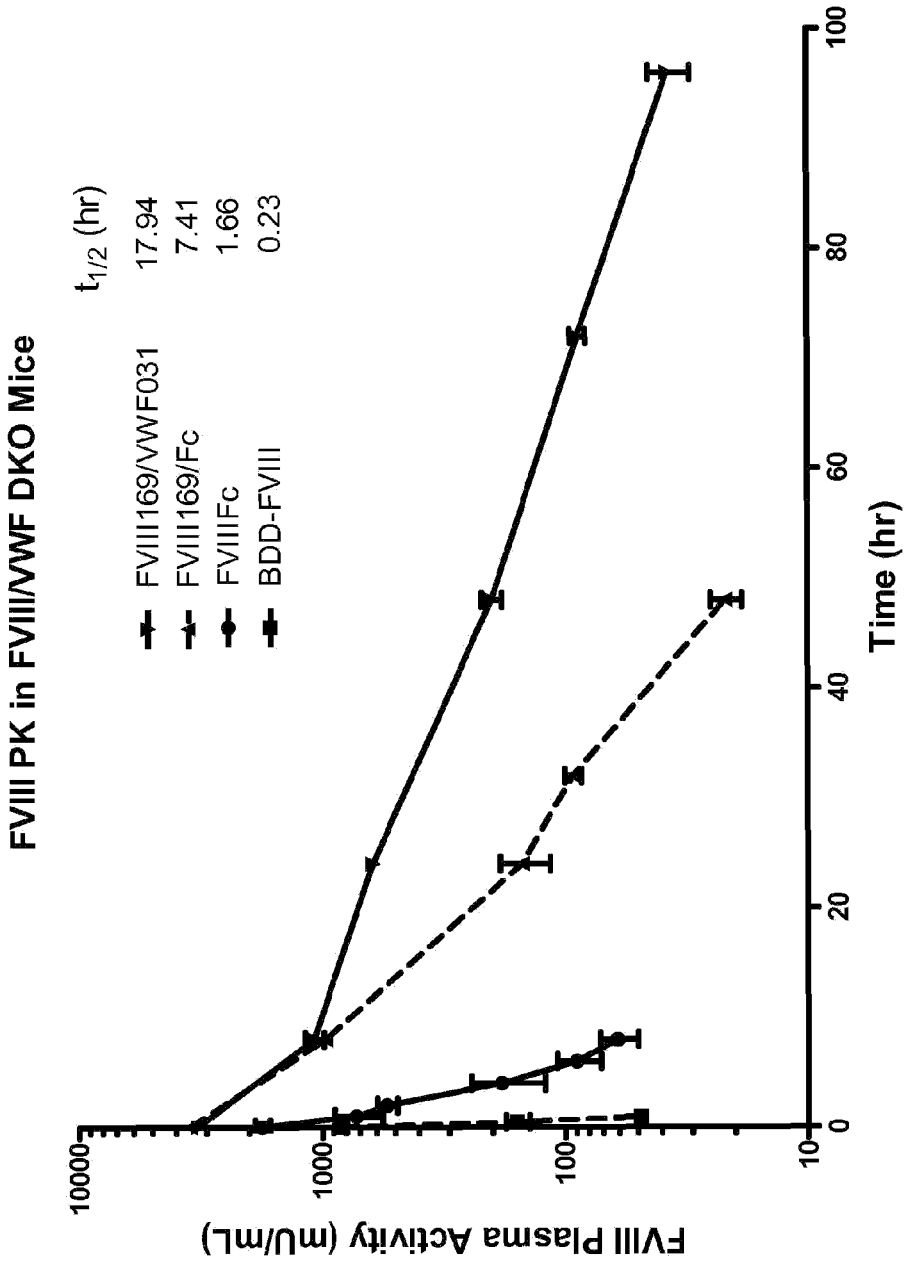


Figure 11: Additive effect of Fc, XTEN and VWF-D'D3 fragment on FVIII half-life extension

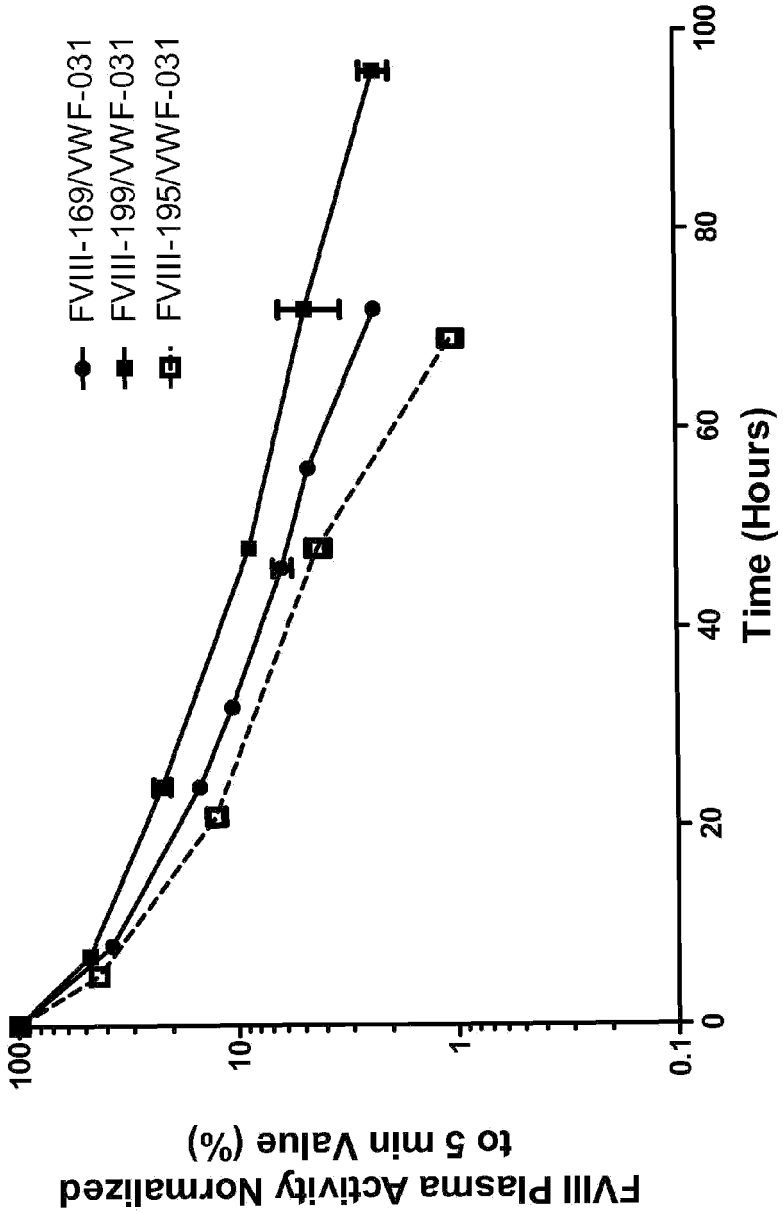


Figure 12A: Effect of different XTEN on rFVIII-XTEN/VWF heterodimer PK in HemA mice

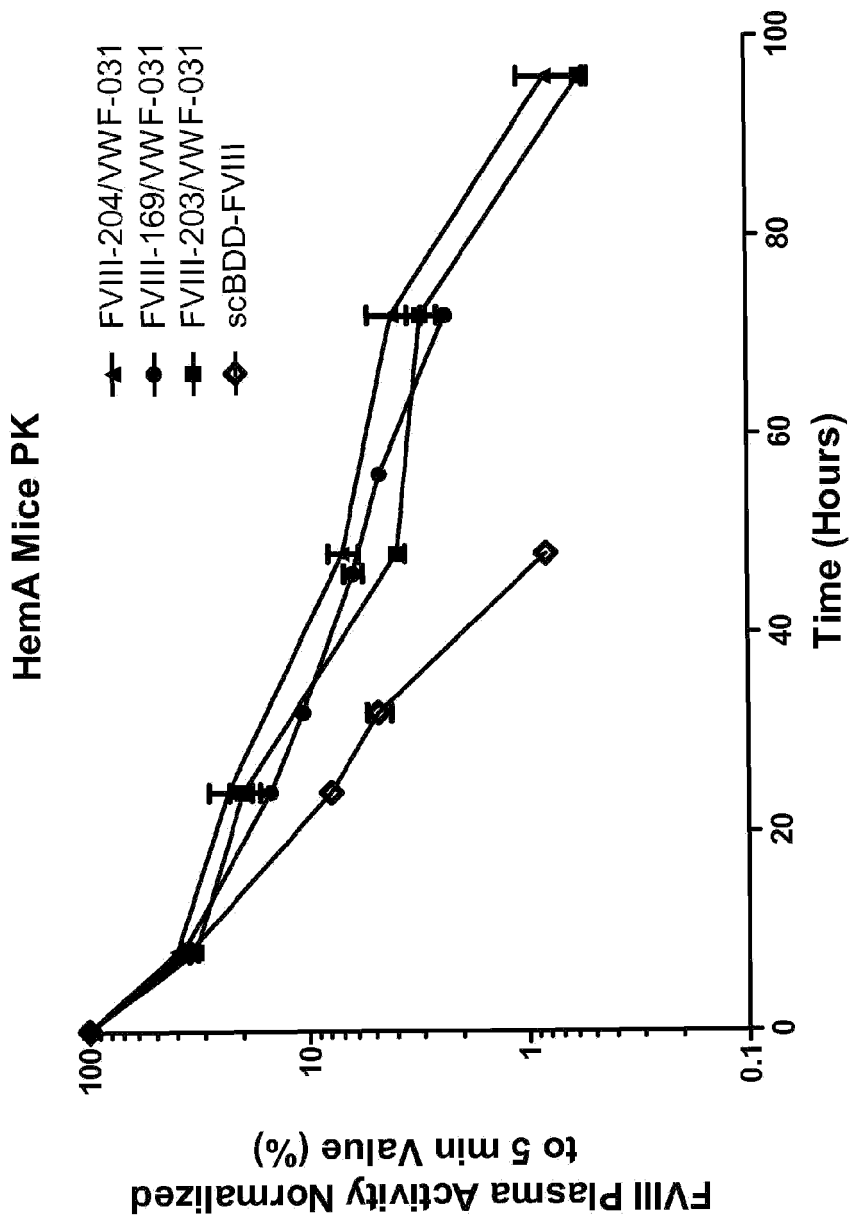


Figure 12B: Effect of different XTEN on rFVIII-XTEN/VWF heterodimer PK in HemA mice

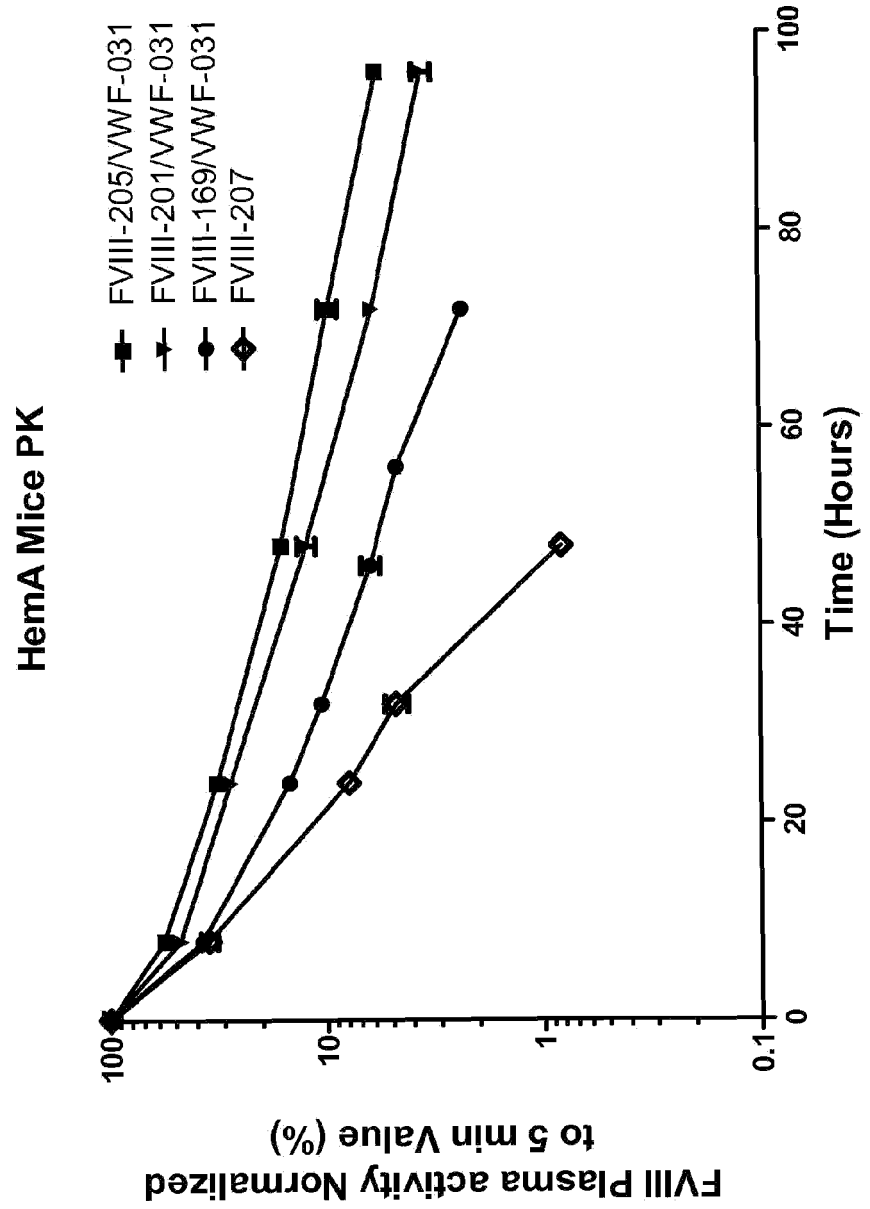


Figure 12C: Effect of different XTEN on rFVIII-XTEN/VWF heterodimer PK in HemA mice

Figure 13: rFVIII-XTEN/VWF-XTEN heterodimer PK in FVIII/VWF DKO mice

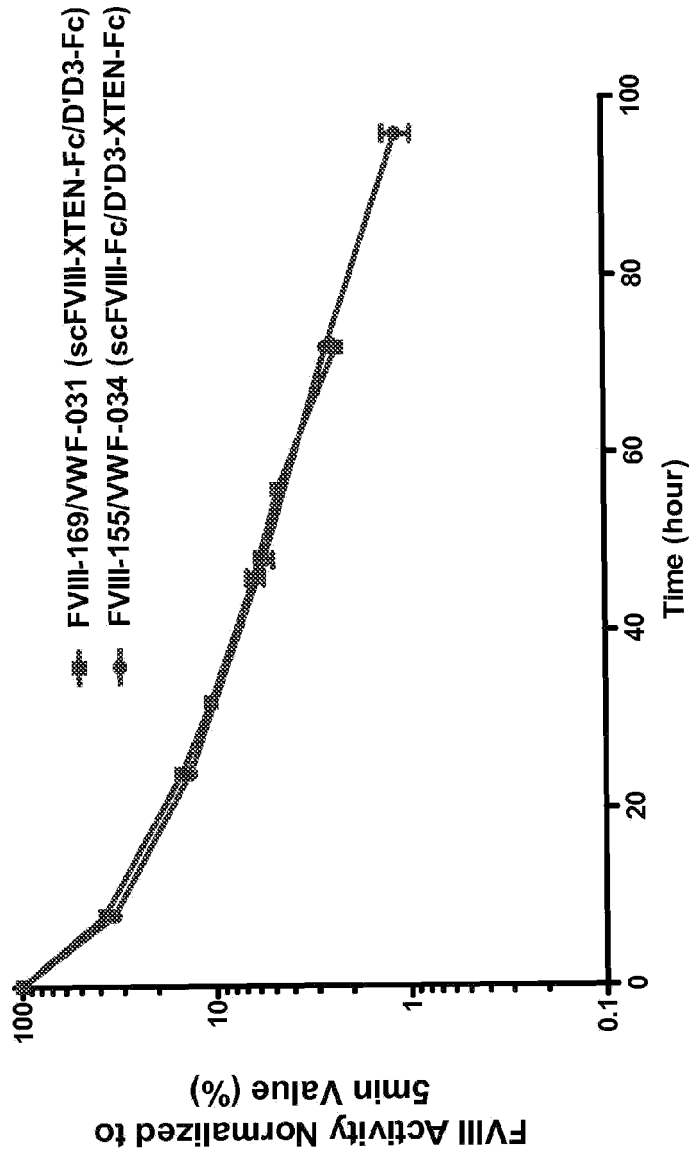


Figure 14. rFVIII-XTEN/VWF Heterodimer PK In HemA Mice

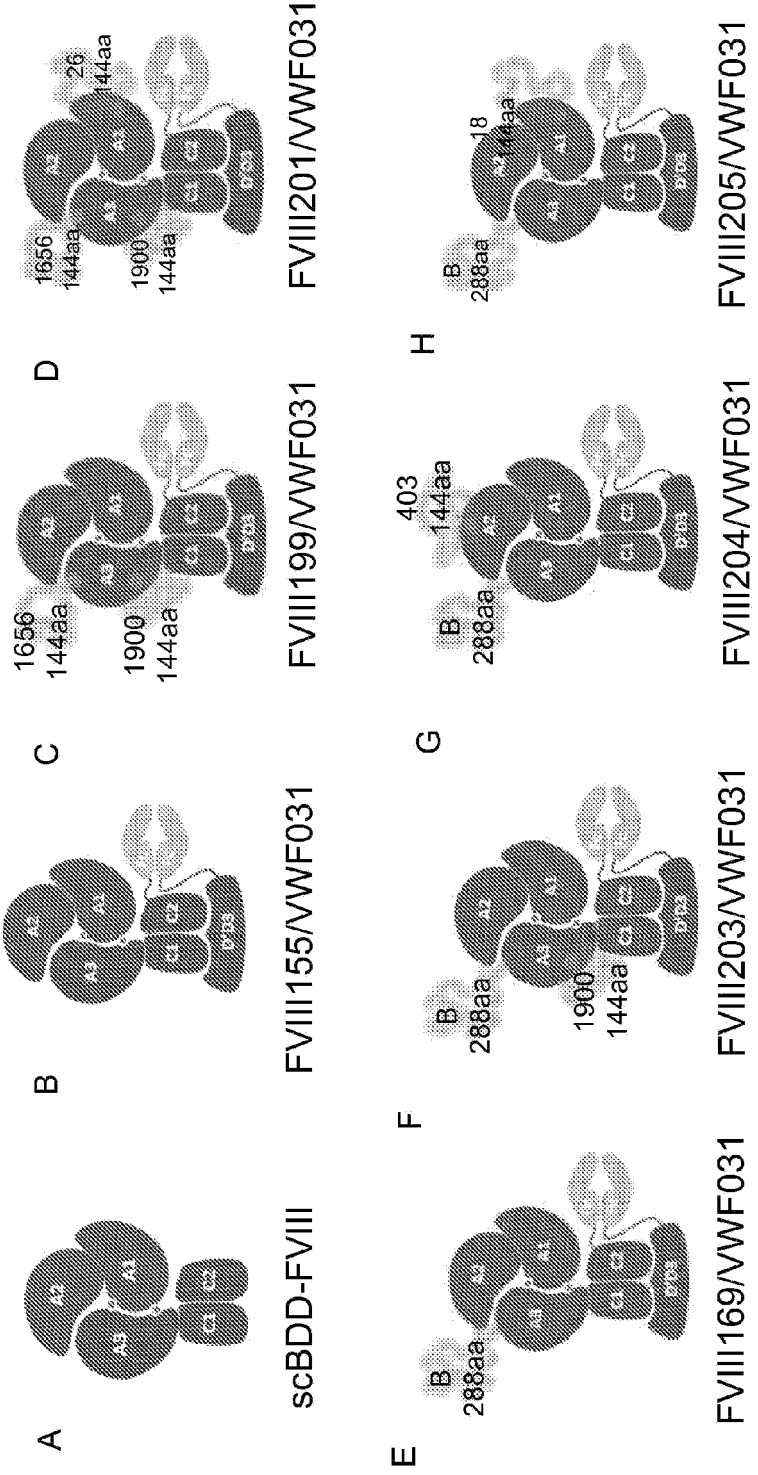


Figure 15:
Half-life extension in HemA mice by rFVIII-XTEN/VWF

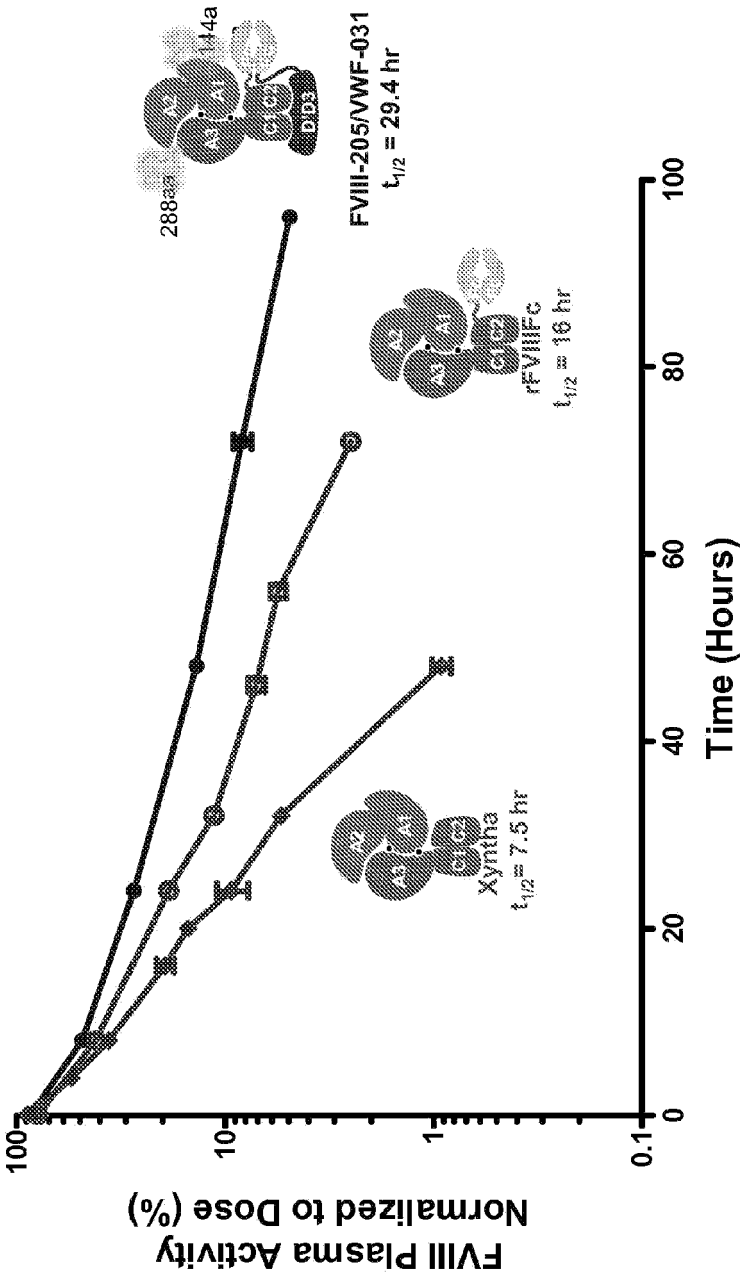


Figure 16: Acute efficacy of FVIII-XTEN-Fc : VWF-Fc heterodimer in HemA mice Tail Clip bleeding model