



(86) Date de dépôt PCT/PCT Filing Date: 2013/06/07
(87) Date publication PCT/PCT Publication Date: 2013/12/12
(85) Entrée phase nationale/National Entry: 2014/11/27
(86) N° demande PCT/PCT Application No.: US 2013/044842
(87) N° publication PCT/PCT Publication No.: 2013/185114
(30) Priorités/Priorities: 2012/06/08 (US61/657,685);
2013/02/01 (US61/759,817); 2013/03/15 (US61/801,603);
2013/05/31 (US61/829,775)

(51) Cl.Int./Int.Cl. *C07K 19/00* (2006.01),
A61K 38/36 (2006.01), *A61K 47/48* (2006.01),
A61P 7/04 (2006.01), *C07K 14/745* (2006.01),
C12N 15/62 (2006.01), *C12N 9/64* (2006.01),
C12P 21/06 (2006.01), *C40B 40/02* (2006.01),
C40B 40/08 (2006.01)

(71) Demandeur/Applicant:
BIOGEN IDEC MA INC., US

(72) Inventeurs/Inventors:
SALAS, JOE, US;
KISTANOVA, ELENA, US;
HONG, VU PHONG, US;
MEZO, ADAM R., US;

(54) Titre : FACTEURS DE COAGULATION CHIMERIQUES
(54) Title: CHIMERIC CLOTTING FACTORS

(57) **Abrégé/Abstract:**

The invention provides chimeric clotting factors comprising an activatable clotting factor and an enhancer moiety. The activatable clotting factor allows the chimeric clotting factor to be activated at the site of coagulation. The enhancer moiety can additionally improve procoagulation activities of the chimeric clotting factors. The chimeric clotting factors can further be improved by fusion to a half-life extender, which improves a pharmacokinetics property of the chimeric clotting factor. The invention also includes methods of making and methods of using these chimeric clotting factors.



(72) Inventeurs(suite)/Inventors(continued): PETERS, ROBERT, US

(74) Agent: GOWLING LAFLEUR HENDERSON LLP

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property
Organization
International Bureau



WIPO | PCT



(10) International Publication Number

WO 2013/185114 A3

(43) International Publication Date
12 December 2013 (12.12.2013)

(51) International Patent Classification:

A61K 38/36 (2006.01) A61P 7/02 (2006.01)

(21) International Application Number:

PCT/US2013/044842

(22) International Filing Date:

7 June 2013 (07.06.2013)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

61/657,685	8 June 2012 (08.06.2012)	US
61/759,817	1 February 2013 (01.02.2013)	US
61/801,603	15 March 2013 (15.03.2013)	US
61/829,775	31 May 2013 (31.05.2013)	US

(71) Applicant: **BIOGEN IDEC MA INC.** [US/US]; 14 Cambridge Center, Cambridge, Massachusetts 02142 (US).

(72) Inventors: **SALAS, Joe**; 9 D'Angelo Road, Wayland, Massachusetts 01778 (US). **KISTANOVA, Elena**; 30 Gardner Road, Apt 3G, Brookline, Massachusetts 02445 (US). **HONG, Vu Phong**; 27 Wheeler Street #217, Cambridge, Massachusetts 02138 (US). **MEZO, Adam R.**; 12449 Meeting House Rd., Carmel, Indiana 46032 (US). **PETERS, Robert**; 51 Newfield Street, West Roxbury, Massachusetts 02132 (US).

(74) Agents: **STEFFE, Eric K.** et al.; Sterne, Kessler, Goldstein & Fox PLLC, 1100 New York Ave NW, Washington, District of Columbia 20005 (US).

(81) Designated States (*unless otherwise indicated, for every kind of national protection available*): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (*unless otherwise indicated, for every kind of regional protection available*): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

- with international search report (Art. 21(3))
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))
- with sequence listing part of description (Rule 5.2(a))

(88) Date of publication of the international search report:

30 January 2014

(54) Title: CHIMERIC CLOTTING FACTORS

(57) Abstract: The invention provides chimeric clotting factors comprising an activatable clotting factor and an enhancer moiety. The activatable clotting factor allows the chimeric clotting factor to be activated at the site of coagulation. The enhancer moiety can additionally improve procoagulation activities of the chimeric clotting factors. The chimeric clotting factors can further be improved by fusion to a half-life extender, which improves a pharmacokinetics property of the chimeric clotting factor. The invention also includes methods of making and methods of using these chimeric clotting factors.



WO 2013/185114 A3

CHIMERIC CLOTTING FACTORS

BACKGROUND OF THE INVENTION

[0001] Initiation of the extrinsic clotting pathway is mediated by the formation of a complex between tissue factor, which is exposed as a result of injury to a vessel wall, and Factor VIIa. This complex then converts Factors IX and X to their active forms (Factor IXa and Xa). Factor Xa converts limited amounts of prothrombin to thrombin on the tissue factor-bearing cell. This resulting thrombin is then able to diffuse away from the tissue-factor bearing cell and activate platelets, and Factors V and VIII, making Factors Va and VIIIa. During the propagation phase of coagulation, Factor Xa is generated by Factor IXa (in complex with factor VIIIa) on the surface of activated platelets. Factor Xa, in complex with the cofactor Factor Va, activates prothrombin into thrombin, generating a thrombin burst. The cascade culminates in the conversion of fibrinogen to fibrin by thrombin, which results in the formation of a fibrin clot. Factor VII and tissue factor are key players in the initiation of blood coagulation.

[0002] Factor VII is a plasma glycoprotein that circulates in blood as a single-chain zymogen, which is catalytically inactive. Although single-chain Factor VII may be converted to two-chain Factor VIIa by a variety of factors in vitro, Factor Xa is an important physiological activator of Factor VII. The conversion of zymogen Factor VII into the activated two-chain molecule occurs by cleavage of the peptide bond linking the Arginine residue at amino acid position 152 and the Ile residue at amino acid position 153. In the presence of tissue factor, phospholipids and calcium ions, the two-chain Factor VIIa activates Factor X or Factor IX. Factor VIIa is thought to be the physiologic initiator of the clotting cascade by acting at the surface of a TF-bearing cell and generating the initial amount of thrombin that then diffuses to platelets to activate and prime them for the propagation phase of thrombin generation. Therapeutically, recombinant FVIIa acts by activating Factor X on the surface of activated platelets, bypassing the need for FIXa or FVIIIa to generate a thrombin burst during the propagation phase of coagulation. Since FVIIa has relatively low affinity for platelets, recombinant FVIIa is dosed at supra-physiological levels. This process is thought to be tissue factor-independent.

[0003] Factor X is also synthesized as a single-chain polypeptide containing the light and heavy chains connected by an Arg-Lys-Arg tripeptide. The single-chain molecule is then converted to the light and heavy chains by cleavage of two (or more) internal peptide bonds. In plasma, these two chains are linked together by a disulfide bond, forming Factor X. Activated Factor X, Factor Xa, participates in the final common pathway whereby prothrombin is converted to thrombin, which in turn converts fibrinogen to fibrin.

[0004] Clotting factors have been administered to patients to improve hemostasis for some time. The advent of recombinant DNA technology has significantly improved treatment for patients with clotting disorders, allowing for the development of safe and consistent protein therapeutics. For example, recombinant activated factor VII has become widely used for the treatment of major bleeding, such as that which occurs in patients having haemophilia A or B, deficiency of coagulation Factors XI or VII, defective platelet function, thrombocytopenia, or von Willebrand's disease.

[0005] Although such recombinant molecules are effective, there is a need for improved versions which localize the therapeutic to sites of coagulation, have improved pharmacokinetic properties, have reduced clearance rates, have improved manufacturability, have reduced thrombogenicity, or have enhanced activity, or more than one of these characteristics.

SUMMARY OF THE INVENTION

[0006] The present invention provides a chimeric protein comprising (i) an activatable clotting factor (Ac), (ii) an enhancer moiety (Em), and (iii) an optionally linker moiety (L or L1) between the activatable clotting factor and the enhancer moiety. The activatable clotting factor and the enhancer moiety can be linked or associated with each other, but may not be chemically crosslinked. The chimeric protein can be represented by formula Ac-L-Em or Em-L-Ac, wherein Ac comprises the activatable clotting factor; L comprises the optional linker moiety; and Em comprises the enhancer moiety.

[0007] In one embodiment, the activatable clotting factor comprises a clotting factor zymogen comprising a heavy chain (HC) and a light chain (LC) and a protease-cleavage site inserted between the HC and the LC. The clotting factor zymogen can be a FVII protein (e.g., FVII, functional fragments, derivatives, or variants thereof) or a FX protein (FX, functional fragments, derivatives, or variants thereof). Embodiments of the present invention

include a chimeric protein further comprising a self-immolative moiety (e.g., PABC) inserted between the protease-cleavage site and the HC. The protease-cleavage site inserted between the HC and the LC can be cleaved by a protease selected from thrombin (factor IIa), factor XIa, factor XIIa, kallikrein, factor VIIa, factor IXa, factor Xa, or any combinations thereof, wherein the protease-cleavage site is not naturally occurring in the clotting factor zymogen.

[0008] In another embodiment, the enhancer moiety comprises a clotting cofactor, a procoagulant peptide, or an antigen-binding moiety. Examples of the clotting cofactors include, but are not limited to, Tissue Factor, a fragment (e.g., soluble tissue factor), a variant, or a derivative thereof or FVa, a fragment, a variant, or derivative thereof. Non-limiting examples of the antigen binding moiety include an antibody or an antigen-binding fragment thereof which is capable of binding to the FVII protein or the FX protein and enhances the activity of FVII or FX, respectively.

[0009] In some embodiments, the chimeric protein further comprises a heterologous moiety (Het) (e.g., a half-life extender) linked to the activatable clotting factor, the linker moiety, or the enhancer moiety. Non-limiting examples of the half-life extender include an immunoglobulin constant region or a portion thereof (e.g., an Fc moiety or an FcRn binding partner), albumin, transferrin, an albumin binding moiety, a PAS sequence, an XTEN sequence, a HES sequence, the β subunit of the C-terminal peptide (CTP) of human chorionic gonadotropin, polyethylene glycol (PEG), hydroxyethyl starch (HES), albumin-binding small molecules, or any combinations thereof. The immunoglobulin constant region or a portion thereof can comprise an Fc moiety or an FcRn binding partner.

[0010] In other embodiments, the chimeric protein comprises a first heterologous moiety (Het1) and a second heterologous moiety (Het2). Either or both of Het1 and Het2 can comprise a half-life extender, e.g., an immunoglobulin constant region or a portion thereof (e.g., an Fc moiety or an FcRn binding partner), albumin, transferrin, an albumin binding moiety, a PAS sequence, an XTEN sequence, a HES sequence, the β subunit of the C-terminal peptide (CTP) of human chorionic gonadotropin, polyethylene glycol (PEG), hydroxyethyl starch (HES), albumin-binding small molecules, or any combinations thereof. Optionally, in certain embodiments, the first heterologous moiety is linked to the activatable clotting factor via a first linker (L1), and the second heterologous moiety is linked to an enhancer moiety via a second linker (L2). The chimeric protein may comprise only one linker (either L1 or L2) or both linkers.

[0011] In yet other embodiments, the chimeric protein comprises a first polypeptide chain and a second polypeptide chain, wherein the first polypeptide chain comprises the activatable clotting factor (Ac) and the second polypeptide chain comprises the enhancer moiety (Em), wherein the first polypeptide chain and the second polypeptide chain are associated with each other. For example, the first polypeptide chain can comprise the activatable clotting factor (Ac), the first heterologous moiety (Het1), and the first optional linker moiety (L1), and the second polypeptide chain can comprise the enhancer moiety (Em), the second heterologous moiety (Het2), and the second optional linker moiety (L2), wherein the first polypeptide chain and the second polypeptide chain are associated with each other.

[0012] In still other embodiments, the chimeric protein has a structure selected from:

- (a) Ac linked to Het1 via the linker moiety, and Em linked to Het2;
- (b) Ac linked to Het1 via the first linker moiety, and Em linked to Het2 via the second linker moiety;
- (c) Ac linked to Het1, and Em linked to Het2 via the linker moiety;
- (d) Ac linked to Het1, and Em linked to Het2;
- (e) Em linked to Het1 via the linker moiety, and Ac linked to Het2;
- (f) Em linked to Het1 via the first linker moiety, and Ac linked to Het2 via the second linker moiety;
- (g) Em linked to Het1, and Ac is linked to Het2 via the linker moiety; or,
- (h) Em linked to Het1, and Ac linked to Het2.

[0013] In yet other embodiments, the chimeric protein comprising two polypeptide chains can comprise:

- (a) the first polypeptide comprises a structure represented by the formula Ac-L1-Het1, and the second polypeptide comprises a structure represented by the formula Em-Het2;
- (b) the first polypeptide comprises a structure represented by the formula Ac-L1-Het1, and the second polypeptide comprises a structure represented by the formula Em-L2-Het2;
- (c) the first polypeptide comprises a structure represented by the formula Ac-Het1, and the second polypeptide comprises a structure represented by the formula Em-Het2;

- (d) the first polypeptide comprises a structure represented by the formula Ac-Het1, and the second polypeptide comprises a structure represented by the formula Em-L1-Het2;
- (e) the first polypeptide comprises a structure represented by the formula Em-L2-Het1, and the second polypeptide comprises a structure represented by the formula Ac-L1-Het2;
- (f) the first polypeptide comprises a structure represented by the formula Em-L1-Het1, and the second polypeptide comprises a structure represented by the formula Ac-Het2;
- (g) the first polypeptide comprises a structure represented by the formula Em-Het1, and the second polypeptide comprises a structure represented by the formula Ac-Het2; and,
- (h) the first polypeptide comprises a structure represented by the formula Em-Het1, and the second polypeptide comprises a structure represented by the formula Ac-L1-Het2; wherein Het1 and Het2 of the two polypeptide chains form a disulfide bond.

[0014] In some embodiments, the chimeric protein is a single polypeptide chain. For example, the chimeric protein can further comprise a scFc linker (X) linked to the enhancer moiety and the first heterologous moiety linked to the activatable clotting factor or the activatable clotting factor and the second heterologous moiety linked to the enhancer moiety. Examples of the single chain chimeric protein can comprise a formula selected from:

- (1) Ac-Het1-X-Em-Het2;
- (2) Ac-Het1-X-Em-L2-Het2;
- (3) Ac-L1-Het1-X-Em-Het2;
- (4) Ac-L1-Het1-X-Em-L2-Het2;
- (5) Het2-Em-X-Het1-Ac;
- (6) Het2-L2-Em-X-Het1-Ac;
- (7) Het2-Em-X-Het1-L1-Ac; or
- (8) Het2-L2-Em-X-Het1-L1-Ac,

wherein (a) Ac is the activatable clotting factor, (b) L1 is the first optional linker moiety; (c) Het1 is the first heterologous moiety; (d) X is the scFc linker; (e) Em is the enhancer moiety; (f) L2 is the optional second linker moiety; (g) Het2 is the second heterologous moiety, and (h) (-) is a peptide bond or one or more amino acids. In one embodiment, the

scFc linker is a processable linker (cscFc), which comprises at least one intracellular processing site. The processable linker may be processed into two or more polypeptide chains by one or more intracellular processing enzymes selected from a yeast Kex2, PCSK1, PCSK2, PCSK3, PCSK4, PCSK5, PCSK6, PCSK7, , or any combinations thereof. In one embodiment, the intracellular processing site is processed by PCSK5.

[0015] In some embodiments, the chimeric protein is polysialylated, pegylated, glycosylated, hesylated, gamma-carboxylated, or any combinations thereof.

[0016] Also included is a nucleic acid molecule encoding the chimeric protein or a complement thereof, a set of nucleic acid molecules comprising a first nucleotide sequence (NA1) and a second nucleotide sequence (NA2), wherein NA1 encodes the first polypeptide of the two chain chimeric protein or a complement thereof, and NA2 encodes the second polypeptide of the two chain chimeric protein or a complement thereof, the vectors comprising the nucleic acid molecule or the set of nucleic acid molecules, or the host cell comprising the vector or the set of vectors.

[0017] The invention is also directed to a pharmaceutical composition comprising the chimeric protein, the nucleic acid molecule, the vector, and the host cell and to methods for treating, ameliorating, or preventing a bleeding disease or disorder in a subject in need thereof comprising administering to the subject an effective amount of the chimeric protein, the nucleic acid molecule or the set of nucleic acid molecules, the vector or the set of vectors, the host cell, or a pharmaceutical composition. The bleeding disease or disorder treatable or preventable by the composition is selected from 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 iliopsoas sheath. The composition of the present invention can also be used to treat, ameliorate, or prevent a coagulation factor deficiency in a mammalian subject comprising administering to the subject an effective amount of the chimeric protein, the nucleic acid molecule or the set of nucleic acid molecules, the vector or the set of vectors, the host cell, or the pharmaceutical composition, wherein the coagulation factor is selected from FVII, FVIIa, FVIII, FIX, or FXI.

[0018] In a specific embodiment, the chimeric protein or the composition is used to treat, ameliorate, or prevent a bleeding disease or disorder in a bypass therapy. In the bypass therapy, the subject may have developed or may be subject to develop an inhibitor against Factor VIII.

[0019] The invention also includes methods of producing a chimeric protein comprising expressing a nucleotide sequence encoding the single chain chimeric protein, which comprises a scFc linker, wherein the scFc linker is cleaved intracellularly by an intracellular processing enzyme. The chimeric protein produced by the nucleotide sequence would comprise two polypeptide chains due to the processing of the intracellular processing site.

BRIEF DESCRIPTION OF THE DRAWINGS

[0020] FIG. 1 illustrates a schematic diagram of an exemplary chimeric protein (e.g., a chimeric clotting factor) comprising a thrombin-activatable or FXIa-activatable clotting factor and an enhancer moiety (sometimes referred to as “an activity enhancing moiety”). FIG. 1A shows a FVII or FX light chain with optional activation peptide for FX linked to a coagulation cascade protease cleavage site (e.g., thrombin cleavage site or FXIa cleavage site), which is further linked to a FVII or FX heavy chain. The FVII or FX heavy chain is then linked to an enhancer moiety via a linker. When the construct in FIG. 1A is dosed as a zymogen (non-active form), the construct is resistant to protease inhibitors upon administration (prior to activation). When the clotting factors are activated at the site of an injury as shown in FIG. 1B, the clotting factors can display high activity stimulated by the enhancer moiety.

[0021] FIG. 2 illustrates a schematic diagram of a chimeric FVII protein comprising a thrombin-activatable molecule and an enhancer moiety. FIG. 2A shows a FVII light chain linked to a thrombin cleavage site, which is further linked to a FVII heavy chain. The FVII heavy chain is then linked to an enhancer moiety via a linker, resulting in a non-active and zymogen form. When dosed in animals, this zymogen is resistant to protease inhibitors in the circulation and can be converted to the activated form (FIG. 2B) at the site of an injury. Activity of the clotting factors can be stimulated by an enhancer moiety. Examples for the enhancer moieties include soluble tissue factor (sTF), procoagulant peptides and antibody fragments.

[0022] FIG. 3 illustrates a schematic diagram of a molecule comprising a thrombin activatable FVII molecule, a sTF molecule as an enhancer moiety and a heterologous moiety (Het), shown as an Fc moiety for half-life extension. The construct in FIG. 3A comprises a first polypeptide chain and a second polypeptide chain, wherein the first polypeptide chain comprises a FVII light chain, a thrombin cleavage site, a FVII heavy chain, a first linker, and a first Fc moiety (Het1) in the N terminus to C terminus order and the second polypeptide chain comprises sTF, a second linker, and a second Fc moiety (Het2) in the N-terminus to C terminus direction. The first linker and the second linker can be the same or different. The first Fc moiety and the second Fc moiety can be the same or different. When the construct in FIG. 3A (i.e., a zymogen (non-active form)) is dosed, the construct is resistant to protease inhibitors upon administration (prior to activation). When the clotting factors are activated by thrombin at the site of an injury, as shown in FIG. 3B, the clotting factors can display high activity stimulated by the enhancer moiety.

[0023] FIG. 4 shows a schematic diagram of generation of the construct in FIG. 4B (similar to FIG. 3A). FIG. 4A (left construct) shows a single polypeptide sequence encoding a FVII light chain, a thrombin cleavage site (ALRPR (SEQ ID NO: 1)), a FVII heavy chain, a first linker, a first Fc moiety (Het1), a first intracellular processing site (e.g., RRRR (SEQ ID NO: 2)), a second linker, a second intracellular processing site (e.g., RKRRKR (SEQ ID NO: 3)), sTF, a third linker, and a second Fc moiety (Het2) in the N-terminus to C-terminus order. A nucleotide sequence (FVIII-133) encoding the single polypeptide sequence can be expressed in a host cell, and the single polypeptide sequence undergoes intracellular processing such that the first intracellular processing site and the second intracellular processing site are cleaved by a propeptide endopeptidase, e.g., PCSK5. The second linker interposed between the first intracellular processing site and the second intracellular processing site can thus be removed by PCSK5. FIG. 4B shows the final construct, after the linker is removed by processing, which may contain a portion of the intracellular processing site which remains after cleavage. This remaining linker portion may comprise a series of amino acids from about 1 to about 10, 1 to about 4. FIG. 4C shows an SDS-PAGE of the thrombin-activatable FVII-Fc/sTF-Fc chimeric protein under either non-reducing condition or reducing condition as indicated.

- [0024] FIG. 5 shows an SDS-PAGE analysis of the thrombin-activatable FVII-Fc/sTF-Fc dimer (FVII-133) under reducing condition. The second lane (*i.e.*, eluate) shows the purified thrombin-activatable FVII-Fc/sTF-Fc dimer.
- [0025] FIG. 6 shows data generated by thrombin generation assays to test the activity of FVII-133 and FVIIaFc. The activities of FVII-133 without or with Tissue Factor (TF) are shown as circle (●) and square (■), respectively. The activities of FVIIaFc without or with TF are shown as triangle (▲) or diamond (◆), respectively. The y-axis shows nanomoles (nM) of thrombin, and the x-axis shows time. The construct FVIIaFc consists of two polypeptide chains, a first chain consisting of an activated FVII (FVIIa) linked to a first Fc region, and a second chain consisting of an Fc region.
- [0026] FIG. 7 shows data generated by ROTEM assays with mouse hemophilia B blood to test the activity of FVII-133 and FVIIaFc. FIGS. 7A and 7B show clotting time and alpha angle for FVII-133. FIGS. 7C and 7D show clotting time and alpha angle of FVIIaFc and vehicle respectively.
- [0027] FIG. 8A-C shows FVII activity measured by ROTEM assay in human hemophilia A blood. FVII-133, FVII-184, and FVIIa were spiked into citrated human blood from hemophilia A donors. Structure of FVII-133 is shown in FIG. 4. FVII-184 is a mutant form of FVII-133 and is insensitive to thrombin activation due to mutation of the Arg residue, which is essential for thrombin cleavage, to Ala. FVIII-184 is otherwise identical to FVII-133. Clotting Time (CT), Clotting Formation Time (CFT), and Alpha Angle for FVII-133 (triangle), FVII-184 (square), and FVIIa (circle) were measured. The baseline clotting time in the hemophilia A donor is shown as diamond (◇). FIGS. 8A, 8B, and 8C show a graph of the results of the clotting time, clotting formation time, and alpha angle, respectively. FVIIa was used as a control for FVIIa activity.
- [0028] FIG. 9 shows FVII-133 ex vivo efficacy in hemB mice by ex vivo ROTEM assays. Clotting Time (CT) was measured on blood collected from mice that were dosed via tail vein injection by vehicle, FVIIa, and FVII-133, respectively.
- [0029] FIG. 10A-B shows the plasma level of FVII and FVII/ATIII complex as a function of time following administration of the proteins. HemB mice were administered i.v. with FVII-133, rFVIIaFc, or rFVIIa. The plasma samples at various time points were collected, and the FVII antigen level (FIG. 10A) and the FVII-133/ATIII or rFVIIaFc-ATIII complex (FIG. 10B) were measured by ELISA. The PK properties, including the

Mean Residence Time (MRT), of the FVII-133 (dotted line, circle) and FVIIaFc (solid line, triangle) were generated by 2 compartmental analysis using Phoenix 6 program.

[0030] FIG. 11 shows *in vitro* clotting time measured by ROTEM assays in human HemA blood. The clotting activity of FVII-212, which has the identical structure as FVII-133, was measured. The proteins were spiked in citrated human HemA blood. The clotting was initiated by Calcium and the clotting time was recorded by ROTEM machine under the NATEM program. X axis shows concentrations of either rFVIIa or FVII-212 in nM, and y axis shows the clotting time.

[0031] FIG. 12 shows *in vitro* clotting time measured by ROTEM assays in mouse HemA blood, which were collected by *vena cava* bleeding. The proteins were spiked into citrated mouse HemA blood. The clotting was initiated by Calcium and the clotting time was recorded in ROTEM machine under NATEM program. X axis shows the concentrations of spiked rFVIIa and FVII-212 in nM, and y axis shows the clotting time.

[0032] FIG. 13 shows *ex vivo* efficacy in HemA mice. FVII-212 (triangle) was administered in HemA mice at 10 nmol/kg. Blood was collected via *vena cava* with citrate and corn trypsin inhibitor (CTI) as an anti-coagulant at various times after dosing, and the clotting activity was measured by ROTEM analyzer under NATEM program. rFVIIa (circle) was used as a control. X axis shows the time (hr) following protein administration, and y axis shows the clotting time.

[0033] FIG. 14 shows pharmacokinetics of rFVIIa (circle), FVII-212 (square), and rFVII/ATIII (triangle) in HemA mice. The concentration of the proteins (y axis) is plotted against time (x axis).

[0034] FIG. 15. shows amidolytic activity of FVII-212 measured before and after thrombin activation using a chromozyme t-PA substrate. FVII-212 with thrombin is represented as inverted triangle (the first line from top to bottom). rFVIIa is represented as circle (the second line from top to bottom). FVII-212 and thrombin are shown as the third and fourth lines (the bottom lines).

[0035] FIG. 16A shows the general organization of a protease-activatable procoagulant compound of the invention. Het2, Pep2, Het1 and L are independently optional components. Pep1 and Pep2 are polypeptides, at least one of which is a clotting factor or a procoagulant peptide. Het1 and Het are heterologous moieties. L is a linker. Additional linkers can connect the different moieties; for example, a linker could be located between Pep2 and Het1 (as

shown in the diagram). Additional protease cleavable substrate and self-immolative spacer groups can be inserted at the N-terminus of other moieties such as polypeptides or heterologous moieties. The diagram shows the optional insertion of such a group at the N-terminus of Pep2. FIG. 16B is a representation of an exemplary procoagulant compound of the invention comprising a protease cleavable substrate (Aa1Aa2Aa3Aa4), a self-immolative spacer and a protein of interest (POI; e.g., a clotting factor or procoagulant peptide); illustrating the fragmentation of the compound and the release of the peptide or protein of interest after proteolytic cleavage of the cleavable substrate and 1,6 spontaneous fragmentation.

[0036] FIG. 17 is a representation of an alternative exemplary protease-activatable procoagulant compound of the invention which comprises an exosite binding peptide (M). The diagram illustrates the release of the peptide or protein of interest (POI; e.g., a clotting factor or procoagulant peptide) and the exosite binding peptide after proteolytic cleavage of a cleavable substrate (Aa1Aa2Aa3Aa4) and 1,6 spontaneous fragmentation.

[0037] FIG. 18 shows the release kinetics of the peptide IVGGQE, which corresponds to the six N-terminal amino acid residues of the heavy chain of the FXa clotting factor, from different procoagulant compounds (Compounds 1, 2, and 3) following treatment with 14 nM thrombin.

[0038] FIG. 19 shows the release kinetics of the peptide IVGGQE, which corresponds to the six N-terminal amino acid residues of the heavy chain of the FXa clotting factor, from different procoagulant compounds (Compounds 1, 4, 5 and 6) following treatment with 1.4 nM thrombin.

[0039] FIG. 20 shows the natural processing of factor VII to yield activated factor (FVIIa).

[0040] FIG. 21 is a representation of exemplary procoagulant compounds of the invention comprising FVIIa clotting factor.

[0041] FIG. 22A-B shows a flow diagram of a cleavable polypeptide, FVII-186 (FIG. 22A) that can be processed by a proprotein convertase (e.g., PACE) to a processed cleavable polypeptide (FIG. 22B). FIG. 22A shows a cleavable polypeptide comprising FVII LC (FVII light chain)-Proprotein Convertase Processing Site by a proprotein convertase (e.g., PACE processing site, e.g., 2X(RKR) (SEQ ID NO: 3))-Linker1-SUMO -Truncated FVII HC (FVII heavy chain without IVGGKV (SEQ ID NO: 60) at the N-terminus)-Linker2-Fc

Region2-Linker3-Fc Region2. FIG. 22B shows a schematic diagram of a cleavable polypeptide that has been processed by PACE. The processed cleavable polypeptide comprises two polypeptide chains, the first chain comprising FVIILC linked to the Proprotein Convertase processing site and the second chain comprising Linker1-SUMO-Truncated FVIIHC (FVII heavy chain without IVGGKV (SEQ ID NO: 60) at the N-terminus)-Linker2-Fc Region1-Linker3-Fc Region2. FIG. 22C demonstrates non-reduced (lane 1) or reduced (lane 2) SDS-PAGE, showing the above constructs and chains. (—) indicates a peptide bond.

[0042] FIG. 23A-C shows a flow diagram of (i) FVII-186 cleavage by a SUMO protease (FIG. 23B) and (ii) its fusion to a thioester peptide (FIG. 23C). FIG. 23A is identical to the construct in FIG. 22B. FIG. 23B shows that, after FVII-186 is cleaved by a SUMO protease, the resulting cleaved polypeptide construct comprises two chains, the first chain comprising FVIILC and Proprotein Convertase Site and the second chain comprising Truncated FVIIHC (FVII heavy chain without IVGGKV (SEQ ID NO: 60) at the N-terminus)-Linker2-Fc Region1-Linker3-Fc Region2. The first chain and the second chain are bound by a disulfide bond. FIG. 23C shows that after the cleaved polypeptide construct in FIG. 23B is ligated with a thioester peptide (D-Phe-Pip-Arg-PABC-IVGGKV-COSBn), the resulting construct comprises two polypeptide chains, the first chain comprising FVIILC and Proprotein Convertase Processing Site and the second chain comprising Thrombin cleavage site-FVIIHC (FVII heavy chain)-Linker2-Fc Region1-Linker3-Fc Region2 (TA-FVII-186). FIG. 23D shows reducing SDS-PAGE indicating the constructs and chains: lane 1 shows marker; lane 2 shows FVII-186; lane 3 shows FVII-186 with SUMO protease reaction; lane 4 shows FVII-186 with SUMO protease reaction and conjugation with a positive control peptide; and lane 5 shows FVII-186 with SUMO protease reaction and conjugation with PABC peptide. (—) indicates a peptide bond.

[0043] FIG. 24 shows FVIIa chromogenic assay after thrombin activation of TA-FVII-186. X axis indicates time (min), and Y axis indicates Absorbance (A405) measurement for FVIIa activity. (x) shows FVIIa activity of a mixture of thrombin and hirudin. (□) indicates FVIIa activity of a mixture of FVII-186, thrombin, and hirudin. (○) indicates FVIIa activity of a mixture of TA-FVII-186, thrombin, and hirudin.

DETAILED DESCRIPTION OF THE INVENTION

[0044] The present invention relates to chimeric proteins comprising an activatable clotting factor and an enhancer moiety. The present invention is based, at least in part, on the development of novel ways to enhance the efficacy, pharmacokinetic properties, and/or manufacturability of clotting factors. The activatable clotting factor is in a form that is activatable at the site of coagulation. For use in bypass therapy, exogenous clotting factors are only efficacious when given in the activated form. However, such activated clotting factors are rapidly inactivated by endogenous pathways (e.g. antithrombin III, TFPI), leading to their fast clearance and a short effective half-life in circulation. Giving higher doses does not solve this problem as it can result in thrombogenic effects. Thus, in one embodiment, the invention pertains to an activity-enhanced chimeric protein constructs which comprise an activatable clotting factor fused to or associated with an enhancer moiety. The "activatable" clotting factor comprises a heavy chain and a light chain of a clotting factor zymogen and a heterologous protease cleavage site (i.e., not naturally occurring in the clotting factor zymogen) inserted between the heavy chain and the light chain. These molecules circulate as enhanced zymogen fusion proteins and have a longer half-life than their activated counterparts due to the lack of inactivation, but can readily be activated at the site of clotting due to the cleavage of the heavy chain and the light chain by a protease that is activated or localized at the site of clotting. Incorporating an enhancer moiety can also improve their procoagulant activities.

[0045] Exemplary constructs of the invention are illustrated in the accompanying Figures and sequence listing. In one embodiment, the invention pertains to a polypeptide having the structure as set forth in the Figures. In another embodiment, the invention pertains to a polypeptide having the sequence set forth in the accompanying sequence listing or the nucleic acid molecule encoding such polypeptides. In one embodiment, the invention pertains to a mature form of a polypeptide having the sequence set forth in the accompanying sequence listing. It will be understood that these constructs and nucleic acid molecules encoding them can be used to improve hemostasis in a subject.

[0046] In order to provide a clear understanding of the specification and claims, the following definitions are provided below.

I. Definitions

[0047] As used herein, the term “protein” or “polypeptide” refers to a polymer of two or more of the natural amino acids or non-natural amino acids.

[0048] The term “amino acid” includes alanine (Ala or A); arginine (Arg or R); asparagine (Asn or N); aspartic acid (Asp or D); cysteine (Cys or C); glutamine (Gln or Q); glutamic acid (Glu or E); glycine (Gly or G); histidine (His or H); isoleucine (Ile or I); leucine (Leu or L); lysine (Lys or K); methionine (Met or M); phenylalanine (Phe or F); proline (Pro or P); serine (Ser or S); threonine (Thr or T); tryptophan (Trp or W); tyrosine (Tyr or Y); and valine (Val or V). Non-traditional amino acids are also within the scope of the invention and include norleucine, omithine, norvaline, homoserine, and other amino acid residue analogues such as those described in Ellman *et al.* Meth. Enzym. 202:301-336 (1991). To generate such non-naturally occurring amino acid residues, the procedures of Noren *et al.* Science 244:182 (1989) and Ellman *et al.*, supra, can be used. Briefly, these procedures involve chemically activating a suppressor tRNA with a non-naturally occurring amino acid residue followed by in vitro transcription and translation of the RNA. Introduction of the non-traditional amino acid can also be achieved using peptide chemistries known in the art. As used herein, the term “polar amino acid” includes amino acids that have net zero charge, but have non-zero partial charges in different portions of their side chains (e.g. M, F, W, S, Y, N, Q, C). These amino acids can participate in hydrophobic interactions and electrostatic interactions. As used herein, the term “charged amino acid” includes amino acids that can have non-zero net charge on their side chains (e.g. R, K, H, E, D). These amino acids can participate in hydrophobic interactions and electrostatic interactions.

[0049] An “amino acid substitution” refers to the replacement of at least one existing amino acid residue in a predetermined amino acid sequence (an amino acid sequence of a starting polypeptide) with a second, different “replacement” amino acid residue. An “amino acid insertion” refers to the incorporation of at least one additional amino acid into a predetermined amino acid sequence. While the insertion will usually consist of the insertion of one or two amino acid residues, the present larger “peptide insertions”, can be made, e.g. insertion of about three to about five or even up to about ten, fifteen, or twenty amino acid residues. The inserted residue(s) may be naturally occurring or non-naturally

occurring as disclosed above. An "amino acid deletion" refers to the removal of at least one amino acid residue from a predetermined amino acid sequence.

[0050] Polypeptides may be either monomers or multimers. For example, in one embodiment, a protein of the invention is a dimer. A dimeric polypeptide of the invention may comprise two polypeptide chains or may consist of one polypeptide chain (e.g., in the case of a scFc molecule). In one embodiment, the dimers of the invention are homodimers, comprising two identical monomeric subunits or polypeptides (e.g., two identical Fc moieties or two identical biologically active moieties). In another embodiment, the dimers of the invention are heterodimers, comprising two non-identical monomeric subunits or polypeptides (e.g., comprising two different clotting factors or portions thereof or one clotting factor only). See, e.g., U.S. patent 7404956, incorporated herein by reference.

[0051] As used herein, the term "peptide linker(s)," "linker(s)," or "linker moiety" refers to a peptide or polypeptide sequence (e.g., a synthetic peptide or polypeptide sequence) which connects two domains in a linear amino acid sequence of a polypeptide chain. In one embodiment, the polypeptides of invention are encoded by nucleic acid molecules that encode peptide linkers which either directly or indirectly connect the two Fc moieties which make up the construct. These linkers are referred to herein as "scFc linkers" and the scFc linker is interposed between the two Fc moieties of a polypeptide which comprises it. If the scFc linker connects two Fc moieties contiguously in the linear polypeptide sequence, it is a "direct" linkage. In contrast, the scFc linkers may link the first Fc moiety to a binding moiety which is, in turn, linked to the second Fc moiety, thereby forming an indirect linkage. These scFc linkers permit the formation of a single chain genetic construct. In one embodiment, the polypeptides also comprise intracellular processing sites which result in the scFc linker being processed (a cscFc linker) and, in one embodiment, substantially excised (e.g., during processing by a cell). Thus, the resulting processed polypeptide is a dimeric molecule comprising at least two amino acid chains and substantially lacking extraneous linker amino acid sequences. In some embodiments, all or substantially all of the linker is excised, while in some embodiments, a portion of the cleavage site may remain, e.g., four arginines of the RRRR cleavage site. In another embodiment, the linker or peptide linker may not typically be cleaved; however in certain embodiments, such cleavage may be desirable. Exemplary positions of the linkers

are shown in the accompanying drawings. Linkers can be located between the activatable clotting factors, enhancing moieties, and/or heterologous moieties, e.g., at the N or C terminus of these moieties. In one embodiment, these linkers are not removed during processing.

[0052] A third type of linker which may be present in an activatable clotting factor is herein referred to as a "cleavable linker" which comprises a heterologous protease-cleavage site (e.g., a factor XIa or thrombin cleavage site) that are not naturally occurring in the clotting factor and which may include additional linkers on either the N terminal or C terminal or both sides of the cleavage site. Exemplary locations for such sites are shown in the accompanying drawings and include, e.g., placement between a heavy chain of a clotting factor zymogen and a light chain of a clotting factor zymogen. In another embodiment, such linkers can further comprises a self-immolative moiety. For example, in one embodiment, a self-immolative moiety linked to a cleavable linker may be fused to the N terminus of the heavy chain of a clotting factor. In such cases, the cleavable linker may include additional linkers at the N terminus of the cleavage site, but requires direct fusion at the C-terminus of the cleavage site to the amino terminus of the heavy chain of the clotting factor.

[0053] As used herein, the term "gly-ser peptide linker" refers to a peptide that consists of glycine and serine residues. An exemplary gly/ser peptide linker comprises the amino acid sequence $(\text{Gly}_4 \text{Ser})_n$ (SEQ ID NO: 4). Another exemplary gly/ser peptide linker comprises the amino acid sequence $\text{S}(\text{Gly}_4 \text{Ser})_n$ (SEQ ID NO: 5) wherein n is an integer that is the same or higher than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 46, 50, 55, 60, 70, 80, 90, or 100.

[0054] In one embodiment, $n=1$. In one embodiment, $n=2$. In another embodiment, $n=3$. In another embodiment, $n=4$. In another embodiment, $n=5$. In yet another embodiment, $n=6$. In another embodiment, $n=7$. In yet another embodiment, $n=8$. In another embodiment, $n=9$. In yet another embodiment, $n=10$. Another exemplary gly/ser peptide linker comprises the amino acid sequence $\text{Ser}(\text{Gly}_4 \text{Ser})_n$ (SEQ ID NO: 5). In one embodiment, $n=1$. In one embodiment, $n=2$. In a preferred embodiment, $n=3$. In another embodiment, $n=4$. In another embodiment, $n=5$. In yet another embodiment, $n=6$.

[0055] "Derivatives" of polypeptides or proteins of the invention are polypeptides or proteins which have been altered so as to exhibit additional features not found on the

native polypeptide or protein. Also included as "derivatives" are those peptides that contain one or more naturally occurring amino acid derivatives of the twenty standard amino acids. A polypeptide or amino acid sequence "derived from" a designated polypeptide or protein refers to the origin of the polypeptide. In one embodiment, the polypeptide or amino acid sequence which is derived from a particular sequence has an amino acid sequence that is essentially identical to that sequence or a portion thereof, wherein the portion consists of at least about 10 to about 20 amino acids, at least about 20 to about 30 amino acids, or at least about 30 to about 50 amino acids, or which is otherwise identifiable to one of ordinary skill in the art as having its origin in the sequence.

[0056] Polypeptides that are "variants" of another peptide may have one or more mutations relative to the starting polypeptide, e.g., one or more amino acid residues which have been substituted with another amino acid residue or which has one or more amino acid residue insertions or deletions. In one embodiment, the polypeptide comprises an amino acid sequence which is not naturally occurring. Such variants necessarily have less than 100% sequence identity or similarity with the starting polypeptide. In another embodiment, the variant will have an amino acid sequence from about 75% to less than 100% amino acid sequence identity or similarity with the amino acid sequence of the starting polypeptide, for example, from about 80% to less than 100%, from about 85% to less than 100%, from about 90% to less than 100% (e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%) and from about 95% to less than 100%, e.g., over the length of the variant molecule. In one embodiment, there is one amino acid difference between a starting polypeptide sequence and the sequence derived therefrom. Identity or similarity with respect to this sequence is defined herein as the percentage of amino acid residues in the candidate sequence that are identical (*i.e.* same residue) with the starting amino acid residues, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity.

[0057] The term "fragment" when referring to polypeptides and proteins of the present invention include any polypeptides or proteins which retain at least some of the properties of the reference polypeptide or protein. Fragments of polypeptides include proteolytic fragments, as well as deletion fragments.

[0058] In one embodiment, polypeptides of the invention comprise an amino acid sequence (*e.g.*, at least one clotting factor or Fc moiety or domain) derived from a human protein sequence. However, polypeptides may comprise one or more amino acids from another mammalian species. For example, a clotting factor, Fc domain, or enhancing moiety may be derived from a non-human species and included in the subject polypeptides. Alternatively, one or more amino acids may be present in a polypeptide which are derived from a non-human species. In a particular embodiment, the polypeptides of the invention are not immunogenic.

[0059] It will also be understood by one of ordinary skill in the art that the polypeptides of the invention may be altered such that they vary in amino acid sequence from the naturally occurring or native polypeptides from which they were derived, while retaining the desirable activity of the native polypeptides. For example, nucleotide or amino acid substitutions leading to conservative substitutions or changes at "non-essential" amino acid residues may be made. An isolated nucleic acid molecule encoding a non-natural variant of a polypeptide derived from an immunoglobulin (*e.g.*, an Fc domain, moiety, or antigen binding site) can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of the immunoglobulin such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations may be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis.

[0060] The polypeptides of the invention may comprise conservative amino acid substitutions at one or more amino acid residues, *e.g.*, at essential or non-essential amino acid residues. 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, a nonessential amino acid residue in a polypeptide may be replaced with another amino acid residue from the same side chain family. In another

embodiment, a string of amino acids can be replaced with a structurally similar string that differs in order and/or composition of side chain family members. Alternatively, in another embodiment, mutations may be introduced randomly along all or part of a coding sequence, such as by saturation mutagenesis, and the resultant mutants can be incorporated into polypeptides of the invention and screened for their ability to bind to the desired target.

[0061] In the context of polypeptides, a "linear sequence" or a "sequence" is the order of amino acids in a polypeptide in an amino to carboxyl terminal direction in which residues that neighbor each other in the sequence are contiguous in the primary structure of the polypeptide.

[0062] As used herein, the terms "linked," "fused", or "fusion" refer to linkage via a peptide bonds (e.g., genetic fusion), chemical conjugation or other means. For example, one way in which molecules or moieties can be linked employs peptide linkers which link the molecules or moieties via peptide bonds. The terms "genetically fused," "genetically linked" or "genetic fusion" are used interchangeably and refer to the co-linear, covalent linkage or attachment of two or more proteins, polypeptides, or fragments thereof via their individual peptide backbones, through genetic expression of a single polynucleotide molecule encoding those proteins, polypeptides, or fragments. Such genetic fusion results in the expression of a single contiguous genetic sequence. Preferred genetic fusions are in frame, i.e., two or more open reading frames (ORFs) are fused to form a continuous longer ORF, in a manner that maintains the correct reading frame of the original ORFs. Thus, the resulting recombinant fusion protein is a single polypeptide containing two or more protein segments that correspond to polypeptides encoded by the original ORFs (which segments are not normally so joined in nature). In this case, the single polypeptide is cleaved during processing to yield dimeric molecules comprising two polypeptide chains.

[0063] 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. In another embodiment, the term "associated with" refers to a covalent, non-peptide bond or a non-covalent bond that is not chemically crosslinked. In some embodiments this association is 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 Waals force, London dispersion force, a mechanical bond, a halogen bond, aurophilicity, intercalation, stacking, entropic force, or chemical polarity.

[0064] As used herein, the term "chemically crosslinked" refers to linking by covalent bonds between acid side chains of amino acids, either directly or via a linker, e.g., a peptide linker. Chemical crosslinking does not include intramolecular or intermolecular disulfide bonds between Fc moieties of a dimeric Fc region, or non-engineered disulfide bonds between an amino acid of the activatable clotting factor and an amino acid of the enhancer moiety. Chemical crosslinking generally takes place by addition of a cross-linking agent, e.g., a heterobifunctional crosslinking agent. Examples of chemical crosslinking includes one or more photo-reactive bonds by chemically connecting photo-Ile, photo-Met, and photo-Leu. *See* Suchanek et al., (2005) *Nature methods*, 2: 261-267.

[0065] As used herein, the term "Fc region" is defined as the portion of a polypeptide which corresponds to the Fc region of native immunoglobulin, i.e., as formed by the dimeric association of the respective Fc domains of its two heavy chains. A native Fc region is homodimeric and comprises two polypeptide chains. 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).

[0066] As used herein, the term “Fc domain” refers to the portion of a single immunoglobulin 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.

[0067] As used herein, the term “Fc domain portion” or “Fc moiety” includes an amino acid sequence of an Fc domain or derived from an Fc domain. In certain embodiments, an Fc moiety comprises at least one of: a hinge (e.g., upper, middle, and/or lower hinge region) domain, a CH2 domain, a CH3 domain, a CH4 domain, or a variant, portion, or fragment thereof. In other embodiments, an Fc moiety comprises a complete Fc domain (i.e., a hinge domain, a CH2 domain, and a CH3 domain). In one embodiment, a Fc moiety comprises a hinge domain (or portion thereof) fused to a CH3 domain (or portion thereof). In another embodiment, an Fc moiety comprises a CH2 domain (or portion thereof) fused to a CH3 domain (or portion thereof). In another embodiment, an Fc moiety consists of a CH3 domain or portion thereof. In another embodiment, an Fc moiety consists of a hinge domain (or portion thereof) and a CH3 domain (or portion thereof). In another embodiment, a Fc moiety consists of a CH2 domain (or portion thereof) and a CH3 domain. In another embodiment, a Fc moiety consists of a hinge domain (or portion thereof) and a CH2 domain (or portion thereof). In one embodiment, an Fc moiety lacks at least a portion of a CH2 domain (e.g., all or part of a CH2 domain).

[0068] 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 chimeric 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. Therefore, in a particular embodiment, 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.

[0069] As used herein, the term "half-life extender" refers to a heterologous moiety which increases the *in vivo* half-life of a protein. *In vivo* half-life of a chimeric clotting factor of the invention can be determined by any method known to those of skill in the art, e.g., FVII activity level assays. In certain embodiments, the half-life extender can comprise an attachment site for a non-polypeptide moiety such as polyethylene glycol (PEG), hydroxyethyl starch (HES), polysialic acid, or any derivatives, variants, or combinations of these elements.

[0070] As used herein the term "moiety" refers to a component part or constituent of a chimeric polypeptide.

[0071] As used herein, the term "enhancer moiety" refers to a molecule, fragment, derivative, or variant thereof or a component of a polypeptide which is capable of enhancing the procoagulant activity of a clotting factor. In one embodiment, a chimeric clotting factor of the invention comprises an "enhancer moiety" which enhances the activity of the polypeptide, e.g., by acting as a cofactor. Such a moiety may be, e.g., a clotting cofactor, such as a soluble tissue factor (sTF), or a Factor Va protein, but does not include a targeting moiety, e.g., a platelet targeting moiety. In another embodiment, the enhancer moiety interacts with the activatable clotting factor, thereby increasing procoagulant activity of the clotting factor. The enhancer moiety may be genetically fused to the construct, chemically conjugated to the construct, or linked to the construct via a linker. For example, enhancer moieties may be attached to a construct of the invention by formation of a bond between the enhancer moiety and an activatable clotting factor of a construct, where the enhancer moiety comprises a first functional group and the activatable clotting factor comprises a second functional group, and where the first and second functional groups are capable of reacting with each other to form a chemical bond. Exemplary enhancer moieties are described in more detail below.

[0072] As used herein, the term "self-immolative moiety" refers to a molecule that can be included in a cleavable linker to enhance its function. In one embodiment, a self-immolative moiety is interposed between a heavy chain of a clotting factor zymogen and a protease cleavage site. Such self-immolating moieties have the advantage that the cleavability of the protease cleavage site is not negatively impacted by the terminal amino acid residue of the first moiety. Exemplary self-immolative moieties are disclosed, e.g.,

in U.S. Patent 7,375,078 and U.S. Patent 7,754,681, which are incorporated herein by reference in their entirety.

[0073] As used herein, the term "heterologous moiety" refers to a moiety that does not naturally occur with the components of the chimeric protein, e.g., an activatable clotting factor, a linker moiety, or an enhancer moiety and/or is linked to or associated with the components of the chimeric protein. In one embodiment, the heterologous moiety is capable of extending the half-life of the activatable clotting factor. In another embodiment, the heterologous moiety increases the hydrodynamic radius of the activatable or activated clotting factor. In other embodiments, a heterologous moiety improves one or more pharmacokinetic properties of the clotting factor without significantly affecting its biological activity or function (e.g., its procoagulant activity). In still other embodiments, the heterologous moiety is a non-polypeptide moiety, e.g., chemical modification or a combination of a peptide or polypeptide and a non-polypeptide moiety. In yet other embodiments, the heterologous moiety is a polypeptide. In some embodiments, the chimeric clotting factor is linked or connected to the heterologous moiety by a linker. Non-limiting examples of heterologous polypeptide moieties comprise an immunoglobulin constant region or a portion thereof, albumin or a fragment thereof, an albumin binding moiety, a PAS sequence, a HAP sequence, transferrin or a fragment thereof, the β subunit of the C-terminal peptide (CTP) of human chorionic gonadotropin, albumin binding small molecule, an XTEN sequence, or two or more combinations thereof. Non-limiting examples of the heterologous non-polypeptide moiety include polyethylene glycol (PEG), polysialic acid, hydroxyethyl starch (HES), a derivative thereof, or any combinations thereof. Exemplary heterologous moieties include, e.g., FcRn binding moieties (e.g., complete Fc regions or portions thereof which bind to FcRn), single chain Fc regions (ScFc regions, e.g., as described in US 2008/0260738, WO 2008/012543, or WO 2008/1439545), processable scFc regions (comprising a cscFc regions as described herein).

[0074] In one embodiment an enhancer moiety for use in a construct of the invention comprises an antibody variant. The term "antibody variant" or "modified antibody" includes an antibody which does not occur in nature and which has an amino acid sequence or amino acid side chain chemistry which differs from that of a naturally-derived antibody by at least one amino acid or amino acid modification as described

herein. As used herein, the term “antibody variant” includes synthetic forms of antibodies which are altered such that they are not naturally occurring, e.g., antibodies that comprise at least two heavy chain portions but not two complete heavy chains (such as, domain deleted antibodies or minibodies); multispecific forms of antibodies (e.g., bispecific, trispecific, etc.) altered to bind to two or more different antigens or to different epitopes on a single antigen); heavy chain molecules joined to scFv molecules; single-chain antibodies; diabodies; triabodies; and antibodies with altered effector function and the like.

[0075] As used herein, the term “Gla domain” refers to the conserved membrane binding motif which is present in vitamin K-dependent proteins, such as as prothrombin, coagulation factors VII, IX and X, proteins C, S, and Z. These proteins require vitamin K for the posttranslational synthesis of γ -carboxyglutamic acid, an amino acid clustered in the N-terminal Gla domain of these proteins. All glutamic residues present in the domain are potential carboxylation sites and many of them are therefore modified by carboxylation. In the presence of calcium ions, the Gla domain interacts with phospholipid membranes that include phosphatidylserine. The Gla domain also plays a role in binding to the FVIIa cofactor, tissue factor (TF). Complexed with TF, the Gla domain of FVIIa is loaded with seven Ca^{2+} ions, projects three hydrophobic side chains in the direction of the cell membrane for interaction with phospholipids on the cell surface, and has significant contact with the C-terminal domain of TF.

[0076] As used herein the term “scFv molecule” includes binding molecules which consist of one light chain variable domain (VL) or portion thereof, and one heavy chain variable domain (VH) or portion thereof, wherein each variable domain (or portion thereof) is derived from the same or different antibodies. scFv molecules preferably comprise an scFv linker interposed between the VH domain and the VL domain. ScFv molecules are known in the art and are described, e.g., in US patent 5,892,019, Ho et al. 1989. *Gene* 77:51; Bird et al. 1988 *Science* 242:423; Pantoliano et al. 1991. *Biochemistry* 30:10117; Milenic et al. 1991. *Cancer Research* 51:6363; Takkinen et al. 1991. *Protein Engineering* 4:837.

[0077] A “scFv linker” as used herein refers to a moiety interposed between the VL and VH domains of the scFv. scFv linkers preferably maintain the scFv molecule in an antigen binding conformation. In one embodiment, a scFv linker comprises or consists of

an scFv linker peptide. In certain embodiments, an scFv linker peptide comprises or consists of a gly-ser peptide linker. In other embodiments, an scFv linker comprises a disulfide bond.

[0078] The term “glycosylation” refers to the covalent linking of one or more carbohydrates to a polypeptide. Typically, glycosylation is a posttranslational event which can occur within the intracellular milieu of a cell or extract therefrom. The term glycosylation includes, for example, N-linked glycosylation (where one or more sugars are linked to an asparagine residue) and/or O-linked glycosylation (where one or more sugars are linked to an amino acid residue having a hydroxyl group (*e.g.*, serine or threonine)). In one embodiment, a molecule of the invention is glycosylated. In another embodiment, a molecule of the invention is aglycosylated. In yet another embodiment, a molecule of the invention has reduced glycosylation as compared to that in a wild type Fc region.

[0079] As used herein the term “disulfide bond” includes the covalent bond formed between two sulfur atoms. The amino acid cysteine comprises a thiol group that can form a disulfide bond or bridge with a second thiol group. In most naturally occurring IgG molecules, the CH1 and CL regions are linked by native disulfide bonds and the two heavy chains are linked by two native disulfide bonds at positions corresponding to 239 and 242 using the Kabat numbering system (position 226 or 229, EU numbering system).

[0080] The term “vector” or “expression vector” is used herein to mean vectors used in accordance with the present invention as a vehicle for introducing into and expressing a desired polynucleotide in a cell. As known to those skilled in the art, such vectors may easily be selected from plasmids, phages, viruses or retroviruses. In general, vectors compatible with the instant invention will comprise a selection marker, appropriate restriction sites to facilitate cloning of the desired gene and the ability to enter and/or replicate in eukaryotic or prokaryotic cells.

[0081] Numerous expression vector systems may be employed to produce the chimeric clotting factors of the invention. For example, one class of vector utilizes DNA elements which are derived from animal viruses such as bovine papilloma virus, polyoma virus, adenovirus, vaccinia virus, baculovirus, retroviruses (RSV, MMTV or MOMLV) or SV40 virus. Additionally, cells which have integrated the DNA into their chromosomes may be selected by introducing one or more markers which allow selection of transfected host

cells. The marker may provide for prototrophy to an auxotrophic host, biocide resistance (e.g., antibiotics) or resistance to heavy metals such as copper. The selectable marker gene can either be directly linked to the DNA sequences to be expressed, or introduced into the same cell by cotransformation. In one embodiment, an inducible expression system can be employed. Additional elements may also be needed for optimal synthesis of mRNA. These elements may include signal sequences, splice signals, as well as transcriptional promoters, enhancers, and termination signals. In one embodiment, a secretion signal, e.g., any one of several well characterized bacterial leader peptides (e.g., *pelB*, *phoA*, or *ompA*), can be fused in-frame to the N terminus of a polypeptide of the invention to obtain optimal secretion of the polypeptide. (Lei *et al.* (1988), *Nature*, 331:543; Better *et al.* (1988) *Science*, 240:1041; Mullinax *et al.*, (1990). *PNAS*, 87:8095).

[0082] The term "host cell" refers to a cell that has been transformed with a vector constructed using recombinant DNA techniques and encoding at least one heterologous gene. In descriptions of processes for isolation of proteins from recombinant hosts, the terms "cell" and "cell culture" are used interchangeably to denote the source of protein unless it is clearly specified otherwise. In other words, recovery of protein from the "cells" may mean either from spun down whole cells, or from the cell culture containing both the medium and the suspended cells. The host cell line used for protein expression is most preferably of mammalian origin; those skilled in the art are credited with ability to preferentially determine particular host cell lines which are best suited for the desired gene product to be expressed therein. Exemplary host cell lines include, but are not limited to, DG44 and DUXB11 (Chinese Hamster Ovary lines, DHFR minus), HELA (human cervical carcinoma), CVI (monkey kidney line), COS (a derivative of CVI with SV40 T antigen), R1610 (Chinese hamster fibroblast) BALBC/3T3 (mouse fibroblast), PerC6 cells), HAK (hamster kidney line), SP2/O (mouse myeloma), P3x63-Ag3.653 (mouse myeloma), BFA-1c1BPT (bovine endothelial cells), RAJI (human lymphocyte) and 293 (human kidney). Host cell lines are typically available from commercial services, the American Tissue Culture Collection or from published literature. The polypeptides of the invention can also be expressed in non-mammalian cells such as bacteria or yeast or plant cells. In this regard it will be appreciated that various unicellular non-mammalian microorganisms such as bacteria can also be transformed; *i.e.* those capable of being grown in cultures or fermentation. Bacteria, which are susceptible

to transformation, include members of the enterobacteriaceae, such as strains of *Escherichia coli* or *Salmonella*; Bacillaceae, such as *Bacillus subtilis*; *Pneumococcus*; *Streptococcus*, and *Haemophilus influenzae*. It will further be appreciated that, when expressed in bacteria, the polypeptides typically become part of inclusion bodies. The polypeptides must be isolated, purified and then assembled into functional molecules.

[0083] In addition to prokaryotes, eukaryotic microbes may also be used. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among eukaryotic microorganisms although a number of other strains are commonly available including *Pichia pastoris*. For expression in *Saccharomyces*, the plasmid YRp7, for example, (Stinchcomb *et al.*, (1979), *Nature*, 282:39; Kingsman *et al.*, (1979), *Gene*, 7:141; Tschemper *et al.*, (1980), *Gene*, 10:157) is commonly used. This plasmid already contains the TRP1 gene which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example ATCC No. 44076 or PEP4-1 (Jones, (1977), *Genetics*, 85:12). The presence of the *trp1* lesion as a characteristic of the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan.

[0084] As used herein the term "endogenous" refers to molecules (e.g. nucleic acid and/or protein molecules) that are naturally present in a cell. In contrast, the term "exogenous" or "heterologous" refers to such molecules that are not normally found in a given context, e.g., in a cell or in a polypeptide. For example, an exogenous or heterologous molecule may be introduced into a cell and are only present after manipulation of the cell, e.g., by transfection or other forms of genetic engineering or a heterologous amino acid sequence may be present in a protein in which it is not naturally found.

[0085] As used herein, the term "cleavage site" or "protease-cleavage site" refers to a site recognized by a protease. In one embodiment, a polypeptide has a protease-cleavage site cleaved by a protease 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: 6) and SVSQTSKLTR (SEQ ID NO: 7). Exemplary thrombin cleavage sites include, e.g., DFLAEGGGVR (SEQ ID NO: 8), TTKIKPR (SEQ ID NO: 9), LVPRG (SEQ ID NO: 10) and ALRPR (SEQ ID NO: 1). Other protease-cleavage sites are described in detail below.

[0086] As used herein, the term “processing site” or “intracellular processing site” refers to a type of enzymatic cleavage site in a polypeptide which is the 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., furin, a yeast Kex2, 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.

[0087] In constructs that include more than one processing or cleavage site, it will be understood that such sites may be the same or different.

[0088] *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.

[0089] As used herein, the phrase “subject that would benefit from administration of a polypeptide” or “subject in need thereof” includes subjects, such as mammalian subjects, that would benefit from administration of polypeptides of the invention, e.g., to improve hemostasis. In one embodiment, the subjects include, but are not limited to, the individuals who have developed a FVIII inhibitor and thus are in need of a bypass therapy. In another embodiment, the subjects also include the individuals who have not

yet developed a FVIII inhibitor, but have a tendency to develop a FVIII inhibitor. The subject can be an adult or a minor (e.g., under 12 years old).

[0090] A “chimeric protein” or “fusion protein”, as used herein, refers to any protein comprised of a first amino acid sequence derived from a first source, bonded, covalently or non-covalently, to a second amino acid sequence derived from a second source, wherein the first and second source are not the same. A first source and a second source that are not the same can include two different biological entities, or two different proteins from the same biological entity, or a biological entity and a non-biological entity. A chimeric protein can include for example, a protein derived from at least 2 different biological sources. A biological source can include any non-synthetically produced nucleic acid or amino acid sequence (e.g. a genomic or cDNA sequence, a plasmid or viral vector, a native virion or a mutant or analog, as further described herein, of any of the above). A synthetic source can include a protein or nucleic acid sequence produced chemically and not by a biological system (e.g. solid phase synthesis of amino acid sequences). A chimeric protein can also include a protein derived from at least 2 different synthetic sources or a protein derived from at least one biological source and at least one synthetic source. A chimeric protein may also comprise a first amino acid sequence derived from a first source, covalently or non-covalently linked to a nucleic acid, derived from any source or a small organic or inorganic molecule derived from any source. The chimeric protein may comprise a linker molecule between the first and second amino acid sequence or between the first amino acid sequence and the nucleic acid, or between the first amino acid sequence and the small organic or inorganic molecule.

[0091] As used herein, the term “clotting factor,” refers to molecules, or analogs thereof, naturally occurring or recombinantly produced which prevent or decrease the duration of a bleeding episode in a subject. In other words, it means molecules having pro-clotting activity, i.e., are responsible for the conversion of fibrinogen into a mesh of insoluble fibrin causing the blood to coagulate or clot. An “activatable clotting factor” is a clotting factor in an inactive form (e.g., in its zymogen form) that is capable of being converted to an active form.

[0092] Clotting activity, as used herein, means the ability to participate in a cascade of biochemical reactions that culminates in the formation of a fibrin clot and/or reduces the severity, duration or frequency of hemorrhage or bleeding episode.

[0093] Hemostasis, as used herein, means the stopping or slowing of bleeding or hemorrhage; or the stopping or slowing of blood flow through a blood vessel or body part.

[0094] 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.

[0095] 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), 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 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.

[0096] 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, or stem cell transplantation

[0097] On-demand treatment 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 iliopsoas 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.

[0098] 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.

[0099] 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, the prophylaxis of one or more symptoms associated with a disease or condition.

[0100] As used herein, the term "solid phase peptide synthesis" refers to the *in vitro* synthesis of polypeptide molecules immobilized on a solid surface. The general principle of SPPS is one of repeated cycles of coupling-wash-deprotection-wash. The free N-terminal amine of a solid-phase attached peptide is coupled to a single N-protected amino acid unit. This unit is then deprotected, revealing a new N-terminal amine to which a further amino acid may be attached. Solid phase peptide synthesis was originally described in Merrifield *et al.*, "Solid Phase Peptide Synthesis. I. The Synthesis of a Tetrapeptide". J. Am. Chem. Soc. 85 (14): 2149-2154 (1963). For example, the compounds of the present disclosure can be synthesised using solid-phase peptide synthesis as described in "Fmoc Solid Phase Peptide Synthesis - A Practical Approach", edited by W. C. Chan, P. D. White, Oxford University Press, New York 2000 and references therein. Solid phase peptide synthesis includes the synthesis of polypeptides comprising natural amino acids, unnatural amino acids including D-amino acids, peptide/protein backbone modification, and conjugation of peptidic and non-peptidic moieties.

II. Chimeric Proteins

[0101] The present invention is directed to a chimeric protein comprising an activatable clotting factor and an enhancer moiety. The activatable clotting factor in the chimeric protein is administered as an inactive form (i.e., zymogen) and is activated by a protease after

administration in vivo, for example, at the site of an injury. Once the activatable clotting factor is activated, the enhancer moiety associated with or linked to the activated clotting factor can enhance the activity of the clotting factor by acting as a partner in the coagulation pathway. Therefore, the chimeric protein of the invention can also be described as an enhanced or improved zymogen or an enhanced or improved zymogen fusion protein (e.g., FVII enhanced zymogen fusion protein or FX enhanced zymogen fusion protein). Examples of the activatable clotting factors useful for the chimeric protein include, but are not limited to, Factor VII or Factor X as described in section (A) below.

[0102] The activatable clotting factor is further improved by bringing an enhancer moiety (e.g., a clotting cofactor, e.g., Tissue Factor) in close proximity to the activatable clotting factor. Thus, when the clotting factor is cleaved into a heterodimer, the enhancer moiety can interact with the clotting factor heterodimer and can induce conformational changes to enhance the procoagulant activities. Examples of the enhancer moiety useful for the invention include, but are not limited to, a clotting cofactor, a procoagulant peptide, or an antigen binding moiety as described in section (B) below. In some embodiments, the enhancer moiety interacts with the clotting factor without cleavage of the clotting factor into a heterodimer.

[0103] While cleavage of a light chain from a heavy chain of a clotting factor makes two-chain activated form of the clotting factor, the clotting factor may still be present as a zymogen-like protein when the N-terminus of the heavy chain is not completely cleaved. One embodiment of the invention includes a chimeric protein comprising a heterodimeric zymogen-like protein comprising a light chain and a heavy chain, wherein the N-terminus of the heavy chain is linked to a protease-cleavage site. The cleavage of the protease-cleavage site at the site of injury can activate the clotting factor in vivo.

[0104] In one embodiment, an activatable clotting factor in a chimeric protein is linked to an enhancer moiety by a covalent bond, e.g., a peptide bond, a disulfide 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. In another embodiment, the linkage between the activatable clotting factor and the enhancer moiety 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 some embodiments, the linkage between the activatable clotting factor and the enhancer moiety is a covalent bond or a non-covalent bond, but is not a chemical crosslinking, e.g., a photo reactive bond. In a particular embodiment, the linkage between the activatable clotting factor and the enhancer moiety is a disulfide bond.

[0105] In one aspect, a chimeric protein comprising an activatable clotting factor and an enhancer moiety further comprises one or more linker moieties. For example, a chimeric protein can comprise a formula of Ac-L-Em or Em-L-Ac, wherein Ac is an activatable clotting factor, L is a linker moiety, and Em is an enhancer moiety. In one embodiment, the linker moiety can be a peptide linker. Non-limiting examples of the peptide linkers are described in section (D) below. In another embodiment, the linker moiety is a low complex polypeptide, e.g., an XTEN sequence. A linker moiety useful for the chimeric protein comprises at least about five, at least about 10, at least about 20, at least about 30, at least about 40, at least about 50, at least about 60, at least about 70, at least about 80, at least about 90, at least about 100, at least about 110, at least about 120 amino acids, at least 150 amino acids, at least 200 amino acids, at least 500 amino acids, at least 1000 amino acids, or at least 2000 amino acids.

[0106] In another aspect, the chimeric protein of the invention comprises an activatable clotting factor, an enhancer moiety, and one or more heterologous moieties (sometimes indicated herein as Het, Het1, or Het2). Heterologous moieties can comprise a heterologous polypeptide moiety, a non-polypeptide moiety, or both. The heterologous polypeptide moiety can be selected from an immunoglobulin constant region or portion thereof, albumin or a fragment, derivative, or variant thereof, an albumin binding moiety, an albumin binding small molecule, a PAS sequence, an XTEN sequence, a HAP sequence, transferrin or a fragment, derivative, or variant thereof, or any combination thereof. In other embodiments, the heterologous moiety is an immunoglobulin constant region or portion thereof, e.g., an Fc moiety. In still other embodiments, the non-polypeptide moiety is selected from polyethylene glycol (PEG), polysialic acid, hydroxyethyl starch (HES), a derivative thereof, or any combinations thereof. The heterologous moiety can be linked to the N-terminus or C-terminus of the activating clotting factor (either the light chain, the heavy chain, or both) or inserted between two amino acids within the activating clotting factor (either the light chain, the heavy chain, or both) or to the N-terminus or C-terminus of the enhancing moiety or

inserted between two amino acids within the enhancing moiety. Examples of the heterologous moiety are described in section (C) below.

[0107] In some embodiments, a chimeric protein comprises two or more heterologous moieties. The chimeric protein comprising two or more heterologous moieties can have a single polypeptide chain, two polypeptide chains, three polypeptide chains, or more. For example, a chimeric protein can comprise a single chain represented by a formula of Ac-Het1-Em-Het2, Het2-Em-Het1-Ac, Ac-Em-Het1-Het2, Het2-Het1-Em-Ac, Het1-Het2-Ac-Em, Em-Ac-Het2-Het1, Het1-Em-Het2-Ac, Ac-Het1-Em-Het2, Em-Het2-Ac-Het1, Het1-Ac-Het2-Em, Het2-Ac-Het1-Em, and Em-Het1-Ac-Het2, wherein Ac is an activatable clotting factor, Het1 is a first heterologous moiety, Em is an enhancer moiety, Het2 is a second heterologous moiety, and (-) is a peptide bond or one or more amino acids.

[0108] The chimeric protein comprising two polypeptide chain can be represented by a formula of Ac-Het1: Em-Het2, Het1-Ac:Het2-Em, Ac-Het1:Het2-Em, or Het1-Ac:Em-Het2, wherein Ac is an activatable clotting factor, Em is an enhancer moiety, Het1 is a first heterologous moiety (e.g., a first Fc moiety), Het2 is a second heterologous moiety (e.g., a second Fc moiety), (-) is a peptide bond or one or more amino acids, and (:) is an association between the two polypeptide chains (e.g., Ac-Het1 and Em-Het2). The association (:) as set forth herein represents a covalent bond or a non-covalent bond, e.g., at least one non-peptide bond. In one embodiment, the association, i.e., (:), is a covalent bond. In another embodiment, the association, i.e., (:), is a non-covalent interaction, e.g., an ionic interaction, a hydrophobic interaction, a hydrophilic interaction, a Van der Waals interaction, a hydrogen bond. In other embodiments, (:) is a non-peptide covalent bond. In still other embodiments, (:) is a peptide bond. In yet other embodiments, (:) in formulas set forth herein represents a physical or chemical association between two sequences, but not a chemical crosslinking, wherein a portion of the first sequence is in close proximity to the second sequence such that the first sequence and the second sequence interacts with each other upon activation of either or both the first sequence and the second sequence.

[0109] Formulas set forth herein are merely non-limiting examples of constructs of the present invention. The orientation of the polypeptide formulas is shown from N-terminus (left) to C-terminus (right). For example, formula Ac-Het1 means formula NH₂-Ac-Het1-COOH. In addition, (:) can be an association or interaction between two polypeptide chains by a covalent bond or a non-covalent bond between any part of the first chain and any part of

the second chain unless otherwise noted. For example, formula Ac-Het1:Em-Het2 has two polypeptide chains, the first chain being Ac-Het1 and the second chain being Em-Het2, wherein Ac in the first chain interacts or associates with Em in the second chain and/or Het1 in the first chain interacts or associates with Het2 in the second chain. In some embodiments, (:) means a covalent, non-peptide bond or non-covalent bond.

[0110] In a further aspect, a chimeric protein of the invention comprises an activatable clotting factor, an enhancer moiety, one or more linker moieties, and one or more heterologous moieties. In one embodiment, the chimeric protein comprises an activatable clotting factor (Ac), an enhancer moiety (Em), one linker moiety (L), and one heterologous moiety (Het), wherein the components are linked to or associated with each other. The chimeric protein can be represented by a formula of Ac-L-Het: Em, Het-L-Ac:Em, Em-L-Het:Ac, Het-L-Em:Ac, Ac-L-Het-Em, or Em-Het-L-Ac. In another embodiment, the chimeric protein comprises an activatable clotting factor (Ac), an enhancer moiety (Em), two linker moieties (L1 and L2), and one heterologous moiety (Het). The chimeric protein can be represented by a formula of Ac-L1-Het-L2-Em and Em-L2-Het-L1-Ac. In other embodiments, the chimeric protein comprises an activatable clotting factor (Ac), an enhancer moiety (Em), two linker moieties (L1 and L2), and two heterologous moieties (Het1 and Het2), wherein the components are linked to or associated with each other. The chimeric protein can be represented by a formula Ac-L1-Het1: Em-L2-Het2, Het1-L2-Ac:Em-L2-Het2, or Het1-L2-Ac:Het2-L2-Em, wherein Ac comprises, consisting essentially of, or consisting of an activatable clotting factor, L1 comprises, consisting essentially of, or consisting of an first optional linker moiety, e.g., a first linker, Het1 comprises, consisting essentially of, or consisting of a first heterologous moiety (e.g., a first Fc moiety), Em comprises, consisting essentially of, or consisting of an enhancer moiety, L2 comprises, consisting essentially of, or consisting of a second optional linker moiety, e.g., a second linker, Het2 comprises, consisting essentially of, or consisting of a second optional heterologous moiety (e.g., a second Fc moiety), (-) comprises, consisting essentially of, or consisting of a peptide bond or one or more amino acids, and (:) is an association between Ac-L1-Het1 and Em-L2-Het2. The association (:) as set forth herein represents a covalent bond or a non-covalent bond, e.g., at least one non-peptide bond. In one embodiment, the association, i.e., (:), is a covalent bond. In a particular embodiment, the association (:) is a disulfide bond between Het1 and Het2. In another embodiment, the association, i.e., (:), is a

non-covalent interaction, e.g., an ionic interaction, a hydrophobic interaction, a hydrophilic interaction, a Van der Waals interaction, a hydrogen bond. In other embodiments, (:) is a non-peptide covalent bond. In still other embodiments, (:) is a peptide bond. In yet other embodiments, (:) in formulas set forth herein represents a physical or chemical association between two sequences, but not a chemical crosslinking, wherein a portion of a first sequence is in close proximity to a second sequence such that the first sequence and the second sequence interacts with each other upon activation of either or both the first sequence and the second sequence.

[0111] In certain aspects, a chimeric protein of the invention comprises a first polypeptide chain and a second polypeptide chain, wherein the first polypeptide chain comprises an activatable clotting factor and the second polypeptide chain comprises an enhancer moiety, wherein the first polypeptide chain and the second polypeptide chain are linked to or associated with each other. The chimeric protein can further comprise a dimeric heterologous moiety region comprising a first heterologous moiety, Het1 (e.g., a first Fc moiety, e.g., F1) and a second heterologous moiety, Het2 (e.g., a second Fc moiety, e.g., F2), wherein the first heterologous moiety is in the first polypeptide chain and the second heterologous moiety is in the second polypeptide chain. For example, a chimeric protein can comprise a structure selected from:

- (a) Ac linked to Het1 via the linker moiety, and Em linked to Het2;
- (b) Ac linked to Het1 via the first linker moiety, and Em linked to Het2 via the second linker moiety ;
- (c) Ac linked to Het1, and Em is linked to Het2 via the linker moiety;
- (d) Ac linked to Het1, and Em linked to Het2;
- (e) Em linked to Het1 via the linker moiety, and Ac linked to Het2;
- (f) Em linked to Het1 via the first linker moiety, and Ac linked to Het2 via the second linker moiety;
- (g) Em linked to Het1, and Ac is linked to Het2 via the linker moiety; or,
- (h) Em linked to Het1, and Ac linked to Het2, wherein Het1 and Het2 form a disulfide bond.

[0112] The chimeric protein comprising two polypeptides can also be represented as set forth below:

(a) the first polypeptide comprises a structure represented by the formula Ac-L1-Het1, and the second polypeptide comprises a structure represented by the formula Em-Het2;

(b) the first polypeptide comprises a structure represented by the formula Ac-L1-Het1, and the second polypeptide comprises a structure represented by the formula Em-L2-Het2;

(c) the first polypeptide comprises a structure represented by the formula Ac-Het1, and the second polypeptide comprises a structure represented by the formula Em-L2-Het2;

(d) the first polypeptide comprises a structure represented by the formula Ac-Het1, and the second polypeptide comprises a structure represented by the formula Em-L1-Het2;

(e) the first polypeptide comprises a structure represented by the formula Em-L2-Het1, and the second polypeptide comprises a structure represented by the formula Ac-L1-Het2;

(f) the first polypeptide comprises a structure represented by the formula Em-L1-Het1, and the second polypeptide comprises a structure represented by the formula Ac-Het2;

(g) the first polypeptide comprises a structure represented by the formula Em-Het1, and the second polypeptide comprises a structure represented by the formula Ac-L1-Het2; and,

(h) the first polypeptide comprises a structure represented by the formula Em-Het1, and the second polypeptide comprises a structure represented by the formula Ac-Het2;

wherein Het1 and Het2 of the two polypeptide chains form a disulfide bond.

[0113] In yet other aspects, the chimeric protein comprises an activatable clotting factor (Ac), an enhancer moiety (Em), three linker moieties (L1, L2, and X), and two heterologous moieties (Het1 and Het2), wherein the components are linked to each other. The chimeric protein can comprise by a formula selected from Ac-Het1-X-Em-Het2 or Het2-Em-X-Het1-Ac, wherein Ac is an activatable clotting factor, Het1 is a first heterologous moiety, X is a scFc linker, Em is an enhancer moiety, and Het2 is a second heterologous moiety. The chimeric protein can also comprise one or more linker moieties. For example, a chimeric

protein can comprise a formula selected from Ac-L1-Het1-X-Em-Het2, Ac-Het1-X-Em-L2-Het2, Ac-L1-Het1-X-Em-L2-Het2, Het2-Em-X-Het1-L1-Ac, Het2-L2-Em-X-Het1-Ac, or Het2-L2-Em-X-Het1-L1-Ac, wherein Ac is an activatable clotting factor, L1 is a first optional linker moiety, Het1 is a first heterologous moiety, X is a scFc linker, Em is an enhancer moiety, L2 is a second optional linker moiety, and Het2 is a second heterologous moiety.

[0114] In one embodiment, either or both of the heterologous moieties (Het1 and Het2) are a heterologous polypeptide moiety, which are the same or different. In another embodiment, either or both of Het1 and Het2 are a non-polypeptide moiety. In other embodiments, either or both of the heterologous moieties (Het1 and Het2) can be a half-life extender. Examples of the half-life extender include, but are not limited to, an immunoglobulin constant region or a portion thereof, albumin, transferrin, an albumin binding moiety, a PAS sequence, a HES sequence, the β subunit of the C-terminal peptide (CTP) of human chorionic gonadotropin, polyethylene glycol (PEG), an XTEN sequence, hydroxyethyl starch (HES), albumin-binding small molecules, von Willebrand Factor or a fragment, derivative, or variant thereof, or any combinations thereof. Examples of the heterologous moiety are shown in section (C) below.

[0115] In another embodiment, the first and second heterologous moieties (Het1 and Het2) are linked to each other by a peptide bond or a linker (e.g., scFc linker (sometimes also indicated as "X")) or associated by a covalent or non-covalent bond, e.g., a disulfide bond. For example, a scFc linker can link a first Fc moiety and a second Fc moiety, thereby forming a dimeric Fc region. The scFc linker can further comprise an intracellular processing site, which enables processing of the chimeric protein when expressed in a host cell. Examples of the scFc linker are shown in section (C.3) below.

[0116] Each component of the chimeric proteins is described below.

A. Activatable Clotting Factors

1. Clotting Factors

[0117] In particular, the invention pertains to improved versions of factors VII and X. These factors are all structurally related in that in each the amino terminal end of the light chain is not amenable to the incorporation of additional moieties. Similarly, the amino terminal end of the heavy chain of these three clotting factors is not amenable to the

incorporation of additional moieties, with the exception of cleavable moieties, i.e., moieties linked via a cleavage site or moieties which consist of a cleavage site. The chimeric clotting factor constructs of the invention were designed based on these shared properties and it will be understood that although factor VII is often shown to illustrate exemplary embodiments of the invention, the subject constructs may be made using factor VII or X. For example, one of skill in the art would understand that the FVII portion of a construct of the invention could be substituted with a FX portion to make an enhanced version of one of these clotting factors.

[0118] Clotting factors given for bypass therapy are efficacious when given in the activated form, since exogenous clotting factors are often not activated with sufficient kinetics to be effective. However, they are also rapidly inactivated by endogenous pathways (e.g., by antithrombin III or TFPI), leading to clearance of the active form and a short effective half-life. In order to prevent rapid inactivation by endogenous enzymes and clearance, the chimeric clotting factor of the invention is constructed as an "activatable" form. Such activatable constructs circulate as an enhanced zymogen with a longer half-life, but can be readily cleaved at the site of clotting when necessary.

[0119] Exemplary chimeric clotting factor constructs of the invention are set forth in the accompanying Figures. The chimeric clotting factor useful for the invention is expressed in inactive form, is subsequently administered as inactive form, and then is activated upon administration in vivo. Inactive forms of Factors VII and X are single chain zymogens. Active forms of Factors VII and X are comprised of dimeric molecules in which the heavy chain and the light chain are linked by a covalent bond, e.g., a disulfide bond.

[0120] An activatable clotting factor comprises a light chain of the clotting factor zymogen linked to a protease-cleavage site, which is further linked to a heavy chain of the clotting factor zymogen. The light chain or the heavy chain of the clotting factor zymogen can include a fragment, a variant, a derivative, or an analog thereof that retains the function of the light chain or the heavy chain of the clotting factor zymogen, respectively.

[0121] In one embodiment, a clotting factor of the invention is a mature form of Factor VII or a variant thereof. Factor VII (FVII, F7; also referred to as Factor 7, coagulation factor VII, serum factor VII, serum prothrombin conversion accelerator, SPCA, proconvertin and eptacog alpha) is a serine protease that is part of the coagulation cascade. FVII includes a Gla domain, two EGF domains (EGF-1 and EGF-2), and a serine protease domain (or peptidase S1 domain) that is highly conserved among all members of the peptidase S1 family of serine

proteases, such as for example with chymotrypsin. FVII occurs as a single chain zymogen (i.e., activatable FVII) and a fully activated two-chain form.

[0122] As used herein, the term "a FVII protein" includes wild-type FVII, mature FVII, full-length FVII, a functional fragment of FVII, a variant, or a derivative thereof. Exemplary FVII variants include those with increased specific activity, e.g., mutations that increase the activity of FVII by increasing its enzymatic activity (K_{cat} or K_m). Such variants have been described in the art and include, e.g., mutant forms of the molecule as described for example in Persson et al. 2001. PNAS 98:13583; Petrovan and Ruf. 2001. J. Biol. Chem. 276:6616; Persson et al. 2001 J. Biol. Chem. 276:29195; Soejima et al. 2001. J. Biol. Chem. 276:17229; Soejima et al. 2002. J. Biol. Chem. 247:49027. In one embodiment, a variant form of FVII includes the mutations. Exemplary mutations include V158D-E296V-M298Q. In another embodiment, a variant form of FVII includes a replacement of amino acids 608-619 (LQQSRKVGDSPN, corresponding to the 170-loop) from the FVII mature sequence with amino acids EASYPGK from the 170-loop of trypsin. High specific activity variants of FIX are also known in the art. For example, Simioni et al. (2009 N.E. Journal of Medicine 361:1671) describe an R338L mutation. Chang et al. (1988 JBC 273:12089) and Pierri et al. (2009 Human Gene Therapy 20:479) describe an R338A mutation. Other mutations are known in the art and include those described, e.g., in Zogg and Brandstetter. 2009 Structure 17:1669; Sichler et al. 2003. J. Biol. Chem. 278:4121; and Sturzebecher et al. 1997. FEBS Lett 412:295. The contents of these references are incorporated herein by reference. Exemplary FVII amino acid and nucleotide sequences are disclosed in the Sequence Listing as a portion of SEQ ID NOs: 44 and 45, respectively.

[0123] Factor VII or Factor X activation occurs when the immediate upstream of a heavy chain of a FVII zymogen or a FX zymogen is cleaved. For example, FVII is activated when the immediate upstream of the first residue of the FVII heavy chain, i.e., Ile-153, is cleaved.

[0124] In one embodiment, a clotting factor of the invention is a mature form of Factor X. Factor X is a vitamin-K dependent glycoprotein of a molecular weight of 58.5 kDa, which is secreted from liver cells into the plasma as a zymogen. Initially factor X is produced as a prepropeptide with a signal peptide consisting in total of 488 amino acids. The signal peptide is cleaved off by signal peptidase during export into the endoplasmic reticulum, the propeptide sequence is cleaved off after gamma carboxylation took place at the first 11 glutamic acid residues at the N-terminus of the mature N-terminal chain. A further processing

step occurs by cleavage between Arg182 and Ser183. This processing step also leads concomitantly to the deletion of the tripeptide Arg180-Lys181-Arg182. The resulting secreted factor X zymogen consists of an N-terminal light chain of 139 amino acids (M, 16,200) and a C-terminal heavy chain of 306 amino acids (M, 42,000) which are covalently linked via a disulfide bridge between Cys172 and Cys342. Further posttranslational processing steps include the .beta.-hydroxylation of Asp103 as well as N- and O-type glycosylation.

Table 1.

Amino acid Sequence of Factor X zymogen (SEQ ID NO: 11)					
MGRPLHLVLL	SASLAGLLLL	GESLFIRREQ	ANNILARVTR	ANSFLEEMKK	GHLERECMEE
TCSYEEAREV	FEDSDKTNEF	WNKYKDGDQC	ETSPCQNQ GK	CKDGLGEYTC	TCLEGFEGKN
CELFTRKLCS	LDNGDCDQFC	HEEQNSVVC S	CARGYTLADN	GKACIPTGPY	PCGKQTLERR
KRSVAQATSS	SGEAPDSITW	KPYDAADLDP	TENPFDLLDF	NQTQPERGDN	NLTRIVGGQE
CKDGECPWQA	LLINEENEGF	CGGTILSEFY	ILTAAHCLYQ	AKRFKVRVGD	RNTEQEEGGE
AVHEVEVVIK	HNRFTKET YD	FDIAVLRLKT	PITFRMNVAP	ACLPERDWAE	STLMTQKTGI
VSGFGRTHEK	GRQSTRLKML	EVPIVDRNSC	KLSSSFIIITQ	NMFCAGYDTK	QEDACQGDSG
GPHVTRFKDT	YFVTGIVSWG	EGCARKGKYG	IYTKVT AFLK	WIDRSMKTRG	LPKAKSHAPE
VITSSPLK					
Nucleotide Sequence Encoding Factor X Zymogen (SEQ ID NO: 12)					
atggggcgcc	cactgcacct	cgctctgctc	agtgcctccc	tggetggcct	cctgctgctc
ggggaaagtc	tgttcatccg	cagggagcag	gccacaaca	tcctggcgag	ggtcacgagg
gccaatccct	ttcttgaaga	gatgaagaaa	ggacacctcg	aaagagagtg	catggaagag
acctgctcat	acgaagaggc	ccgcgaggtc	tttgaggaca	gcgacaagac	gaatgaattc
tggaataaat	acaaagatgg	cgaccagtgt	gagaccagtc	cttgccagaa	ccagggcaaa
tgtaaagacg	gcctcgggga	atacacctgc	acctgtttag	aaggattcga	aggcaaaaac
tgtgaattat	tcacacggaa	gctctgcagc	ctggacaacg	gggactgtga	ccagttctgc
cacgaggaac	agaactctgt	gggtgtgctc	tgcgcccgcg	ggtacacct	ggctgacaac
ggcaaggcct	gcattcccac	agggccctac	ccctgtggga	aacagacct	ggaacgcagg
aagaggtcag	tgcccaggc	caccagcagc	agcggggagg	cccctgacag	catcacatgg
aagccatatg	atgcagccga	cctggacccc	accgagaacc	ccttcgacct	gcttgacttc
aaccagacgc	agcctgagag	gggcgacaac	aacctcacca	ggatcgtggg	aggccaggaa
tgcaaggacg	gggagtgtcc	ctggcaggcc	ctgctcatca	atgaggaaaa	cgagggtttc
tgtggtggaa	ccattctgag	cgagttctac	atcctaacgg	cagcccactg	tctctaccaa
gccaagagat	tcaaggtgag	ggtaggggac	cggaacacgg	agcaggagga	gggcggtgag
gcggtgcacg	aggtggaggt	ggtcatcaag	cacaaccggg	tcacaaagga	gacctatgac
ttcgacatcg	ccgtgctccg	gctcaagacc	cccatcacct	tcgcgatgaa	cgtggcgccct
gcctgcctcc	ccgagcgtga	ctgggcgag	tcacgcgtga	tgacgcagaa	gacggggatt
gtgagcggct	tcgggcgcac	ccacgagaag	ggccggcagt	ccaccaggct	caagatgctg
gaggtgccct	acgtggacgc	caacagctgc	aagctgtcca	gcagcttcat	catcaccacg
aacatgtttc	gtgccggcta	cgacaccaag	caggaggatg	cctgccaggg	ggacagcggg
ggeccgcacg	tcaccgcctt	caaggacacc	tacttcgtga	caggcatcgt	cagctgggga
gagggctgtg	cccgttaagg	gaagtacggg	atctacacca	aggtcacccg	cttctcaag
tggtatcgaca	ggtccatgaa	aaccaggggc	ttgcccaggg	ccaagagcca	tgccccggag
gtcataacgt	cctctccatt	aaagtga			

[0125] It will be understood that in addition to wild type (WT) versions of these clotting factors or biologically active portions thereof, the present invention may also employ precursor truncated forms thereof that have activity, allelic variants and species variants, variants encoded by splice variants, and other variants, including polypeptides that have at least 40%, 45%, 50%, 55%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the mature form of the clotting factor and which retain the ability to promote clot formation. For example, modified FVII polypeptides and variants thereof which retain at least one activity of a FVII, such as TF binding, factor X binding, phospholipid binding, and/or coagulant activity of a FVII may be employed. By retaining activity, the activity can be altered, such as reduced or increased, as compared to a wild-type clotting factor so long as the level of activity retained is sufficient to yield a detectable effect. Exemplary sequences of clotting factors that can be used in the constructs of the invention are found in the accompanying sequence listing.

[0126] Exemplary modified polypeptides include, but are not limited to, tissue-specific isoforms and allelic variants thereof, synthetic molecules prepared by translation of nucleic acids, proteins generated by chemical synthesis, such as syntheses that include ligation of shorter polypeptides, through recombinant methods, proteins isolated from human and non-human tissue and cells, chimeric polypeptides and modified forms thereof. The instant clotting factors may also consist of fragments or portions of WT molecules that are of sufficient length or include appropriate regions to retain at least one activity (upon activation if needed) of a full-length mature polypeptide. Exemplary clotting factor variants are known in the art.

[0127] In one embodiment, activatable clotting factors are modified to lack a Gla domain. In the case of Factor VII, the Gla domain is present at the amino terminus of the light chain and consists of amino acids 1-35. The GLA domain is responsible for the high-affinity binding of calcium ions. It starts at the N-terminal extremity of the mature form of proteins and ends with a conserved aromatic residue. A conserved Gla-x(3)-Gla-x-Cys motif is found in the middle of the domain which seems to be important for substrate recognition by the carboxylase.

[0128] Using stopped-flow fluorescence kinetic measurements in combination with surface plasmon resonance analysis, the Gla domain has been found to be important in the sequence of events whereby the protease domain of FVIIa initiates contact with sTF

(Biochemical and Biophysical Research Communications. 2005. 337:1276). In addition, clearance of clotting factors may be significantly mediated through Gla interactions, e.g., on liver cells and clearance receptors, e.g., EPCR.

[0129] Therefore, the Gla domain is responsible for mediating clearance of clotting factors via multiple pathways, such as binding to liver cells, clearance receptors such as EPCR, etc. Thus, eliminating the Gla domain has beneficial effects on half-life of the clotting factors. The Gla domain of factor VII comprises the uncommon amino acid γ -carboxyglutamic acid (Gla), which plays a vital role in the binding of clotting factors to negatively charged phospholipid surfaces.

[0130] Exemplary clotting factors are those of mammalian, e.g., human, origin. The sequences of exemplary clotting factors are presented in the accompanying sequence listing, e.g., alone or in the context of a chimeric clotting factor construct.

2. Protease-Cleavage Site

[0131] A protease-cleavage site linking a light chain of a clotting factor zymogen and a heavy chain of the clotting factor zymogen can be selected from any protease-cleavage site known in the art. In one embodiment, the protease-cleavage site is cleaved by a protease selected from factor XIa, factor XIIa, kallikrein, factor VIIa, factor IXa, factor Xa, factor IIa (thrombin), or any combinations thereof. The protease-cleavage sites allow the light chain and the heavy chain of the clotting factor to be cleaved and dissociated from each other at the site of injury. Exemplary FXIa cleavage sites include, e.g., KLTR (SEQ ID NO: 13), DFTR (SEQ ID NO: 14), TQSFNDFTR (SEQ ID NO: 6) and SVSQTSKLTR (SEQ ID NO: 7). Exemplary thrombin cleavage sites include, e.g., DFLAEGGGVR (SEQ ID NO: 8), TTKIKPR (SEQ ID NO: 9), LVPRG (SEQ ID NO: 10) and ALRPR (SEQ ID NO: 1).

[0132] In some embodiments, the protease-cleavage site can be combined with an intracellular processing site for efficient cleavage and activation. For example, an activatable clotting factor in the chimeric protein may comprise a heterodimer, which comprises a light chain of a clotting factor associated with a heavy chain of the clotting factor by a covalent bond, wherein the N-terminus of the heavy chain of the clotting factor is linked to a protease-cleavage site. The protease-cleavage site can be cleaved off at the site of coagulation, thus activating the clotting factor. Such constructs can be designed by inserting an intracellular processing site between the light chain of the clotting factor zymogen and the protease-

cleavage site, which is linked to the heavy chain of the clotting factor zymogen. The intracellular processing site inserted therein can be processed (cleaved) by an intracellular processing enzyme upon expression in a host cell, thereby allowing formation of a zymogen-like heterodimer. Examples of the intracellular processing enzymes include furin, a yeast Kex2, 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.

3. Self-Immolative Moiety

[0133] In certain embodiments, the protease-cleavage site is linked to a heavy chain of a clotting factor zymogen via a self-immolative moiety. The term "self-immolative moiety" as used herein refers to a bifunctional chemical moiety which is capable of covalently linking together two spaced moieties (e.g., a heavy chain of a clotting factor and a protein-cleavage site) into a normally stable tripartate molecule. The self-immolative moiety will spontaneously separate from the second moiety (e.g., a heavy chain of a clotting factor) if it is bound to the first moiety (e.g., a protein-cleavage site) is cleaved.

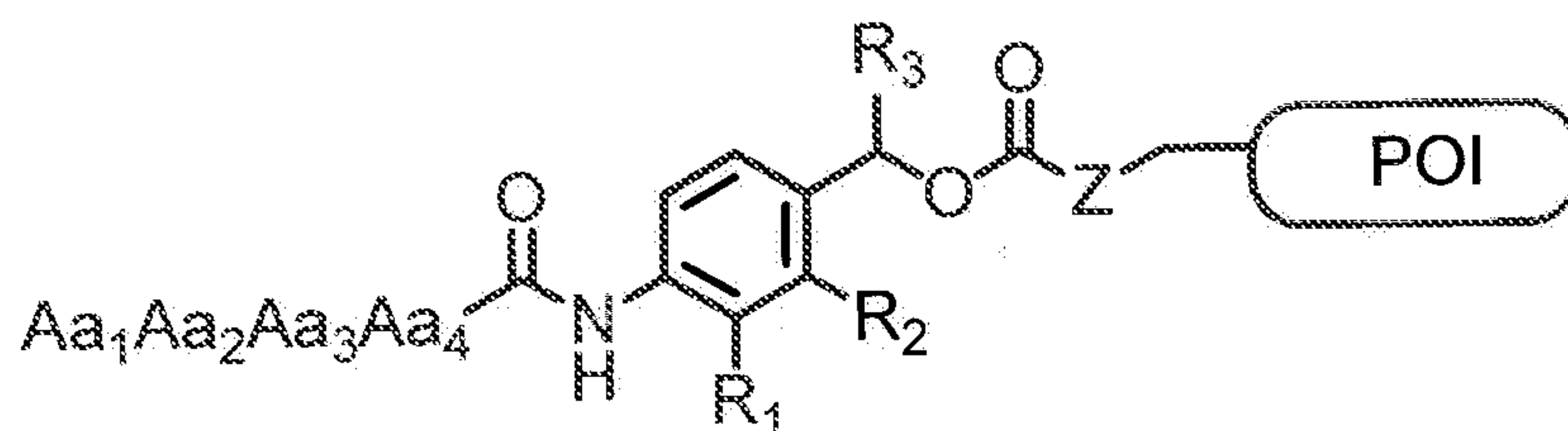
[0134] In some aspects, the self-immolative moiety comprises an aminobenzyl carbamate group, an aminobenzyl ether group, or an aminobenzyl carbonate group. In one aspect, the self-immolative moiety is p-amino benzyl carbamate (PABC).

[0135] P-amino benzyl carbamate (PABC) is the most efficient and most widespread connector linkage for self-immolative site-specific prodrug activation (see, e.g., Carl *et al.* J. Med. Chem. 24:479-480 (1981); WO 1981/001145; Rautio *et al.*, Nature Reviews Drug Discovery 7:255-270 (2008); Simplicio *et al.*, Molecules 13:519-547 (2008);). PABC allows the release of any amine drugs, peptides, and proteins upon cleavage by a protease and 1,6 spontaneous fragmentation.

[0136] The aromatic ring of the aminobenzyl group may optionally be substituted with one or more (e.g., R₁ and/or R₂) substituents on the aromatic ring, which replace a hydrogen that is otherwise attached to one of the four non-substituted carbons that form the ring. As used herein, the symbol "R_x" (e.g., R₁, R₂, R₃, R₄) is a general abbreviation that represents a substituent group as described herein.

[0137] Substituent groups can improve the self-immolative ability of the p-aminobenzyl group (Hay *et al.*, J. Chem Soc., Perkin Trans. 1:2759-2770 (1999); see also, Sykes *et al.* J. Chem. Soc., Perkin Trans. 1:1601-1608 (2000)).

[0138] The following formula shows the general topology of a p-amino benzyl immolative linker and the relative locations of an exemplary protease-cleavage site (Aa₁Aa₂Aa₃Aa₄) and a heavy chain of a clotting factor (POI). The formula indicates possible locations of R substituent groups (R₁, R₂, R₃).



(Formula I)

[0139] The substituents, which may be a single atom, *e.g.*, a halogen, or a multi-atom group, *e.g.*, methyl, are selected in order to impact the stability of the aminobenzyl or the decomposition product thereof. Electron withdrawal from the ring may be used to facilitate the spontaneous decomposition of the aminobenzyl group from the drug after cleavage of the bond between the amino group of the aminobenzyl group and the adjacent peptide linkage. Exemplary aromatic group R₁, R₂, or R₃ substituents include, for example, F, Cl, I, Br, OH, methyl, methoxy, NO₂, NH₂, NO³⁺, NHCOCH₃, N(CH₃)₂, NHCOCF₃, alkyl, haloalkyl, C₁-C₈ alkylhalide, carboxylate, sulfate, sulfamate, sulfonate, etc. (see, *e.g.*, U.S. Patent Nos. 7,091,186 and 7,659,241). The p-aminobenzyl linker can comprise a heteroatom Z connected to the amino terminus of the peptide or protein of interest protein. The term heteroatom, as used herein, includes oxygen (O), nitrogen (N), sulfur (S), silicon (Si), boron (B) and phosphorus (P). In one embodiment, the heteroatoms in Z are O, S or N.

[0140] In some embodiments, only one of the four non-substituted carbons in the p-aminobenzyl ring is substituted. In some other embodiments, two of the four non-substituted carbons in the p-aminobenzyl ring are substituted. In other embodiments, three of the four non-substituted carbons in the p-aminobenzyl ring are substituted. In some embodiments, the four non-substituted carbons in the p-aminobenzyl ring are substituted.

[0141] Self-immolative elimination can take place, *e.g.*, via 1,4 elimination, 1,6 elimination (*e.g.* PABC), 1,8 elimination (*e.g.* p-amino-cinnamyl alcohol), cyclisation-

elimination (*e.g.*, 4-aminobutanol ester and ethylenediamines), etc. In some aspects, the self-immolative moiety can comprise, *e.g.*, an cinnamyl, naphthyl, or biphenyl groups (see, *e.g.*, Blencowe *et al.* Polym. Chem. 2:773-790 (2011)). In some aspects, the self-immolative moiety comprises a heterocyclic ring (see, *e.g.*, U.S. Patent Nos. 7,375,078; 7,754,681). Numerous homoaromatic (see, *e.g.*, Carl *et al.* J. Med. Chem. 24:479 (1981); Senter *et al.* J. Org. Chem. 55:2975 (1990); Taylor *et al.* J. Org. Chem. 43:1197 (1978); Andrianomenjanahary *et al.* Bioorg. Med. Chem. Lett. 2:1903 (1992)), and coumarin (see, *e.g.*, Weinstein *et al.* Chem. Commun. 46:553 (2010)), furan, thiophene, thiazole, oxazole, isoxazole, pyrrole, pyrazole (see, *e.g.*, Hay *et al.* J. Med. Chem. 46:5533 (2003)), pyridine (see, *e.g.*, Perry-Feigenbaum *et al.* Org. Biomol. Chem. 7:4825 (2009)), imidazone (see, *e.g.*, Nailor *et al.* Bioorg. Med. Chem. Lett. Z:1267 (1999); Hay and Denny, Tetrahedron Lett. 38:8425 (1997)), and triazole (see, *e.g.*, Bertrand and Gesson, J. Org. Chem. 72:3596 (2007)) based heteroaromatic groups that are self-immolative under both aqueous and physiological conditions are known in the art. See also, U.S. Pat Nos. 7,691,962; 7,091,186; U.S. Pat. Publ. Nos. US2006/0269480; US2010/0092496; US2010/0145036; US2003/0130189; US2005/0256030)

[0142] Where substituent groups in the self-immolative linkers are specified by their conventional chemical formulae, written from left to right, they equally encompass the chemically identical substituents, which would result from writing the structure from right to left. For example, “-CH₂O-” is intended to also recite “-OCH₂-”. Substituent groups in self-immolative, for example, R₁ and/or R₂ substituents in a p-aminobenzyl self-immolative linker as discuss above can include, *e.g.*, alkyl, alkylene, alkenyl, alkynyl, alkoxy, alkylamino, alkylthio, heteroalkyl, cycloalkyl, heterocycloalkyl, aryl, arylalkyl, aryloxy, heteroaryl, etc. When a compound of the present disclosure includes more than one substituent, then each of the substituents is independently chosen.

B. Enhancer Moieties (Em)

[0143] The present invention provides an improved or enhanced activatable clotting factor such that by fusing the activatable clotting factor to an “enhancer moiety,” the properties of an activatable clotting factor of the invention are improved compared to the activatable clotting factor which is not fused to the enhancer moiety. The improved properties include a procoagulant activity of the clotting factor. The increase in the procoagulant activity is relative to the free, or un-fused, activatable clotting factor. An

enhancer moiety can be any molecule which has the ability to enhance the procoagulant activity of a clotting factor. The enhancer moiety useful for the invention can have a physical interaction with the activatable clotting factor, and the physical interaction can induce increase in procoagulant activity.

[0144] The chimeric protein of the invention can comprise one or more than one enhancer moieties. Additionally, two or more enhancer moieties may be linked to each other (*e.g.*, via a linker) in series, and the tandem array operably linked to a construct of the invention. When two or more enhancer moieties are present in a chimeric clotting factor of the invention, the moieties may be the same or different.

[0145] In one embodiment, the enhancer moiety is located on the C- terminus of the heavy chain of factor VII or factor X. In another embodiment, the enhancer moiety is located on the N-terminus of the light chain of factor VII or factor X. In other embodiments, the enhancer moiety is located on the C-terminus of the light chain of factor VII or factor X. In embodiments in which an Fc domain or portion thereof is employed, the enhancer moiety may be positioned at the N or C terminus of the second Fc moiety, or the C-terminus of either or both Fc moieties.

[0146] In one embodiment, an enhancer moiety is not genetically fused directly to a construct, but rather is linked via a linker or a chemical bond to the construct. For example, enhancer moieties may be attached to a construct of the invention by formation of a bond between the enhancer moiety and an Fc moiety of a construct, where the enhancer moiety comprises a first functional group and the Fc moiety comprises a second functional group, and where the first and second functional groups are capable of reacting with each other to form a chemical bond (see, *e.g.*, U.S. patent 7381408).

[0147] In certain embodiments, the enhancer moieties of the invention can be blood coagulation pathway proteins (*e.g.*, cofactors), procoagulant peptides, or antigen binding molecules. Examples of enhancer moieties are found in the instant examples and Figures. Other molecules useful as enhancer moieties can readily be selected by one of skill in the art based upon the teaching herein.

1. Clotting Cofactors

[0148] An enhancer moiety useful for the chimeric protein can be a clotting cofactor. The "clotting cofactor" as used herein means a clotting factor that forms a complex with

another clotting factor, e.g., Factor VII or Factor X, and becomes an activated complex having procoagulant activity. For example, a clotting cofactor for FVII is Tissue Factor, which forms the TF-FVIIa complex. A clotting cofactor for FX is FVa, which forms the prothrombinase complex and thereby activates prothrombin to thrombin.

[0149] In one embodiment, the clotting factor zymogen is a FVII protein, and the clotting cofactor is a Tissue Factor (TF) polypeptide. Tissue Factor initiates blood coagulation by forming a complex with circulating factor VII or VIIa. The [TF:VIIa] complex activates factors IX or X by specific limited proteolysis. TF plays a role in normal hemostasis by initiating the cell-surface assembly and propagation of the coagulation protease cascade. TF is also known as coagulation factor III, thromboplastin, CD142, and F3. The full-length tissue factor polypeptide has Accession Number P13726-1 in UniProtKB entry and consists of the signal peptide (amino acids 1 to 32), the extracellular domain (amino acids 33 to 251), the transmembrane domain (amino acids 252 to 274) and the cytoplasmic domain (amino acids 275 to 295), total of 295 amino acids. The nucleotide and amino acid sequences of Tissue Factor are represented herein as SEQ ID NO: 16 and SEQ ID NO: 15, respectively. An isoform of Accession Number P13726-1 (No. P13726-2) contains a substitution of amino acids 199-238: TAKTNTNEFL...TVNRKSTDSP → YSTSLELWYL...WGRAGRRTPH and a deletion of amino acids 239 to 295. Variants of human Tissue Factor include, but are not limited to, the polypeptides with the following mutations: T36A, I145V, R163W, or G281E. Also included is PCSK1 from a different species, e.g., mouse, rat, monkey, dog, drosophila, or porcine. As used herein, a tissue factor polypeptide refers to a polypeptide comprising the soluble ectodomain of Tissue Factor (sTF) (approximately amino acids 33-251), or functional variants, fragments, analogues, or derivatives thereof. sTF lacks the transmembrane and cytoplasmic domains. The full length sequence of mature human Tissue Factor is disclosed in Spicer et al. Proc. Natl. Acad. Sci, USA, 84, 5148-5152 (1987).

Table 2. Tissue Factor Sequences

Tissue Factor Amino Acid Sequence (SEQ ID NO: 15)- isoform 1					
METPAWPRVP	RPETAVARTL	LLGWVFAQVA	GASGTTNTVA	AYNLTWKSTN	FKTILEWEPK
PVNQVYTVQI	STKSGDWKSK	CFYTTDTECD	LTDEIVKDVK	QTYLARVFSY	PAGNVESTGS
AGEPLYENSP	EFTPYLETNL	GQPTIQSFEQ	VGTKVNVTV	DERTLVRN	TFSLRDVFG
KDLIYTLYYW	KSSSSGKKA	KTNTNEFLID	VDKGENYCFS	VQAVIPSRTV	NRKSTDSPVE

CMGQEKGEFR EIFYIIGAVV FVVIILVIIL AISLHKCRKA GVGQSWKENS PLNVS

Tissue Factor Nucleic Acid Sequence (SEQ ID NO: 16)

ATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCCGTCGCTCGGACGCTCCTGCTCGG
CTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTTAACTT
GGAAATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCCGTCAATCAAGTCTACACTGTT
CAAATAAGCACTAAGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAACAGACACAGAGTGTGACCT
CACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTCTTCTCCTACCCGGCAGGGA
ATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAAGTCCCCAGAGTTCACACCTTACCTG
GAGACAAACCTCGGACAGCCAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGT
AGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCCTAAGCCTCCGGGATGTTTTTGGCAAGG
ACTTAATTTATACACTTTATTATTGGAAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAAACACT
AATGAGTTTTTGTATTGATGTGGATAAAGGAGAAAACACTACTGTTTCAGTGTTCAAGCAGTGATTCCCTC
CCGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCA
GAGAAATATTCTACATCATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTGCATCATCCTGGCTATA
TCTCTACACAAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCCACTGAATGTTTC
ATAA

[0150] The tissue factor polypeptide used for the present invention comprises an amino acid sequence, which is at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to amino acids 33-251 of SEQ ID NO: 15, (sTF), wherein the amino acid sequence is capable of forming a complex with FVII or FVIIa. The term "TF protein" as used herein includes full-length TF, functional fragments (e.g., an extracellular domain), variants, analogues, or derivatives thereof. The term "soluble TF" as used herein includes any functional fragments, variants, analogues, or derivatives thereof that retain one or more activities of the complete extracellular domain of TF. In one embodiment, soluble TF (and its functional fragments, variants, analogues, or derivatives thereof) is capable of binding to FVII. In another embodiment, soluble TF can act as a clotting cofactor for FVII.

[0151] In another embodiment, the clotting factor zymogen is a FX protein, and the clotting cofactor is a FVa protein. A FVa protein serves as a critical cofactor for the prothrombinase activity of factor Xa that results in the activation of prothrombin to thrombin. Factor Va, the activated form of factor V, is composed of a heavy chain and a light chain, non-covalently bound. The interaction between the two chains is calcium-dependent. Factor V is also known as coagulation factor V, activated protein C cofactor, proaccelerin, and labile factor and can be cleaved into two chains, a heavy chain and a light chain. The full-length Factor V polypeptide has Accession No. P12259 in UniProtKB entry and consists of the signal peptide (amino acids 1 to 28), the heavy chain (amino acids 29 to 737), the activation peptide (also called as connecting region, amino acids 734 to 1573), and the light chain

(amino acids 1574 to 2224). The nucleotide and amino acid sequences of FV are represented herein as SEQ ID NO: 18 and SEQ ID NO: 17, respectively. Variants of human Factor V include, but are not limited to, the polypeptides with the following mutations: G15S, D107H, R334G, R334T, I387T, M413T, R513K, R534Q, C613R, S775A, S781R, P809S, N817T, K858R, H865R, T915S, K925E, N969S, R980L, H1146Q, L1285I, H1327R, L1397F, P1404S, E1530A, T1685S, Y1730C, L1749V, M1764V, M1820I, R2102C, R2102H, M2148T, K2185R, or D2222G. Also included is a Factor V protein from a different species, e.g., mouse, rat, monkey, dog, drosophila, or porcine.

Table 3. Factor V Sequences

Factor V Amino Acid Sequence (SEQ ID NO: 17)

```

MFPGCPRLWV LVVLGTSWVG WGSQGTEAAQ LRQFYVAAQG ISWSYRPEPT NSSLNLSVTS
FKKIVYREYE PYFKKEKPQS TISGLLGPTL YAEVGDIKLV HFKNKADKPL SIHPQGIRYS
KLSEGASYLD HTFPAEKMDD AVAPGREYTY EWSISEDSPG THDDPPCLTH IYYSHENLIE
DFNSGLIGPL LICKKGTLTE GGTQKTFDKQ IVLLFAVFDE SKSWSQSSSL MYTVNGYVNG
TMPDITVCAH DHISWHLLGM SSGPELFSIH FNGQVLEQNH HKVSAITLVS ATSTTANMTV
GPEGKWISS LTPKHLQAGM QAYIDIKNCP KKTRNLKKIT REQRRHMKRW EYFIAAEEVI
WDYAPVIPAN MDKKYRSQHL DNFSNQIGKH YKKVMYTQYE DESFTKHTVN PNMKEDGILG
PIIRAQVRDT LKIVFKNMAS RPYSIYPHGV TFSPYEDEVN SSFTSGRNNT MIRAVQPGET
YTYKWNILEF DEPTENDAQC LTRPYSDVD IMRDIASGLI GLLICKSRS LDRRGIQRAA
DIEQQAVFAV FDENKSWYLE DNINKFCENP DEVKRDDPKF YESNIMSTIN GYVPESITTL
GFCFDDTVQW HFCSVGTQNE ILTIHFTGHS FIYGKRHEDT LTLFPMRGES VTVTMDNVGT
WMLTSMNSSP RSKKLRLKFR DVKCIPDDDE DSYEIFEPPE STVMATRKMH DRLEPEDEES
DADYDYQNRL AAALGIRSER NSSLNQEEEE FNLTALEN GTEFVSSNTD IIVGSNYSSP
SNISKFTVNN LAEPQKAPSH QQATTAGSPL RHLIGKNSVL NSSTAETHSSP YSEDPIEDPL
QPDVTGIRLL SLGAGEFKSQ EHAKHKGPKV ERDQAAKHRF SWMKLLAHKV GRHLSQDTGS
PSGMRPWEDL PSQDTGSPSR MRPWKDPPSD LLLKQSNSS KILVGRWHLA SEKGSYEIIQ
DTDEDTAVNN WLISPQNASR AWGESTPLAN KPGKQSGHPK FPRVRHKSLO VRQDGGKSRL
KKSQFLIKTR KKKKEKHTHH APLSPRTFHP LRSEAYNTFS ERRLKHSLVL HKSNETSLPT
DLNQTLPSMD FGWIASLPDH NQNSSNDTGQ ASCPPGLYQT VPPEEHYQTF PIQDPDQMHS
TSDPSHRSSS PELSEMLEYD RSHKSFPTDI SQMSPSSEHE VWQTVISPD L SQVTLSPELS
QTNLSPDLSH TTLSPELIQR NLSPALGQMP ISPDLSHTTL SPDLSHHTLS LDLSQTNLSP
ELSQTNLSPA LGQMPLSPDL SHTTSLDFS QTNLSPELSH MTLSPELSQT NLSPALGQMP
ISPDESHTTL SLDFSQTNLS PELSQTNLSP ALGQMPLSPD PSHTTSLDL SQTNLSPELS
QTNLSPDLSE MPLFADLSQI PLTPDLDMQT LSPDLGETDL SPNFGQMSLS PDL SQVTLSP
DISDTTLLPD LSQISPPPD L DQIFYPSESS QSLLLQEFNE SFPYPDLGQM PSPSSPTLND

```

TELSKEFNPL VIVGLSKDGT DYIELIPKEE VQSSDDYAE IDYVPYDDPY KTDVVRTNINS
 SRDPDNIAAW YLRNNGNRR NYXIAAEEIS WDYSEFVQRE TDIEDSDDIP EDTTYKKVVF
 RKYLDSTFTK RDPGEYEEH LGILGPIIRA EVDDVIOVRF KNLASRPYSL HANGLSYEKS
 SEGKTYEDDS PEWFKEDNAV QPNSSYTYVW HATERSGPES PGSACRAWAY YSAVNPEKDI
 HSGLIGPLLI CQKGILHKDS NMPMDMREFV LLEMTFDEKK SWYYEKKRS SWRLTSSEMK
 KSHEFHAING MIYSLPGLKM YEQEWVRLHL LNIGGSQDIH VVHFHGQTLL ENGNKQHQLG
 VWPLLPGSFK TLEMKASKPG WWLLNTEVGE NQRAGMQTFP LIMDRDCRMP MGLSTGLISD
 SQIKASEFLG YWEPRLARLN NGGSYNAWSV EKLAEEFASK PWIQVDMQKE VIITGIQTQG
 AKHYLKSCYT TEFYVAYSSN QINWQIFKGN STRNVMYFNG NSDASTIKEN QFDPPIVARY
 IRISPTRAYN RPTLRLELQG CEVNGCSTPL GMENGKIENK QITASSEKKS WWGDYWEPR
 ARLNAQGRVN AWQAKANNK QWLEIDLLKI KKITAITQG CKSLSEMYV KSYTHYSEQ
 GVEWKPYPLK SSMVDKIFEG NTNTKGHVKN FFPPIISRF IRVIPKTWNQ SIALRLELFG
 CDIY

Factor V Nucleic Acid Sequence (SEQ ID NO: 18)

ATGTT CCCAGGCTGC CCACGCCTCT GGGTCCTGGT
 GGTCTTGGGC ACCAGCTGGG TAGGCTGGGG GAGCCAAGGG ACAGAAGCGG CACAGCTAAG
 GCAGTTCTAC GTGGCTGCTC AGGGCATCAG TTGGAGCTAC CGACCTGAGC CCACAAACTC
 AAGTTTGAAT CTTTCTGTAA CTTCTTTTAA GAAAATTGTC TACAGAGAGT ATGAACCATA
 TTTTAAGAAA GAAAAACCAC AATCTACCAT TTCAGGACTT CTTGGGCCTA CTTTATATGC
 TGAAGTCGGA GACATCATAA AAGTTCACCT TAAAAATAAG GCAGATAAGC CCTTGAGCAT
 CCATCCTCAA GGAATTAGGT ACAGTAAATT ATCAGAAGGT GCTTCTTACC TTGACCACAC
 ATTCCTGCG GAGAAGATGG ACGACGCTGT GGCTCCAGGC CGAGAATACA CCTATGAATG
 GAGTATCAGT GAGGACAGTG GACCCACCCA TGATGACCCT CCATGCCTCA CACACATCTA
 TTAATCCCAT GAAAATCTGA TCGAGGATTT CAACTCGGGG CTGATTGGGC CCCTGCTTAT
 CTGTAAAAAA GGGACCCTAA CTGAGGGTGG GACACAGAAG ACGTTTGACA AGCAAATCGT
 GCTACTATTT GCTGTGTTTG ATGAAAGCAA GAGCTGGAGC CAGTCATCAT CCCTAATGTA
 CACAGTCAAT GGATATGTGA ATGGGACAAT GCCAGATATA ACAGTTTGTG CCCATGACCA
 CATCAGCTGG CATCTGCTGG GAATGAGCTC GGGGCCAGAA TTATTCTCCA TTCATTTCAA
 CGGCCAGGTC CTGGAGCAGA ACCATCATAA GGTCTCAGCC ATCACCCTTG TCAGTGCTAC
 ATCCACTACC GCAAATATGA CTGTGGGCCC AGAGGGAAAG TGGATCATAT CTTCTCTCAC
 CCCAAACAT TTGCAAGCTG GGATGCAGGC TTACATTGAC ATTAAAAACT GCCCAAAGAA
 AACCAGGAAT CTTAAGAAAA TAACTCGTGA GCAGAGGCGG CACATGAAGA GGTGGGAATA
 CTTTATTGCT GCAGAGGAAG TCATTGTTGGA CTATGCACCT GTAATACCAG CGAATATGGA
 CAAAAAATAC AGGTCTCAGC ATTTGGATAA TTTCTCAAAC CAAATTGGAA AACATTATAA
 GAAAGTTATG TACACACAGT ACGAAGATGA GTCCTTCACC AAACATACAG TGAATCCCAA
 TATGAAAGAA GATGGGATTT TGGGTCCTAT TATCAGAGCC CAGGTCAGAG ACACACTCAA
 AATCGTGTTT AAAAATATGG CCAGCCGCCC CTATAGCATT TACCCTCATG GAGTGACCTT
 CTGCTCTTAT GAAGATGAAG TCAACTCTTC TTTCACCTCA GGCAGGAACA ACACCATGAT
 CAGAGCAGTT CAACCAGGGG AAACCTATAC TTATAAGTGG AACATCTTAG AGTTTGATGA
 ACCACAGAA AATGATGCCC AGTGCTTAAC AAGACCATAC TACAGTGACG TGGACATCAT
 GAGAGACATC GCCTCTGGGC TAATAGGACT ACTTCTAATC TGTAAGAGCA GATCCCTGGA
 CAGGCGAGGA ATACAGAGGG CAGCAGACAT CGAACAGCAG GCTGTGTTTG CTGTGTTTGA
 TGAGAACAAA AGCTGGTACC TTGAGGACAA CATCAACAAG TTTTGTGAAA ATCCTGATGA
 GGTGAAACGT GATGACCCCA AGTTTTATGA ATCAAACATC ATGAGCACTA TCAATGGCTA
 TGTGCCTGAG AGCATAACTA CTCTTGATT CTGCTTTGAT GACACTGTCC AGTGGCACTT
 CTGTAGTGTG GGGACCCAGA ATGAAATTTT GACCATCCAC TTCACTGGGC ACTCATTCAT
 CTATGGAAAG AGGCATGAGG ACACCTTGAC CCTCTTCCCC ATGCGTGGAG AATCTGTGAC
 GGTCACAATG GATAATGTTG GAACTTGAT GTTAACTTCC ATGAATTCTA GTCCAAGAAG
 CAAAAAGCTG AGGCTGAAAT TCAGGGATGT TAAATGTATC CCAGATGATG ATGAAGACTC
 ATATGAGATT TTTGAACCTC CAGAATCTAC AGTCATGGCT ACACGGAAAA TGCATGATCG

TTTAGAACCT	GAAGATGAAG	AGAGTGATGC	TGACTATGAT	TACCAGAACA	GACTGGCTGC
AGCATTAGGA	ATCAGGTCAT	TCCGAAACTC	ATCATTGAAT	CAGGAAGAAG	AAGAGTTCAA
TCTTACTGCC	CTAGCTCTGG	AGAATGGCAC	TGAATTCGTT	TCTTCAAACA	CAGATATAAT
TGTTGGTTCA	AATTATTCTT	CCCCAAGTAA	TATTAGTAAG	TTCAGTGTCA	ATAACCTTGC
AGAACCTCAG	AAAGCCCCCT	CTCACCAACA	AGCCACCACA	GCTGGTTCCC	CACTGAGACA
CCTCATGGC	AAGAACTCAG	TTCTCAATTC	TTCCACAGCA	GAGCATTCCA	GCCCATATTC
TGAAGACCCT	ATAGAGGATC	CTCTACAGCC	AGATGTCACA	GGGATACGTC	TACTTTCACT
TGGTGCTGGA	GAATTCAAAA	GTCAAGAACA	TGCTAAGCAT	AAGGGACCCA	AGGTAGAAAG
AGATCAAGCA	GCAAAGCACA	GGTTCTCCTG	GATGAAATTA	CTAGCACATA	AAGTTGGGAG
ACACCTAAGC	CAAGACACTG	GTTCTCCTTC	CGGAATGAGG	CCCTGGGAGG	ACCTTCCTAG
CCAAGACACT	GGTTCTCCTT	CCAGAATGAG	GCCCTGGAAG	GACCTCTCTA	GTGATCTGTT
ACTCTTAAAA	CAAAGTAACT	CATCTAAGAT	TTTGGTTGGG	AGATGGCATT	TGGCTTCTGA
GAAAGGTAGC	TATGAAATAA	TCCAAGATAC	TGATGAAGAC	ACAGCTGTTA	ACAATTGGCT
GATCAGCCCC	CAGAATGCCT	CACGTGCTTG	GGGAGAAAGC	ACCCCTCTTG	CCAACAAGCC
TGGAAAGCAG	AGTGGCCACC	CAAAGTTTCC	TAGAGTTAGA	CATAAATCTC	TACAAGTAAG
ACAGGATGGA	GGAAAGAGTA	GACTGAAGAA	AAGCCAGTTT	CTCATTAAAG	CACGAAAAAA
GAAAAAAGAG	AAGCACACAC	ACCATGCTCC	TTTATCTCCG	AGGACCTTTC	ACCCCTCTAG
AAGTGAAGCC	TACAACACAT	TTTCAGAAAG	AAGACTTAAG	CATTTCGTTG	TGCTTCATAA
ATCCAATGAA	ACATCTCTTC	CCACAGACCT	CAATCAGACA	TTGCCCTCTA	TGGATTTTGG
CTGGATAGCC	TCACTTCCTG	ACCATAATCA	GAATTCCTCA	AATGACACTG	GTCAGGCAAG
CTGTCTCTCA	GGTCTTTATC	AGACAGTGCC	CCCAGAGGAA	CACTATCAAA	CATTCCCCAT
TCAAGACCCT	GATCAAATGC	ACTCTACTTC	AGACCCCACT	CACAGATCCT	CTTCTCCAGA
GCTCAGTGAA	ATGCTTGAGT	ATGACCGAAG	TCACAAGTCC	TTCCCCACAG	ATATAAGTCA
AATGTCCCCT	TCTTCAGAAC	ATGAAGTCTG	GCAGACAGTC	ATCTCTCCAG	ACCTCAGCCA
GGTGACCCTC	TCTCCAGAAC	TCAGCCAGAC	AAACCTCTCT	CCAGACCTCA	GCCACACGAC
TCTCTCTCCA	GAACTCATTTC	AGAGAAACCT	TTCCCCAGCC	CTCGGTCAGA	TGCCCCATTT
TCCAGACCTC	AGCCATACAA	CCCTTTCTCC	AGACCTCAGC	CATACAACCC	TTTCTTTAGA
CCTCAGCCAG	ACAAACCTCT	CTCCAGAACT	CAGTCAGACA	AACCTTTCTC	CAGCCCTCGG
TCAGATGCCC	CTTTCTCCAG	ACCTCAGCCA	TACAACCCTT	TCTCTAGACT	TCAGCCAGAC
AAACCTCTCT	CCAGAACTCA	GCCATATGAC	TCTCTCTCCA	GAACTCAGTC	AGACAAACCT
TTCCCCAGCC	CTCGGTCAGA	TGCCCCATTT	TCCAGACCTC	AGCCATACAA	CCCTTTCTCT
AGACTTCAGC	CAGACAAACC	TCTCTCCAGA	ACTCAGTCAA	ACAAACCTTT	CCCCAGCCCT
CGGTCAGATG	CCCCCTTCTC	CAGACCCCAAG	CCATACAACC	CTTTCTCTAG	ACCTCAGCCA
GACAAACCTC	TCTCCAGAAC	TCAGTCAGAC	AAACCTTTCC	CCAGACCTCA	GTGAGATGCC
CCTCTTTGCA	GATCTCAGTC	AAATTCCCCCT	TACCCCAAGC	CTCGACCAGA	TGACACTTTC
TCCAGACCTT	GGTGAGACAG	ATCTTTCCCC	AAACTTTGGT	CAGATGTCCC	TTTCCCCAGA
CCTCAGCCAG	GTGACTCTCT	CTCCAGACAT	CAGTGACACC	ACCCCTTCTCC	CGGATCTCAG
CCAGATATCA	CCTCCTCCAG	ACCTTGATCA	GATATTCTAC	CCTTCTGAAT	CTAGTCAGTC
ATTGCTTCTT	CAAGAATTTA	ATGAGTCTTT	TCCTTATCCA	GACCTTGGTC	AGATGCCATC
TCCTTCATCT	CCTACTCTCA	ATGATACTTT	TCTATCAAAG	GAATTTAATC	CACTGGTTAT
AGTGGGCCTC	AGTAAAGATG	GTACAGATTA	CATTGAGATC	ATTCCAAAGG	AAGAGGTCCA
GAGCAGTGAA	GATGACTATG	CTGAAATTGA	TTATGTGCCC	TATGATGACC	CCTACAAAAC
TGATGTTAGG	ACAAACATCA	ACTCCTCCAG	AGATCCTGAC	AACATTGCAG	CATGGTACCT
CCGCAGCAAC	AATGGAAACA	GAAGAAATTA	TTACATTGCT	GCTGAAGAAA	TATCCTGGGA
TTATTAGAAA	TTTGTACAAA	GGGAAACAGA	TATTGAAGAC	TCTGATGATA	TTCCAGAAGA
TACCACATAT	AAGAAAGTAG	TTTTTGGAAA	GTACCTCGAC	AGCACTTTTA	CCAAACGTGA
TCCTCGAGGG	GAGTATGAAG	AGCATCTCGG	AATTCTTGGT	CCTATTATCA	GAGCTGAAGT
GGATGATGTT	ATCCAAGTTC	GTTTTAAAAA	TTTAGCATCC	AGACCGTATF	CTCTACATGC
CCATGGACTT	TCCTATGAAA	AATCATCAGA	GGGAAAGACT	TATGAAGATG	ACTCTCCTGA
ATGGTTTAAG	GAAGATAATG	CTGTTTACGC	AAATAGCAGT	TATACCTACG	TATGGCATGC
CACTGAGCGA	TCAGGGCCAG	AAAGTCCTGG	CTCTGCTGTG	CGGGCTTGGG	CCTACTACTC
AGCTGTGAAC	CCAGAAAAAG	ATATTCACTC	AGGCTTGATA	GGTCCCCCTC	TAATCTGCCA
AAAAGGAATA	CTACATAAGG	ACAGCAACAT	GCCTATGGAC	ATGAGAGAAAT	TTGTCTTACT
ATTTATGACC	TTTGATGAAA	AGAAGAGCTG	GTACTATGAA	AAGAAGTCCC	GAAGTTCTTG
GAGACTCACA	TCCTCAGAAA	TGAAAAAATC	CCATGAGTTT	CACGCCATTA	ATGGGATGAT
CTACAGCTTG	CCTGGCCTGA	AAATGTATGA	GCAAGAGTGG	GTGAGGTTAC	ACCTGCTGAA
CATAGGCGGC	TCCCAAGACA	TTCACGTGGT	TCACTTTCAC	GGCCAGACCT	TGCTGGAAAA
TGGCAATAAA	CAGCAACAGT	TAGGGGTCTG	GCCCCCTCTG	CCTGGTTTCT	TTAAAACTCT
TGAAATGAAG	GCATCAAAAC	CTGGCTGGTG	GCTCCTAAAC	ACAGAGGTTG	GAGAAAAACCA

GAGAGCAGGG	ATGCAAACGC	CATTTCTTAT	CATGGACAGA	GACTGTAGGA	TGCCAATGGG
ACTAAGCACT	GGTATCATAT	CTGATTCACA	GATCAAGGCT	TCAGAGTTTC	TGGGTACTG
GGAGCCCAGA	TTAGCAAGAT	TAAACAATGG	TGGATCTTAT	AATGCTTGGA	GTGTAGAAAA
ACTTGCAGCA	GAATTTGCCT	CTAAACCTTG	GATCCAGGTG	GACATGCAAA	AGGAAGTCAT
AATCACAGGG	ATCCAGACCC	AAGGTGCCAA	ACACTACCTG	AAGTCCTGCT	ATACCACAGA
GTTCTATGTA	GCTTACAGTT	CCAACCAGAT	CAACTGGCAG	ATCTTCAAAG	GGAACAGCAC
AAGGAATGTG	ATGTATTTTA	ATGGCAATTC	AGATGCCTCT	ACAATAAAAG	AGAATCAGTT
TGACCCACCT	ATTGTGGCTA	GATATATTAG	GATCTCTCCA	ACTCGAGCCT	ATAACAGACC
TACCCTTCGA	TTGGAACCTG	AAGGTTGTGA	GGTAAATGGA	TGTTCCACAC	CCCTGGGTAT
GGAAAATGGA	AAGATAGAAA	ACAAGCAAAT	CACAGCTTCT	TCGTTTAAGA	AATCTTGGTG
GGGAGATTAC	TGGGAACCCT	TCCGTGCCCC	TCTGAATGCC	CAGGGACGTG	TGAATGCCTG
GCAAGCCAAG	GCAAACAACA	ATAAGCAGTG	GCTAGAAATT	GATCTACTCA	AGATCAAGAA
GATAACGGCA	ATTATAACAC	AGGGCTGCAA	GTCTCTGTCC	TCTGAAATGT	ATGTAAAGAG
CTATACCATC	CACTACAGTG	AGCAGGGAGT	GGAATGGAAA	CCATACAGGC	TGAAATCCTC
CATGGTGGAC	AAGATTTTTG	AAGGAAATAC	TAATACCAAA	GGACATGTGA	AGAACTTTTT
CAACCCCCCA	ATCATTTCCA	GGTTTATCCG	TGTCATTCTT	AAAACATGGA	ATCAAAGTAT
TGCACTTCGC	CTGGAACCTC	TTGGCTGTGA	TATTTACTAG		

[0152] The FVa protein used for the present invention comprises a heterodimer comprising a heavy chain and a light chain, wherein the heavy chain comprises a first amino acid sequence, which is at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to amino acids 29 to 737 of SEQ ID NO: 17 and the light chain comprises a second amino acid sequence, which is at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to amino acids 1574 to 2224 of SEQ ID NO: 18, wherein the first amino acid sequence and the second amino acid sequence when formed the heterodimer is capable of forming a complex with FX or FXa. The FVa protein as used herein includes full-length FVa, mature FVa, functional fragments, variants, analogues, or derivatives thereof.

2. Procoagulant Peptides

[0153] In other embodiments, the enhancer moiety is a procoagulant peptide. A "procoagulant peptide" is a low molecular weight compound (e.g., peptides or peptide derivatives) with pro-coagulant activity that can be used for the treatment of bleeding diathesis (e.g., blood coagulation disorders/coagulopathies, such as hemophilia A) or for the treatment of deficiencies in at least one of FV, FVII, FVIII, FIX, FX, FXI, and vWF. In some embodiments, when a procoagulant peptide is used as an enhancer moiety, it is capable of increasing the catalytic activity of the clotting factor to which it is fused.

[0154] In one embodiment, the procoagulant peptide comprises a compound that includes:

(a) an amino acid sequence including Formula II:



or (b) a retro-, an inverso- or a retro-inverso variant of the amino acid sequence of (a).

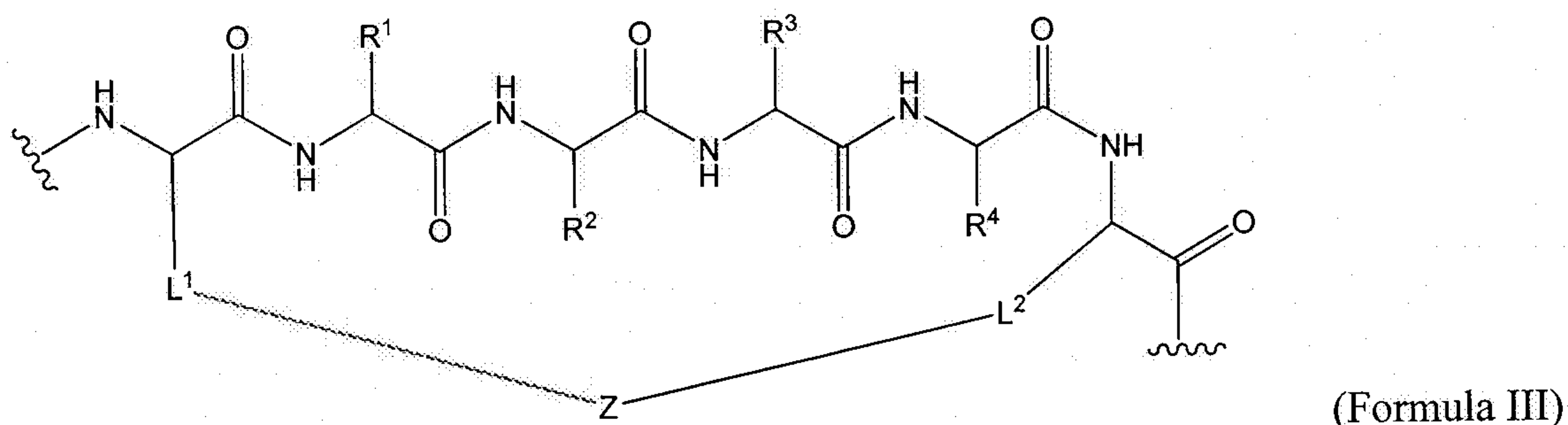
The present disclosure further provides pharmaceutically acceptable salts of the above compound.

[0155] In Formula II, C^1 and C^2 are amino acids having a side chain, wherein the side chains of C^1 and C^2 are linked to form a loop. In one example, the side chains of C^1 and C^2 are covalently linked (e.g., via a disulfide bond or an amide bond).

[0156] In Formula II, one, two or three additional amino acids can be inserted anywhere between C^1 and C^2 . In one example according to any of the above embodiments, one or two additional amino acids are optionally inserted into Formula (I) anywhere between C^1 and C^2 . In another example, one amino acid is optionally inserted into Formula II anywhere between C^1 and C^2 . In another example, no amino acid is inserted between C^1 and C^2 .

[0157] In Formula II, L is L-leucine, A is L-alanine, S is L-serine, and Y is L-tyrosine. In Formula II, one, two or three of L, A, S, and Y are optionally replaced with an independently selected replacement amino acid. In one example, one or two of L, A, S, and Y are optionally replaced with an independently selected replacement amino acid. In another example, exactly one of L, A, S, and Y is optionally replaced with an independently selected replacement amino acid.

[0158] In another embodiment, the enhancer moiety in a chimeric protein comprises a compound that contains a peptide of Formula III:



or a retro-, an inverso- or a retro-inverso variant thereof.

[0159] In Formula III, R^1 , R^2 , R^3 and R^4 are members independently selected from amino acid side chains. In Formula III, L^1 and L^2 are linker groups independently selected from straight or branched alkylene, and straight or branched heteroalkylene.

[0160] In Formula III, Z is a linking moiety. In one example, Z is selected from an amino group, an amide group, a disulfide group, a diselenide group, a -S-Se- group, alkylene, e.g., (C₂-C₄)alkylene, alkenyl, e.g., (C₂-C₄)alkenyl, alkynyl, e.g., (C₂-C₄)alkynyl, cycloalkyl (e.g., (C₃-C₈)cycloalkyl containing from 1 to 4 double bonds), heterocycloalkyl (e.g., 3- to 8-membered heterocyclic ring comprising from 1 to 6 heteroatoms selected from O, S and N), aryl (e.g., (C₃-C₇)aryl), and heteroaryl (e.g., 3- to 8-membered heteroaryl comprising from 1 to 6 heteroatoms selected from O, S and N).

[0161] Exemplary synthetic procoagulant peptides include, for example:

KLTCLASYCWLF	(SEQ ID NO: 19);
RRAPGKLTCLASYCWLFWTGIA	(SEQ ID NO: 20);
RRAPGKLQCLASYCWLFWTGIA	(SEQ ID NO: 21);
PRIRTVGPGRSASGKLTCLASYCWLFWTGIA	(SEQ ID NO: 22);
SKQGRPISPDRRAAGKLTCLASYCWLFWTGIA	(SEQ ID NO: 23);
PRIRTVGPGRSASGKSTCLASYCWLFWTGIA	(SEQ ID NO: 24);
SRIRTVSPGRSASGKSTCLASYCWLFWTGIA	(SEQ ID NO: 25); or
PRSRTVGPGRSASGKSTCLASYCWLFWTGIA	(SEQ ID NO: 26).

[0162] Exemplary procoagulant peptides are additionally disclosed in U.S. 61/495,818, U.S. 61/600,237, U.S. 61/605,540, U.S. 61/496,540, U.S. 61/496,543, U.S. 61/496,544, U.S. 61/496,541, and U.S. 61/496,542, each of which is incorporated herein by reference in its entirety.

3. Antibodies or Antigen Binding Sites

[0163] In other embodiments, the enhancer moiety comprises at least one antigen binding moiety (e.g., an antigen binding site of an antibody, antibody variant, or antibody fragment), a receptor binding portion of ligand, or a ligand binding portion of a receptor. Exemplary antigen binding molecules that can be used as enhancer moieties are disclosed in Andersen LM et al., J Biol Chem. 287: 8994-9001 (Jan. 2012), incorporated herein by reference in its entirety, which discloses FVII activating antibodies and antibody derivatives used for increasing the procoagulant activity of FVIIa and for treating blood coagulation disorders such as hemophilia A and hemorrhagic diathesis.

[0164] The term "antigen-binding moiety" refers to a polypeptide fragment of an immunoglobulin, antibody, or antibody variant which binds antigen or competes with intact antibody (i.e., with the intact antibody from which they were derived) for antigen

binding (i.e., specific binding). Antigen binding portions can be produced by recombinant or biochemical methods that are well known in the art. Exemplary antigen-binding portions include Fv, Fab, Fab', and (Fab')₂ as well as scFv molecules.

[0165] In other embodiments, a chimeric clotting factor of the invention may comprise an enhancer moiety comprising a binding site from single chain binding molecule (e.g., a single chain variable region or scFv). Techniques described for the production of single chain antibodies (U.S. Pat. No. 4,694,778; Bird, Science 242:423-442 (1988); Huston et al., Proc. Natl. Acad. Sci. USA 85:5879-5883 (1988); and Ward et al., Nature 334:544-554 (1989)) can be adapted to produce single chain binding molecules. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain antibody. Techniques for the assembly of functional Fv fragments in E coli may also be used (Skerra et al., Science 242:1038-1041 (1988)).

[0166] In certain embodiments, a chimeric clotting factor of the invention may comprise an enhancer moiety comprising one or more binding sites or regions comprising or consisting of a single chain variable region sequence (scFv). Single chain variable region sequences comprise a single polypeptide having one or more antigen binding sites, e.g., a VL domain linked by a flexible linker to a VH domain. ScFv molecules can be constructed in a VH-linker-VL orientation or VL-linker-VH orientation. The flexible linker that links the VL and VH domains that make up the antigen binding site preferably comprises from about 10 to about 50 amino acid residues. In one embodiment, the peptide linker is a gly-ser peptide linker. An exemplary gly/ser peptide linker is of the formula (Gly₄Ser)_n, wherein n is a positive integer (e.g., 1, 2, 3, 4, 5, or 6). Other peptide linkers are known in the art. Antibodies having single chain variable region sequences (e.g. single chain Fv antibodies) and methods of making said single chain antibodies are well-known in the art (see e.g., Ho et al. 1989. Gene 77:51; Bird et al. 1988 Science 242:423; Pantoliano et al. 1991. Biochemistry 30:10117; Milenic et al. 1991. Cancer Research 51:6363; Takkinen et al. 1991. Protein Engineering 4:837).

[0167] In certain embodiments, a scFv molecule employed in a chimeric clotting factor of the invention is a stabilized scFv molecule. In one embodiment, the stabilized cFv molecule may comprise a scFv linker interposed between a VH domain and a VL domain, wherein the VH and VL domains are linked by a disulfide bond between an amino acid in

the VH and an amino acid in the VL domain. In other embodiments, the stabilized scFv molecule may comprise a scFv linker having an optimized length or composition. In yet other embodiments, the stabilized scFv molecule may comprise a VH or VL domain having at least one stabilizing amino acid substitution(s). In yet another embodiment, a stabilized scFv molecule may have at least two of the above listed stabilizing features.

[0168] Stabilized scFv molecules have improved protein stability or impart improved protein stability to the polypeptide to which it is operably linked. Preferred scFv linkers of the invention improve the thermal stability of a chimeric clotting factor of the invention by at least about 2 °C or 3 °C as compared to a conventional polypeptide. Comparisons can be made, for example, between the scFv molecules of the invention. In certain embodiments, the stabilized scFv molecule comprises a (Gly4Ser)₄ scFv linker and a disulfide bond which links VH amino acid 44 and VL amino acid 100. Other exemplary stabilized scFv molecules which may be employed in the chimeric clotting factor of the invention are described in US Provisional Patent Application No. 60/873,996, filed on December 8, 2006 or US Patent Application No. 11/725,970, filed on March 19, 2007, each of which is incorporated herein by reference in its entirety.

[0169] Chimeric clotting factor of the invention may comprise a variable region or portion thereof (e.g. a VL and/or VH domain) derived from an antibody using art recognized protocols. For example, the variable domain may be derived from antibody produced in a non-human mammal, e.g., murine, guinea pig, primate, rabbit or rat, by immunizing the mammal with the antigen or a fragment thereof. See Harlow & Lane, *supra*, incorporated by reference for all purposes. The immunoglobulin may be generated by multiple subcutaneous or intraperitoneal injections of the relevant antigen (e.g., purified tumor associated antigens or cells or cellular extracts comprising such antigens) and an adjuvant. This immunization typically elicits an immune response that comprises production of antigen-reactive antibodies from activated splenocytes or lymphocytes.

[0170] While the variable region may be derived from polyclonal antibodies harvested from the serum of an immunized mammal, it is often desirable to isolate individual lymphocytes from the spleen, lymph nodes or peripheral blood to provide homogenous preparations of monoclonal antibodies (MAbs) from which the desired variable region is derived. Rabbits or guinea pigs are typically used for making polyclonal antibodies. Mice are typically used for making monoclonal antibodies. Monoclonal antibodies can

be prepared against a fragment by injecting an antigen fragment into a mouse, preparing "hybridomas" and screening the hybridomas for an antibody that specifically binds to the antigen. In this well-known process (Kohler et al., (1975), Nature, 256:495) the relatively short-lived, or mortal, lymphocytes from the mouse which has been injected with the antigen are fused with an immortal tumor cell line (e.g. a myeloma cell line), thus, producing hybrid cells or "hybridomas" which are both immortal and capable of producing the antibody genetically encoded by the B cell. The resulting hybrids are segregated into single genetic strains by selection, dilution, and regrowth with each individual strain comprising specific genes for the formation of a single antibody. They produce antibodies which are homogeneous against a desired antigen and, in reference to their pure genetic parentage, are termed "monoclonal".

[0171] Hybridoma cells thus prepared are seeded and grown in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, parental myeloma cells. Those skilled in the art will appreciate that reagents, cell lines and media for the formation, selection and growth of hybridomas are commercially available from a number of sources and standardized protocols are well established. Generally, culture medium in which the hybridoma cells are growing is assayed for production of monoclonal antibodies against the desired antigen. Preferably, the binding specificity of the monoclonal antibodies produced by hybridoma cells is determined by immunoprecipitation or by an in vitro assay, such as a radioimmunoassay (RIA) or enzyme-linked immunosorbent assay (ELISA). After hybridoma cells are identified that produce antibodies of the desired specificity, affinity and/or activity, the clones may be subcloned by limiting dilution procedures and grown by standard methods (Goding, Monoclonal Antibodies: Principles and Practice, pp 59-103 (Academic Press, 1986)). It will further be appreciated that the monoclonal antibodies secreted by the subclones may be separated from culture medium, ascites fluid or serum by conventional purification procedures such as, for example, affinity chromatography (e.g., protein-A, protein-G, or protein-L affinity chromatography), hydroxylapatite chromatography, gel electrophoresis, or dialysis.

[0172] DNA encoding the desired monoclonal antibody or binding site thereof may be readily isolated and sequenced using any of the conventional procedures described supra for the isolation of constant region domain sequences (e.g., by using oligonucleotide

probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The isolated and subcloned hybridoma cells serve as a preferred source of such DNA. More particularly, the isolated DNA (which may be synthetic as described herein) may be used to clone the desired variable region sequences for incorporation in the chimeric clotting factor of the invention.

[0173] In other embodiments, the binding site is derived from a fully human antibody. Human or substantially human antibodies may be generated in transgenic animals (e.g., mice) that are incapable of endogenous immunoglobulin production (see e.g., U.S. Pat. Nos. 6,075,181, 5,939,598, 5,591,669 and 5,589,369, each of which is incorporated herein by reference). For example, it has been described that the homozygous deletion of the antibody heavy-chain joining region in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of a human immunoglobulin gene array to such germ line mutant mice will result in the production of human antibodies upon antigen challenge. Another preferred means of generating human antibodies using SCID mice is disclosed in U.S. Pat. No. 5,811,524 which is incorporated herein by reference. It will be appreciated that the genetic material associated with these human antibodies may also be isolated and manipulated as described herein.

[0174] In other aspects, the polypeptides of the invention may comprise antigen binding sites, or portions thereof, derived from modified forms of antibodies. Exemplary such forms include, e.g., minibodies, diabodies, triabodies, nanobodies, camelids, Dabs, tetravalent antibodies, intradiabodies (e.g., Jendreyko et al. 2003. J. Biol. Chem. 278:47813), fusion proteins (e.g., antibody cytokine fusion proteins, proteins fused to at least a portion of an Fc receptor), and bispecific antibodies. Other modified antibodies are described, for example in U.S. Pat. No. 4,745,055; EP 256,654; Faulkner et al., Nature 298:286 (1982); EP 120,694; EP 125,023; Morrison, J. Immun. 123:793 (1979); Kohler et al., Proc. Natl. Acad. Sci. USA 77:2197 (1980); Raso et al., Cancer Res. 41:2073 (1981); Morrison et al., Ann. Rev. Immunol. 2:239 (1984); Morrison, Science 229:1202 (1985); Morrison et al., Proc. Natl. Acad. Sci. USA 81:6851 (1984); EP 255,694; EP 266,663; and WO 88/03559. Reassorted immunoglobulin chains also are known. See, for example, U.S. Pat. No. 4,444,878; WO 88/03565; and EP 68,763 and references cited therein.

[0175] In another embodiment, a chimeric clotting factor of the invention comprises an antigen binding site or region which is a diabody or an antigen binding site derived

therefrom. Diabodies are dimeric, tetravalent molecules each having a polypeptide similar to scFv molecules, but usually having a short (e.g., less than 10 and preferably 1-5) amino acid residue linker connecting both variable domains, such that the VL and VH domains on the same polypeptide chain cannot interact. Instead, the VL and VH domain of one polypeptide chain interact with the VH and VL domain (respectively) on a second polypeptide chain (see, for example, WO 02/02781). In one embodiment, a chimeric clotting factor of the invention comprises a diabody which is operably linked to the N-terminus and/or C-terminus of at least one genetically-fused Fc region (i.e., scFc region).

[0176] In certain embodiments, a chimeric clotting factor of the invention comprises a single domain binding molecule (e.g. a single domain antibody) as an enhancer moiety. Exemplary single domain molecules include an isolated heavy chain variable domain (VH) of an antibody, i.e., a heavy chain variable domain, without a light chain variable domain, and an isolated light chain variable domain (VL) of an antibody, i.e., a light chain variable domain, without a heavy chain variable domain. Exemplary single-domain antibodies employed in the binding molecules of the invention include, for example, the Camelid heavy chain variable domain (about 118 to 136 amino acid residues) as described in Hamers-Casterman, et al., *Nature* 363:446-448 (1993), and Dumoulin, et al., *Protein Science* 11:500-515 (2002). Other exemplary single domain antibodies include single VH or VL domains, also known as Dabs® (Domantis Ltd., Cambridge, UK). Yet other single domain antibodies include shark antibodies (e.g., shark Ig-NARs). Shark Ig-NARs comprise a homodimer of one variable domain (V-NAR) and five C-like constant domains (C-NAR), wherein diversity is concentrated in an elongated CDR3 region varying from 5 to 23 residues in length. In camelid species (e.g., llamas), the heavy chain variable region, referred to as VHH, forms the entire antigen-binding domain. The main differences between camelid VHH variable regions and those derived from conventional antibodies (VH) include (a) more hydrophobic amino acids in the light chain contact surface of VH as compared to the corresponding region in VHH, (b) a longer CDR3 in VHH, and (c) the frequent occurrence of a disulfide bond between CDR1 and CDR3 in VHH. Methods for making single domain binding molecules are described in US Patent Nos 6,005,079 and 6,765,087, both of which are incorporated herein by reference. Exemplary single domain antibodies comprising VHH domains include Nanobodies® (Ablynx NV, Ghent, Belgium).

C. Heterologous Moieties (e.g., Het1, Het2, ... , Het_n)

[0177] Some embodiments of the invention comprise one or more heterologous moieties (indicated herein as “Het1” or “Het2”). In other embodiments, the chimeric protein of the invention can comprise two heterologous moieties (“Het1” and “Het2”). In yet other embodiments, the chimeric protein of the invention can comprise more than two heterologous moieties, e.g., three, four, five, or more than five heterologous moieties. In some embodiments, all the heterologous moieties are identical. In some embodiments, at least one heterologous moiety is different from the other heterologous moieties. In some embodiments, the chimeric protein of the invention can comprise two, three or more than three heterologous moieties in tandem. In other embodiments, the chimeric protein of the invention can comprise two, three, or more than heterologous moieties wherein at least an additional moiety (e.g., an activatable clotting factor, a linker moiety, a protease-cleavage site, a self-immolative moiety, an enhancer moiety, or combinations thereof) is interposed between two heterologous moieties.

[0178] A heterologous moiety can comprise a heterologous polypeptide moiety, or a heterologous non-polypeptide moiety, or both. In one specific embodiment, Het1 is a first heterologous moiety, e.g., a half-life extending molecule which is known in the art. In some embodiments, Het2 is a second heterologous moiety that can also be a half-life extending molecule which is known in the art. In some aspects, the heterologous moiety comprises a combination of a heterologous polypeptide and a non-polypeptide moiety.

[0179] In certain embodiments, the first heterologous moiety (e.g., a first Fc moiety) and the second heterologous moiety (e.g., a second Fc moiety) are associated with each other to form a dimer. In one embodiment, the second heterologous moiety is a second Fc moiety, wherein the second Fc moiety is linked to or associated with the first heterologous moiety, e.g., the first Fc moiety. For example, the second heterologous moiety (e.g., the second Fc moiety) can be linked to the first heterologous moiety (e.g., the first Fc moiety) by a linker or associated with the first heterologous moiety by a covalent or non-covalent bond.

[0180] In some embodiments, the Het1 and Het2 heterologous moieties are peptides and polypeptides with either unstructured or structured characteristics that are associated with the prolongation of *in vivo* half-life when incorporated in a chimeric protein of the invention. Non-limiting examples include albumin, albumin fragments, Fc fragments of

immunoglobulins, the β subunit of the C-terminal peptide (CTP) of human chorionic gonadotropin, a HAP sequence, an XTEN sequence, a transferrin or a fragment thereof, a PAS polypeptide, polyglycine linkers, polyserine linkers, albumin-binding moieties, or any fragments, derivatives, variants, or combinations of these polypeptides. In other related aspects a heterologous moiety can include an attachment site (e.g., a cysteine amino acid) for a non-polypeptide moiety such as polyethylene glycol (PEG), hydroxyethyl starch (HES), polysialic acid, or any derivatives, variants, or combinations of these elements. In some aspects, a heterologous moiety consisting of a cysteine amino acid that function as an attachment site for a non-polypeptide moiety such as polyethylene glycol (PEG), hydroxyethyl starch (HES), polysialic acid, or any derivatives, variants, or combinations of these elements.

[0181] In some embodiments, the heterologous moiety 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. In other embodiments, the heterologous moiety is a polypeptide comprising, consisting essentially of, or consisting of about 100 to about 200 amino acids, about 200 to about 300 amino acids, about 300 to about 400 amino acids, about 400 to about 500 amino acids, about 500 to about 600 amino acids, about 600 to about 700 amino acids, about 700 to about 800 amino acids, about 800 to about 900 amino acids, or about 900 to about 1000 amino acids.

[0182] In certain embodiments, a heterologous moiety improves one or more pharmacokinetic properties of the chimeric protein without significantly affecting the biological activity or function of the activatable clotting factor and/or the enhancer moiety (e.g., procoagulant activity of a clotting factor or a fragment thereof, or of activity enhancing property of an enhancer moiety).

[0183] In certain embodiments, a heterologous moiety increases the *in vivo* and/or *in vitro* half-life of the clotting factor of the invention. In other embodiments, a heterologous moiety facilitates visualization or localization of the clotting factor of the invention or a fragment thereof (e.g., a fragment comprising a heterologous moiety after proteolytic cleavage of the activatable clotting factor). Visualization and/or location of the chimeric protein of the invention or a fragment thereof can be *in vivo*, *in vitro*, *ex vivo*, or combinations thereof.

[0184] In other embodiments, a heterologous moiety increases stability of the chimeric protein of the invention or a fragment thereof (e.g., a fragment comprising a heterologous moiety after proteolytic cleavage of the activatable clotting factor). As used herein, the term "stability" refers to an art-recognized measure of the maintenance of one or more physical properties of the activatable clotting factor in response to an environmental condition (e.g., an elevated or lowered temperature). In certain aspects, the physical property can be the maintenance of the covalent structure of the chimeric protein (e.g., the absence of proteolytic cleavage, unwanted oxidation or deamidation). In other aspects, the physical property can also be the presence of the chimeric protein in a properly folded state (e.g., the absence of soluble or insoluble aggregates or precipitates). In one aspect, the stability of the chimeric protein is measured by assaying a biophysical property of the chimeric protein, for example thermal stability, pH unfolding profile, stable removal of glycosylation, solubility, biochemical function (e.g., ability to bind to a protein, receptor or ligand), etc., and/or combinations thereof. In another aspect, biochemical function is demonstrated by the binding affinity of the interaction. In one aspect, a measure of protein stability is thermal stability, i.e., resistance to thermal challenge. Stability can be measured using methods known in the art, such as, HPLC (high performance liquid chromatography), SEC (size exclusion chromatography), DLS (dynamic light scattering), etc. Methods to measure thermal stability include, but are not limited to differential scanning calorimetry (DSC), differential scanning fluorimetry (DSF), circular dichroism (CD), and thermal challenge assay.

[0185] In certain aspects, a chimeric protein of the invention comprises at least one half-like extender, i.e., a heterologous moiety which increases the in vivo half-life of the chimeric protein with respect to the in vivo half-life of the corresponding chimeric protein lacking such heterologous moiety. In vivo half-life of a chimeric protein can be determined by any method known to those of skill in the art, e.g., activity assays (chromogenic assay or one stage clotting aPTT assay), ELISA, etc.

[0186] In some embodiments, the presence of one or more half-life extenders results in the half-life of the chimeric protein to be increased compared to the half-life of the corresponding protein lacking such one or more half-life extenders. The half-life of the chimeric protein comprising a half-life extender 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 *in vivo* half-life of the corresponding chimeric protein lacking such half-life extender.

[0187] In one embodiment, the half-life of the chimeric protein comprising a half-life extender 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 *in vivo* half-life of the corresponding protein lacking such half-life extender. In another embodiment, the half-life of chimeric protein comprising a half-life extender 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 the *in vivo* half-life of the corresponding protein lacking such half-life extender.

[0188] In other embodiments, the half-life of the chimeric protein comprising a half-life extender 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.

[0189] In still other embodiments, the half-life of the chimeric protein comprising a half-life extender 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.

[0190] In some embodiments, the average half-life per subject of the chimeric protein comprising a half-life extender 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.

1. An immunoglobulin Constant Region or a Portion Thereof

[0191] In another aspect, a heterologous moiety comprises one or more immunoglobulin constant region or a portion thereof (e.g., an Fc moiety). In one embodiment, a chimeric protein comprises an activatable clotting factor, an enhancer moiety, and at least two heterologous moieties, a first heterologous moiety comprises a first immunoglobulin constant region or a portion thereof (e.g., a first Fc moiety), which is linked to the activatable clotting factor and a second heterologous moiety comprises a second immunoglobulin constant region or a portion thereof (e.g., a second Fc moiety), which is linked to the enhancer moiety. The first immunoglobulin constant region or a portion thereof and the second immunoglobulin constant region or a portion thereof can form a covalent bond (e.g., a disulfide bond), thereby placing the activatable clotting factor and the enhancer moiety close in proximity to allow interaction between the activated clotting factor and the enhancer moiety at the site of injury.

[0192] An immunoglobulin 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.

[0193] An immunoglobulin 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 one embodiment, an immunoglobulin constant region or a portion thereof is derived from a human immunoglobulin. It is understood, however, that the immunoglobulin constant region or a portion thereof may be derived from an immunoglobulin 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 immunoglobulin constant region or a portion thereof may be derived from any immunoglobulin class, including IgM, IgG, IgD, IgA and IgE, and any immunoglobulin isotype, including IgG1, IgG2, IgG3 and IgG4. In one embodiment, the human isotype IgG1 is used.

[0194] A variety of the immunoglobulin 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.

[0195] The sequences of the immunoglobulin 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 immunoglobulin 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, which is incorporated by reference herein.

[0196] An immunoglobulin constant region used herein can include all domains and the hinge region or portions thereof. In one embodiment, the immunoglobulin constant region or a portion thereof comprises CH2 domain, CH3 domain, and a hinge region, i.e., an Fc domain or an FcRn binding partner.

[0197] An immunoglobulin 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 immunoglobulin that binds to FcRn.

[0198] 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 immunoglobulin 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.

[0199] 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 immunoglobulins or immunoglobulin 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.

[0200] 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 immunoglobulin 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.

[0201] 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.

[0202] An FcRn binding partner region is a molecule or 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 K_A 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.

[0203] 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.

[0204] The Fc moieties denoted as F, F1, or F2 herein may be obtained from a number of different sources. In one embodiment, an Fc moiety of the polypeptide is derived from a human immunoglobulin. It is understood, however, that an Fc moiety may be derived from an immunoglobulin 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 polypeptide of the Fc domains or portions thereof may be derived

from any immunoglobulin class, including IgM, IgG, IgD, IgA and IgE, and any immunoglobulin isotype, including IgG1, IgG2, IgG3 and IgG4. In another embodiment, the human isotype IgG1 is used.

[0205] In certain embodiments, the Fc variant confers a change in at least one effector function imparted by an Fc moiety 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.

[0206] The Fc moiety 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, each of which is incorporated by reference herein. 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.

[0207] The Fc moiety 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 γ 1) 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 moieties. Moreover, one of the Fc moiety of a construct of the invention may be mutated and the other Fc moiety of the construct not mutated at all, or they both may be mutated but with different mutations.

[0208] Certain of the above mutations may confer new functionality upon the Fc moiety 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 Fc γ RI, Fc γ RIIA, Fc γ RIIB, and Fc γ RIIIA, 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).

[0209] 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.

[0210] In one embodiment, the immunoglobulin constant region or a portion thereof, e.g., an Fc moiety, is a polypeptide including the sequence PKNSSMISNTP (SEQ ID NO: 27) and optionally further including a sequence selected from HQSLGTQ (SEQ ID NO: 28), HQNLSDGK (SEQ ID NO: 29), HQNISDGK (SEQ ID NO: 30), or VISSHLGQ (SEQ ID NO: 31) (U.S. Pat. No. 5,739,277).

[0211] 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 an activatable clotting factor and the second polypeptide comprising the enhancer moiety together so that upon activation of the clotting factor, the enhancer moiety is available to enhance activity of the clotting factor. The hinge region or a portion thereof can further be linked to one or more domains of CH1, CH2, CH3, a fragment thereof, or any combinations thereof.

[0212] In certain embodiments, the immunoglobulin constant region or a portion thereof is hemi-glycosylated. For example, the chimeric protein comprising two Fc moieties or FcRn binding partners may contain a first, glycosylated, Fc moiety (e.g., a glycosylated

CH2 region) or FcRn binding partner and a second, aglycosylated, Fc moiety (e.g., an aglycosylated CH2 region) or FcRn binding partner. In one embodiment, a linker may be interposed between the glycosylated and aglycosylated Fc moieties. In another embodiment, the Fc moiety or FcRn binding partner is fully glycosylated, i.e., all of the Fc moieties are glycosylated. In other embodiments, the Fc moiety may be aglycosylated, i.e., none of the Fc moieties are glycosylated.

[0213] In certain embodiments, a chimeric protein of the invention comprises an amino acid substitution to an immunoglobulin 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.

[0214] 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 exhibits reduced transport across the epithelium of kidney glomeruli from the vasculature. In another embodiment, the chimeric protein of the invention exhibits 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 moiety 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 moiety 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 which is incorporated by reference herein.

[0215] An Fc moiety 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 moiety or FcRn binding partner of the chimeric protein linked to an activatable clotting factor or an enhancer moiety may comprise an Fc moiety 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).

[0216] In one embodiment, a 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 portion thereof independently selected from the Ig constant region or portion thereof described herein. In one embodiment, the Fc domains of a dimeric Fc region are the same. In another embodiment, at least two of the Fc domains are different. For example, the Fc moieties 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 moieties 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 moieties 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).

2. scFc Regions

[0217] In one embodiment, the invention provides for unprocessed chimeric polypeptides comprising an activatable clotting factor, an enhancer moiety, and at least one genetically fused Fc region or portion thereof within a single polypeptide chain (i.e., polypeptides comprising a single-chain Fc (scFc) region). The unprocessed polypeptides comprise at least two immunoglobulin constant regions or portions thereof (e.g., Fc moieties or domains (e.g., 2, 3, 4, 5, 6, or more Fc moieties or domains)) within the same linear polypeptide chain that are capable of folding (e.g., intramolecularly or intermolecularly folding) to form one functional scFc region which is linked by an Fc peptide linker. For example, in one embodiment, a polypeptide of the invention is capable of binding, via its scFc region, to at least one Fc receptor (e.g. an FcRn, an FcγR receptor (e.g., FcγRIII), or a complement protein (e.g. C1q)) in order to improve half-life or trigger an immune effector function (e.g., antibody-dependent cytotoxicity (ADCC), phagocytosis, or complement-dependent cytotoxicity (CDCC) and/or to improve manufacturability).

[0218] A variety of polypeptides of alternative designs are within the scope of the invention. For example, in one embodiment, a polypeptide comprises the moieties:

A-F1-P1-L-P2-B-F2 ()

in linear sequence from the amino to carboxy terminus wherein A, if present, is an activatable clotting factor or portion thereof, F1 is a first immunoglobulin constant region or a portion thereof, P1 is a first intracellular processing site, L is a scFc linker, P2 is a second intracellular processing site; B is an enhancer moiety, F2 is a second immunoglobulin constant region or a portion thereof; and “-” represents a peptide bond. Formula () comprises at least a P1 or a P2 and optionally both. P1 and P2, if both present, can be the same or different. Formula () comprises at least a F1, a F2, or both. F1 and F2, if both present, can be the same or different.

3. CTP

[0219] In certain aspects, a chimeric protein of the invention comprises at least one heterologous moiety comprising one β subunit of the C-terminal peptide (CTP) of human chorionic gonadotropin or fragment, variant, or derivative thereof. One or more CTP peptides inserted into a recombinant protein is known to increase the *in vivo* half-life of that protein. See, e.g., U.S. Patent No. 5,712,122, incorporated by reference herein in its entirety.

[0220] Exemplary CTP peptides include DPRFQDSSSSKAPPSLPSPSRLPGPSDTPIL (SEQ ID NO: 32) or SSSSKAPPSLPSPSRLPGPSDTPILPQ. (SEQ ID NO: 33). See, e.g., U.S. Patent Application Publication No. US 2009/0087411 A1, incorporated by reference.

4. XTEN Sequence

[0221] In some embodiments, a heterologous moiety in the chimeric protein comprises one or more XTEN sequences, fragments, variants, or derivatives thereof. 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 heterologous moiety, XTENs can serve as a half-life extension moiety. In addition, XTEN can provide desirable properties including but are not limited to enhanced pharmacokinetic parameters and solubility characteristics.

[0222] The incorporation of a heterologous moiety comprising an XTEN sequence into a chimeric protein of the invention can confer to the chimeric protein 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.

[0223] In certain aspects, an XTEN sequence can improve pharmacokinetic properties such as extending *in vivo* half-life or increasing total exposure (area under the curve (AUC)), so that a chimeric protein of the invention displays prolonged efficacy for controlling bleeds compared to a chimeric protein with the same but without the XTEN heterologous moiety.

[0224] Examples of XTEN sequences that can be used as heterologous moieties in chimeric proteins of the invention are disclosed, *e.g.*, in US Pat Nos. 7,855,279 and 7,846,445, U.S. Patent Publication Nos. 2009/0092582 A1, 2010/0239554 A1, 2010/0323956 A1, 2011/0046060 A1, 2011/0046061 A1, 2011/0077199 A1, 2013/0017997 A1, or 2012/0263701 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, or International Application No. PCT/US2011/48517, filed August 19, 2011, each of which is incorporated by reference herein in its entirety.

5. Albumin or Fragment, Derivative, or Variant Thereof

[0225] In certain embodiments, the chimeric protein of the invention comprises a heterologous moiety comprising albumin or a functional fragment thereof. Human serum albumin (HSA, or HA), a protein of 609 amino acids in its full-length form, is responsible for a significant proportion of the osmotic pressure of serum and also functions as a carrier of endogenous and exogenous ligands. The term "albumin" as used herein includes full-length albumin or a functional fragment, variant, derivative, or analog thereof. Examples of albumin or the fragments or variants thereof are disclosed in US Pat. Publ. Nos. 2008/0194481A1, 2008/0004206 A1, 2008/0161243 A1, 2008/0261877 A1, or 2008/0153751 A1 or PCT Appl. Publ. Nos. 2008/033413 A2, 2009/058322 A1, or 2007/021494 A2, which are incorporated herein by reference in their entireties.

[0226] In one embodiment, the chimeric protein of the invention comprises albumin, a fragment, or a variant thereof which is further linked to a heterologous moiety selected from an immunoglobulin constant region or portion thereof (*e.g.*, an Fc region), a PAS sequence, HES, PEG, or any combinations thereof.

6. Albumin Binding Moiety

[0227] In certain embodiments, the heterologous moiety is an albumin binding moiety, which comprises an albumin binding peptide, a bacterial albumin binding domain, an albumin-binding antibody fragment, or any combinations thereof.

[0228] For example, the albumin binding protein can be a bacterial albumin binding protein, an antibody or an antibody fragment including domain antibodies (see U.S. Pat. No. 6,696,245). An albumin binding protein, for example, can be a bacterial albumin

binding domain, such as the one of streptococcal protein G (Konig, T. and Skerra, A. (1998) *J. Immunol. Methods* 218, 73-83). Other examples of albumin binding peptides that can be used as conjugation partner are, for instance, those having a Cys-Xaa₁-Xaa₂-Xaa₃-Xaa₄-Cys consensus sequence, wherein Xaa₁ is Asp, Asn, Ser, Thr, or Trp; Xaa₂ is Asn, Gln, His, Ile, Leu, or Lys; Xaa₃ is Ala, Asp, Phe, Trp, or Tyr; and Xaa₄ is Asp, Gly, Leu, Phe, Ser, or Thr (SEQ ID NO: 34) as described in US patent application 2003/0069395 or Dennis et al. (Dennis et al. (2002) *J. Biol. Chem.* 277, 35035-35043).

[0229] Domain 3 from streptococcal protein G, as disclosed by Kraulis *et al.*, FEBS Lett. 378:190-194 (1996) and Linhult *et al.*, Protein Sci. 11:206-213 (2002) is an example of a bacterial albumin-binding domain. Examples of albumin-binding peptides include a series of peptides having the core sequence DICLPRWGCLW (SEQ ID NO: 35). See, *e.g.*, Dennis *et al.*, J. Biol. Chem. 2002, 277: 35035-35043 (2002). Examples of albumin-binding antibody fragments are disclosed in Muller and Kontermann, Curr. Opin. Mol. Ther. 9:319-326 (2007); Roovers *et al.*, Cancer Immunol. Immunother. 56:303-317 (2007), and Holt *et al.*, Prot. Eng. Design Sci., 21:283-288 (2008), which are incorporated herein by reference in their entireties. An example of such albumin binding moiety is 2-(3-maleimidopropanamido)-6-(4-(4-iodophenyl)butanamido) hexanoate ("Albu" tag) as disclosed by Trusset *et al.*, Bioconjugate Chem. 20:2286-2292 (2009).

[0230] Fatty acids, in particular long chain fatty acids (LCFA) and long chain fatty acid-like albumin-binding compounds can be used to extend the *in vivo* half-life of chimeric proteins of the invention. An example of a LCFA-like albumin-binding compound is 16-(1-(3-(9-(((2,5-dioxopyrrolidin-1-yl)oxy) carbonyloxy)-methoxy)-7-sulfo-9H-fluoren-2-ylamino)-3-oxopropyl)-2,5-dioxopyrrolidin-3-ylthio) hexadecanoic acid (see, *e.g.*, WO 2010/140148).

7. PAS Sequence

[0231] In other embodiments, at least one heterologous moiety is a PAS sequence. A PAS sequence, as used herein, means an amino acid sequence comprising mainly alanine and serine residues or comprising mainly alanine, serine, and proline residues, the amino acid sequence forming random coil conformation under physiological conditions. Accordingly, the PAS sequence is a building block, an amino acid polymer, or a sequence cassette comprising, consisting essentially of, or consisting of alanine, serine, and proline which can be used as a part of the heterologous moiety in the chimeric protein. Yet, the

skilled person is aware that an amino acid polymer also may form random coil conformation when residues other than alanine, serine, and proline are added as a minor constituent in the PAS sequence. The term "minor constituent" as used herein means that amino acids other than alanine, serine, and proline may be added in the PAS sequence to a certain degree, e.g., up to about 12%, i.e., about 12 of 100 amino acids of the PAS sequence, up to about 10%, i.e. about 10 of 100 amino acids of the PAS sequence, up to about 9%, i.e., about 9 of 100 amino acids, up to about 8%, i.e., about 8 of 100 amino acids, about 6%, i.e., about 6 of 100 amino acids, about 5%, i.e., about 5 of 100 amino acids, about 4%, i.e., about 4 of 100 amino acids, about 3%, i.e., about 3 of 100 amino acids, about 2%, i.e., about 2 of 100 amino acids, about 1%, i.e., about 1 of 100 of the amino acids. The amino acids different from alanine, serine and proline may be selected from Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Thr, Trp, Tyr, or Val.

[0232] Under physiological conditions, the PAS sequence stretch forms a random coil conformation and thereby can mediate an increased *in vivo* and/or *in vitro* stability to the chimeric protein. Since the random coil domain does not adopt a stable structure or function by itself, the biological activity mediated by the activatable clotting factor in the chimeric protein is essentially preserved. In other embodiments, the PAS sequences that form random coil domain are biologically inert, especially with respect to proteolysis in blood plasma, immunogenicity, isoelectric point/electrostatic behaviour, binding to cell surface receptors or internalisation, but are still biodegradable, which provides clear advantages over synthetic polymers such as PEG.

[0233] Non-limiting examples of the PAS sequences forming random coil conformation comprise an amino acid sequence selected from ASPAAPAPASPAAPAPSAPA (SEQ ID NO: 36), AAPASPAPAAPSAPAPAAPS (SEQ ID NO: 37), APSSPSPSAPSSPSPASPSS (SEQ ID NO: 38), APSSPSPSAPSSPSPASPS (SEQ ID NO: 39), SSPSAPSPSSPASPSPPSPA (SEQ ID NO: 40), AASPAAPSAPPAAASPAAPSAPPA (SEQ ID NO: 41), ASAAAPAAASAAASAPSAAA (SEQ ID NO: 42) or any combinations thereof. Additional examples of PAS sequences are known from, e.g., US Pat. Publ. No. 2010/0292130 A1 and PCT Appl. Publ. No. WO 2008/155134 A1.

8. HAP Sequence

[0234] In certain embodiments, at least one heterologous moiety is a glycine-rich homo-amino-acid polymer (HAP). The HAP sequence can comprise a repetitive sequence of glycine, which has at least 50 amino acids, at least 100 amino acids, 120 amino acids, 140 amino acids, 160 amino acids, 180 amino acids, 200 amino acids, 250 amino acids, 300 amino acids, 350 amino acids, 400 amino acids, 450 amino acids, or 500 amino acids in length. In one embodiment, the HAP sequence is capable of extending half-life of a moiety fused to or linked to the HAP sequence. Non-limiting examples of the HAP sequence includes, but are not limited to $(\text{Gly})_n$, $(\text{Gly}_4\text{Ser})_n$ or $\text{S}(\text{Gly}_4\text{Ser})_n$, wherein n is 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20. In one embodiment, n is 20, 21, 22, 23, 24, 25, 26, 26, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40. In another embodiment, n is 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, or 200.

9. Transferrin or Fragment thereof

[0235] In certain embodiments, at least one heterologous moiety is transferrin or a fragment thereof. Any transferrin may be used to make the chimeric proteins of the invention. As an example, wild-type human TF (TF) is a 679 amino acid protein, of approximately 75 KDa (not accounting for glycosylation), with two main domains, N (about 330 amino acids) and C (about 340 amino acids), which appear to originate from a gene duplication. See GenBank accession numbers NM001063, XM002793, M12530, XM039845, XM 039847 and S95936 (www.ncbi.nlm.nih.gov/), all of which are herein incorporated by reference in their entirety. Transferrin comprises two domains, N domain and C domain. N domain comprises two subdomains, N1 domain and N2 domain, and C domain comprises two subdomains, C1 domain and C2 domain.

[0236] In one embodiment, the transferrin heterologous moiety includes a transferrin splice variant. In one example, a transferrin splice variant can be a splice variant of human transferrin, e.g., Genbank Accession AAA61140. In another embodiment, the transferrin portion of the chimeric protein includes one or more domains of the transferrin sequence, e.g., N domain, C domain, N1 domain, N2 domain, C1 domain, C2 domain or any combinations thereof.

10. Polymer, *e.g.*, Polyethylene Glycol (PEG)

[0237] In other embodiments, at least one heterologous moiety is a soluble polymer known in the art, including, but not limited to, polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, or polyvinyl alcohol. In some embodiments, the chimeric protein comprising a PEG heterologous moiety further comprises a heterologous moiety selected from an immunoglobulin constant region or portion thereof (*e.g.*, an Fc region), a PAS sequence, HES, albumin, fragment, or variant thereof, or any combinations thereof. In still other embodiments, the chimeric protein comprises an activatable clotting factor or fragment thereof and a PEG heterologous moiety, wherein the chimeric protein further comprises a heterologous moiety selected from an immunoglobulin constant region or portion thereof (*e.g.*, an Fc moiety), a PAS sequence, HES, albumin, fragment, or variant thereof, or any combinations thereof. In yet other embodiments, the chimeric protein comprises a clotting factor or fragment thereof, a second clotting factor or fragment thereof, and a PEG heterologous moiety, wherein the chimeric protein further comprises a heterologous moiety selected from an immunoglobulin constant region or portion thereof (*e.g.*, an Fc moiety), a PAS sequence, HES, albumin, fragment, or variant thereof, or any combinations thereof. In other embodiments, the chimeric protein comprises a clotting factor or fragment thereof, a synthetic procoagulant polypeptide, and a PEG heterologous moiety, wherein the chimeric protein further comprises a heterologous moiety selected from an immunoglobulin constant region or portion thereof (*e.g.*, an Fc region), a PAS sequence, HES, albumin, fragment, or variant thereof, or any combinations thereof. In other embodiments, the chimeric protein comprises two synthetic procoagulant peptides and a PEG heterologous moiety, wherein the chimeric protein further comprises a heterologous moiety selected from an immunoglobulin constant region or portion thereof (*e.g.*, an Fc region), a PAS sequence, HES, albumin, fragment, or variant thereof, or any combinations thereof. In yet another embodiment, the chimeric protein comprises a clotting factor or fragment thereof, a clotting factor cofactor (*e.g.*, Factor Va if the clotting factor is Factor X; or Tissue Factor if the clotting factor is Factor VII), and a PEG heterologous moiety, wherein the chimeric protein further comprises a heterologous moiety selected from an immunoglobulin constant region or portion thereof (*e.g.*, an Fc

region), a PAS sequence, HES, albumin, fragment, or variant thereof, or any combinations thereof.

[0238] Also provided by the invention are chimeric proteins of the invention comprising heterologous moieties which may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Pat. No. 4,179,337). Such heterologous moieties for modification can be selected from water soluble polymers including, but not limited to, polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol, or any combinations thereof.

[0239] The polymer can be of any molecular weight, and can be branched or unbranched. For polyethylene glycol, in one embodiment, the molecular weight is between about 1 kDa and about 100 kDa for ease in handling and manufacturing. Other sizes may be used, depending on the desired profile (e.g., the duration of sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the polyethylene glycol to a protein or analog). For example, the polyethylene glycol may have an average molecular weight of about 200, 500, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 8500, 9000, 9500, 10,000, 10,500, 11,000, 11,500, 12,000, 12,500, 13,000, 13,500, 14,000, 14,500, 15,000, 15,500, 16,000, 16,500, 17,000, 17,500, 18,000, 18,500, 19,000, 19,500, 20,000, 25,000, 30,000, 35,000, 40,000, 45,000, 50,000, 55,000, 60,000, 65,000, 70,000, 75,000, 80,000, 85,000, 90,000, 95,000, or 100,000 kDa.

[0240] In some embodiments, the polyethylene glycol may have a branched structure. Branched polyethylene glycols are described, for example, in U.S. Pat. No. 5,643,575; Morpurgo *et al.*, *Appl. Biochem. Biotechnol.* 56:59-72 (1996); Vorobjev *et al.*, *Nucleosides Nucleotides* 18:2745-2750 (1999); and Caliceti *et al.*, *Bioconjug. Chem.* 10:638-646 (1999), each of which is incorporated herein by reference in its entirety.

[0241] The number of polyethylene glycol moieties attached to each chimeric protein of the invention (i.e., the degree of substitution) may also vary. For example, the PEGylated chimeric protein may be linked, on average, to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, or more polyethylene glycol molecules. Similarly, the average degree of substitution within ranges such as 1-3, 2-4, 3-5, 4-6, 5-7, 6-8, 7-9, 8-10, 9-11, 10-12, 11-13, 12-14, 13-15, 14-16, 15-17, 16-18, 17-19, or 18-20 polyethylene glycol moieties per protein

molecule. Methods for determining the degree of substitution are discussed, for example, in Delgado *et al.*, *Crit. Rev. Thera. Drug Carrier Sys.* 9:249-304 (1992).

[0242] In some embodiments, the chimeric protein can be PEGylated. A PEGylated chimeric protein comprises at least one polyethylene glycol (PEG) molecule. In other embodiments, the polymer can be water-soluble. Non-limiting examples of the polymer can be poly(alkylene oxide), poly(vinyl pyrrolidone), poly(vinyl alcohol), polyoxazoline, or poly(acryloylmorpholine). Additional types of polymer-conjugation to clotting factors are disclosed in U.S. Patent No. 7,199,223. See also, Singh *et al.* *Curr. Med. Chem.* 15:1802-1826 (2008).

11. Hydroxyethyl Starch (HES)

[0243] In certain embodiments, at least one heterologous moiety is a polymer, e.g., hydroxyethyl starch (HES) or a derivative thereof. Hydroxyethyl starch (HES) is a derivative of naturally occurring amylopectin and is degraded by alpha-amylase in the body. HES is a substituted derivative of the carbohydrate polymer amylopectin, which is present in corn starch at a concentration of up to 95% by weight. HES exhibits advantageous biological properties and is used as a blood volume replacement agent and in hemodilution therapy in the clinics (Sommermeyer *et al.*, *Krankenhauspharmazie*, 8(8), 271-278 (1987); and Weidler *et al.*, *Arzneim.-Forschung/Drug Res.*, 41, 494-498 (1991)).

[0244] Amylopectin contains glucose moieties, wherein in the main chain alpha-1,4-glycosidic bonds are present and at the branching sites alpha-1,6-glycosidic bonds are found. The physical-chemical properties of this molecule are mainly determined by the type of glycosidic bonds. Due to the nicked alpha-1,4-glycosidic bond, helical structures with about six glucose-monomers per turn are produced. The physico-chemical as well as the biochemical properties of the polymer can be modified via substitution. The introduction of a hydroxyethyl group can be achieved via alkaline hydroxyethylation. By adapting the reaction conditions it is possible to exploit the different reactivity of the respective hydroxy group in the unsubstituted glucose monomer with respect to a hydroxyethylation. Owing to this fact, the skilled person is able to influence the substitution pattern to a limited extent.

[0245] HES is mainly characterized by the molecular weight distribution and the degree of substitution. The degree of substitution, denoted as DS, relates to the molar

substitution, is known to the skilled people. See Sommermeyer *et al.*, *Krankenhauspharmazie*, 8(8), 271-278 (1987), as cited above, in particular p. 273.

[0246] In one embodiment, hydroxyethyl starch has a mean molecular weight (weight mean) of from 1 to 300 kD, from 2 to 200kD, from 3 to 100 kD, or from 4 to 70kD. hydroxyethyl starch can further exhibit a molar degree of substitution of from 0.1 to 3, preferably 0.1 to 2, more preferred, 0.1 to 0.9, preferably 0.1 to 0.8, and a ratio between C2:C6 substitution in the range of from 2 to 20 with respect to the hydroxyethyl groups. A non-limiting example of HES having a mean molecular weight of about 130 kD is a HES with a degree of substitution of 0.2 to 0.8 such as 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, or 0.8, preferably of 0.4 to 0.7 such as 0.4, 0.5, 0.6, or 0.7. In a specific embodiment, HES with a mean molecular weight of about 130 kD is VOLUVEN[®] from Fresenius. VOLUVEN[®] is an artificial colloid, employed, e.g., for volume replacement used in the therapeutic indication for therapy and prophylaxis of hypovolemia. The characteristics of VOLUVEN[®] are a mean molecular weight of 130,000+/-20,000 D, a molar substitution of 0.4 and a C2:C6 ratio of about 9:1. In other embodiments, ranges of the mean molecular weight of hydroxyethyl starch are, e.g., 4 to 70 kD or 10 to 70 kD or 12 to 70 kD or 18 to 70 kD or 50 to 70 kD or 4 to 50 kD or 10 to 50 kD or 12 to 50 kD or 18 to 50 kD or 4 to 18 kD or 10 to 18 kD or 12 to 18 kD or 4 to 12 kD or 10 to 12 kD or 4 to 10 kD. In still other embodiments, the mean molecular weight of hydroxyethyl starch employed is in the range of from more than 4 kD and below 70 kD, such as about 10 kD, or in the range of from 9 to 10 kD or from 10 to 11 kD or from 9 to 11 kD, or about 12 kD, or in the range of from 11 to 12 kD) or from 12 to 13 kD or from 11 to 13 kD, or about 18 kD, or in the range of from 17 to 18 kD or from 18 to 19 kD or from 17 to 19 kD, or about 30 kD, or in the range of from 29 to 30, or from 30 to 31 kD, or about 50 kD, or in the range of from 49 to 50 kD or from 50 to 51 kD or from 49 to 51 kD.

[0247] In certain embodiments, the heterologous moiety can be a mixture of hydroxyethyl starches having different mean molecular weights and/or different degrees of substitution and/or different ratios of C2: C6 substitution. Therefore, mixtures of hydroxyethyl starches may be employed having different mean molecular weights and different degrees of substitution and different ratios of C2: C6 substitution, or having different mean molecular weights and different degrees of substitution and the same or about the same ratio of C2:C6 substitution, or having different mean molecular weights

and the same or about the same degree of substitution and different ratios of C2:C6 substitution, or having the same or about the same mean molecular weight and different degrees of substitution and different ratios of C2:C6 substitution, or having different mean molecular weights and the same or about the same degree of substitution and the same or about the same ratio of C2:C6 substitution, or having the same or about the same mean molecular weights and different degrees of substitution and the same or about the same ratio of C2:C6 substitution, or having the same or about the same mean molecular weight and the same or about the same degree of substitution and different ratios of C2:C6 substitution, or having about the same mean molecular weight and about the same degree of substitution and about the same ratio of C2:C6 substitution.

12. Polysialic Acids (PSA)

[0248] In certain embodiments, at least one heterologous moiety is a polymer, e.g., polysialic acids (PSAs) or a derivative thereof. Polysialic acids (PSAs) are naturally occurring unbranched polymers of sialic acid produced by certain bacterial strains and in mammals in certain cells Roth J., et al. (1993) in *Polysialic Acid: From Microbes to Man*, eds Roth J., Rutishauser U., Troy F. A. (Birkhäuser Verlag, Basel, Switzerland), pp 335–348.. They can be produced in various degrees of polymerisation from n=about 80 or more sialic acid residues down to n=2 by limited acid hydrolysis or by digestion with neuraminidases, or by fractionation of the natural, bacterially derived forms of the polymer. The composition of different polysialic acids also varies such that there are homopolymeric forms i.e. the alpha-2,8-linked polysialic acid comprising the capsular polysaccharide of *E. coli* strain K1 and the group-B meningococci, which is also found on the embryonic form of the neuronal cell adhesion molecule (N-CAM). Heteropolymeric forms also exist—such as the alternating alpha-2,8 alpha-2,9 polysialic acid of *E. coli* strain K92 and group C polysaccharides of *N. meningitidis*. Sialic acid may also be found in alternating copolymers with monomers other than sialic acid such as group W135 or group Y of *N. meningitidis*. Polysialic acids have important biological functions including the evasion of the immune and complement systems by pathogenic bacteria and the regulation of glial adhesiveness of immature neurons during foetal development (wherein the polymer has an anti-adhesive function) Cho and Troy, *P.N.A.S., USA*, 91 (1994) 11427-11431, although there are no known receptors for polysialic acids in mammals. The alpha-2,8-linked polysialic acid of *E. coli* strain K1 is also known as

‘colominic acid’ and is used (in various lengths) to exemplify the present invention. Various methods of attaching or conjugating polysialic acids to a polypeptide have been described (for example, see U.S. Pat. No. 5,846,951; WO-A-0187922, and US 2007/0191597 A1, which are incorporated herein by reference in their entireties.

13. Clearance Receptors

[0249] In certain aspects, the *in vivo* half-life of an activatable clotting factor in a chimeric protein of the invention can be extended where the chimeric protein comprises at least one heterologous molecule comprising a clearance receptor, fragment, variant, or derivative thereof. In specific aspects wherein the therapeutic peptide is Factor X, soluble forms of clearance receptors, such as the low density lipoprotein-related protein receptor LRP1, or fragments thereof, can block binding of Factor X to clearance receptors and thereby extend its *in vivo* half-life.

[0250] LRP1 is a 600 kDa integral membrane protein that is implicated in the receptor-mediate clearance of a variety of proteins, such as Factor X. See, *e.g.*, Narita et al., Blood 91:555-560 (1998).

D. Linker Moieties (L, L1, or L2)

[0251] Linker moieties useful for the present invention can be either a peptide linker or a non-peptide linker. In one embodiment, the peptide linker can be synthetic.

[0252] As used herein, the term “peptide linkers” refers to a peptide or polypeptide sequence (*e.g.*, a synthetic peptide or polypeptide sequence) which connects two domains in a linear amino acid sequence of a polypeptide chain. The polypeptides of invention are encoded by nucleic acid molecules that encode peptide linkers which either directly or indirectly connect the two immunoglobulin constant regions or portions thereof (*e.g.*, Fc moieties) which make up the construct. These linkers are referred to herein as “scFc linkers”. If the scFc linker connects two Fc moieties contiguously in the linear polypeptide sequence, it is a “direct” linkage. In contrast, the scFc linkers may link the first Fc moiety to a binding moiety which is, in turn, linked to the second Fc moiety, thereby forming an indirect linkage. These scFc linkers (X) result in the formation of a single chain genetic construct. However, in one embodiment, the scFc polypeptides also comprise intracellular processing sites which result in the scFc linker being cleavable (an cscFc linker) and, in one embodiment, substantially excised (*e.g.*, during processing by a

cell). Thus, the processed molecule is a dimeric molecule comprising at least two amino acid chains and substantially lacking extraneous linker amino acid sequences. In some embodiments, all or substantially all of the linker is excised, while in some embodiments, a portion of the intracellular processing site may remain, e.g., four arginines of the RRRR cleavage site.

[0253] In another embodiment, another type of peptide linker, herein referred to as a “linker moiety” may be used to connect different moieties, e.g., an activatable clotting factor to an enhancer moiety, an activatable clotting factor to a heterologous moiety, and/or an enhancer moiety to a heterologous moiety. This type of peptide linkers may provide flexibility to the polypeptide molecule. Linkers are not typically cleaved, however such cleavage may be desirable. Exemplary positions of linkers are shown in the accompanying drawings. Linkers can be located between the activatable clotting factor and the enhancer moiety, the activatable clotting factor and the heterologous moiety linked thereto, or the enhancer moiety and the heterologous moiety linked thereto, e.g., at the N or C terminus of these moieties. In one embodiment, these linkers are not removed during processing.

[0254] A third type of linker which may be present in a chimeric protein of the invention is a protease cleavable linker which comprises a cleavage site (i.e., a protease cleavage site substrate, e.g., a factor XIa, Xa, or thrombin cleavage site) and which may include additional linkers on either the N-terminal or C-terminal or both sides of the cleavage site. These cleavable linkers when incorporated into a clotting factor zymogen result in a chimeric molecule having a heterologous cleavage site. Exemplary locations for such sites are shown in the accompanying drawings and include, e.g., between the light chain and heavy chain of the clotting factor zymogen, between the heavy chain of the clotting factor zymogen and a first heterologous moiety, between the enhancer moiety and a second heterologous moiety.

[0255] In one embodiment, an unprocessed polypeptide of the instant invention comprises two or more Fc domains or moieties linked via a cscFc linker to form an Fc region comprised in a single polypeptide chain. The cscFc linker is flanked by at least one intracellular processing site, i.e., a site cleaved by an intracellular enzyme. Cleavage of the polypeptide at the at least one intracellular processing site results in a polypeptide which comprises at least two polypeptide chains. In one embodiment, an cscFc linker

links F1 or F2 to, e.g., an activatable clotting factor, optionally via an intracellular processing site or an enhancer moiety via an intracellular processing site.

[0256] As is set forth above, other peptide linkers may optionally be used in a construct of the invention, e.g., to connect an activatable clotting factor or an enhancer moiety to an Fc moiety. Some exemplary locations of linkers that can be used in connection with the invention include, e.g., polypeptides comprising GlySer amino acids such as those set forth in the accompanying figures and described in more detail below. In one embodiment, a linker may be adjacent to one or more moieties each independently selected from activatable clotting factor, heterologous moiety, e.g., Fc, cleavage site, and an enhancer moiety.

[0257] In one embodiment, the peptide linker is synthetic, i.e., non-naturally occurring. In one embodiment, a peptide linker includes peptides (or polypeptides) (which may or may not be naturally occurring) which comprise an amino acid sequence that links or genetically fuses a first linear sequence of amino acids to a second linear sequence of amino acids to which it is not naturally linked or genetically fused in nature. For example, in one embodiment the peptide linker may comprise non-naturally occurring polypeptides which are modified forms of naturally occurring polypeptides (e.g., comprising a mutation such as an addition, substitution or deletion). In another embodiment, the peptide linker may comprise non-naturally occurring amino acids. In another embodiment, the peptide linker may comprise naturally occurring amino acids occurring in a linear sequence that does not occur in nature. In still another embodiment, the peptide linker may comprise a naturally occurring polypeptide sequence.

[0258] For example, in certain embodiments, a peptide linker can be used to fuse identical Fc moieties, thereby forming a homodimeric scFc region. In other embodiments, a peptide linker can be used to fuse different Fc moieties (e.g. a wild-type Fc moiety and an Fc moiety variant), thereby forming a heterodimeric scFc region.

[0259] In another embodiment, a peptide linker comprises or consists of a gly-ser linker. In one embodiment, a scFc or cscFc linker comprises at least a portion of an immunoglobulin hinge and a gly-ser linker. As used herein, the term "gly-ser linker" refers to a peptide that consists of glycine and serine residues. An exemplary gly/ser linker comprises an amino acid sequence of the formula (Gly₄Ser)_n (SEQ ID NO: 4), wherein *n* is a positive integer (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10). An example of gly/ser

linker is (Gly₄Ser)₂ (SEQ ID NO: 4), (Gly₄Ser)₄ (SEQ ID NO: 4), or (Gly₄Ser)₆ (SEQ ID NO: 4). Another exemplary gly-ser linker is GGGSSGGGSG (SEQ ID NO: 43). In certain embodiments, said gly-ser linker may be inserted between two other sequences of the peptide linker (*e.g.*, any of the peptide linker sequences described herein). In other embodiments, a gly-ser linker is attached at one or both ends of another sequence of the peptide linker (*e.g.*, any of the peptide linker sequences described herein). In yet other embodiments, two or more gly-ser linker are incorporated in series in a peptide linker. In one embodiment, a peptide linker of the invention comprises at least a portion of an upper hinge region (*e.g.*, derived from an IgG1, IgG2, IgG3, or IgG4 molecule), at least a portion of a middle hinge region (*e.g.*, derived from an IgG1, IgG2, IgG3, or IgG4 molecule) and a series of gly/ser amino acid residues (*e.g.*, a gly/ser linker such as (Gly₄Ser)_n (SEQ ID NO: 4)).

[0260] Peptide linkers of the invention are at least one amino acid in length and can be of varying lengths. In one embodiment, a peptide linker of the invention is from about 1 to about 50 amino acids in length. As used in this context, the term “about” indicates +/- two amino acid residues. Since linker length must be a positive integer, the length of from about 1 to about 50 amino acids in length, means a length of from 1-3 to 48-52 amino acids in length. In another embodiment, a peptide linker of the invention is from about 10 to about 20 amino acids in length. In another embodiment, a peptide linker of the invention is from about 15 to about 50 amino acids in length. In another embodiment, a peptide linker of the invention is from about 20 to about 45 amino acids in length. In another embodiment, a peptide linker of the invention is from about 15 to about 35 or about 20 to about 30 amino acids in length. In another embodiment, a peptide linker of the invention is from about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 40, 50, 60, 70, 80, 90, 100, 500, 1000, or 2000 amino acids in length. In one embodiment, a peptide linker of the invention is 20 or 30 amino acids in length.

[0261] In some embodiments, the peptide linker can comprise at least two amino, at least three, at least four, at least five, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, or at least 100 amino acids. In other embodiments, the peptide linker can comprise at least 200, at least 300, at least 400, at least 500, at least 600, at least 700, at least 800, at least 900, or at least 1,000 amino acids.

In some embodiments, the peptide 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 peptide 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.

[0262] Peptide linkers can be introduced into polypeptide sequences using techniques known in the art. Modifications can be confirmed by DNA sequence analysis. Plasmid DNA can be used to transform host cells for stable production of the polypeptides produced.

III. Preparation of Polypeptides

[0263] A variety of methods are available for recombinantly producing a chimeric protein of the invention. In one embodiment, the invention relates to a nucleic acid construct comprising a nucleic acid sequence encoding the chimeric proteins of the invention. It will be understood that because of the degeneracy of the code, a variety of nucleic acid sequences will encode the amino acid sequence of the polypeptide. The desired polynucleotide can be produced by *de novo* solid-phase DNA synthesis or by PCR mutagenesis of an earlier prepared polynucleotide.

[0264] Oligonucleotide-mediated mutagenesis is one method for preparing a substitution, in-frame insertion, or alteration (*e.g.*, altered codon) to introduce a codon encoding an amino acid substitution (*e.g.*, into an Fc variant moiety). For example, the starting polypeptide DNA is altered by hybridizing an oligonucleotide encoding the desired mutation to a single-stranded DNA template. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that incorporates the oligonucleotide primer. In one embodiment, genetic engineering, *e.g.*, primer-based PCR mutagenesis, is sufficient to incorporate an alteration, as defined herein, for producing a polynucleotide encoding a polypeptide of the invention.

[0265] For recombinant production, a polynucleotide sequence encoding the chimeric protein is inserted into an appropriate expression vehicle, *i. e.*, a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence,

or in the case of an RNA viral vector, the necessary elements for replication and translation.

[0266] The nucleic acid encoding the chimeric protein is inserted into the vector in proper reading frame. The expression vector is then transfected into a suitable target cell which will express the polypeptide. Transfection techniques known in the art include, but are not limited to, calcium phosphate precipitation (Wigler et al. 1978, Cell 14 : 725) and electroporation (Neumann et al. 1982, EMBO, J. 1 : 841). A variety of host-expression vector systems may be utilized to express the chimeric proteins described herein in eukaryotic cells. In one embodiment, the eukaryotic cell is an animal cell, including mammalian cells (e. g. 293 cells, PerC6, CHO, BHK, Cos, HeLa cells). When the chimeric protein is expressed in a eukaryotic cell the DNA encoding the chimeric protein may also code for a signal sequence that will permit the chimeric protein to be secreted. One skilled in the art will understand that while the protein is translated the signal sequence is cleaved by the cell to form the mature chimeric protein. Various signal sequences are known in the art e. g., native factor VII signal sequence, native factor IX signal sequence and the mouse IgK light chain signal sequence. Alternatively, where a signal sequence is not included the chimeric protein can be recovered by lysing the cells.

[0267] The chimeric protein of the invention can be synthesized in a transgenic animal, such as a rodent, goat, sheep, pig, or cow. The term "transgenic animals" refers to non-human animals that have incorporated a foreign gene into their genome. Because this gene is present in germline tissues, it is passed from parent to offspring. Exogenous genes are introduced into single-celled embryos (Brinster et al. 1985, Proc. Natl. Acad. Sci. USA 82 : 4438). Methods of producing transgenic animals are known in the art including transgenics that produce immunoglobulin molecules (Wagner et al. 1981, Proc. Natl. Acad. Sci. USA 78: 6376; McKnight et al. 1983, Cell 34 : 335; Brinster et al. 1983, Nature 306: 332; Ritchie et al. 1984, Nature 312: 517; Baldassarre et al. 2003, Theriogenology 59 : 831 ; Robl et al. 2003, Theriogenology 59: 107; Malassagne et al. 2003, Xenotransplantation 10 (3): 267).

[0268] The expression vectors can encode for tags that permit for easy purification or identification of the recombinantly produced protein. Examples include, but are not limited to, vector pUR278 (Ruther et al. 1983, EMBO J. 2: 1791) in which the chimeric protein described herein coding sequence may be ligated into the vector in frame with the

lac z coding region so that a hybrid protein is produced; pGEX vectors may be used to express proteins 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 (e. g. PreCission Protease (Pharmacia, Peapack, N. J.)) for easy removal of the tag after purification.

[0269] For the purposes of this invention, numerous expression vector systems may be employed. These expression vectors are typically replicable in the host organisms either as episomes or as an integral part of the host chromosomal DNA. Expression vectors may include expression control sequences including, but not limited to, promoters (*e.g.*, naturally-associated or heterologous promoters), enhancers, signal sequences, splice signals, enhancer elements, and transcription termination sequences. Preferably, the expression control sequences are eukaryotic promoter systems in vectors capable of transforming or transfecting eukaryotic host cells. Expression vectors may also utilize DNA elements which are derived from animal viruses such as bovine papilloma virus, polyoma virus, adenovirus, vaccinia virus, baculovirus, retroviruses (RSV, MMTV or MOMLV), cytomegalovirus (CMV), or SV40 virus. Others involve the use of polycistronic systems with internal ribosome binding sites.

[0270] Commonly, expression vectors contain selection markers (*e.g.*, ampicillin-resistance, hygromycin-resistance, tetracycline resistance or neomycin resistance) to permit detection of those cells transformed with the desired DNA sequences (see, *e.g.*, Itakura *et al.*, US Patent 4,704,362). Cells which have integrated the DNA into their chromosomes may be selected by introducing one or more markers which allow selection of transfected host cells. The marker may provide for prototrophy to an auxotrophic host, biocide resistance (*e.g.*, antibiotics) or resistance to heavy metals such as copper. The selectable marker gene can either be directly linked to the DNA sequences to be expressed, or introduced into the same cell by cotransformation.

[0271] A preferred expression vector is NEOSPLA (U.S. Patent No. 6,159,730). This vector contains the cytomegalovirus promoter/enhancer, the mouse beta globin major promoter, the SV40 origin of replication, the bovine growth hormone polyadenylation sequence, neomycin phosphotransferase exon 1 and exon 2, the dihydrofolate reductase gene and leader sequence. This vector has been found to result in very high level

expression of antibodies upon incorporation of variable and constant region genes, transfection in cells, followed by selection in G418 containing medium and methotrexate amplification. Vector systems are also taught in U.S. Pat. Nos. 5,736,137 and 5,658,570, each of which is incorporated by reference in its entirety herein. This system provides for high expression levels, e.g., > 30 pg/cell/day. Other exemplary vector systems are disclosed e.g., in U.S. Patent No. 6,413,777.

[0272] In other embodiments the polypeptides of the invention of the instant invention may be expressed using polycistronic constructs. In these expression systems, multiple gene products of interest such as multiple polypeptides of multimer binding protein may be produced from a single polycistronic construct. These systems advantageously use an internal ribosome entry site (IRES) to provide relatively high levels of polypeptides of the invention in eukaryotic host cells. Compatible IRES sequences are disclosed in U.S. Pat. No. 6,193,980 which is also incorporated herein. Those skilled in the art will appreciate that such expression systems may be used to effectively produce the full range of polypeptides disclosed in the instant application.

[0273] More generally, once the vector or DNA sequence encoding a polypeptide has been prepared, the expression vector may be introduced into an appropriate host cell. That is, the host cells may be transformed. Introduction of the plasmid into the host cell can be accomplished by various techniques well known to those of skill in the art. These include, but are not limited to, transfection (including electrophoresis and electroporation), protoplast fusion, calcium phosphate precipitation, cell fusion with enveloped DNA, microinjection, and infection with intact virus. See, Ridgway, A. A. G. "Mammalian Expression Vectors" Chapter 24.2, pp. 470-472 Vectors, Rodriguez and Denhardt, Eds. (Butterworths, Boston, Mass. 1988). Most preferably, plasmid introduction into the host is via electroporation. The transformed cells are grown under conditions appropriate to the production of the light chains and heavy chains, and assayed for heavy and/or light chain protein synthesis. Exemplary assay techniques include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), or fluorescence-activated cell sorter analysis (FACS), immunohistochemistry and the like.

[0274] As used herein, the term "transformation" shall be used in a broad sense to refer to the introduction of DNA into a recipient host cell that changes the genotype and consequently results in a change in the recipient cell.

[0275] Along those same lines, "host cells" refers to cells that have been transformed with vectors constructed using recombinant DNA techniques and encoding at least one heterologous gene. In descriptions of processes for isolation of polypeptides from recombinant hosts, the terms "cell" and "cell culture" are used interchangeably to denote the source of polypeptide unless it is clearly specified otherwise. In other words, recovery of polypeptide from the "cells" may mean either from spun down whole cells, or from the cell culture containing both the medium and the suspended cells.

[0276] The host cell line used for protein expression is most preferably of mammalian origin; those skilled in the art are credited with ability to preferentially determine particular host cell lines which are best suited for the desired gene product to be expressed therein. Exemplary host cell lines include, but are not limited to, DG44 and DUXB11 (Chinese Hamster Ovary lines, DHFR minus), HELA (human cervical carcinoma), CVI (monkey kidney line), COS (a derivative of CVI with SV40 T antigen), R1610 (Chinese hamster fibroblast) BALBC/3T3 (mouse fibroblast), HAK (hamster kidney line), SP2/O (mouse myeloma), P3.times.63-Ag3.653 (mouse myeloma), BFA-1c1BPT (bovine endothelial cells), RAJI (human lymphocyte), PerC6, and 293 (human kidney). Host cell lines are typically available from commercial services, the American Tissue Culture Collection or from published literature.

[0277] In one embodiment, a host cell endogenously expresses an enzyme (or the enzymes) necessary to cleave a scFc linker (e.g., if such a linker is present and contains intracellular processing site(s)) during processing to form the mature polypeptide. During this processing, the scFc linker may be substantially removed to reduce the presence of extraneous amino acids. In another embodiment of the invention, a host cell is transformed to express one or more enzymes which are exogenous to the cell such that processing of a scFc linker occurs or is improved.

[0278] In one embodiment an enzyme which may be endogenously or exogenously expressed by a cell is a member of the furin family of enzymes. Complete cDNA and amino acid sequences of human furin (i.e., PACE) were published in 1990. Van den Ouweland A M et al. (1990) Nucleic Acids Res. 18:664; Erratum in: Nucleic Acids Res. 18:1332 (1990).

[0279] U.S. Pat. No. 5,460,950, issued to Barr et al., describes recombinant PACE and the coexpression of PACE with a substrate precursor polypeptide of a heterologous protein to improve expression of active, mature heterologous protein.

[0280] U.S. Pat. No. 5,935,815, issued to van de Ven et al., likewise describes recombinant human furin (i.e., PACE) and the coexpression of furin with a substrate precursor polypeptide of a heterologous protein to improve expression of active, mature heterologous protein. Possible substrate precursors disclosed in this patent include a precursor of Factor IX. Other family members in the mammalian furin/ subtilisin/Kex2p-like proprotein convertase (PC) family in addition to PACE are reported to include 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). While these various members share certain conserved overall structural features, they differ in their tissue distribution, subcellular localization, cleavage specificities, and preferred substrates. For a review, see Nakayama K (1997) *Biochem J.* 327:625-35. Similar to PACE, these proprotein convertases generally include, beginning from the amino terminus, a signal peptide, a propeptide (that may be autocatalytically cleaved), a subtilisin-like catalytic domain characterized by Asp, His, Ser, and Asn/Asp residues, and a Homo B domain that is also essential for catalytic activity and characterized by an Arg-Gly-Asp (RGD) sequence. PACE, PACE4, and PC5 also include a Cys-rich domain, the function of which is unknown. In addition, PC5 has isoforms with and without a transmembrane domain; these different isoforms are known as PC5B and PC5A, respectively. Comparison between the amino acid sequence of the catalytic domain of PACE and the amino acid sequences of the catalytic domains of other members of this family of proprotein convertases reveals the following degrees of identity: 70 percent for PC4; 65 percent for PACE4 and PC5; 61 percent for PC1/PC3; 54 percent for PC2; and 51 percent for LPC/PC7/PC8/SPC7. Nakayama K (1997) *Biochem J.* 327:625-35.

[0281] PACE and PACE4 have been reported to have partially overlapping but distinct substrates. In particular, PACE4, in striking contrast to PACE, has been reported to be incapable of processing the precursor polypeptide of FIX. Wasley L C et al. (1993) *J Biol Chem.* 268:8458-65; Rehemtulla A et al. (1993) *Biochemistry.* 32:11586-90.

- [0282] U.S. Pat. No. 5,840,529, issued to Seidah et al., discloses nucleotide and amino acid sequences for human PC7 and the notable ability of PC7, as compared to other PC family members, to cleave HIV gp160 to gp120 and gp41.
- [0283] Nucleotide and amino acid sequences of rodent PC5 were first described as PC5 by Lusson J et al. (1993) Proc Natl Acad Sci USA 90:6691-5 and as PC6 by Nakagawa T et al. (1993) J Biochem (Tokyo) 113:132-5. U.S. Pat. No. 6,380,171, issued to Day et al., discloses nucleotide and amino acid sequences for human PC5A, the isoform without the transmembrane domain. The sequences of these enzymes and method of cloning them are known in the art.
- [0284] Genes encoding the polypeptides of the invention can also be expressed in non-mammalian cells such as bacteria or yeast or plant cells. In this regard it will be appreciated that various unicellular non-mammalian microorganisms such as bacteria can also be transformed; i.e., those capable of being grown in cultures or fermentation. Bacteria, which are susceptible to transformation, include members of the enterobacteriaceae, such as strains of *Escherichia coli* or *Salmonella*; *Bacillaceae*, such as *Bacillus subtilis*; *Pneumococcus*; *Streptococcus*, and *Haemophilus influenzae*. It will further be appreciated that, when expressed in bacteria, the polypeptides typically become part of inclusion bodies. The polypeptides must be isolated, purified and then assembled into functional molecules.
- [0285] In addition to prokaryotes, eukaryotic microbes may also be used. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among eukaryotic microorganisms although a number of other strains are commonly available.
- [0286] For expression in *Saccharomyces*, the plasmid YRp7, for example, (Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)) is commonly used. This plasmid already contains the TRP1 gene which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example ATCC No. 44076 or PEP4-1 (Jones, Genetics, 85:12 (1977)). The presence of the *trp1* lesion as a characteristic of the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan.
- [0287] Other yeast hosts such *Pichia* may also be employed. Yeast expression vectors having expression control sequences (e.g., promoters), an origin of replication, termination sequences and the like as desired. Typical promoters include 3-

phosphoglycerate kinase and other glycolytic enzymes. Inducible yeast promoters include, among others, promoters from alcohol dehydrogenase, isocytchrome C, and enzymes responsible for methanol, maltose, and galactose utilization.

[0288] Alternatively, polypeptide-coding nucleotide sequences can be incorporated in transgenes for introduction into the genome of a transgenic animal and subsequent expression in the milk of the transgenic animal (see, *e.g.*, Deboer *et al.*, US 5,741,957, Rosen, US 5,304,489, and Meade *et al.*, US 5,849,992). Suitable transgenes include coding sequences for polypeptides in operable linkage with a promoter and enhancer from a mammary gland specific gene, such as casein or beta lactoglobulin.

[0289] *In vitro* production allows scale-up to give large amounts of the desired polypeptides. 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, chromatography over DEAE-cellulose or (immuno-)affinity chromatography, *e.g.*, after preferential biosynthesis of a synthetic hinge region polypeptide or prior to or subsequent to the HIC chromatography step described herein. An affinity tag sequence (*e.g.* a His(6) tag) may optionally be attached or included within the polypeptide sequence to facilitate downstream purification.

[0290] In one embodiment, a host cell of the invention comprises a genetic construct encoding a polypeptide comprising a scFc linker and one or more enzymes that can process a cscFc linker. The construct and the enzyme(s) can be expressed using a single vector or two vectors. The chimeric protein produced by the genetic construct encoding a scFc linker can thus have an additional polypeptide chain due to the intracellular processing. In some embodiments, the chimeric protein may contain the cleaved protease cleavage site (*e.g.*, RRRR).

[0291] In one embodiment, the invention pertains to nucleic acid molecules which encode a polypeptide of the invention. In one embodiment, the nucleic acid molecule encodes a chimeric protein comprising an enhancer moiety and an activatable clotting factor selected from activatable FVII or activatable FX, wherein the enhancer moiety enhances

activities of FVII and FX. In another embodiment, the nucleic acid molecule encodes a chimeric protein comprising an enhancer moiety, an activatable clotting factor, and optionally a linker moiety between the activatable clotting factor and the enhancer moiety.

[0292] In another embodiment, the invention pertains to a nucleic acid molecule encoding a polypeptide comprising FVII, which FVII which comprises a heterologous enzymatic cleavage site activatable by a component of the clotting cascade.

[0293] Once expressed, the chimeric clotting factor can be purified according to standard procedures of the art, including ammonium sulfate precipitation, affinity column chromatography, HPLC purification, gel electrophoresis and the like (see generally Scopes, Protein Purification (Springer-Verlag, N.Y., (1982)) and see specifically the methods used in the instant Examples. Substantially pure proteins of at least about 90 to 95% homogeneity are preferred, and 98 to 99% or more homogeneity most preferred, for pharmaceutical uses.

[0294] In other embodiments, the chimeric clotting factor can be produced by combining recombinant DNA technology with chemical synthesis. For example, the present invention includes a method of transfecting a host cell with a polynucleotide encoding a chimeric clotting factor comprising a light chain of a clotting factor, a protease cleavable site (e.g., SUMO), a truncated heavy chain of the clotting factor, an optional linker, and an enhancer moiety. Small Ubiquitin-like Modifier (or SUMO) is a member of the ubiquitin (Ub) and ubiquitin-like (Ubl) family. Post-translational attachment of SUMO to target proteins occurs through an enzymatic cascade analogous to the ubiquitin conjugation cascade (E1-E2-E3 enzymes), ultimately resulting in formation of an isopeptide bond between the Ub/Ubl C-terminal residue and substrate lysine residue.

[0295] SUMO Protease, a highly active cysteinyl protease also known as Ulp, is a recombinant fragment of Ulp1 (Ubl-specific protease 1) from *Saccharomyces cerevisiae*. SUMO Protease cleaves in a highly specific manner, recognizing the tertiary structure of the ubiquitin-like (UBL) protein, SUMO, rather than an amino acid sequence. The protease can be used to cleave SUMO from recombinant fusion proteins. The sequence of the SUMO protein comprises:

SLQDSEVNQEAKPEVKPEVKPETHNLKVSDGSSEIFFKIKKTTPLRRLMEAFKR
QGKEMDSLRFYDGIQADQAPEDLDMEDNDIIEAHREQIGG (SEQ ID NO: 65)

[0296] In some embodiments, the present invention includes a method of transfecting a host cell with a polynucleotide encoding a chimeric clotting factor comprising a light chain of a clotting factor, an optional intracellular processing site, a protease cleavable site (e.g., SUMO), a truncated heavy chain of the clotting factor, an optional linker, and an enhancer moiety, wherein the chimeric clotting factor is expressed. In certain embodiments, the truncated heavy chain does not comprise one or more amino acids from the N-terminus corresponding to the wild type heavy chain. The heavy chain is missing one or more amino acids to expose a naturally occurring cysteine residue on FVII or FX for chemical ligation to a thioester peptide. In one embodiment, the amino acids missing from the truncated heavy chain are six amino acids, e.g., IVGGKV (SEQ ID NO: 60) for FVII or IVGGQE (SEQ ID NO: 61) for FX. In another embodiment, the amino acids missing from the truncated heavy chain are 11 amino acids, e.g., IVGGKVCPKGE (SEQ ID NO: 62) for FVII or IVGGQECKDGE (SEQ ID NO: 63) for FX. In other embodiments, the host cell further comprises a polynucleotide sequence encoding an intracellular processing enzyme, thereby processing the light chain of the clotting factor from the chimeric clotting factor. The light chain of the clotting factor can form a disulphide bond with the heavy chain of the clotting factor.

[0297] In certain embodiments, the method further comprises combining (or adding) a SUMO protease to the recombinantly expressed chimeric clotting factor, wherein the SUMO protease cleaves SUMO from the chimeric clotting factor. The cleavage of SUMO can expose the N-terminus of the truncated heavy chain of the clotting factor (e.g., Cys) for further reaction.

[0298] In other embodiments, the method further comprises adding a thioester peptide to be linked to the N-terminus of the truncated heavy chain of the clotting factor, e.g., at Cys. In one embodiment, the thioester peptide can comprise a thrombin cleavage site (e.g., D-Phe-Pip-Arg). In another embodiment, the thioester peptide comprises a thrombin cleavage site (e.g., D-Phe-Pip-Arg) and a self-immolative linker (e.g., PABC). In other embodiments, the thioester peptide comprises a thrombin cleavage site (e.g., D-Phe-Pip-Arg), a self-immolative linker (e.g., PABC), and the one or more amino acids identical to the amino acids missing from the N-terminus of the truncated heavy chain of the clotting factor. In one embodiment, the one or more amino acids in the thioester peptide comprises six amino acids missing from the truncated heavy chain (e.g.,

IVGGKV (SEQ ID NO: 60) for FVII or IVGGQE (SEQ ID NO: 61) for FX). In another embodiment, the one or more amino acids in the thioester peptide comprises 11 amino acids missing from the truncated heavy chain (e.g., IVGGKVCPKGE (SEQ ID NO: 62) for FVII or IVGGQECKDGE (SEQ ID NO: 63) for FX). Therefore, when the thioester peptide is fused to the truncated heavy chain of the clotting factor, the chimeric clotting factor can comprise an activatable clotting factor, an optional linker, and an enhancing moiety, wherein the activatable clotting factor comprises the thrombin cleavage site (e.g., D-Phe-Pip-Arg), the self-immolative linker (e.g., PABC), and the full-length heavy chain of the clotting factor.

IV. Methods of Administering Polypeptides of the Invention

[0299] The invention also relates to a method of treating, ameliorating, or preventing a hemostatic disorder to a subject comprising administering a therapeutically effective amount of a chimeric protein of the Invention. The treatment, amelioration, and prevention by the chimeric protein can be a bypass therapy. The subject in the bypass therapy may have already developed an inhibitor to a clotting factor, e.g., Factor VIII, or is subject to developing a clotting factor inhibitor.

[0300] Compositions for administration to a subject include nucleic acid molecules which comprise a nucleotide sequence encoding a chimeric clotting factor of the invention (for gene therapy applications) as well as polypeptide molecules.

[0301] In one embodiment, a chimeric protein composition of the invention is administered in combination with at least one other agent that promotes hemostasis. Said other agent that promotes hemostasis in a therapeutic with demonstrated clotting activity. As an example, but not as a limitation, hemostatic agent can include Factor V, Factor VII, Factor VIII, Factor IX, Factor X, Factor XI, Factor XII, Factor XIII, prothrombin, or fibrinogen or activated forms of any of the preceding. The clotting factor of hemostatic agent can also include anti-fibrinolytic drugs, e.g., epsilon-amino-caproic acid, tranexamic acid.

[0302] In one embodiment of the invention, the composition (e.g., the polypeptide or nucleic acid molecule encoding the polypeptide) is one in which the clotting factor is present in activatable form when administered to a subject. Such an activatable molecule can be activated in vivo at the site of clotting after administration to a subject.

- [0303] The chimeric protein of the invention can be administered intravenously, subcutaneously, intramuscularly, or via any mucosal surface, e.g., orally, sublingually, buccally, sublingually, nasally, rectally, vaginally or via pulmonary route. The chimeric protein can be implanted within or linked to a biopolymer solid support that allows for the slow release of the chimeric protein to the desired site.
- [0304] 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.
- [0305] For buccal and sublingual administration the composition may take the form of tablets, lozenges or fast dissolving films according to conventional protocols.
- [0306] For administration by inhalation, the chimeric proteins for use according to the present invention are conveniently delivered in the form of an aerosol spray from a pressurized pack or nebulizer (e.g. in PBS), with a suitable 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.
- [0307] In one embodiment, the route of administration of the polypeptides of the invention is parenteral. The term parenteral as used herein includes intravenous, intraarterial, intraperitoneal, intramuscular, subcutaneous, rectal or vaginal administration. The intravenous form of parenteral administration is preferred. While all these forms of administration are clearly contemplated as being within the scope of the invention, a form for administration would be a solution for injection, in particular for intravenous or intraarterial injection or drip. Usually, a suitable pharmaceutical composition for injection may comprise a buffer (e.g. acetate, phosphate or citrate buffer),

a surfactant (e.g. polysorbate), optionally a stabilizer agent (e.g. human albumin), etc. However, in other methods compatible with the teachings herein, the polypeptides can be delivered directly to the site of the adverse cellular population thereby increasing the exposure of the diseased tissue to the therapeutic agent.

[0308] Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. In the subject invention, pharmaceutically acceptable carriers include, but are not limited to, 0.01-0.1M and preferably 0.05M phosphate buffer or 0.8% saline. Other common parenteral vehicles include sodium phosphate solutions, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers, such as those based on Ringer's dextrose, and the like. Preservatives and other additives may also be present such as for example, antimicrobials, antioxidants, chelating agents, and inert gases and the like.

[0309] More particularly, pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. In such cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It should be stable under the conditions of manufacture and storage and will preferably be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (e.g., glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity 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.

[0310] Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols, such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be

brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

[0311] In any case, sterile injectable solutions can be prepared by incorporating an active compound (*e.g.*, a polypeptide by itself or in combination with other active agents) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated herein, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle, which 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, which yields a powder of an active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof. The preparations for injections are processed, filled into containers such as ampoules, bags, bottles, syringes or vials, and sealed under aseptic conditions according to methods known in the art. Further, the preparations may be packaged and sold in the form of a kit. Such articles of manufacture will preferably have labels or package inserts indicating that the associated compositions are useful for treating a subject suffering from, or predisposed to clotting disorders.

[0312] 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.

[0313] Effective doses of the compositions of the present invention, for the treatment of conditions vary depending upon many different factors, including means of administration, target site, physiological state of the patient, whether the patient is human or an animal, other medications administered, and whether treatment is prophylactic or therapeutic. Usually, the patient is a human but non-human mammals including transgenic mammals can also be treated. Treatment dosages may be titrated using routine methods known to those of skill in the art to optimize safety and efficacy.

[0314] In one embodiment, the dose of a biologically active moiety (*e.g.*, comprising FVII), can range from about 90 to 270 ug/kg or 0.090 to 0.270 mg/kg. In another embodiment, the dose of a biologically active moiety (*e.g.*, comprising FX), can range from about 1 µg/kg to 400mg/kg.

[0315] Dosages can range from 1000 ug/kg to 0.1 ng/kg body weight. In one embodiment, the dosing range is 1ug/kg to 100 ug/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 Vlla-rTF 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).

[0316] Doses intermediate in the above ranges are also intended to be within the scope of the invention. Subjects can be administered such doses daily, on alternative days, weekly or according to any other schedule determined by empirical analysis. An exemplary treatment entails administration in multiple dosages over a prolonged period, for example, of at least six months. In some methods, two or more polypeptides may be administered simultaneously, in which case the dosage of each polypeptide administered falls within the ranges indicated.

[0317] Polypeptides of the invention can be administered on multiple occasions. Intervals between single dosages can be daily, weekly, monthly or yearly. Intervals can also be irregular as indicated by measuring blood levels of modified polypeptide or antigen in the patient. Alternatively, polypeptides can be administered as a sustained release formulation, in which case less frequent administration is required. Dosage and frequency vary depending on the half-life of the polypeptide in the patient.

[0318] The dosage and frequency of administration can vary depending on whether the treatment is prophylactic or therapeutic. In prophylactic applications, compositions containing the polypeptides of the invention or a cocktail thereof are administered to a patient not already in the disease state to enhance the patient's resistance or minimize effects of disease. Such an amount is defined to be a "prophylactic effective dose." A relatively low dosage is administered at relatively infrequent intervals over a long period of time. Some patients continue to receive treatment for the rest of their lives.

[0319] Polypeptides of the invention can optionally be administered in combination with other agents that are effective in treating the disorder or condition in need of treatment (e.g., prophylactic or therapeutic).

[0320] As used herein, the administration of polypeptides of the invention in conjunction or combination with an adjunct therapy means the sequential, simultaneous, coextensive,

concurrent, concomitant or contemporaneous administration or application of the therapy and the disclosed polypeptides. Those skilled in the art will appreciate that the administration or application of the various components of the combined therapeutic regimen may be timed to enhance the overall effectiveness of the treatment. A skilled artisan (e.g. a physician) would be readily be able to discern effective combined therapeutic regimens without undue experimentation based on the selected adjunct therapy and the teachings of the instant specification.

[0321] It will further be appreciated that the polypeptides of the instant invention may be used in conjunction or combination with an agent or agents (e.g. to provide a combined therapeutic regimen). Exemplary agents with which a polypeptide of the invention may be combined include agents that represent the current standard of care for a particular disorder being treated. Such agents may be chemical or biologic in nature. The term “biologic” or “biologic agent” refers to any pharmaceutically active agent made from living organisms and/or their products which is intended for use as a therapeutic.

[0322] The amount of agent to be used in combination with the polypeptides of the instant invention may vary by subject or may be administered according to what is known in the art. See for example, Bruce A Chabner *et al.*, *Antineoplastic Agents*, in GOODMAN & GILMAN'S THE PHARMACOLOGICAL BASIS OF THERAPEUTICS 1233-1287 ((Joel G. Hardman *et al.*, eds., 9th ed. 1996). In another embodiment, an amount of such an agent consistent with the standard of care is administered.

[0323] As previously discussed, the polypeptides of the present invention, may be administered in a pharmaceutically effective amount for the *in vivo* treatment of clotting disorders. In this regard, it will be appreciated that the polypeptides of the invention can be formulated to facilitate administration and promote stability of the active agent. Preferably, pharmaceutical compositions in accordance with the present invention comprise a pharmaceutically acceptable, non-toxic, sterile carrier such as physiological saline, non-toxic buffers, preservatives and the like. Of course, the pharmaceutical compositions of the present invention may be administered in single or multiple doses to provide for a pharmaceutically effective amount of the polypeptide.

[0324] In one embodiment, a chimeric clotting factor of the invention can be administered as a nucleic acid molecule. Nucleic acid molecules can be administered using techniques known in the art, including via vector, plasmid, liposome, DNA

injection, electroporation, gene gun, intravenously injection or hepatic artery infusion. Vectors for use in gene therapy embodiments are known in the art.

[0325] In keeping with the scope of the present disclosure, the chimeric clotting factors of the invention may be administered to a human or other animal in accordance with the aforementioned methods of treatment in an amount sufficient to produce a therapeutic or prophylactic effect.

[0326] The chimeric proteins of the invention have many uses as will be recognized by one skilled in the art, including, but not limited to methods of treating a subject with a disease or condition. The disease or condition can include, but is not limited to, hemostatic disorders.

[0327] In one embodiment, the invention relates to a method of treating a subject having a hemostatic disorder comprising administering a therapeutically effective amount of at least one chimeric protein of the invention.

[0328] The chimeric proteins of the invention treat or prevent a hemostatic disorder by promoting the formation of a fibrin clot. The chimeric protein of the invention can activate any member of a coagulation cascade. The clotting factor can be a participant in the extrinsic pathway, the intrinsic pathway or both.

[0329] A chimeric protein of the invention can be used to treat hemostatic disorders, e.g., those known to be treatable with the particular clotting factor present in the chimeric protein. The hemostatic disorders that may be treated by administration of the chimeric protein of the invention include, but are not limited to, hemophilia A, hemophilia B, von Willebrand's disease, Factor XI deficiency (PTA deficiency), Factor XII deficiency, as well as deficiencies or structural abnormalities in fibrinogen, prothrombin, Factor V, Factor VII, Factor X, or Factor XIII.

[0330] In one embodiment, the hemostatic disorder is an inherited disorder. In one embodiment, the subject has hemophilia A, and the chimeric protein comprises protease-activatable Factor VII linked to or associated with an enhancer moiety. In another embodiment, the subject has hemophilia A and the chimeric clotting factor comprises protease-activatable Factor VII linked to or associated with an enhancer moiety. In another embodiment, the subject has hemophilia B and the chimeric protein comprises protease-activatable Factor VII or Factor X linked to or associated with an enhancer moiety. In another embodiment, the subject has inhibitory antibodies to Factor VIII or

Factor VIIIa and the chimeric clotting factor comprises protease-activatable Factor VII linked to or associated with an enhancer moiety. In yet another embodiment, the subject has inhibitory antibodies against Factor IX or Factor IXa and the chimeric protein comprises protease-activatable Factor VII linked to or associated with an enhancer moiety. In other embodiments, the subject has inhibitory antibodies to Factor VIII or Factor VIIIa and the chimeric clotting factor comprises protease-activatable Factor X linked to or associated with an enhancer moiety. In yet another embodiment, the subject has inhibitory antibodies against Factor IX or Factor IXa and the chimeric protein comprises protease-activatable Factor X linked to or associated with an enhancer moiety.

[0331] The chimeric clotting factor of the invention can be used to prophylactically treat a subject with a hemostatic disorder. The chimeric clotting factor of the invention can be used to treat an acute bleeding episode in a subject with a hemostatic disorder.

[0332] In one embodiment, the hemostatic disorder is the result of a deficiency in a clotting factor, e.g., Factor VII, Factor IX, or Factor VIII. In another embodiment, the hemostatic disorder can be the result of a defective clotting factor.

[0333] In another embodiment, the hemostatic disorder can be 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 autoimmune disease, or pregnancy. The acquired disorder can result from old age or from medication to treat an underlying secondary disorder (e.g. cancer chemotherapy).

[0334] The invention also relates to methods of treating a subject that does not have a hemostatic disorder or a secondary disease or condition resulting in acquisition of a hemostatic disorder. The invention thus relates to a method of treating a subject in need of a general hemostatic agent comprising administering a therapeutically effective amount of at least one chimeric protein of the invention. For example, 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, or stem cell transplantation.

[0335] In another embodiment, the chimeric protein of the invention 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.

[0336] This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patents and published patent applications cited throughout this application are incorporated herein by reference.

EXAMPLES

[0337] Throughout the examples, the following materials and methods were used unless otherwise stated.

Example 1. Cloning of FVII-133

[0338] The DNA sequence comprising nucleotides from the HindIII site to the first EcoRI site of FVII-133 was synthesized and subcloned into the HindIII/EcoRI sites of pBUD-CE4.1 (Invitrogen), generating an intermediate construct. Next, the DNA region comprising nucleotides from the first EcoRI site to the second EcoRI site of FVII-133 was synthesized and subcloned into the EcoRI sites of the intermediate construct to generate FVII-133 (FIG. 4A).

Example 2. Transient expression of FVII-133

[0339] For expression of FVII-133, HEK-293-F cells were grown in Freestyle media (Invitrogen) supplemented with vitamin K3 (Sigma Aldrich, St. Louis, MO) to 2 µg/liter (growth media) as suspension cells at 37° C/10% CO₂. Cells were subcultured every three to four days by seeding at cell density of 5x10⁵ cells/ml.

[0340] Twenty-four hours prior to transfection, cells were seeded at a density of 7x10⁵ cells/ml in growth media. On the day of transfection, a transfection solution was made with a volume equal to 5% of the total volume of the cell culture to be transfected. In the transfection solution DNA was added (final concentration 20 mg/L) to a freshly made solution of PEI (60 mg/L) in growth media. The solution was swirled for 30 seconds and incubated for five minutes at room temperature before adding directly to the cell culture. Four hours later a volume equal to the cell culture volume of OptiCHO (Invitrogen) supplemented with vitamin K3 and 200 mM L-glutamine was added to the cells. The cell culture was allowed to grow as shown above and daily media samples were taken to assess protein expression. On the day of harvest, the cells were spun down and the media filtered in preparation for protein purification or protein analysis by protein A pulldown. For expression of FVII-133, a plasmid encoding FVII-133 was cotransfected with a plasmid encoding the propeptide endopeptidase PC5 to ensure cleavage of the propeptide endopeptidase sites in the linker connecting the Fc to sTF (FIG. 4A).

Example 3. Analysis of protein generated from transient transfections

[0341] For analysis of protein from transient transfections, the conditioned media from cotransfections of FVII-133 with PC5 was subjected to protein A immunoprecipitation. Briefly, cell culture supernatant was mixed with approximately 50 μ l of protein A-Sepharose 50% slurry and incubated at 4°C with rocking for 1 hour, then centrifuged to pellet the protein A beads. Beads were washed twice by resuspending in 1 ml of PBS, spinning and aspirating. The beads were resuspended with sodium dodecylsulfate-polyacrylamide gel electrophoresis (SDS-PAGE) buffer under reducing or nonreducing conditions, heated for 5 minutes at 100°C, spun down and loaded on SDS-PAGE gels and run according to standard protocols. Under nonreducing conditions, 1 band with the expected molecular weight for the thrombin-activatable FVII-Fc/sTF-Fc dimer was observed (FIG. 4C). Under reducing conditions 2 bands were observed representing the thrombin-activatable FVII-Fc subunit and the sTF-Fc subunit.

Example 4. Small scale purification of FVII-133

[0342] FcRn Load Adjustment Buffer (0.5ml) were added to 5 ml of filtered conditioned media from cells transiently transfected with FVII-133. The pH-adjusted media (~5.5 ml) was concentrated using a 30,000 MWCO, 15 ml centrifugal filter units (catalog # UFC 903008). The media was centrifuged for 10' at 4000 rpm to ~200 μ l volume, transferred to a tube and the volume adjusted to 400 μ l with equilibration buffer. 10 μ l of FcRn resin were added and the mixture was rotated overnight at 4°C. The conditioned media with resin was loaded into mini-column and centrifuged for 30" at 2000 rpm. The column was washed extensively with equilibration buffer. The protein was eluted with 30 μ l of elution buffer. Elution Buffer contains 50 mM Tris, 250 mM NaCl, and 0.02% Tween-80 @ pH 7.5. FcRn Load Adjustment Buffer contains 0.5M MES and 0.2% Tween-80 @ pH 6.0. FcRn resin contains soluble FcRn conjugated to Sepharose 4 Fast Flow. Equilibration buffer contains 10 mM MES, 250 mM NaCl, 0.02% Tween-80 @ pH 6.2

[0343] The eluted material was analyzed by SDS PAGE under reducing conditions. Two bands with the expected molecular weight for the thrombin-activatable FVII-Fc and sTF-Fc subunits were observed (FIG. 5).

Example 5. Activity of FVII-133 by Prothrombin Time assay

[0344] The activity of the FVIIaFc and purified FVII-133 was determined by the prothrombin time using Dade Innovin reagents (Siemens catalog number 539196), which measure the activity of total FVII, including FVIIa. Manufacturer recommendations were followed. We observed an activity of approximately 10, 000 IU/mg for FVIIaFc but the activity of FVII-133 was below the level of quantitation. Therefore, in the absence of thrombin, FVII-133 remained as a zymogen and inactive form.

Example 6. Activity of FVII-133 and FVIIaFc in thrombin generation assays

[0345] Thrombin generation assays were performed in a Fluoroskan Ascent fluorometer (Thermo Scientific) and reagents and analysis software from Thrombinoscope, according to manufacturer's recommendations. Briefly, human platelets were washed in 5.4 mM trisodium citrate, 146 mM NaCl, pH 6.8 and resuspended in FVIII-deficient human plasma (Siemens) to generate platelet-rich plasma (PRP) at a platelet concentration of 2×10^8 platelets/ml. Each reaction contained FVIII-deficient PRP, calibrator (Thrombinoscope) or Tyrode's buffer (15 mM Hepes pH 7.4, 138 mM NaCl, 2.7 mM KCl, 1 mM $MgCl_2$, 5.5 mM dextrose, 1 mg/ml BSA), FVII-133 or FVIIaFc (50 nM final concentration), and lipidated tissue factor (PRP reagent at a 1/8 dilution, Thrombinoscope) where indicated. Tissue factor, as a complex with endogenous FVIIa, is expected to activate the reaction by inducing the generation of small amounts of thrombin. As shown in FIG. 6, FVII-133 displayed much greater activity than FVIIaFc in the presence or in the absence of tissue factor (TF). Interestingly FVII-133 showed similar activity in the presence or in the absence of TF, but prothrombin time assays show that FVII-133 has no activity in the absence of thrombin. This suggests that trace amounts of thrombin or TF (that can in turn generate thrombin with endogenous FVIIa) in the PRP are sufficient to activate FVII-133. Furthermore, these data show that FVII-133 has the potential for high activity once activated.

Example 7. Activity of FVII-133 and FVIIaFc in Rotational thromboelastometry assays

[0346] Citrated blood from FIX-deficient mice was used for these experiments. Thromboelastography was carried out in a ROTEM analyzer (Pentapharm) according to the manufacturer's recommendations. Briefly, 280 ul of blood were transferred to a

prewarmed ROTEM plastic cup and spiked with FVIIaFc or FVII-133 to a final concentration of 50 nM. EXTEM reagent (TF and Calcium) was added to initiate the reaction.. Clotting time (CT) and alpha angle were measured. As shown in FIG. 7, both FVII-133 and FVIIaFc displayed clotting times and alpha angles that were significantly lower or higher, respectively, than vehicle. Lower clotting times and higher alpha angles indicate increased hemostatic activity. These data show that FVII-133 can display high activity when activated by thrombin.

Example 8. Generation of alternative chimeric clotting factors comprising an activatable FVII and an enhancer moiety.

[0347] Constructs will be generated for the expression of thrombin-activatable FVII followed by a linker and an enhancer moiety (also referred to as “an enhancer moiety”) as illustrated in FIG. 2. In one embodiment, the enhancer moiety will be soluble tissue factor (residues 1-219 from mature sequence). In another embodiment, the enhancer moiety will be procoagulant peptides SYN3731 or SYN3524 (see Int'l Appl. No. PCT/US2012/041777, filed June 9, 2012 and published as WO 2012/170969, which is incorporated herein by reference in its entirety). In another embodiment the enhancer moiety will be an antibody fragment derived from antibodies that increase the activity of FVIIa. For example, antibodies that enhance the activity of FVIIa were described in Andersen LM et al. J Biol Chem. 287: 8994-9001 (Jan. 24, 2012). These constructs will be transiently expressed in mammalian cells, purified and tested for activity (prothrombin time, thrombin generation and ROTEM assays) as previously described.

Example 9. *In vitro* activity of FVII-133 in human hemophilia A blood by rotational thromboelastometry assays

[0348] To determine the clotting activity, FVII-133 protein was spiked into citrated human whole blood from hemophilia A donors. Clot was initiated by adding CaCl₂; the clotting time, clotting formation time, and α -angle were measured on the ROTEM analyzer (Pentapharm) following the manufacturer's recommendations. FVIIa and FVII-184 were tested in parallel; whereas FVIIa was used as a comparator for activity, FVII-184 was employed as a control for determining the contribution of endogenous FVIIa that could be activated by the fusion protein itself, because FVII-184 was designed to be insensitive to thrombin activation by mutating the Arg essential for the thrombin cleavage

site to Ala, but otherwise the same as FVII-133. As shown in FIG. 8, the clotting time in this hemophilia A donor recorded to be 2500 sec. Spiking FVII-133 in the whole blood resulted in a much shorter clotting time in a dose dependent manner. The clotting time recorded on 10 and 2 nM of FVII-133 was shorter than that of 50, 10nM of rFVIIa respectively. Based on its clotting time profile, the activity of FVII-133 was estimated to be at least 10-fold higher than that of FVIIa. The faster clotting time of FVII-133 correlated with its shorter clotting formation time and higher α -angle, which agree with the higher hemostatic activity of FVII-133. Inactivating the thrombin cleavage site of FVII133 considerably reduced the activity; as the activity of FVII-184, which only became detectable at 50 nM, was much lower than that of FVIIa, indicating the activity of FVII-133 was indeed contributed by its own thrombin activated FVIIa, but not by the endogenous FVII/FVIIa.

Example 10. *Ex vivo* efficacy of FVII-133 in hemB mice by ROTEM analysis

[0349] To assess the *ex vivo* efficacy, hemophilia B (hemB) mice were dosed at 20 nmol/kg of FVII-133 or control protein rFVIIa via tail vein injection. At 2.5 hour after dosing, blood was collected in CTI at 9:1 ratio from mice via vena cava bleeding. Blood was re-calcified, and immediately measured on the ROTEM analyzer. As shown in FIG. 9, whereas the average clotting time in hemB blood measured was about 1800 sec, the clotting time of whole blood from mice injected with FVII-133 was much shorter, approaching 500 sec, indicating that FVII-133 was active in vivo.

Example 11. Improved PK profile of FVII-133 over rFVIIaFc

[0350] FVII-133 was designed to circulate as FVII zymogen, thus it is predicted to be less susceptible to antithrombin III (ATIII) mediated clearance. To evaluate the pharmacokinetic properties of FVII-133, the purified FVII-133, rFVIIaFc and rFVIIa were administrated intravenously into hemB mice (n=4) at 10 nmol/kg, and plasma samples were collected via vena cava bleeding at various times and analyzed for FVII antigen, and FVII-ATIII complex by ELISA assays. Pharmacokinetic parameters were assessed by PK modeling using Phoenix program (Pharsight). Since rFVIIa was cleared much more rapidly than either FVII-133 or rFVIIaFc (FIG.10A), we used rFVIIaFc as a comparator for the pharmacokinetic analysis of FVII-133 (FIG. 10B). Plasma

concentration of the protein versus time curve was found to best fit in a two compartmental model; all the PK parameters indicated a marked improvement of FVII-133 over rFVIIaFc, with longer terminal half-life (Beta half life of 16.56 hour vs 7.78 hour, respectively) and longer mean residence time (MRT 19.29 hour vs 7.45 hour) as shown in Table 4.

Table 4. PK Parameters: FVII-133 vs FVIIaFc

Treatment	Alpha $t_{1/2}$ (hour)	Beta $t_{1/2}$ (hour)	MRT (hour)	CL (mL/hour/kg)	Vss (mL/kg)	AUC (hour*pmol/mL)
FVII-133	0.43	16.56	19.29	17.59	339.31	738.96
FVIIaFc	1.41	7.78	7.45	73.15	544.79	273.42

[0351] In addition, whereas a significant amount of rFVIIaFc/ATIII complex was detected, the FVII-133/ATIII complex in plasma was almost undetectable. Together, these results indicated that FVII-133 successfully escaped the ATIII-mediated clearance, leading to a marked improvement in PK profile over rFVIIaFc.

Example 12. Prolonged *Ex vivo* Efficacy of FVII-212 over rFVIIa in HemA Mice

[0352] FVII-212 is identical to FVII-133, but encoded by an improved expression vector. Similar to FVII-133, FVII-212 displayed higher *in vitro* clotting activity than rFVIIa in human HemA blood per ROTEM assays (FIG. 11). In mouse HemA blood, however, the activity of FVII-212 was found to be similar to rFVIIa (FIG. 12), indicating FVII-212 is less active in mouse than human.

[0353] To assess the *ex vivo* efficacy of FVII-212 and corroborate the finding by example 10 (*ex vivo* efficacy of FVII-133 in HemB mice), FVII-212 was administrated in HemA mice at 10 nmol/kg; blood was sampled at various times, and the clotting activity was measured by ROTEM analyzer under NATEM program. rFVIIa was included in parallel as a comparator. As shown in FIG. 13, although the clotting time from the blood collected at 5 min following dosing was similar between rFVII-212 and rFVIIa treated groups, the blood collected from the later time points of FVII-212 group clotted faster than that from the corresponding time point of rFVIIa group. The results indicate the prolonged *ex-vivo* efficacy of FVII-212 compared to rFVIIa.

[0354] As indicated in Example 11, FVII-133 displayed improved PK properties over rFVIIaFc in HemB mice, which were thought to contribute to the prolonged efficacy of this protein. Similar to FVII-133 in HemB mice, the clearance of FVII-212 in HemA mice was considerably slower than that of rFVIIa (FIG. 14), represented by a longer terminal half-life of about 18 hours (compared to the half-life about 1 hour in HemA plasma of rFVIIa when measured by rFVIIa's activity) as well as the absence of rFVII-212-ATIII complex in treated HemA mice.

[0355] Taken together, this example extended the previous finding and demonstrated that 1) FVII-212 displays prolonged *ex vivo* efficacy over rFVIIa in HemA mice; 2) the prolonged efficacy of FVII-212 is resulted from its improved PK properties; and 3) resistance to ATIII inhibition contributes, at least partly, to the PK improvement in FVII-212.

Example 13. Amidolytic Activity of FVII-212

[0356] Amidolytic activity of FVII-212 was measured before and after thrombin activation using a chromozyme t-PA substrate. For thrombin activation, FVII-212 (100 nM) was treated with thrombin (50 nM) for 20 minutes at 37° C. Thrombin was subsequently inhibited with hirudin (250 nM).

[0357] As FIG. 15 shows, FVII-212 displayed no activity prior to thrombin activation. Following thrombin activation, the amidolytic activity associated with FVII-212 was greater than that observed for equal molar levels of rFVIIa. These data demonstrate that the activity of FVII-212 is dependent on thrombin activation.

Example 14. Thrombin-Activatable Procoagulant Compounds with PABC Self-Immolative Linker

[0358] Six different peptides, designated Compound 1 to 6, were used in the experiments disclosed herein (TABLE 5). The sequence in Compounds 1 to 6 reproduces the coupling of a thrombin cleavable substrate and a self-immolative spacer to the N-terminus of a clotting factor or a fragment thereof, in this specific example, FX. These compounds comprise the six N-terminal amino acid residues of the heavy chain of the FXa clotting factor, Ile-Val-Gly-Gly-Gln-Glu, and serve as a model to show the applicability of the procoagulant compound design disclosed herein to clotting factors.

TABLE 5

Compound	Structure
1	(D-Phe)-Pip-Arg-PABC-Ile-Val-Gly-Gly-Gln-Glu-NH ₂
2	(D-Phe)-Pip-Arg-Ile-Val-Gly-Gly-Gln-Glu-NH ₂
3	Ala-Leu-Arg-Pro-Arg-Ile-Val-Gly-Gly-Gln-Glu-NH ₂
4	(D-Phe)-Pro-Arg-PABC-Ile-Val-Gly-Gly-Gln-Glu-NH ₂
5	Ala-Leu-Val-Pro-Arg-PABC-Ile-Val-Gly-Gly-Gln-Glu-NH ₂
6	Ala-Leu-Val-Pro-Arg-Ile-Val-Gly-Gly-Gln-Glu-NH ₂

Pip is pipecolic acid. (D-Phe) is D-Phenyl alanine. The sequences of the thrombin substrate are underlined.

The location of the PABC self-immolative linker is indicated by a box.

[0359] FIG. 18 depicts the cleavage of Compounds 1, 2 and 3 by 14 nM thrombin. In this specific example, 50 μ L of peptide (1 mM) in water was added to 900 μ L PBS, followed by 50 μ L of thrombin (278 nM, 10 μ g/mL), giving the following approximate initial concentrations: thrombin = 14 nM, peptide = 50 μ M. The mixture was incubated at room temperature. Aliquots (95 μ L) at various time points were quenched with 5 μ L of hirudin (2 μ M) and injected into the HPLC (C-18 column, CH₃CN/H₂O, 0 to 70% over 12 minutes, 60°C 0.5 mL/min, λ = 280 nm). The decreases of peptide peak areas were used to calculate yield.

[0360] Compared to Compounds 2 and 3, the construct incorporating the thrombin-cleavable synthetic substrate D-Phe-Pip-Arg and the self-immolative spacer PABC (Compound 1) was a better substrate for thrombin. The incorporation of PABC to Compound 1 led to at least 10-fold increase in cleavage rate compared to that of Compound 2.

[0361] FIG. 19 depicts the cleavage of Compounds 1, 4, 5 and 6 by 1.4 nM thrombin. Compounds 1, 4 and 5 incorporate PABC and different thrombin-cleavable substrates. 50 μ L of peptide (1 mM) in water was added to 900 μ L PBS. The mixture was incubated at 37°C for 30min, followed by 50 μ L of thrombin (27.8 nM, 1 μ g/mL), giving the following approximate initial concentrations: thrombin = 1.4 nM, peptide = 50 μ M. The mixture was incubated at 37°C. Aliquots (95 μ L) at various time points were quenched with 5 μ L of hirudin (2 μ M) and injected into the HPLC (C-18 column, CH₃CN/H₂O, 0 to 70% over 12 minutes, 60°C 0.5 mL/min, λ = 280 nm). The decreases of peptide peak areas were used to calculate yield.

[0362] Compound 1 was a better substrate for thrombin than Compounds 4 and 5. At 1.4 nM, a physiological relevant concentration of thrombin, 30% of Compound 1 was quickly

cleaved and released. In contrast, thrombin-mediated release of peptide IVGGQE from Compound 6 without PABC linker was not observed.

Example 15. Thrombin activatable FVII-186 with SUMO cleavage site

[0363] For cloning of FVII-186, the DNA sequence comprising nucleotides from the HindIII site to the EcoRI site of FVII-186 (Table #) was synthesized. The DNA was subcloned into the HindIII/EcoRI sites of pcDNA.

[0364] To transiently express FVII-186, HEK-293-F cells were grown in suspension in FREESTYLE[®] media (Invitrogen) supplemented with vitamin K3 (Sigma Aldrich, St. Louis, MO) to 2 µg/liter (growth media) as suspension cells at 37° C/10% CO₂. Cells were subcultured every three to four days by seeding at cell density of 5x10⁵ cells/ml. Twenty-four hours prior to transfection, cells were seeded at a density of 7x10⁵ cells/ml in growth media. On the day of transfection, a transfection solution was made with a volume equal to 5% of the total volume of the cell culture to be transfected. In the transfection solution, DNA was added (final concentration 20 mg/L) to a freshly made solution of PEI (60 mg/L) in growth media. The solution was swirled for 30 seconds and incubated for five minutes at room temperature before adding directly to the cell culture. Four hours later a volume equal to the cell culture volume of OPTICHO[™] (Invitrogen) supplemented with vitamin K3 and 200 mM L-glutamine was added to the cells. The cell culture was allowed to grow as shown above and daily media samples were taken to assess protein expression. On the day of harvest, the cells were spun down, and the media filtered in preparation for protein purification or protein analysis by protein A pulldown. For expression of FVII-186, a plasmid encoding FVII-186 was cotransfected with a plasmid encoding the proprotein convertase PACE to ensure intracellular processing and cleavage of the proprotein convertase cleavage sites (2X(RKR) SEQ ID NO: 3) in the linker connecting the FVII light chain to SUMO (FIG. 22).

[0365] To purify FVII-186, conditioned medium was loaded onto a 25-mL column of Q SEPHAROSE[®] Fast Flow (GE HealthCare Life Sciences) after adjustment of pH to 7.4 with 2.0 M Tris, pH 8.0. Column was washed with 10 mM MES, 50mM NaCl, pH 6.5. The protein was eluted with 10 mM MES, 100 mM NaCl, 20 mM CaCl₂, pH 6.5. The fractions containing FVII-186 were pooled and loaded onto a 25-mL column of rhFcRn-sepharose after adjustment of pH to 6.2 with 0.5 M MES, pH 5.5. After washing with 50

mM MES, 100 mM NaCl, pH 6.2, the bound material was eluted with 10 mM Tris, 250 mM NaCl, pH 8.0 and analyzed with SDS-PAGE.

[0366] FVII-186 was cleaved by a SUMO protease as follows. FVII-186 (0.83 mg/mL, 10 μ L) was incubated with 10 μ L of 100 mM HEPES, 20 mM CaCl_2 , 0.004% Tween 80 containing 0.4 mM oxidized Glutathione (GSSG), 20 mM Glutathione (GSH), 0.2 U/ μ L SUMO protease (Invitrogen Cat. No.12588-018) for 48 hours at room temperature. Reducing SDS-PAGE (FIG. 23, lane 3) showed almost complete conversion of FVII-186 to the desired FVIIIHC.

[0367] For SUMO protease cleavage of FVII-186 and native chemical ligation with a thioester peptide, FVII-186 (0.83 mg/mL, 10 μ L) was incubated with 10 μ L of 100 mM HEPES, 20 mM CaCl_2 , 0.004% Tween 80 containing 0.4 mM SYN470 as a positive control peptide, 0.4 mM GSSG, 20 mM GSH, 0.2 U/ μ L SUMO protease (Invitrogen Cat. No.12588-018) for 48 hours at room temperature. Reducing SDS-PAGE (Figure #, lane 4) showed complete disappearance of the FVIIIHC band and a single new band as the conjugate of the positive peptide control and the FVIIIHC.

[0368] In order to synthesize Thrombin Activatable FVII-186 (TA-FVII-186), FVII-186 (0.83 mg/mL, 200 μ L) was incubated with 200 μ L of 100 mM HEPES, 20 mM CaCl_2 , 0.004% Tween 80 containing 0.4 mM FVII-PABC peptide (i.e., D-Phe-Pip-Arg-PABC-IVGGKV-COSBn) (SEQ ID NO: 66), 0.4 mM GSSG, 20 mM GSH, 0.2 U/ μ L SUMO protease (Invitrogen Cat. No.12588-018) for 48 hours at room temperature and analyzed by reducing SDS-PAGE (FIG. 23, lane 5). Reaction mixture was placed in a 0.5 mL dialysis cassette with 10k MWCO and dialyzed against 1 L of 10 mM Tris, 250 mM NaCl, pH 8.0 containing 0.4 mM GSSG, 2 mM GSH for 24 hours at 4° C. The conjugate was further purified by rhFcRn- sepharose column as described.

[0369] FVIIa Chromogenic assay was performed after Thrombin cleavage and activation of TA-FVII-186 (FIG. 24). This assay measures the FX activation activity by measuring the ability of FVIIa to activate FX, as determined by measuring levels of a chromogenic substrate that is cleaved by activated FX (FXa). TA-FVII-186 (200 nM) was activated with Thrombin (140 nM) for 20 minutes at 37° C. Hirudin was added to quench Thrombin. sTF-PL mixture (A STACLOT® FVII-rTF kit), FX, and PEFACHROME® FXa substrate were added and reaction was monitored by measuring absorbance at 405 nm. FVII-186 missing the six N-terminal amino acids was not active in the presence of

thrombin. Only TA-FVII-186 with a thrombin cleavage site connected to the complete heavy chain FVII showed activity after thrombin cleavage. The resulted activity demonstrated that the FVII PABC peptide was successfully conjugated to the N-terminal cysteine of the truncated heavy chain of FVII, the crucial N-terminal isoleucine residue was generated upon cleavage by thrombin, and the formed protein had the essential structure for activity.

[0370] The present invention has been described above with the aid of functional building blocks illustrating the implementation of specified functions and relationships thereof. The boundaries of these functional building blocks have been arbitrarily defined herein for the convenience of the description. Alternative boundaries can be defined so long as the specified functions and relationships thereof are appropriately performed.

[0371] 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.

[0372] The breadth and scope of the present invention should not be limited by any of the above-described exemplary embodiments, but should be defined only in accordance with the following claims and their equivalents. 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.

[0373] All patents and publications cited herein are incorporated by reference herein in their entirety.

SEQUENCES

SEQ ID NO: 44 DNA sequence of FVII-133

```
1 AAGCTTGCCG CCACCATGGT CTCCCAGGCC CTCAGGCTCC TCTGCCTTCT GCTTGGGCTT
  TTCGAACGGC GGTGGTACCA GAGGGTCCGG GAGTCCGAGG AGACGGAAGA CGAACCCGAA
61 CAGGGCTGCC TGGCTGCAGT CTTCGTAACC CAGGAGGAAG CCCACGGCGT CCTGCACCGG
  GTCCCGACGG ACCGACGTCA GAAGCATTGG GTCCTCCTTC GGGTGCCGCA GGACGTGGCC
121 CGCCGGCGCG CCAACGCGTT CCTGGAGGAG CTGCGGCCGG GCTCCCTGGA GAGGGAGTGC
  GCGGCCGCGC GGTTCGCAA GGACCTCCTC GACGCCGGCC CGAGGGACCT CTCCCTCACG
181 AAGGAGGAGC AGTGCTCCTT CGAGGAGGCC CGGGAGATCT TCAAGGACGC GGAGAGGACG
  TTCCTCCTCG TCACGAGGAA GCTCCTCCGG GCCCTCTAGA AGTTCCTGCG CCTCTCCTGC
241 AAGCTGTTCT GGATTTCTTA CAGTGATGGG GACCAGTGTG CCTCAAGTCC ATGCCAGAAT
  TTCGACAAGA CCTAAAGAAT GTCACTACCC CTGGTCACAC GGAGTTCAGG TACGGTCTTA
301 GGGGGCTCCT GCAAGGACCA GCTCCAGTCC TATATCTGCT TCTGCCTCCC TGCCTTCGAG
  CCCCCGAGGA CGTTCCTGGT CGAGGTCAGG ATATAGACGA AGACGGAGGG ACGGAAGCTC
361 GGCCGGAAC TGTGAGACGA CAAGGATGAC CAGCTGATCT GTGTGAACGA GAACGGCGGC
  CCGGCCTTGA CACTCTGCGT GTTCCTACTG GTCGACTAGA CACACTTGCT CTTGCCGCCG
421 TGTGAGCAGT ACTGCAGTGA CCACACGGGC ACCAAGCGCT CCTGTCGGTG CCACGAGGGG
  ACACTCGTCA TGACGTCACT GGTGTGCCCC TGGTTCGCGA GGACAGCCAC GGTGCTCCCC
481 TACTCTCTGC TGGCAGACGG GGTGTCTGTC ACACCCACAG TTGAATATCC ATGTGGAAAA
  ATGAGAGACG ACCGTCTGCC CCACAGGACG TGTGGGTGTC AACTTATAGG TACACCTTTT
541 ATACCTATTC TAGAAAAAAG AAATGCCAGC AAACCCCAAG GCGCCCTGCG GCCCCGGATT
  TATGGATAAG ATCTTTTTC TTTACGGTCG TTTGGGGTTC CGCGGGACGC CGGGGCCTAA
601 GTGGGGGGCA AGGTGTGCCC CAAAGGGGAG TGTCCATGGC AGGTCCTGTT GTTGGTGAAT
  CACCCCCCGT TCCACACGGG GTTTCCTCCTC ACAGGTACCG TCCAGGACAA CAACCACTTA
661 GGAGCTCAGT TGTGTGGGGG GACCCTGATC AACACCATCT GGGTGGTCTC CGCGGCCAC
  CCTCGAGTCA ACACACCCCC CTGGGACTAG TTGTGGTAGA CCCACCAGAG GCGCCGGGTG
721 TGTTCGACA AAATCAAGAA CTGGAGGAAC CTGATCGCGG TGCTGGGCGA GCACGACCTC
  ACAAAGCTGT TTTAGTTCTT GACCTCCTTG GACTAGCGCC ACGACCCGCT CGTGCTGGAG
781 AGCGAGCACG ACGGGGATGA GCAGAGCCGG CGGGTGGCGC AGGTCATCAT CCCCAGCACG
  TCGCTCGTGC TGCCCCACT CGTCTCGGCC GCCCACC GCGCTGCTCC GCCTGCACCA GCCCCTGGTC
841 TACGTCCCGG GCACCACCAA CCACGACATC GCGCTGCTCC GCCTGCACCA GCCCCTGGTC
  ATGCAGGGCC CGTGGTGGTT GGTGCTGTAG CGCGACGAGG CGGACGTGGT CGGGCACCAG
901 CTCACTGACC ATGTGGTGCC CCTCTGCCTG CCCGAACGGA CGTTCCTCTGA GAGGACGCTG
  GAGTGACTGG TACACCACGG GGAGACGGAC GGGCTTGCTT GCAAGAGACT CTCCTGCGAC
961 GCCTTCGTGC GCTTCTCATT GGTGAGCGGC TGGGGCCAGC TGCTGGACCG TGGCGCCACG
  CGGAAGCACG CGAAGAGTAA CCAGTCGCCG ACCCCGGTCG ACGACCTGGC ACCCGGGTGC
1021 GCCCTGGAGC TCATGGTCCT CAACGTGCCG CGGCTGATGA CCCAGGACTG CCTGCAGCAG
  CGGGACCTCG AGTACCAGGA GTTGACGGG GCCGACTACT GGGTCCTGAC GGACGTCGTC
1081 TCACGGAAGG TGGGAGACTC CCCAAATATC ACGGAGTACA TGTTCCTGTGC CGGCTACTCG
  AGTGCCTTCC ACCCTCTGAG GGGTTTATAG TGCCTCATGT ACAAGACACG GCCGATGAGC
1141 GATGGCAGCA AGGACTCCTG CAAGGGGGAC AGTGGAGGCC CACATGCCAC CCACTACCGG
  CTACCGTCGT TCCTGAGGAC GTTCCCCCTG TCACCTCCGG GTGTACGGTG GGTGATGGCC
1201 GGCACGTGGT ACCTGACGGG CATCGTCAGC TGGGGCCAGG GCTGCGCAAC CGTGGGCCAC
  CCGTGCACCA TGGACTGCCC GTAGCAGTCG ACCCCGGTCC CGACGCGTTG GCACCCGGTG
1261 TTTGGGGTGT ACACCAGGGT CTCCCAGTAC ATCGAGTGGC TGCAAAAGCT CATGCGCTCA
  AAACCCACA TGTGGTCCCA GAGGGTCATG TAGCTCACCG ACGTTTTTCGA GTACGCGAGT
1321 GAGCCACGCC CAGGAGTCCT CCTGCGAGCC CCATTTCCTG GTGGCGGTGG CTCCGGCGGA
  CTCGGTGC GGTCCTCAGGA GGACGCTCGG GGTAAAGGGC CACCGCCACC GAGGCCGCCT
1381 GGTGGGTCCG GTGGCGGCGG ATCAGGTGGG GGTGGATCAG GCGGTGGAGG TTCCGGTGGC
  CCACCCAGGC CACCGCCGCC TAGTCCACCC CCACCTAGTC CGCCACCTCC AAGGCCACCG
1441 GGGGGATCCG ACAAACCTCA CACATGCCCA CCGTGCCCG CTCCGGAACCT CCTGGGAGGA
  CCCCCTAGGC TGTTTTGAGT GTGTACGGGT GGCACGGGTC GAGGCCTTGA GGACCCTCCT
1501 CCGTCAGTCT TCCTCTTCCC CCAAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT
  GGCAGTCAGA AGGAGAAGGG GGGTTTTGGG TTCCTGTGGG AGTACTAGAG GGCCTGGGGA
1561 GAGGTCACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG
  CTCCAGTGTA CGCACCACCA CCTGCACTCG GTGCTTCTGG GACTCCAGTT CAAGTTGACC
1621 TACGTGGACG GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC
  ATGCACCTGC CGCACCTCCA CGTATTACGG TTCTGTTTCG GCGCCCTCCT CGTCATGTTG
1681 AGCACGTACC GTGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG
  TCGTGCATGG CACACCAGTC GCAGGAGTGG CAGGACGTGG TCCTGACCGA CTTACCGTTC
1741 GAGTACAAGT GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC
  CTCATGTTCA CGTTCCAGAG GTTGTTCGG GAGGGTCCGG GGTAGCTCTT TTGGTAGAGG
1801 AAAGCCAAAG GGCAGCCCCG AGAACCACAG GTGTACACCC TGCCCCCATC CCGGGATGAG
```

TTTCCGGTTTC CCGTCGGGGC TCTTGGTGTC CACATGTGGG ACGGGGGTAG GGCCCTACTC
 1861 CTGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG GCTTCTATCC CAGCGACATC
 GACTGGTTCT TGGTCCAGTC GGACTGGACG GACCAGTTTC CGAAGATAGG GTCGCTGTAG
 1921 GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAACT ACAAGACCAC GCCTCCCGTG
 CGGCACCTCA CCCTCTCGTT ACCCGTCGGC CTCTTGTTGA TGTTCTGGTG CGGAGGGCAC
 1981 TTGGACTCCG ACGGCTCCTT CTTCTCTAC AGCAAGCTCA CCGTCGACAA GAGCAGGTGG
 AACCTGAGGC TGCCGAGGAA GAAGGAGATG TCGTTCGAGT GGCAGCTGTT CTCGTCCACC
 2041 CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG
 GTCGTCCCTT TGCAGAAGAG TACGAGGCAC TACGTACTCC GAGACGTGTT GGTGATGTGC
 2101 CAGAAGAGCC TCTCCCTGTC TCCGGGTAAA CGGCGCCGCC GGAGCGGCGG TGGAGGTTC
 GTCTTCTCGG AGAGGGACAG AGGCCCATTT GCCGCGGCGG CCTCGCCGCC ACCTCCAAGG
 2161 GGTGGCGGCG GATCAGGTGG CGGCGGATCA GGTGGGGGTG GATCAGGTGG CGGGGGATCC
 CCACCGCCGC CTAGTCCACC GCCGCCTAGT CCACCCCCAC CTAGTCCACC GCCCCCTAGG
 2221 AGGAAGAGGA GGAAGAGGTC AGGCACTACA AATACTGTGG CAGCATATAA TTTAACTTGG
 TCCTTCTCCT CTTTCTCCAG TCCGTGATGT TTATGACACC GTCGTATATT AAATTGAACC
 2281 AAATCAACTA ATTTCAAGAC AATTTTGGAG TGGGAACCCA AACCCGTCAA TCAAGTCTAC
 TTTAGTTGAT TAAAGTTCTG TTAAAACCTC ACCCTTGGGT TTGGGCAGTT AGTTCAGATG
 2341 ACTGTTCAA TAAGCACTAA GTCAGGAGAT TGGAAAAGCA AATGCTTTTA CACAACAGAC
 TGACAAGTTT ATTCGTGATT CAGTCCTCTA ACCTTTTTCGT TTACGAAAAT GTGTTGTCTG
 2401 ACAGAGTGTG ACCTCACCAG CGAGATTGTG AAGGATGTGA AGCAGACGTA CTTGGCACGG
 TGTCTCACAC TGGAGTGGCT GCTCTAACAC TTCCTACACT TCGTCTGCAT GAACCGTGCC
 2461 GTCTTCTCCT ACCCGGCAGG GAATGTGGAG AGCACCGGTT CTGCTGGGGA GCCTCTGTAT
 CAGAAGAGGA TGGGCCGTCC CTTACACCTC TCGTGGCCAA GACGACCCCT CGGAGACATA
 2521 GAGAACTCCC CAGAGTTCAC ACCTTACCTG GAGACAAACC TCGGACAGCC AACAATTCAG
 CTCTTGAGGG GTCTCAAGTG TGGAAATGGAC CTCTGTTTGG AGCCTGTCCG TTGTTAAGTC
 2581 AGTTTTGAAC AGGTGGGAAC AAAAGTGAAT GTGACCGTAG AAGATGAACG GACTTTAGTC
 TCAAACTTG TCCACCCTTG TTTTCACTTA CACTGGCATC TTCTACTTGC CTGAAATCAG
 2641 AGAAGGAACA ACACCTTCCT AAGCCTCCGG GATGTTTTTG GCAAGGACTT AATTTATACA
 TCTTCCTTGT TGTGAAAGGA TTCGGAGGCC CTACAAAAC CGTTCCTGAA TTAAATATGT
 2701 CTTTATTATT GGAAATCTTC AAGTTCAGGA AAGAAAACAG CCAAAACAAA CACTAATGAG
 GAAATAATAA CCTTTAGAAG TTCAAGTCCT TTCTTTTGTG GGTTTTGTTC GTGATTACTC
 2761 TTTTTGATTG ATGTGGATAA AGGAGAAAAC TACTGTTTCA GTGTTCAAGC AGTGATTCCT
 AAAAATAAC TACACCTATT TCCTCTTTTG ATGACAAAGT CACAAGTTCG TCACTAAGGG
 2821 TCCCGAACAG TTAACCGGAA GAGTACAGAC AGCCCGGTAG AGTGTATGGG CCAGGAGAAA
 AGGGCTTGTC AATTGGCCTT CTCATGTCTG TCGGGCCATC TCACATACCC GGTCTCTTTT
 2881 GGGGAATTCA GAGAAGGTGG CGGCGGATCA GGTGGGGGTG GATCAGGCGG TGGAGGTTC
 CCCCTTAAGT CTCTTCCACC GCCGCCTAGT CCACCCCCAC CTAGTCCGCC ACCTCCAAGG
 2941 GGTGGCGGCG GATCAGGTGG CGGCGGATCA GGTGGGGGTG GATCAGGTGG CGGCGGATCA
 CCACCGCCGC CTAGTCCACC GCCGCCTAGT CCACCCCCAC CTAGTCCACC GCCGCCTAGT
 3001 GGTGGCGGGG GATCAGACAA AACTCACACA TGCCACCGT GCCCAGCACC GGAATCCTG
 CCACCGCCCC CTAGTCTGTT TTGAGTGTGT ACGGGTGGCA CGGGTCGTGG CCTTGAGGAC
 3061 GCGGACCGT CAGTCTTCCT CTTCCCCCA AAACCCAAGG ACACCCCTCAT GATCTCCCGG
 CCGCCTGGCA GTCAGAAGGA GAAGGGGGGT TTTGGGTTC TGTGGGAGTA CTAGAGGGCC
 3121 ACCCCTGAGG TCACATGCGT GGTGGTGGAC GTGAGCCACG AAGACCTGA GGTCAAGTTC
 TGGGGAATCC AGTGTACGCA CCACCACCTG CACTCGGTGC TTCTGGGACT CCAGTTCAAG
 3181 AACTGGTACG TGGACGGCGT GGAGGTGCAT AATGCCAAGA CAAAGCCGCG GGAGGAGCAG
 TTGACCATGC ACCTGCCGCA CCTCCACGTA TTACGGTTCT GTTTCGGCGC CCTCCTCGTC
 3241 TACAACAGCA CGTACCGTGT GGTGAGCGTC CTCACCGTCC TGCACCAGGA CTGGCTGAAT
 ATGTTGTCTG GCATGGCACA CCAGTCGCAG GAGTGGCAGG ACGTGGTCCT GACCGACTTA
 3301 GGCAAGGAGT ACAAGTGCAA GGTCTCCAAC AAAGCCCTCC CAGCCCCCAT CGAGAAAACC
 CCGTTCCTCA GTTTCACGTT CCAGAGGTG TTTCCGGAGG GTCGGGGGTA GCTCTTTTGG
 3361 ATCTCCAAAG CCAAAGGGCA GCCCCGAGAA CCACAGGTGT ACACCTGCC CCCATCCCGG
 TAGAGTTTTC GGTTCCTCGT CGGGGCTCTT GGTGTCCACA TGTGGGACGG GGGTAGGGCC
 3421 GATGAGCTGA CCAAGAACCA GGTGAGCCTG ACCTGCCTGG TCAAAGGCTT CTATCCCAGC
 CTACTCGACT GGTTCCTTGGT CCAGTCGGAC TGGACGGACC AGTTTCCGAA GATAGGGTCG
 3481 GACATCGCCG TGGAGTGGGA GAGCAATGGG CAGCCGGAGA ACAACTACAA GACCACGCCT
 CTGTAGCGGC ACCTCACCCCT CTCGTTACCC GTCGGCCTCT TGTGATGTT CTGGTGCGGA
 3541 CCCGTGTTGG ACTCCGACGG CTCCTTCTTC CTCTACAGCA AGCTCACCGT GGACAAGAGC
 GGGCACAACC TGAGGCTGCC GAGGAAGAAG GAGATGTCGT TCGAGTGGCA CCTGTTCTCG
 3601 AGGTGGCAGC AGGGGAACGT CTTCTCATGC TCCGTGATGC ATGAGGCTCT GCACAACCAC
 TCCACCGTCG TCCCCTTGCA GAAGAGTACG AGGCACTACG TACTCCGAGA CGTGTTGGTG
 3661 TACACGCAGA AGAGCCTCTC CCTGTCTCCG GGTAAATGAG AATTC
 ATGTGCGTCT TCTCGGAGAG GGACAGAGGC CCATTTACTC TTAAG

SEQ ID NO: 45: FVII-133 amino acid sequence. Signal sequence is shown in dotted underline, propeptide is wave underlined, thrombin cleavage site inserted between the light and heavy chains is double underlined, linker region connecting FVII to Fc region is underlined, linker with proprotein convertase processing sites connecting the Fc and sTF is shown in bold, and linker region connecting sTF to Fc is in dashed underline. The light chain expands from residues 39 to 189, the heavy chain from residues 195 to 448 and sTF from residues 742 to 960.

```

1  MVSQALRLLC LLLGLQGCLA AVFVTQEEAH GVLHRRRRAN AFLEELRPGS LERECKEEQC
61  SFEEAREIFK DAERTKLFWI SYSDGDQCAS SPCQNGGSCK DQLQSYICFC LPAFEGRNCE
121 THKDDQLICV NENGGCEQYC SDHTGTRKSC RCHEGYSLLA DGVSCPTPTVE YPCGKIPILE
181 KRNASKPQGA LRPRIVGGKV CPKGECPWQV LLLVNGAQLC GGTINTIYV VSAAHCFDKI
241 KNWRNLIAVL GEHDLSEHDG DEQSRRAQV IIPSTYVPGT TNHDIALRL HQPVVLTDHV
301 VPLCLPERTF SERTLAFVRF SLVSGWGQLL DRGATAELM VLNVPRLMTQ DCLQQSRKVG
361 DSPNITEYMF CAGYSDGSKD SCKGDSGGPH ATHYRGTWYL TGIVSWGQGC ATVGHFVYVT
421 RVSQYIEWLQ KLMRSEPRPG VLLRAPFPGG GSGSGGSGSG GSGSGGSGSG GSGSGGSGDK
481 THTCPPCPAP ELLGGPSVFL FPPKPKDTLM ISRTPEVTCV VVDVSHEDPE VKFNWYVDGV
541 EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ
601 PREPQVYTLF PSRDELTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG
661 SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSL LSPGKRRRRS GGGSGGGGS
721 GGGSGGGGS GGGSRKRRK RSGTTNTVAA YNLTKSTNF KTILEWEPKP VNQVYTVQIS
781 TKSQDWKSKC FYTTDTECDL TDEIVKDVQK TYLARVFSYP AGNVESTGSA GEPLYENSPE
841 FTPYLETNLG OPTIQSFEQV GTKVNVTVED ERTLVRNNT FLSLRDVFGK DLIYTLYYWK
901 SSSSGKKTA TNTNEFLIDV DKGNYCFSV QAVIPSRV N RKSTDSPEV MGQEKGEFRE
961 GGGSGGGGS GGGSGGGGS GGGSGGGGS GGGSGGGGS DKTHTCPPCP APELLGGPSV
1021 FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
1081 RVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKISKAK QPREPQVYT LPPSRDELTK
1141 NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS DGSFFLYSKL TVDKSRWQQG
1201 NVFSCSVMHE ALHNHYTQKS LSLSPGK*

```

SEQ ID NO: 46 DNA sequence of FVII-184.

```

1  AAGCTTGCCG CCACCATGGT CTCCCAGGCC CTCAGGCTCC TCTGCCTTCT GCTTGGGCTT
   TTCGAACGGC GGTGGTACCA GAGGGTCCGG GAGTCCGAGG AGACGGAAGA CGAACCCGAA
61  CAGGGCTGCC TGGCTGCAGT CTTCTGTAACC CAGGAGGAAG CCCACGGCGT CCTGCACCGG
   GTCCCGACGG ACCGACGTCA GAAGCATTGG GTCCTCCTTC GGGTGCCGCA GGACGTGGCC
121 CGCCGGCGCG CCAACGCGTT CCTGGAGGAG CTGCGGCCGG GCTCCCTGGA GAGGGAGTGC
   GCGGCCGCGC GGTGCGCAA GGACCTCCTC GACGCCGGCC CGAGGGACCT CTCCCTCACG
181 AAGGAGGAGC AGTGCTCCTT CGAGGAGGCC CGGGAGATCT TCAAGGACGC GGAGAGGACG
   TTCCTCCTCG TCACGAGGAA GCTCCTCCGG GCCCTCTAGA AGTTCCTGCG CCTCTCCTGC
241 AAGCTGTTCT GGATTTCTTA CAGTGATGGG GACCAAGTGT CCTCAAGTCC ATGCCAGAAT
   TTCGACAAGA CCTAAAGAAT GTCACATACC CTGGTCACAC GGAGTTCAGG TACGGTCTTA
301 GGGGGCTCCT GCAAGGACCA GCTCCAGTCC TATATCTGCT TCTGCCTCCC TGCCTTCGAG
   CCCCCGAGGA CGTTCCTGGT CGAGGTCAGG ATATAGACGA AGACGGAGGG ACGGAAGCTC
361 GGCCGGAACG GTGAGACGCA CAAGGATGAC CAGCTGATCT GTGTGAACGA GAACGGCGGC
   CCGGCCCTGA CACTCTGCGT GTTCTACTG GTCGACTAGA CACACTTGCT CTTGCCGCCG
421 TGTGAGCAGT ACTGCAGTGA CCACACGGGC ACCAAGCGCT CCTGTGCGTG CCACGAGGGG
   AACTCGTCA TGACGTCAC TGTGTGCCCC TGGTTCGCGA GGACAGCCAC GGTGCTCCCC
481 TACTCTCTGC TGGCAGACGG GGTGTCCTGC ACACCCACAG TTGAATATCC ATGTGGAAAA
   ATGAGAGACG ACCGTCTGCC CCACAGGACG TGTGGGTGTC AACTTATAGG TACACCTTTT
541 ATACCTATTC TAGAAAAAAG AAATGCCAGC AAACCCCAAG GCGCCCTGCG GCCCGCCATT
   TATGGATAAG ATCTTTTTTC TTTACGGTCG TTTGGGGTTC CGCGGGACGC CGGGCGGTAA
601 GTGGGGGGCA AGGTGTGCCC CAAAGGGGAG TGTCCATGGC AGGTCTGTG GTTGGTGAAT
   CACCCCCCGT TCCACACGGG GTTTCCTCCT ACAGGTACCG TCCAGGACAA CAACCACTTA
661 GGAGCTCAGT TGTGTGGGGG GACCCTGATC AACACCATCT GGGTGGTCTC CGCGGCCAC
   CCTCGAGTCA ACACACCCCC CTGGGACTAG TTGTGGTAGA CCCACCAGAG GCGCCGGGTG
721 TGTTTCGACA AAATCAAGAA CTGGAGGAAC CTGATCGCGG TGCTGGGCGA GCACGACCTC
   ACAAAGCTGT TTTAGTTCTT GACCTCCTTG GACTAGCGCC ACGACCCGCT CGTGCTGGAG
781 AGCGAGCACG ACGGGGATGA GCAGAGCCGG CGGGTGGCGC AGGTCATCAT CCCCAGCACG
   TCGCTCGTGC TGCCCCTACT CGTCTCGGCC GCCCACCAGC TCCAGTAGTA GGGTCTGTGC

```

841 TACGTCCCGG GCACCACCAA CCACGACATC GCGCTGCTCC GCCTGCACCA GCCCGTGGTC
 ATGCAGGGCC CGTGGTGGTT GGTGCTGTAG CGCGACGAGG CGGACGTGGT CGGGCACCAG
 901 CTCACTGACC ATGTGGTGCC CCTCTGCCTG CCCGAACGGA CGTTCTCTGA GAGGACGCTG
 GAGTGACTGG TACACCACGG GGAGACGGAC GGGCTTGCCT GCAAGAGACT CTCCTGCGAC
 961 GCCTTCGTGC GCTTCTCATT GGTGAGCGGC TGGGGCCAGC TGCTGGACCG TGGCGCCACG
 CGGAAGCACG CGAAGAGTAA CCAAGTCGCC ACCCCGGTCG ACGACCTGGC ACCGCGGTGC
 1021 GCCCTGGAGC TCATGGTCCCT CAACGTGCCC CGGCTGATGA CCCAGGACTG CCTGCAGCAG
 CGGGACCTCG AGTACCAGGA GTTGACACGGG GCCGACTACT GGGTCCCTGAC GGACGTCGTC
 1081 TCACGGAAGG TGGGAGACTC CCCAAATATC ACGGAGTACA TGTTCTGTGC CGGCTACTCG
 AGTGCCTTCC ACCCTCTGAG GGGTTTATAG TGCCTCATGT ACAAGACACG GCCGATGAGC
 1141 GATGGCAGCA AGGACTCCTG CAAGGGGGAC AGTGGAGGCC CACATGCCAC CCACTACCGG
 CTACCGTCGT TCCTGAGGAC GTTCCCCCTG TCACCTCCGG GTGTACGGTG GGTGATGGCC
 1201 GGCACGTGGT ACCTGACGGG CATCGTCAGC TGGGGCCAGG GCTGCGCAAC CGTGGGCCAC
 CCGTGCACCA TGGACTGCCC GTAGCAGTCG ACCCCGGTCC CGACGCGTTG GCACCCGGTG
 1261 TTTGGGGTGT ACACCAGGGT CTCCCAGTAC ATCGAGTGGC TGCAAAAGCT CATGCGCTCA
 AAACCCACA TGTGGTCCCA GAGGGTCATG TAGCTCACCG ACGTTTTCGA GTACGCGAGT
 1321 GAGCCACGCC CAGGAGTCCT CCTGCGAGCC CCATTTCCCG GTGGCGGTGG CTCCGGCGGA
 CTCGGTGC GG GTCCCTCAGGA GGACGCTCGG GGTAAAGGGC CACCGCCACC GAGGCCGCCT
 1381 GGTGGGTCCG GTGGCGGGCG ATCAGGTGGG GGTGGATCAG GCGGTGGAGG TTCCGGTGGC
 CCACCCAGGC CACCGCCGCC TAGTCCACCC CCACCTAGTC CGCCACCTCC AAGGCCACCG
 1441 GGGGGATCCG ACAAACCTCA CACATGCCCA CCGTGCCCAG CTCCGGAACCT CCTGGGAGGA
 CCCCCTAGGC TGTTTTGAGT GTGTACGGGT GGCACGGGTC GAGGCCCTGA GGACCCTCCT
 1501 CCGTCAGTCT TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT
 GGCAGTCAGA AGGAGAAGGG GGGTTTTGGG TTCCTGTGGG AGTACTAGAG GGCTTGGGGA
 1561 GAGGTCACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG
 CTCAGTGTA CGCACCAACA CCTGCACTCG GTGCTTCTGG GACTCCAGTT CAAGTTGACC
 1621 TACGTGGACG GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC
 ATGCACCTGC CGCACCTCCA CGTATTACGG TTCTGTTTTG GCGCCCTCCT CGTCATGTTG
 1681 AGCACGTACC GTGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG
 TCGTGATGG CACACCAGTC GCAGGAGTGG CAGGACGTGG TCCTGACCGA CTTACCGTTC
 1741 GAGTACAAGT GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC
 CTCATGTTCA CGTTCCAGAG GTTGTTCGGG GAGGGTCGGG GGTAGCTCTT TTGGTAGAGG
 1801 AAAGCCAAAG GGCAGCCCCG AGAACCACAG GTGTACACCC TGCCCCCATC CCGGGATGAG
 TTTCCGTTTC CCGTCGGGGC TCTTGGTGTC CACATGTGGG ACGGGGGTAG GGCCCTACTC
 1861 CTGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG GCTTCTATCC CAGCGACATC
 GACTGGTTCT TGGTCCAGTC GGAAGTGGAC GACCAGTTTC CGAAGATAGG GTCGCTGTAG
 1921 GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAAC ACAAAGACCAC GCCTCCCGTG
 CGGCACCTCA CCCTCTCGTT ACCCGTCGGC CTCTTGTGTA TGTTCTGGTG CGGAGGGCAC
 1981 TTGGACTCCG ACGGCTCCTT CTTCTCTAC AGCAAGCTCA CCGTCGACAA GAGCAGGTGG
 AACCTGAGGC TGCCGAGGAA GAAGGAGATG TCGTTCGAGT GGCAGCTGTT CTCGTCCACC
 2041 CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG
 GTCGTCCCTC TGCAGAAAG TACGAGGCAC TACGTACTCC GAGACGTGTT GGTGATGTGC
 2101 CAGAAGAGCC TCTCCCTGTC TCCGGGTAAA CGGCGCCGCC GGAGCGGCGG TGGAGGTTCC
 GTCTTCTCGG AGAGGGACAG AGGCCCATTT GCCGCGGCGG CCTCGCCGCC ACCTCCAAGG
 2161 GGTGGCGGCG GATCAGGTGG CGGCGGATCA GGTGGGGGTG GATCAGGTGG CGGGGGATCC
 CCACCGCCGC CTAGTCCACC GCCGCTAGT CCACCCCCAC CTAGTCCACC GCCCCCTAGG
 2221 AGGAAGAGGA GGAAGAGGTC AGGCACTACA AATACTGTGG CAGCATATAA TTAACTTGG
 TCCTTCTCCT CTTTCTCCAG TCCGTGATGT TTATGACACC GTCGTATATT AAATTGAACC
 2281 AAATCAACTA ATTTCAAGAC AATTTTGGAG TGGGAACCCA AACCCGTCAA TCAAGTCTAC
 TTTAGTTGAT TAAAGTTCTG TTAAACCTC ACCCTTGGGT TTGGGCAGTT AGTTCAGATG
 2341 ACTGTTCAAA TAAGCACTAA GTCAGGAGAT TGGAAAAGCA AATGCTTTTA CACAACAGAC
 TGACAAGTTT ATTCGTGATT CAGTCCTCTA ACCTTTTTCG TTACGAAAAT GTGTTGTCTG
 2401 ACAGAGTGTG ACCTCACCAG CGAGATTGTG AAGGATGTGA AGCAGACGTA CTTGGCACGG
 TGTCTCACAC TGGAGTGGCT GCTCTAACAC TTCTTACACT TCGTCTGCAT GAACCGTGCC
 2461 GTCTTCTCCT ACCCGGCAGG GAATGTGGAG AGCACCGGTT CTGCTGGGGA GCCTCTGTAT
 CAGAAGAGGA TGGGCCGTCC CTTACACCTC TCGTGGCCAA GACGACCCCT CGGAGACATA
 2521 GAGAACTCCC CAGAGTTCAC ACCTTACCTG GAGACAAACC TCGGACAGCC AACAAATTCAG
 CTCTTGAGGG GTCTCAAGTG TGGAAATGGAC CTCTGTTTGG AGCCTGTGCG TTGTTAAGTC
 2581 AGTTTTGAAC AGGTGGGAAC AAAAGTGAAT GTGACCGTAG AAGATGAACG GACTTTAGTC
 TCAAACTTG TCCACCCTTG TTTTCACTTA CACTGGCATC TTCTACTTGC CTGAAATCAG
 2641 AGAAGGAACA ACACTTTCCT AAGCCTCCGG GATGTTTTTG GCAAGGACTT AATTTATACA
 TCTTCTTGT TGTGAAAGGA TTCGGAGGCC CTACAAAAC CGTTCCTGAA TTAAATATGT
 2701 CTTTATTATT GGAAATCTTC AAGTTCAGGA AAGAAAACAG CCAAAACAAA CACTAATGAG
 GAAATAATAA CCTTTAGAAG TTCAAGTCCT TTCTTTTGTG GGTTTTGTGTT GTGATTACTC
 2761 TTTTGTGATT ATGTGGATAA AGGAGAAAAC TACTGTTTCA GTGTTCAAGC AGTGATTCCC
 AAAAATAAC TACACCTATT TCCTCTTTTG ATGACAAAGT CACAAGTTCG TCACTAAGGG

- 124 -

```

2821 TCCCGAACAG TTAACCGGAA GAGTACAGAC AGCCCGGTAG AGTGTATGGG CCAGGAGAAA
      AGGGCTTGTC AATTGGCCTT CTCATGTCTG TCGGGCCATC TCACATACCC GGTCTCTTTT
2881 GGGGAATTCA GAGAAGGTGG CGGCGGATCA GGTGGGGGTG GATCAGGCGG TGGAGGTTC
      CCCCTTAAGT CTCTTCCACC GCCGCCTAGT CCACCCCCAC CTAGTCCGCC ACCTCCAAGG
2941 GGTGGCGGCG GATCAGGTGG CGGCGGATCA GGTGGGGGTG GATCAGGTGG CGGCGGATCA
      CCACCGCCGC CTAGTCCACC GCCGCCTAGT CCACCCCCAC CTAGTCCACC GCCGCCTAGT
3001 GGTGGCGGGG GATCAGACAA AACTCACACA TGCCCACCGT GCCCAGCACC GGAATCCTG
      CCACCGCCCC CTAGTCTGTT TTGAGTGTGT ACGGGTGGCA CGGGTCTGTG CCTTGAGGAC
3061 GGCAGGACCGT CAGTCTTCCT CTTCCCCCCA AAACCCAAGG ACACCCCTCAT GATCTCCCGG
      CCGCCTGGCA GTCAGAAGGA GAAGGGGGGT TTTGGGTTC TGTGGGAGTA CTAGAGGGCC
3121 ACCCCTGAGG TCACATGCGT GGTGGTGGAC GTGAGCCACG AAGACCCTGA GGTCAAGTTC
      TGGGGACTCC AGTGTACGCA CCACCACCTG CACTCGGTGC TTCTGGGACT CCAGTTCAAG
3181 AACTGGTACG TGGACGGCGT GGAGGTGCAT AATGCCAAGA CAAAGCCGCG GGAGGAGCAG
      TTGACCATGC ACCTGCCGCA CCTCCACGTA TTACGGTTCT GTTTCGGCGC CCTCCTCGTC
3241 TACAACAGCA CGTACCGTGT GGTGAGCGTC CTCACCGTCC TGCACCAGGA CTGGCTGAAT
      ATGTTGTCGT GCATGGCACA CCAGTCGCAG GAGTGGCAGG ACGTGGTCCT GACCGACTTA
3301 GGCAAGGAGT ACAAGTGCAA GGTCTCCAAC AAAGCCCTCC CAGCCCCCAT CGAGAAAACC
      CCGTTCCTCA TGTTACGTT CCAGAGGTTG TTTCCGGGAGG GTCGGGGGTA GCTCTTTTGG
3361 ATCTCCAAAG CCAAAGGGCA GCCCCGAGAA CCACAGGTGT ACACCCTGCC CCCATCCCGG
      TAGAGGTTTC GGTTTCCCGT CGGGGCTCTT GGTGTCCACA TGTGGGACGG GGGTAGGGCC
3421 GATGAGCTGA CCAAGAACCA GGTCAGCCTG ACCTGCCTGG TCAAAGGCTT CTATCCCAGC
      CTACTCGACT GGTTCTTGGT CCAGTCGGAC TGGACGGACC AGTTTCCGAA GATAGGGTCG
3481 GACATCGCCG TGGAGTGGGA GAGCAATGGG CAGCCGGAGA ACAACTACAA GACCACGCCT
      CTGTAGCGGC ACCTCACCTT CTCGTTACCC GTCGGCCTCT TGTGATGTT CTGGTGCGGA
3541 CCCGTGTTGG ACTCCGACGG CTCCTTCTTC CTCTACAGCA AGCTCACCGT GGACAAGAGC
      GGGCACAACC TGAGGCTGCC GAGGAAGAAG GAGATGTCGT TCGAGTGGCA CCTGTTCTCG
3601 AGGTGGCAGC AGGGGAACGT CTTCTCATGC TCCGTGATGC ATGAGGCTCT GCACAACCAC
      TCCACCGTCG TCCCCTTGCA GAAGAGTACG AGGCACTACG TACTCCGAGA CGTGTGTTGGT
3661 TACACGCAGA AGAGCCTCTC CCTGTCTCCG GGTAAATGA
      ATGTGCGTCT TCTCGGAGAG GGACAGAGGC CCATTTACT

```

SEQ ID NO: 47 FVII-184 amino acid sequence. Signal sequence is shown in dotted underline, propeptide is wave underlined, the mutated thrombin cleavage site inserted between the light and heavy chains is double underlined with the Arg to Ala mutation (residue 194) in bold, linker region connecting FVII to Fc region is underlined, linker with proprotein convertase processing sites connecting the Fc and sTF is shown in bold, and linker region connecting sTF to Fc is in dashed underline. The light chain expands from residues 39 to 189, the heavy chain from residues 195 to 448 and sTF from residues 742 to 960.

```

1  MVSQALRLLC LLLGLQGCLA AVFVTQEEAH GVLHRRRRAN AFLEELRPGS LERECKEEQC
61  SFEEAREIFK DAERTKLFWI SYSDGDQCAS SPCQNGGSK DQLQSYICFC LPAFEGRNCE
121 THKDDQLICV NENGGEQYVC SDHTGTRKSC RCHEGYSLA DGVSCTPTVE YPCGKPILE
181 KRNASKPQGA LRPAIVGGKV CPKGECPWQV LLLVNGAQLC GGTINTIIV VSAAHCFDKI
241 KNWRNLIAVL GEHDLSEHDG DEQSRRVAQV IIPSTYVPGT TNHDIALRL HQPVVLTDHV
301 VPLCLPERTF SERTLAFVRF SLVSGWGQLL DRGATALELM VLNVPRLMTQ DCLQQSRKVG
361 DSPNITEYMF CAGYSDGSKD SCKGDSGGPH ATHYRGTYL TGIVSWGQGC ATVGHFVYT
421 RVSQYIEWLQ KLMRSEPRPG VLLRAPFPGG GSGGGGSGG GSGGGGSGG GSGGGGSGDK
481 THTCPPCPAP ELLGGPSVFL FPPKPKDTLM ISRTPEVTCV VVDVSHEDPE VKFNWYVDGV
541 EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ
601 PREPQVYTL PPSRDELTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG
661 SFFLYSKLTV DKSRWQQGNV FSCSVMEAL HNHYTQKSL LSPGKRRRRS GGGGSGGGGS
721 GGGGSGGGGS GGGSRKRRK RSGTTNTVAA YNLTKWSTNF KTIWEWPKP VNQVYTVQIS
781 TKSQDWKSKC FYTTDTECDL TDEIVKDVQ TYLARVFSYP AGNVESTGSA GEPLYENSPE
841 FTPYLETNLG OPTIQSFQV GTKVNVTVED ERTLVRNNT FLSLRDVFGK DLIYTYLYWK
901 SSSSGKKTAK TNTNEFLIDV DKGENYCFV QAVIPSRVN RKSTDSPVEC MGQEKGEFRE
961 GGGGSGGGGS GGGGSGGGGS GGGGSGGGGS GGGGSGGGGS DKTHTCPPCP APELLGGPSV
1021 FLFPPKPKDT LMISRTPEVT CVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
1081 RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK
1141 NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLD DGSFFLYSKL TVDKSRWQQG

```

- 125 -

1201 NVFSCSVMHE ALHNHYTQKS LSLSPGK*

SEQ ID NO: 32

>CTP peptide 1

DPRFQDSSSSKAPPPSLPSPSRLPGPSDTPIL

SEQ ID NO: 33

>CTP peptide 2

SSSSKAPPPSLPSPSRLPGPSDTPILPQ

SEQ ID NO: 36

>PAS peptide 1

ASPAAPAPASPAAPAPSAPA

SEQ ID NO: 37

>PAS peptide 2

AAPASPAPAAAPSAPAPAAAPS

SEQ ID NO: 38

>PAS peptide 3

APSSPSPSAPSSPSPASPS

SEQ ID NO: 39

>PAS peptide 4

APSSPSPSAPSSPSPASPS

SEQ ID NO: 40

>PAS peptide 5

SSPSAPSPSSPASPSPSSPA

SEQ ID NO: 41

>PAS peptide 6

AASPAAPSAPPAAASPAAPSAPPA

SEQ ID NO: 42

>PAS peptide 7

ASAAAPAAASAAASAPSAAA

SEQ ID NO: 35

>Albumin Binding Peptide Core Sequence

DICLPRWGCLW

SEQ ID NO: 48

>GFP protein sequence (Genbank ID AAG34521.1)

MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTTGKLPVPWPTL
 VTTFGYGVQCFAARYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV
 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSGVQLAD
 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITHGMDELYKSR
 TSGSPGLQEFDIKLIDTVDLSCN

SEQ ID NO: 49

>Example: Single-chain Human IgG1 Fc. (Fc sequences with Gly/Ser linker underlined.)

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD
 GVEVHNAKTKPREEQYNSTYRVSVLTVQLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAK
 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS
 DGSFFLYSKLTVDKSRWQQGNVFCSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGG

GSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 50

>Mature human albumin protein sequence (derived from NCBI Ref. Sequence NP_000468):

RGVFRRDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFEDHVKLVNEVTEFAKTCV
ADESAENC DKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNP NLPR
LVRPEVDVMCTAFHDNEETFLKKYLYE IARRHPYFYAPELLFFAKRYKAAFTECCQAADK
AACLLPKLDEL RDEGKASSAKQRLK CASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKL
VTDLTKVHTECCHGDLLECADRADLAKYICENQDSTISSKLKECCEKPLLEKSHCIAEVE
NDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVL LLLRLAKTYE
TTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNC ELFQLG EYKFQNALLVRYTKK
VPQVSTPTLVEVSRNLGKVGSKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT
KCTTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVK
HKPKATKEQLKAVMDDFAAFVEKCKKADDKETCF AE EGKKLVAASQAALGL

SEQ ID NO: 51

>Albumin binding peptide 1

RLIEDICLPRWGCLWEDD

SEQ ID NO: 52

>Albumin binding peptide 2

QRLMEDICLPRWGCLWEDDF

SEQ ID NO: 53

>Albumin binding peptide 3

QGLIGDICLPRWGCLWGDSVK

SEQ ID NO: 54

>Albumin binding peptide 4

GEWWEDICLPRWGCLWEEED

SEQ ID NO: 55

>Cysteine-containing peptide

GGSGGCGGGS

SEQ ID NO: 56

>Human LRP1 sequence (signal peptide and transmembrane segment underlined;
NCBI Reference Sequence: CAA32112)

MLTPFLL LLL LLL LLL SALVAAIDA PKTCS PKQFACRDQITCISKGWRC DGERDCPDGSDEA
PEICFQSKAQRCQPN EHNCLGTEL CVPM SRLCNGVQDCMDGSDEGPHCRELQGNCSRLGC
QHHCVP TLDGPTCYCNSS FQLQADGETCKDFDECSVYGTCSQLCTNTDGSFICGCVEGYL
LQPDNRSC KAKNEPVD RPPVLL IANSONILATYLSGAQVSTITPTSTRQTTAMDFS YANE
TVCWVHV GDSAAQTQLKCARMPGLKGFVDEHTINI SL SLHHVEQMAIDWLTGNFYFVDDI
DDRIFVCNRNGDTCVTLLDLELYNPKGIALDPAMGKVFFTDYGOIPKVERCDMDGQNR TK
LVDSKIVFFPHGITL DLVSRLVY WADAYLDYIEVV DYE GKG RQTIIQ GILIEHLYGLTVFE
NYLYATNSDNANAQQKTSVIRVNRFNST EYQV VTRVDKGGALHIYHORRQPRVRSHACEN
DQYGKPGGCS DICLLANSHKARTCRCSRSGFSLGSDGKSCKKPEHELFVY GKG RFGIIRG
MDMGAKVPDEHMIPIENLMNPRALDFHAETGFIYFADTTSYLIGRQKIDGTERETILKDG
IHNVEGVAVDWMGDNL YWTD DGP KKTISVARLEKAAQTRKTLIEGKMTHPRAIVVDPLNG
WMYWTDWEE DPKDSRRGRLE RAWMDGSHRDI FVTSKTVLWPNGLSLDIPAGRLYWVDAFY
DRIETILLNGTDRKIVYEGPELNHAFGLCHHGNYLFWTEYRSGSVYRLERGVGGAPPTVT
LLRSERPPIFEIRMYDAQQQQVG TNKCRV NNGGCS SLCLATPGSRQCACAEDQVLDADGV
TCLANPSYVPPPQCQPG EFACANSRCIQERWKCDGDNDCLDNSDEAPALCHQHTCPSDRF
KCENNRCI PNRLCDGDNDCGNSEDES NATCSARTCPPNQFSCASGRCLPISWTCDLDDD
CGDRSDESAS CAYPTCFPLTQFTCNNGRCININWRCNDND CGDNDSD EAGCSHSCSSTQF

KCNSGRCIPEHWTCDGDNDGCDYSEDETHANCTNQATRPPGGCHTDEFQCRLDGLCIPLRW
 RCDGDTDCMDSSDEKSCEGVTHVCDPSVKFGCKDSARCISKAWVCDGDNDCEDNSDEENC
 ESLACRPPSHPCANNTSVCLPPDKLCDGNDDCGDGSDEGELCDQCSLNNGGCSHNCSVAP
 GEGIVCSCPLGMELGPDNHTCQIQSYCAKHLKCSQKCDQNKFSVKCSCYEGWVLEPDGES
 CRSLDPFKPFIIIFSNRHEIRRIDLHKG DYSVLPGLRNTIALDFHLSQSALYWTDVVEDK
 IYRGKLLDNGALTSFEVVIQYGLATPEGLAVDWIAGNIYWVESNLDQIEVAKLDGTLRTT
 LLAGDIEHFRAIALDPRDGILFWTDWDASLPRIEASMSGAGRRTVHRETGSGGWPNGLT
 VDYLEKRILWIDARSDAIYSARYDGS GHMEVLRGHEFLSHPPFAVTLYGGEVYWTDWRTNT
 LAKANKWTGHNVTVVQRTNTQPFDLQVYHPSRQPMAPNPCEANGGQGPCSHLCLINYNRT
 VSCACPHLMKLHKDNTTCYEFKKFLLYARQMEIRGVDLDAPYYNYIISFTVPDIDNVTVL
 DYDAREQRVYWSVVRTQAIKRAFINGTG VETVVSADLPNAHGLAVDWVSRNLFWTSYDTN
 KKQINVARLDG SFKNVAVQGLEQPHGLVHPLRGKLYWTDGDNISMANMDG SNRTLLFSG
 QKGPVGLAIDFPESKLYWISSGNHTINRCNLDGSGLEVIDAMRSQ LGKATALAIMGDKLW
 WADQVSEKMGTC SKADGSGSVVLNRNSTTLMHMKVYDESIQLDHKG TNPCSVNNGDCSQL
 CLPTSETTRSCMCTAGYSLRSGQQACEGVGSFLLYSVHEGIRGIPLDPNDKSDALVPVSG
 TSLAVGIDFHAENDTIYWVDMGLSTISRARDQ TWREDVVTNGIGRVEGIAVDWIAGNIY
 WTDQGFVDVIEVARLNGSFRYVVISQGLDKPRAITVHPEKGYLFWTEWGQYPRIERSRLDG
 TERVVLVNVSISWPNGISVDYQDGKLYWCDARTDKIERIDLETGENREVVLSSNNMDMFS
 VSVFEDFIYWSDRTHANGSIKRGSKDNATDSVPLRTGIGVQLKDIKVFNDRQKGTNVCA
 VANGGCQQLCLYRGRGQRACACAHGMLAEDGASCREYAGYLLYSERTILKSIHLSDERNL
 NAPVQPFEDPEHMKNVIALAFDYRAGTSPGTPNRIFFSDIHFGNIQQINDDGSRRTIVE
 NVGSVEGLAYHRGWDTLYWTSYTTSTITRHTVDQTRPGA FERETVITMSGDDHPRAFLD
 ECQNLFWTNWNEQHPSIMRAALSGANVLT LIEKDIRTPNGLAIDHRAEKLYFSDATLDK
 IERCEYDGS HRYVILKSEPVHPFGLAVYGEHIFWTDWVRRAVQRANKHVGSNMKLLRVDI
 PQQPMGIIAVANDTNSCELSPCRINNGGCQDLCLLTHQGHVNCSCRGRILQDDLT CRAV
 NSSCRAQDEFECANGECINFSLTCDGVPHCKDKSDEKPSYCNSRRCKKTFRQCSNGRCVS
 NMLWCNGADDCGDGSD EIPCNKTACGVGEFRCDGT CIGNSSRCNQFVDCEDASDEMNC S
 ATDCSSYFRLGVKGVLFQPCERTSLCYAPSWVCDGANDCGDYSDERDCPGVKRPRCPLNY
 FACPSGRICIPMSWTCDEDDCEHGEDETHCNKFCSEAQFECQNHRCISKQWLC DGSDDCG
 DGSDEAAHCEGKTCGPSSFSCPGTHVCVPERWLC DGDKDCADGADESIAAGCLYNSTCDD
 REFMQNRQCI PKHFVCDHDCADGSD ESPECEYPTCGPSEFR CANGRCLSSRQWECDG
 ENDCHDQSD EAPKNPHCTSP EHKCNASSQFLCSSGR CVAEALLCNGQDDCGDSSDERGCH
 INECLSRKLSGCSQDCEDLKIGFKRCRPGFRLKDDGRTCADVDECSTTFPCSQRCINTH
 GSYKCLC VEGYAPRGDPHSCKAVTDEEPFLIFANRYYLRLKNLDGSNYTLLKQGLNNAV
 ALDFDYREQMIYWTDVTTQGS MIRRMHLNGSNVQVLHRTGLSNPDGLAVDWVGGNLYWCD
 KGRDTIEVSKLNGAYRTVLVSSGLREPRALVVDVQNGYLYWTDWGDHSLIGRIGMDGSSR
 SVIVDTKITWPNGLTLDYVTERIYWADAREDYIEFASLDGSNRHVLSQDIPHIFALT LF
 EDYVYWTDWETKSINRAHKT TGTNKTLLISTLHRPMDLHV FHALRQPDVPNHPCKVNNGG
 CSNLCLLSPGGGHK CACPTNFYLGSDGRTCVSNCTASQFVCKNDKCI PFWWKCDTEDDCG
 DHSDEPPDCPEFKCRPGQFQCSTGICTNPAFICDGDND CQDNDSEANCDIHVCLPSQFKC
 TTNTRCIPGIFRCNGQDNCGDGEDERDCPEVTCAPNQFQCSITKRCIPRVWVCDRDND CV
 DGSDEPANCTQMT CGVDEFRCCKDSGRICIPARWKCDGEDDCGDGSD EPKEECDERTCEPYQ
 FRCKNNRCVPGRWQCDYDND CGDNDSEESCTPRPCSESEFSCANGRCIAGRWKCDGDHDC
 ADGSDEKDCTPRCDMDQFQCKSGHCIPLRWRCADADCM DGSDEEACGTGVRTCP LDEFQ
 CNNTLCKPLAWKCDGEDDCGDNSDENPEECARFVCPPNRPFRCKNDRVCLWIGRQCDGTD
 NCGDGTDEEDCEPPTAHTTHCKDKKEFLCRNQRC LSSSLRCNMFD DCGDGSDEEDCSIDP
 KLTSCATNASICGDEARCVRTEKAAYCACRSGFHTVPGQPGCQDINECLRFGTCSQLCNN
 TKGGHLCSCARNFMKTHNTCKAEGSEYQVLYIADDNEIRSLFP GHPHSAYEQAFQGD ESV
 RIDAMDVHV KAGRVYWTNWHTGTISYRSLPPAAPPTTSNRHRRQIDRGVTHLNI SGLKMP
 RGIAIDWVAGNVYWTD SGRDVIEVAQMKG ENRKTLISGMIDEPHAI VVDPLRGTM YWSDW
 GNHPKIETAAMDGTLRETLVQDNIQWPTGLAVDYHNERLYWADAKLSVIGSIRLNGTDPI
 VAADSKRGLSHPPFSIDVFEDYIYGVTYINN RVFKIHKFGHSPLVNL TGGLSHASDVVL YH
 QHKQPEVTNPNCDRKKCEWLCLLSPSGPVCTCPNGKRLDNGTCVPVPSPTPPPDAPRPGTC
 NLQCFNGGSCFLNARRQPKCRCQPRYTGDKCELDQCWEHCRNGGTCAASPSGMPTCRCPT
 GFTGPKCTQQVCAGYCANNSTCTVNQGNQPPCRLPGFLGDRCQYRQCSGYCENFGTCQM
 AADGSRQCRCTAYFEGSRCEVNKCSRCLEGACVVNKQSGDVTCNCTDGRVAPSCLTCVGH
 CSNGGSCTMNSKMMPECQCPHMTGPRCEEHVFSQQQPGH IASILIP LLLLLLLLLLVLVAGV
 VFWYKRRVQGA KGFQHQ RMTNGAMNVEIGNPTYKMYEGGEPDDVGGLLDADFALDPDKPT
 NFTNPVYATLYMGGHGSRHSLASTDEKRELLGRGPEDEIGDPLA

- 128 -

SEQ ID NO: 57

>Biotin Acceptor Peptide (BAP)

LNDIFFEAQKIEWH

SEQ ID NO: 58

>Lipocate Acceptor Peptide 2 (LAP2)

GFEIDKVVYDLDA

SEQ ID NO: 4

>HAPylation motif, n= 1 to 400

(Gly4Ser)n

SEQ ID NO: 59

>CTP

DSSSSKAPPPSLPSPSRLLPGPSDTPILPQ

SEQ ID NO: 65

>SUMO

SLQDSEVNQEAKPEVKPEVKPETHINLKVSDGSSEIFFKIKKTTPLRLMEAFKR

QGKEMDSLRFYDGIHQADQAPEDLDMEDNDIIEAHREQIGG

SEQ ID NO: 66

>FVII-PABC Peptide

D-Phe-Pip-Arg-PABC-IVGGKV-COSBn

WHAT IS CLAIMED IS:

1. A chimeric protein comprising (i) an activatable clotting factor (Ac), (ii) an enhancer moiety (Em), and (iii) an optionally linker moiety (L or L1) between the activatable clotting factor and an enhancer moiety.

2. The chimeric protein according to claim 1, wherein the activatable clotting factor and the enhancer moiety are linked or associated with each other, but are not chemically crosslinked.

3. The chimeric protein according to claim 1 or 2, comprising a structure represented by formula Ac-L-Em or Em-L-Ac, wherein Ac comprises the activatable clotting factor; wherein L comprises the optional linker moiety; and wherein Em comprises the enhancer moiety.

4. The chimeric protein according to any one of claims 1 to 3, wherein the activatable clotting factor comprises a clotting factor zymogen comprising a heavy chain (HC) and a light chain (LC) and a protease-cleavage site inserted between the HC and the LC.

5. The chimeric protein according any one of claims 1 to 4, wherein the enhancer moiety comprises a clotting cofactor, a procoagulant peptide, or an antigen-binding moiety.

6. The chimeric protein according to claim 4 or 5, wherein the clotting factor zymogen is a FVII protein or a FX protein.

7. The chimeric protein according to claim 5 or 6, wherein the procoagulant peptide is synthetic.

8. The chimeric protein according to claim 5 or 6, wherein the procoagulant peptide comprises (a) an amino acid sequence comprising formula C¹LASYC²

wherein

L is L-leucine;

A is L-alanine;

S is L-serine;

Y is L-tyrosine;

one or two of L, A, S, and Y are optionally replaced with a replacement amino acid independently selected from D- and L-amino acids;

one additional amino acid is optionally inserted into Formula (I), anywhere between C¹ and C²; and

C¹ and C² are independently selected from amino acids having a side chain, wherein the side chains of C¹ and C² are linked to form a loop; or

(b) a retro-, an inverso- or a retro-inverso variant of the amino acid sequence of (a).

9. The chimeric protein according to any one of claims 4 to 6, wherein:

(a) the clotting factor zymogen comprises a FVII protein, and the clotting cofactor comprises a Tissue Factor protein; or

(b) the clotting factor zymogen comprises a FX protein, and the clotting cofactor comprises a FVa protein.

10. The chimeric protein according to claim 9, wherein the Tissue Factor protein is a soluble Tissue Factor (sTF).

11. The chimeric protein according to any one of claims 5 to 10, wherein the antigen-binding moiety comprises an antibody or an antigen-binding fragment thereof which is capable of binding to the FVII protein or the FX protein and enhances the activity of the FVII protein or the FX protein, respectively.

12. The chimeric protein according to claim 11, further comprising a self-immolative moiety inserted between the protease-cleavage site and the HC.

13. The chimeric protein according to any one of claims 4 to 12, wherein the protease-cleavage site is cleaved by a protease selected from the group consisting of thrombin (factor IIa), factor XIa, factor XIIa, kallikrein, factor VIIa, factor IXa, and factor Xa, wherein the protease-cleavage site is not naturally occurring in the clotting factor zymogen.

14. The chimeric protein according to claim 12 or 13, wherein the self-immolative moiety comprises p-amino benzyl carbamate (PABC), a p-amino benzyl ether (PABE), or a p-amino benzyl carbonate.

15. The chimeric protein according to any one of claims 1 to 14, further comprising a heterologous moiety (Het).

16. The chimeric protein according to claim 15, wherein the heterologous moiety (Het) is a half-life extender.

17. The chimeric protein according to claim 16, wherein the half-life extender comprises an immunoglobulin constant region or a portion thereof, albumin, transferrin, an albumin binding moiety, a PAS sequence, a HES sequence, the β subunit of the C-terminal peptide (CTP) of human chorionic gonadotropin, polyethylene glycol (PEG), hydroxyethyl starch (HES), albumin-binding small molecules, or any combinations thereof.

18. The chimeric protein according to claim 16, wherein the immunoglobulin constant region or a portion thereof comprises an Fc moiety or an FcRn binding partner.

19. The chimeric protein according to any one of claims 1 to 18, further comprising a second heterologous moiety (Het2) and, optionally, a second linker moiety (L2), which is identical to or different from the first linker moiety (L or L1).

20. The chimeric protein according to claim 19, wherein the second heterologous moiety (Het2) comprises a half-life extender.

21. The chimeric protein according to claim 20, wherein the half-life extender comprises an immunoglobulin constant region or a portion thereof, albumin, transferrin, an albumin binding moiety, a PAS sequence, a HES sequence, the β subunit of the C-terminal peptide (CTP) of human chorionic gonadotropin, polyethylene glycol (PEG), hydroxyethyl starch (HES), albumin-binding small molecules, or any combinations thereof.

22. The chimeric protein according to claim 21, wherein the immunoglobulin constant region or a portion thereof comprises an Fc moiety or an FcRn binding partner.

23. The chimeric protein according to any one of claims 1 to 22, wherein the chimeric protein comprises a first polypeptide chain and a second polypeptide chain, wherein the first polypeptide chain comprises the activatable clotting factor (Ac) and the second polypeptide chain comprises the enhancer moiety (Em), wherein the first polypeptide chain and the second polypeptide chain are associated with each other.

24. The chimeric protein according to any one of claims 19 to 22, wherein the chimeric protein comprises a first polypeptide chain and a second polypeptide chain, wherein the first polypeptide chain comprises the activatable clotting factor (Ac), the first heterologous moiety (Het1), and the first optional linker moiety (L1), and the second polypeptide comprises

the enhancer moiety (Em), the second heterologous moiety (Het2), and the second optional linker moiety (L2), wherein the first polypeptide chain and the second polypeptide chain are associated with each other.

25. The chimeric protein according to claim 24, wherein the chimeric protein has a structure selected from the group consisting of:

- (a) Ac linked to Het1 via the linker moiety , and Em linked to Het2;
- (b) Ac linked to Het1 via the first linker moiety, and Em linked to Het2 via the second linker moiety ;
- (c) Ac linked to Het1, and Em is linked to Het2 via the linker moiety;
- (d) Ac linked to Het1, and Em linked to Het2;
- (e) Em linked to Het1 via the linker moiety, and Ac linked to Het2;
- (f) Em linked to Het1 via the first linker moiety, and Ac linked to Het2 via the second linker moiety;
- (g) Em linked to Het1, and Ac is linked to Het2 via the linker moiety; and,
- (h) Em linked to Het1 , and Ac linked to Het2.

26. The chimeric protein according to claim 25, which comprises two polypeptides wherein:

- (a) the first polypeptide comprises a structure represented by the formula Ac-L1-Het1, and the second polypeptide comprises a structure represented by the formula Em-Het2;
- (b) the first polypeptide comprises a structure represented by the formula Ac-L1-Het1, and the second polypeptide comprises a structure represented by the formula Em-L2-Het2;
- (c) the first polypeptide comprises a structure represented by the formula Ac-Het1, and the second polypeptide comprises a structure represented by the formula Em-Het2;

- (d) the first polypeptide comprises a structure represented by the formula Ac-Het1, and the second polypeptide comprises a structure represented by the formula Em-L1-Het2;
- (e) the first polypeptide comprises a structure represented by the formula Em-L1-Het2, and the second polypeptide comprises a structure represented by the formula Ac-Het1;
- (f) the first polypeptide comprises a structure represented by the formula Em-L2-Het1, and the second polypeptide comprises a structure represented by the formula Ac-L1-Het2;
- (g) the first polypeptide comprises a structure represented by the formula Em-Het1, and the second polypeptide comprises a structure represented by the formula Ac-L1-Het2; and,
- (h) the first polypeptide comprises a structure represented by the formula Em-Het1, and the second polypeptide comprises a structure represented by the formula Ac-Het2;

wherein Het1 and Het2 of the two polypeptide chains form a disulfide bond.

27. The chimeric protein according to any one of claims 1 to 26, comprising at least one linker moiety .

28. The chimeric protein according to any one of claims 18 to 27, comprising at two linker moieties.

29. The chimeric protein according to claim 28, wherein the two linker moieties are the same.

30. The chimeric protein according to claim 28, wherein the two linker moieties are different.

31. The chimeric protein according to any one of claims 27 to 30, wherein at least one linker moiety has an amino acid sequence comprising about 10 to about 50 amino acids.

32. The chimeric protein according to claim 31, wherein the at least one linker moiety has an amino acid sequence comprising about 20 to about 30 amino acids.

33. The chimeric protein according to any one of claims 1 to 32, wherein the linker moiety comprises a gly/ser peptide.

34. The chimeric protein according to claim 33, wherein the gly/ser peptide comprises an amino acid sequence of formula $(\text{Gly}_4\text{Ser})_n$ or $\text{Ser}(\text{Gly}_4\text{Ser})_n$, wherein n is a positive integer selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9 and 10.

35. The chimeric protein according to claim 34, wherein the $(\text{Gly}_4\text{Ser})_n$ peptide comprises an amino acid sequence selected from the group consisting of $(\text{Gly}_4\text{Ser})_6$, $\text{Ser}(\text{Gly}_4\text{Ser})_6$, $(\text{Gly}_4\text{Ser})_4$ and $\text{Ser}(\text{Gly}_4\text{Ser})_4$.

36. The chimeric protein according to claim 35, wherein the $(\text{Gly}_4\text{Ser})_n$ peptide is a $(\text{Gly}_4\text{Ser})_6$ peptide.

37. The chimeric protein according to any one of claims 1 to 22, which is a single polypeptide chain.

38. The chimeric protein according to claim 37, further comprising a scFc linker (X) linked to the enhancer moiety and the first heterologous moiety or the activatable clotting factor and the second heterologous moiety.

39. The chimeric protein according to claim 38, comprising a formula selected from the group consisting of:

- (1) Ac-Het1-X-Em-Het2;
- (2) Ac-Het1-X-Em-L2-Het2;
- (3) Ac-L1-Het1-X-Em-Het2;
- (4) Ac-L1-Het1-X-Em-L2-Het2;
- (5) Het2-Em-X-Het1-Ac;
- (6) Het2-L2-Em-X-Het1-Ac;
- (7) Het2-Em-X-Het1-L1-Ac; and
- (8) Het2-L2-Em-X-Het1-L1-Ac

, wherein

(a) Ac is the activatable clotting factor,

(b) L1 is the first optional linker moiety ;

- (c) Het1 is the first heterologous moiety;
- (d) X is the scFc linker;
- (e) Em is the enhancer moiety;
- (f) L2 is the optional second linker moiety ;
- (g) Het2 is the second heterologous moiety; and
- (h) (-) is a peptide bond or one or more amino acids. .

40. The chimeric protein according to claim 39, wherein each of Het1 or Het2 is a half-life extender.

41. The chimeric protein according to claim 40, wherein Het1 and Het2 are an Fc moiety or an FcRn binding moiety, wherein Het1 and E2 are the same or different.

42. The chimeric protein according to any one of claims 39 to 41, wherein the scFc linker is a processable linker (cscFc).

43. The chimeric protein according to claim 42, wherein the cscFc linker comprises at least one intracellular processing site.

44. The chimeric protein according to claim 42 or 43, wherein the cscFc linker comprises two intracellular processing sites which are recognized by the same or by different intracellular processing enzymes.

45. The chimeric protein according to claim 44, wherein the intracellular processing site is recognized by a intracellular processing enzyme selected from the group consisting of a yeast Kex2, PCSK1, PCSK2, PCSK3, PCSK4, PCSK5, PCSK6, or PCSK7.

46. The chimeric protein according to claim 44 or 45, wherein the at least one intracellular processing site is processed by PCSK5.

47. The chimeric protein according to claim 44 or 45, wherein each of the two intracellular processing sites is processed by PCSK5.

48. The chimeric protein according to claim 47, wherein the two intracellular processing sites are the same.

49. The chimeric protein according to claim 47, wherein the two intracellular processing sites are different.

50. The chimeric protein according to any one of claims 43 to 49, wherein the intracellular processing site processed by the intracellular processing enzyme comprises the amino sequence R-X-[R/K]-R, wherein X can be any amino acid, and [R/K] indicated that the amino acid can be R or K.

51. The chimeric protein according to claim 50, wherein each of the PCSK5 enzymatic cleavage sites independently comprises the sequence RRRR (SEQ ID NO: 2) or (RKR)_n (SEQ ID NO: 3), where n is 2.

52. The chimeric protein according to claim 51, wherein the PCSK5 enzymatic cleavage site at the C-terminal end of the cscFc linker comprises the sequence RRRR (SEQ ID NO: 2) and the PCSK5 enzymatic cleavage site at the N-terminal end of the cscFc linker comprises the sequence (RKR)₂ (SEQ ID NO: 3).

53. The chimeric protein according to any one of claims 38 to 52, wherein the scFc linker has a length of about 10 to about 50 amino acids.

54. The chimeric protein according to any one of claims 38 to 52, wherein the scFc linker has a length of about 20 to about 30 amino acids.

55. The chimeric protein according to any one of claims 38 to 52, wherein the scFc linker comprises a gly/ser peptide.

56. The chimeric protein according to claim 55, wherein the gly/ser peptide comprises an amino acid sequence of formula (Gly₄Ser)_n or Ser(Gly₄Ser)_n, wherein n is a positive integer selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9 and 10.

57. The chimeric protein according to claim 55, wherein the (Gly₄ Ser)_n peptide comprises an amino acid sequence selected from the group consisting of (Gly₄Ser)₆, Ser(Gly₄Ser)₆, (Gly₄Ser)₄ and Ser(Gly₄Ser)₄.

58. The chimeric protein according to claim 57, wherein the (Gly₄ Ser)_n peptide is a (Gly₄Ser)₆ peptide.

59. The chimeric protein according to any one of claims 4 to 58, wherein the clotting factor zymogen is a FVII protein.

60. The chimeric protein according to claim 59, wherein the FVII protein is a high specific activity variant of Factor VII.

61. The chimeric protein according to any one of claim 4 to 58, wherein the clotting factor zymogen is a FX protein.

62. The chimeric protein according to claim 61, wherein the FX protein is a high specific activity variant of Factor X.

63. The chimeric protein according to any of claims 1 to 62, wherein the activatable clotting factor is activated *in vivo*.

64. The chimeric protein according to any one of claims 4 to 63, wherein the protease-cleavage site is a thrombin cleavage site.

65. The chimeric protein according to claim 64, wherein the thrombin cleavage site comprises an amino acid sequence selected from the group consisting of TQSFNDFTR (SEQ ID NO: 6), SVSQTSKLTR (SEQ ID NO: 7), TTKIKPR (SEQ ID NO: 9), LVPRG (SEQ ID NO: 10), and ALRPR (SEQ ID NO: 1).

66. The chimeric protein according to any one of claims 4 to 65, wherein the protease cleavage site is a FXIa cleavage site.

67. The chimeric protein according to claim 66, wherein the FXIa cleavage site comprises the amino acid sequence of KLTR (SEQ ID NO: 13) or DFTR (SEQ ID NO: 14).

68. The chimeric protein according to any one of claims 4 to 67, wherein an intracellular processing site is inserted between the light chain of the clotting factor zymogen and the protease-cleavage site.

69. The chimeric protein according to claim 68, wherein the intracellular processing site is cleaved by an intracellular processing enzyme selected from the group consisting of a yeast Kex2, PCSK1, PCSK2, PCSK3, PCSK4, PCSK5, PCSK6, and PCSK7.

70. The chimeric protein according to claim 69, wherein the intracellular processing enzyme is PCSK5.

71. The chimeric protein according to any one of claims 12 to 70, wherein the self-immolative moiety comprises an aromatic ring.

72. The chimeric protein according to claim 71, wherein the aromatic ring is selected from the group consisting of benzyl, cinnamyl, naphthyl, and biphenyl.

73. The chimeric protein according to claim 71 or 72, wherein the aromatic ring is heterocyclic.

74. The chimeric protein according to any one of claims 71 to 73, wherein the aromatic ring comprises at least one substituent.

75. The chimeric protein according to claim 74, wherein the at least one substituent is selected from the group consisting of F, Cl, I, Br, OH, NO₂, NH₂, NO³⁺, NHCOCH₃, N(CH₃)₂, NHCOCF₃, alkyl, haloalkyl, C₁-C₈ alkylhalide, carboxylate, sulfate, sulfamate, or sulfonate.

76. The chimeric protein according to claim 75, wherein at least one C in the aromatic group is substituted with N, O, or C-R₁, wherein R₁ is independently selected from F, Cl, I, Br, OH, NO₂, NH₂, NO³⁺, NHCOCH₃, N(CH₃)₂, NHCOCF₃, alkyl, haloalkyl, C₁-C₈ alkylhalide, carboxylate, sulfate, sulfamate, or sulfonate.

77. The chimeric protein according to any one of claims 10 to 76, wherein the soluble TF comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to amino acids 1 to 219 of the mature TF peptide (i.e., amino acids 33 to 251 of SEQ ID NO: 15).

78. The chimeric protein according to any one of claims 18 to 87, further comprising at least one additional heterologous moiety.

79. The chimeric protein according to any one of claims 1 to 78, which is polysialylated, pegylated, glycosylated, hesylated, gamma-carboxylated, or any combinations thereof.

80. A nucleic acid molecule encoding a chimeric protein according to any one of claims 1 to 79 or a complement thereof.

81. A set of nucleic acid molecules comprising a first nucleotide sequence (NA1) and a second nucleotide sequence (NA2), wherein NA1 encodes the first polypeptide of the chimeric protein according to any one of claims 23-37 and 59-79 or a complement thereof, and NA2 encodes the second polypeptide of the chimeric protein according to any one of claims 23-37 and 59-79 or a complement thereof.

82. A vector comprising the nucleic acid molecule or molecules of claim 80 or 81 or a complement thereof.

83. A set of vectors comprising a first vector (V1) and a second vector (V2), wherein V1 comprises the NA1 or a complement thereof according to claim 81 and V2 comprises the NA2 or a complement thereof according to claim 81.

84. The vector or the set of vectors according to claim 82 or 83, further comprising a nucleotide sequence encoding an intracellular processing enzyme which processes at least one of the intracellular processing sites in the chimeric protein or a complement thereof.

85. A host cell comprising the vector according to any one of claims 82 to 84.

86. The host cell of claim 85, which is a HEK293 cell, a BHK cell, or a CHO cell.

87. A method for producing a chimeric protein comprising culturing the host cell according to claim 85 or 86 and recovering the chimeric protein from the culture medium.

88. A pharmaceutical composition comprising the chimeric protein of any one of claims 1 to 79, the nucleic acid molecule or the set of nucleic acid molecules according to claim 80 or 81, the vector or the set of vectors of any one of claims 82 to 84 and a pharmaceutically acceptable carrier.

89. A method for treating, ameliorating, or preventing a bleeding disease or disorder in a subject in need thereof, comprising administering to the subject an effective amount of the chimeric protein according to any one of claims 1 to 79, the nucleic acid molecule or the set of nucleic acid molecules according to claim 80 or 81, the vector or the set of vectors according to any of claims 82 to 84, the host cell according to any one of claims 85 or 86, or a pharmaceutical composition according to claim 85.

90. The method according to claim 89, wherein the bleeding disease or disorder is caused by a blood coagulation disorder.

91. The method according to claim 90, wherein the blood coagulation disorder is hemophilia A or hemophilia B.

92. The method according to any one of claims 89 to 91, wherein the bleeding disease or disorder is selected from 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 iliopsoas sheath.

93. A method of treating, ameliorating, or preventing a coagulation factor deficiency in a mammalian subject comprising administering to the subject an effective amount of the chimeric protein according to any one of claims 1 to 79, the nucleic acid molecule or the set of nucleic acid molecules according to claim 80 or 81, the vector or the set of vectors according to any of claims 82 to 84, the host cell according to any one of claims 85 or 86, or the pharmaceutical composition of claim 88, wherein the coagulation factor is selected from the group consisting of FVII, FVIIa, FVIII, FIX, and FXI.

94. The method according to any one of claims 89 to 93 wherein the treating, ameliorating, or preventing is a bypass therapy.

95. The method according to any one of claims 89 to 94, wherein the subject has developed or is subject to develop an inhibitor against Factor VIII.

96. The method according to any one of claims 89 to 95, wherein the subject is a human subject.

97. The chimeric protein according to any one of claims 1 to 79, the nucleic acid molecule or the set of nucleic acid molecules according to claim 80 or 81, the vector or the set of vectors according to any of claims 82 to 84, the host cell according to claim 85 or 86, or the pharmaceutical composition of claim 88 for treating, ameliorating, or preventing a subject having a blood coagulation disorder.

98. Use of the chimeric protein according to any one of claims 1 to 79, the nucleic acid molecule or the set of nucleic acid molecules according to claim 80 or 81, the vector or the set of vectors according to any of claims 82 to 84, the host cell according to claim 85 or 86, or the pharmaceutical composition of claim 88 for the manufacture of a medicament for the treatment, prevention, or amelioration of a blood coagulation disorder.

99. A method for making the chimeric protein to any one of claims 1 to 79, the method comprising using solid-phase peptide synthesis.

100. The method according to claim 99, comprising using orthogonal solid-phase peptide synthesis.

101. A chimeric protein comprising a linear structure from amino terminus to carboxy terminus represented by the formula Ac-L1-Em, wherein Ac is a protease activatable FVII clotting factor, Em is soluble tissue factor, and L1 is a linker moiety comprising a gly/ser peptide

connecting the carboxy terminus of Ac and the amino terminus of Em; wherein the protease activatable FVII clotting factor Ac comprises a light chain (LC) and a heavy chain (HC), and a thrombin-cleavage site inserted between the carboxy terminus of the LC and the amino terminus of the HC.

102. A chimeric protein comprising two polypeptides, the first polypeptide having a linear structure from amino terminus to carboxy terminus represented by the formula Ac-L1-Het1, and the second polypeptide having a linear structure from amino terminus to carboxy terminus represented by the formula Em-L2-Het2, wherein:

- (a) Ac is a protease activatable FVII clotting factor;
- (b) Het1 is an Fc moiety of a dimeric Fc region; and,
- (c) L1 is a linker moiety comprising a gly/ser peptide connecting the carboxy terminus of Ac and the amino terminus of Het1;
- (d) Em is a soluble tissue factor;
- (e) Het2 is an Fc moiety of a dimeric Fc region; and,
- (f) L2 is a linker moiety comprising a gly/ser peptide connecting the amino terminus of Het2 and the carboxy terminus of Em;

wherein the Het1 and Het2 moieties form a dimeric Fc region; and,

wherein the protease activatable FVII clotting factor Ac comprises a light chain (LC) and a heavy chain (HC), and a thrombin-cleavage site inserted between the carboxy terminus of the LC and the amino terminus of the HC.

103. A chimeric protein comprising a linear structure from amino terminus to carboxy terminus represented by the formula Ac-L1-Het1-X-Em-L2-Het2 wherein:

- (a) Ac is a protease activatable FVII clotting factor;
- (b) Het1 is an Fc moiety of a dimeric Fc region;
- (c) L1 is a linker moiety comprising a gly/ser peptide connecting the carboxy terminus of Ac and the amino terminus of Het1;
- (d) X is a cleavable scFc linker connecting the carboxy terminus of Het1 and the amino terminus of Em;
- (e) Em is a soluble tissue factor;
- (f) L2 is a linker moiety comprising a gly/ser peptide connecting the carboxy terminus of Em and the amino terminus of Het2; and,
- (g) Het2 is an Fc moiety of a dimeric Fc region;

wherein the Het1 and Het2 form a dimeric Fc region;

wherein the protease activatable FVII clotting factor Ac comprises a light chain (LC) and a heavy chain (HC), and a thrombin-cleavage site inserted between the carboxy terminus of the LC and the amino terminus of the HC; and,

wherein the cscFc cleavable linker comprises a gly/ser peptide flanked by two PCSK5 enzymatic cleavage sites, which are an amino terminal site comprising the sequence RRRR (SEQ ID NO: 2) and a carboxy terminal site comprising the sequence (RKR)₂ (SEQ ID NO: 3).

104. A method of producing a chimeric protein comprising expressing a nucleotide sequence encoding the chimeric protein of any one of claims 38 to 79, wherein the scFc linker is cleaved intracellularly by an intracellular processing enzyme.

105. The method of claim 104, further purifying the chimeric protein.

106. The method of claim 105, wherein the chimeric protein has two polypeptide chains covalently associated with each other.

FIG. 1

Activatable clotting factor fused to enhancer moiety

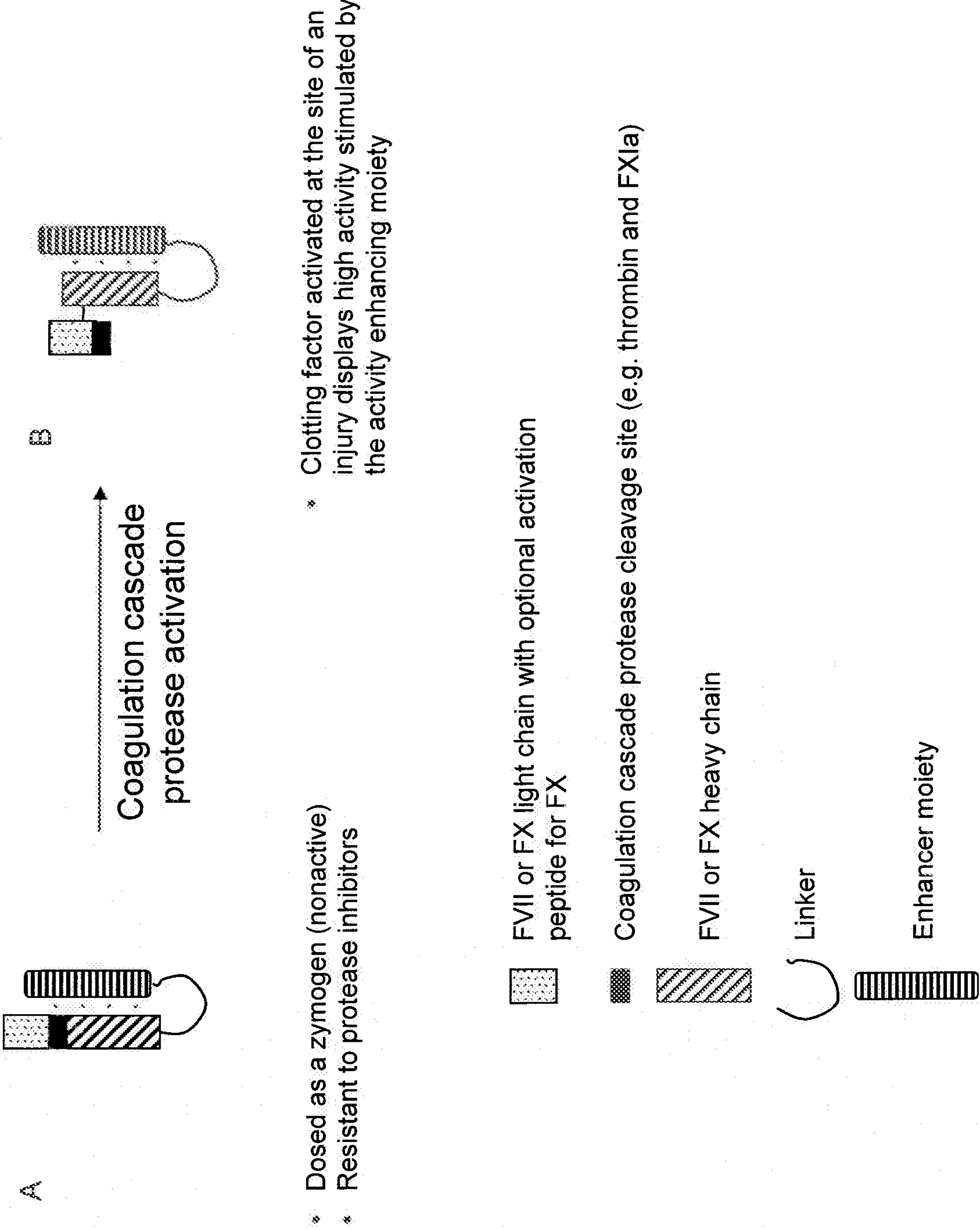


FIG. 2

Thrombin-activatable FVII fused to activity-enhancing moiety

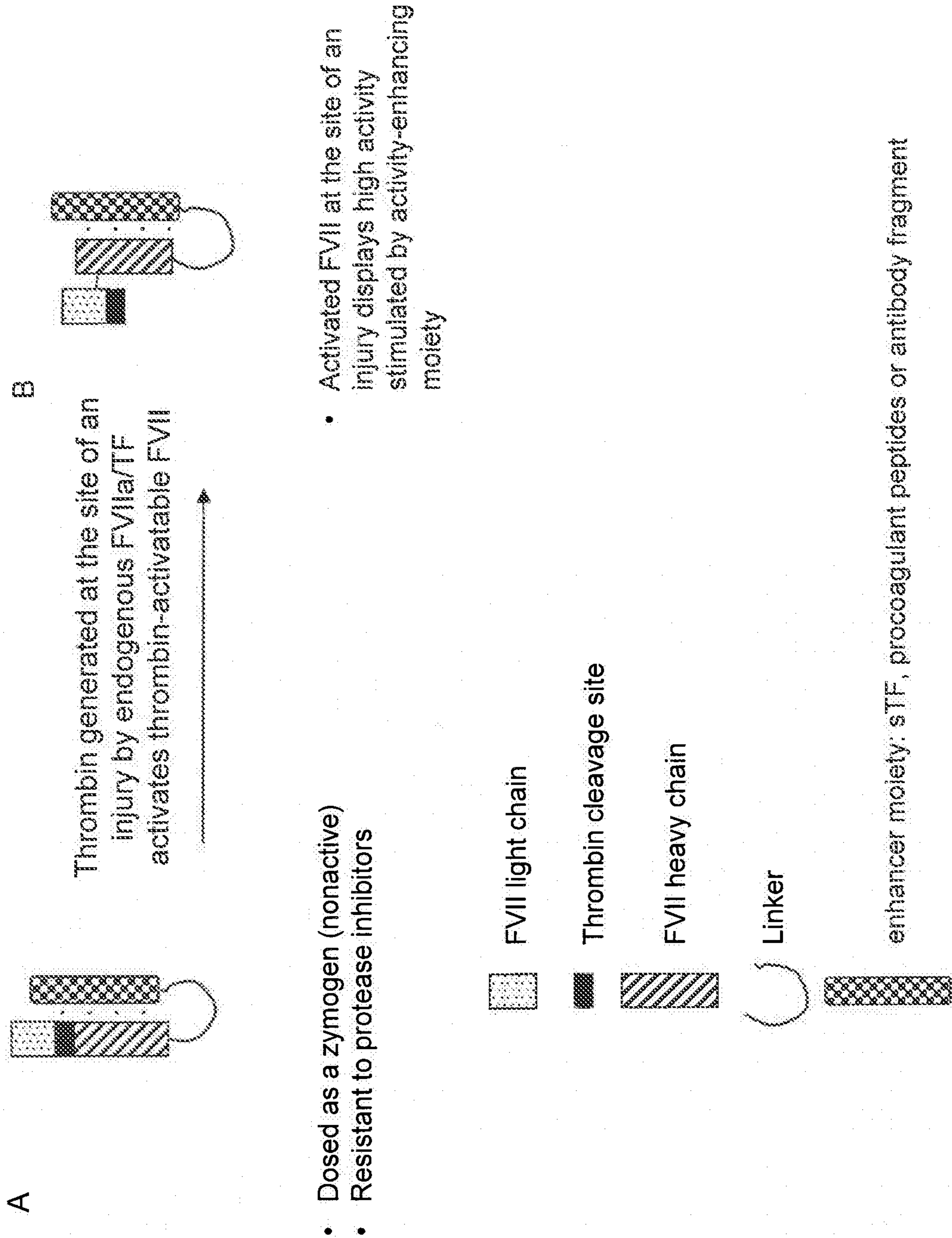
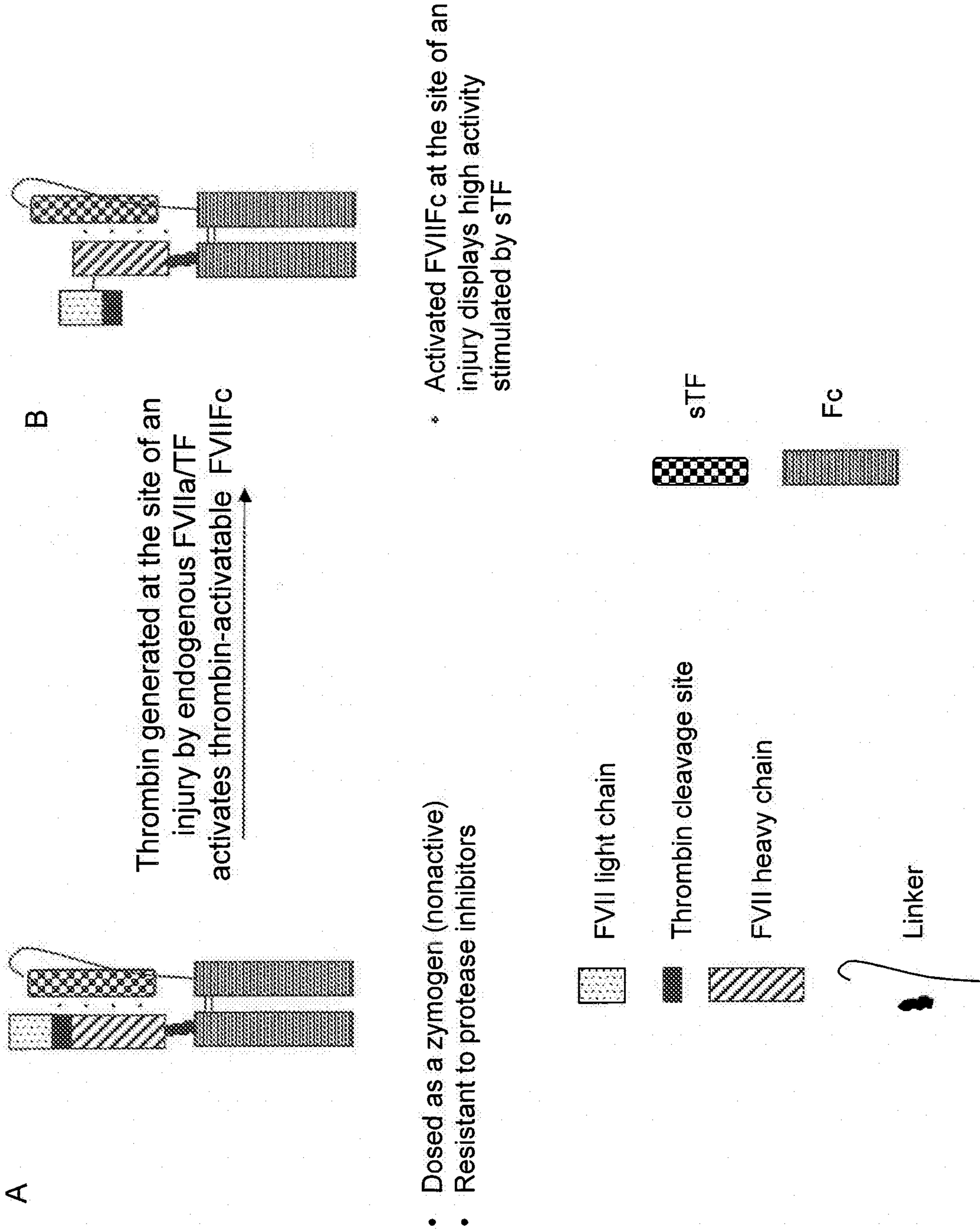


FIG. 3

Thrombin-activatable FVIIFc Fused to Soluble Tissue Factor-Fc



4/25

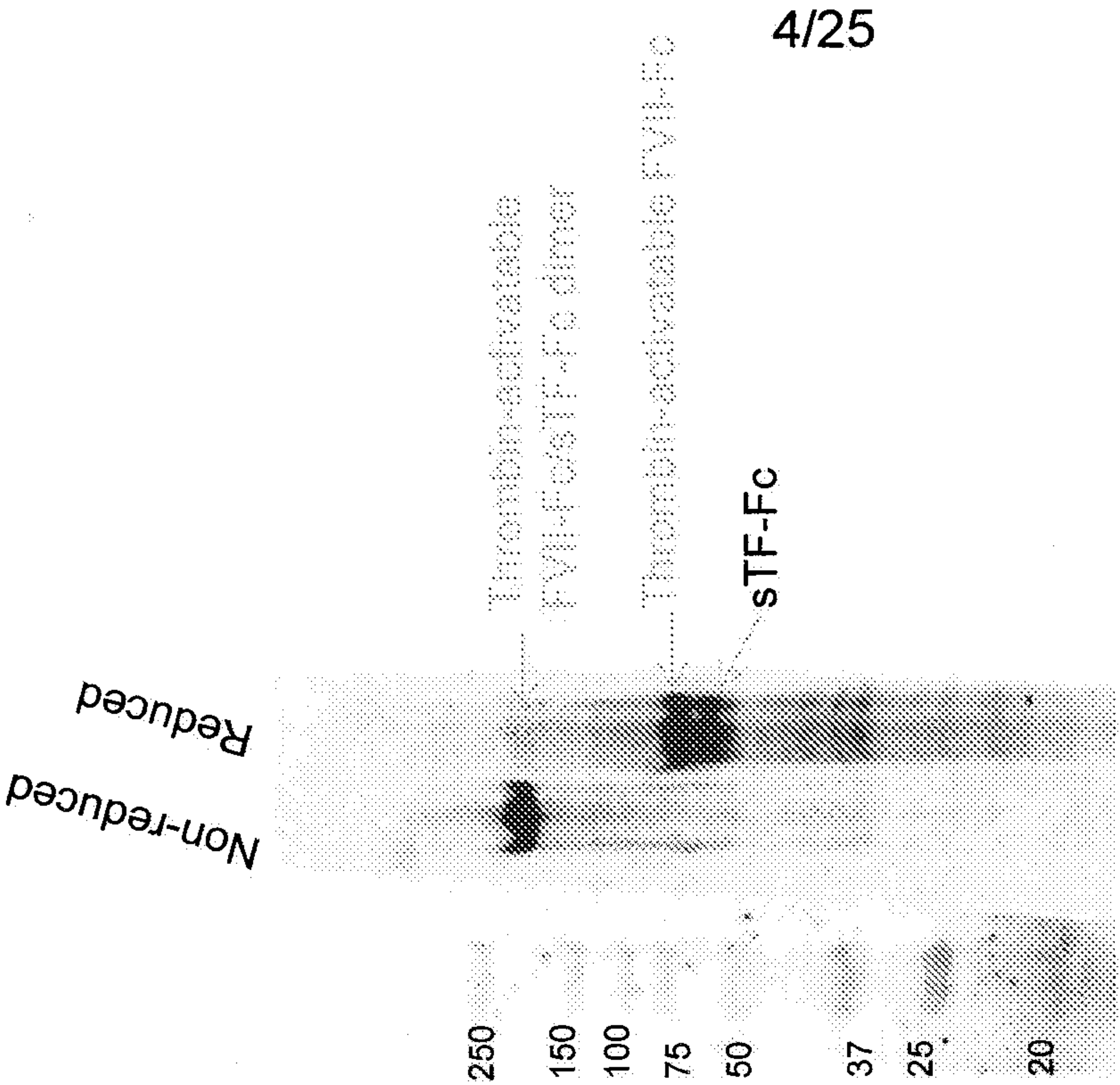
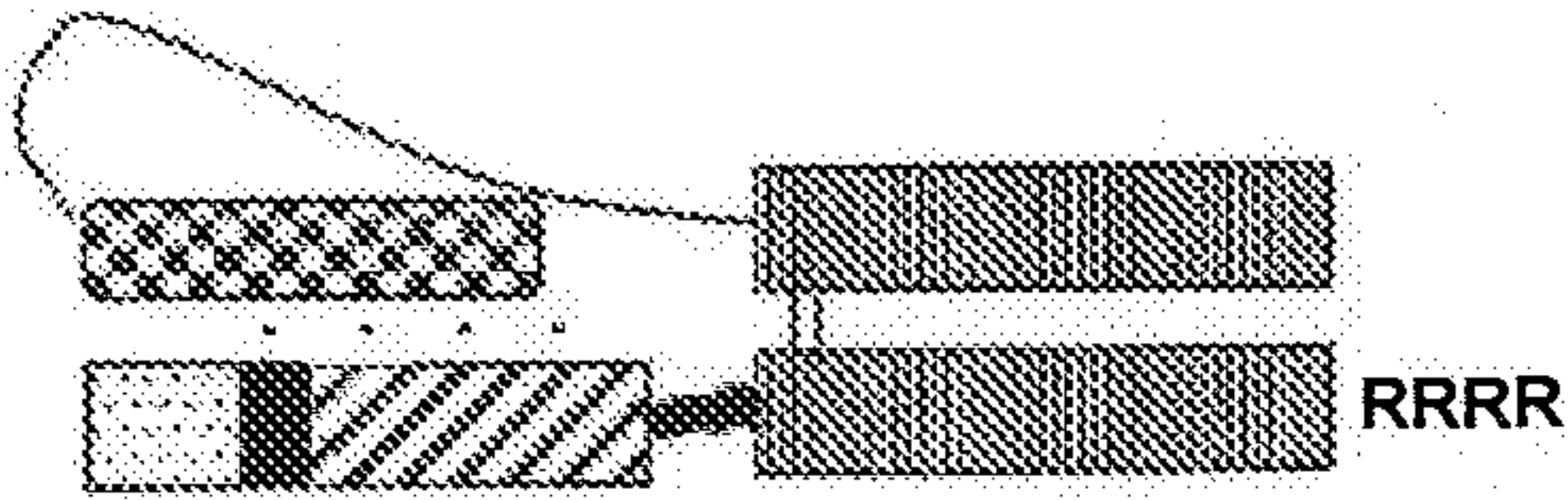


FIG. 4

C

B



PC5

Intracellular processing of propeptide endopeptidase (PC5) cleavage sites and linker removal

FVII-133

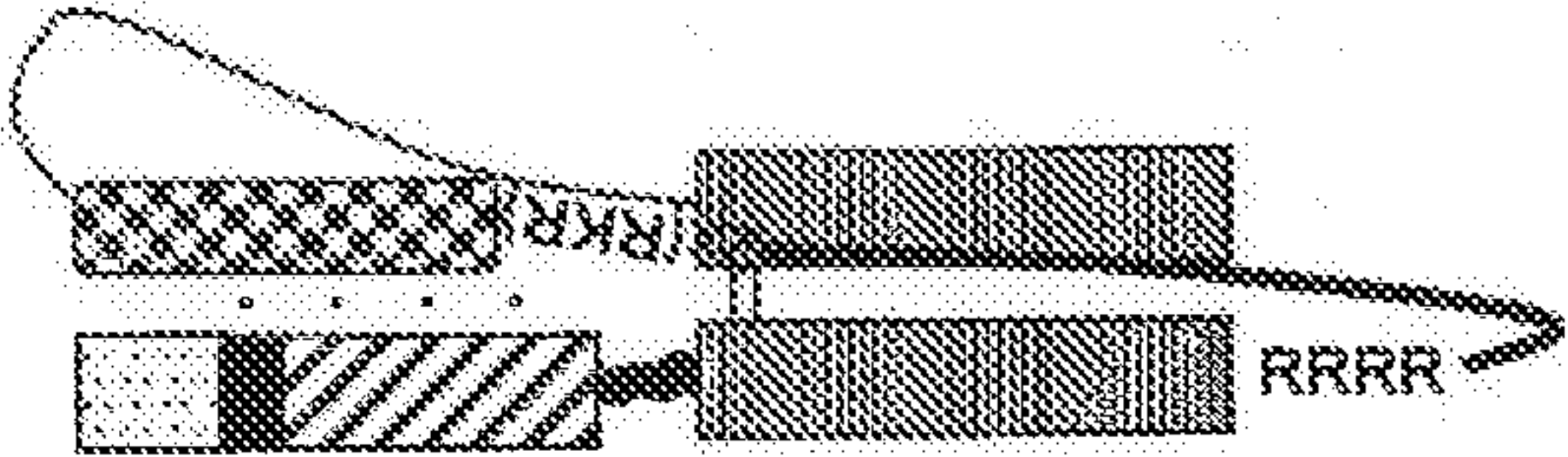
Propeptide endopeptidase cleavage sites

RRRR 2x(RKR)

sTF

Fc

A



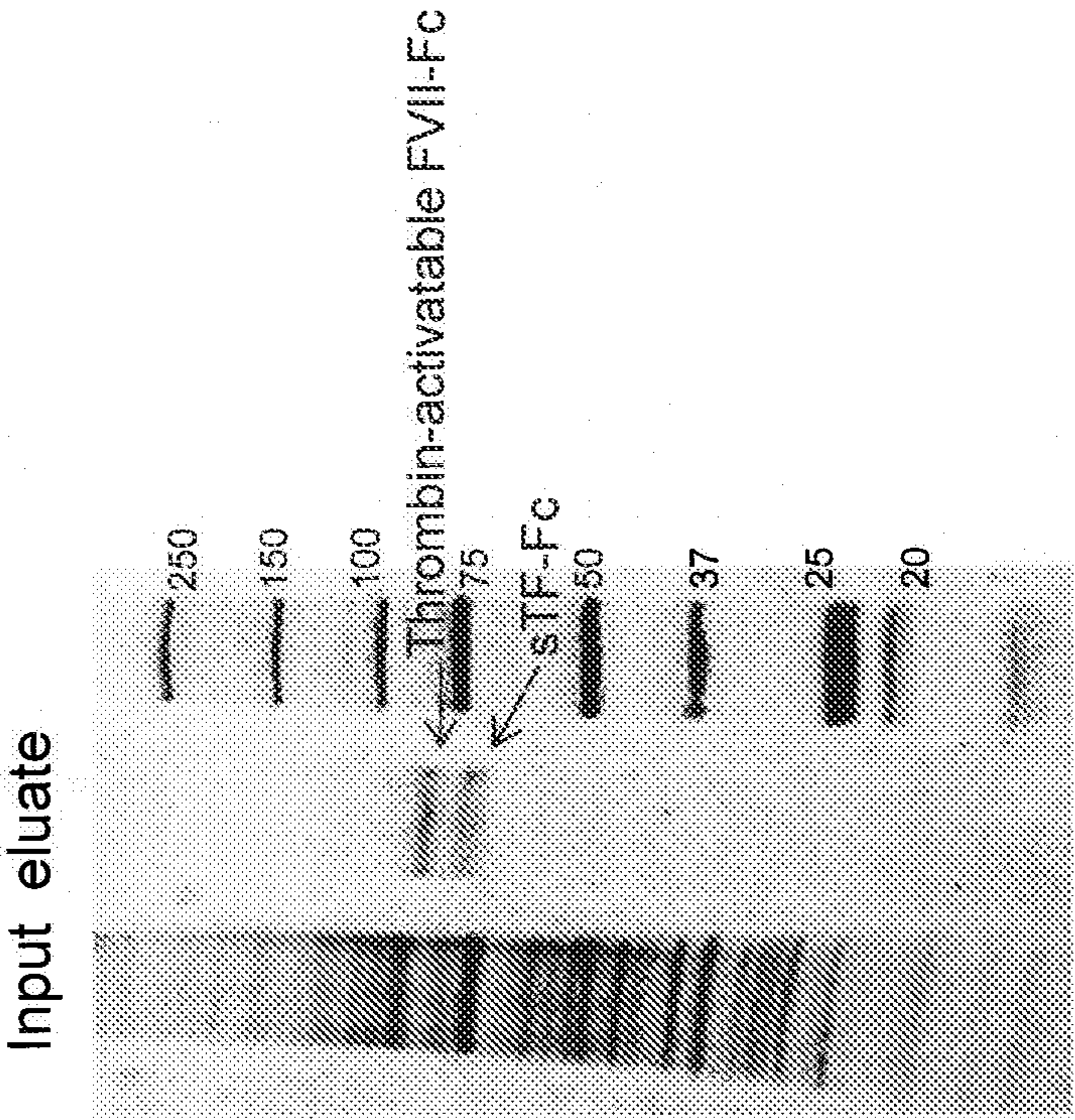
FVII light chain

Thrombin cleavage site (ALRPR)

FVII heavy chain

Linker

FIG. 5



SDS PAGE analysis of purified FVII-133

6/25

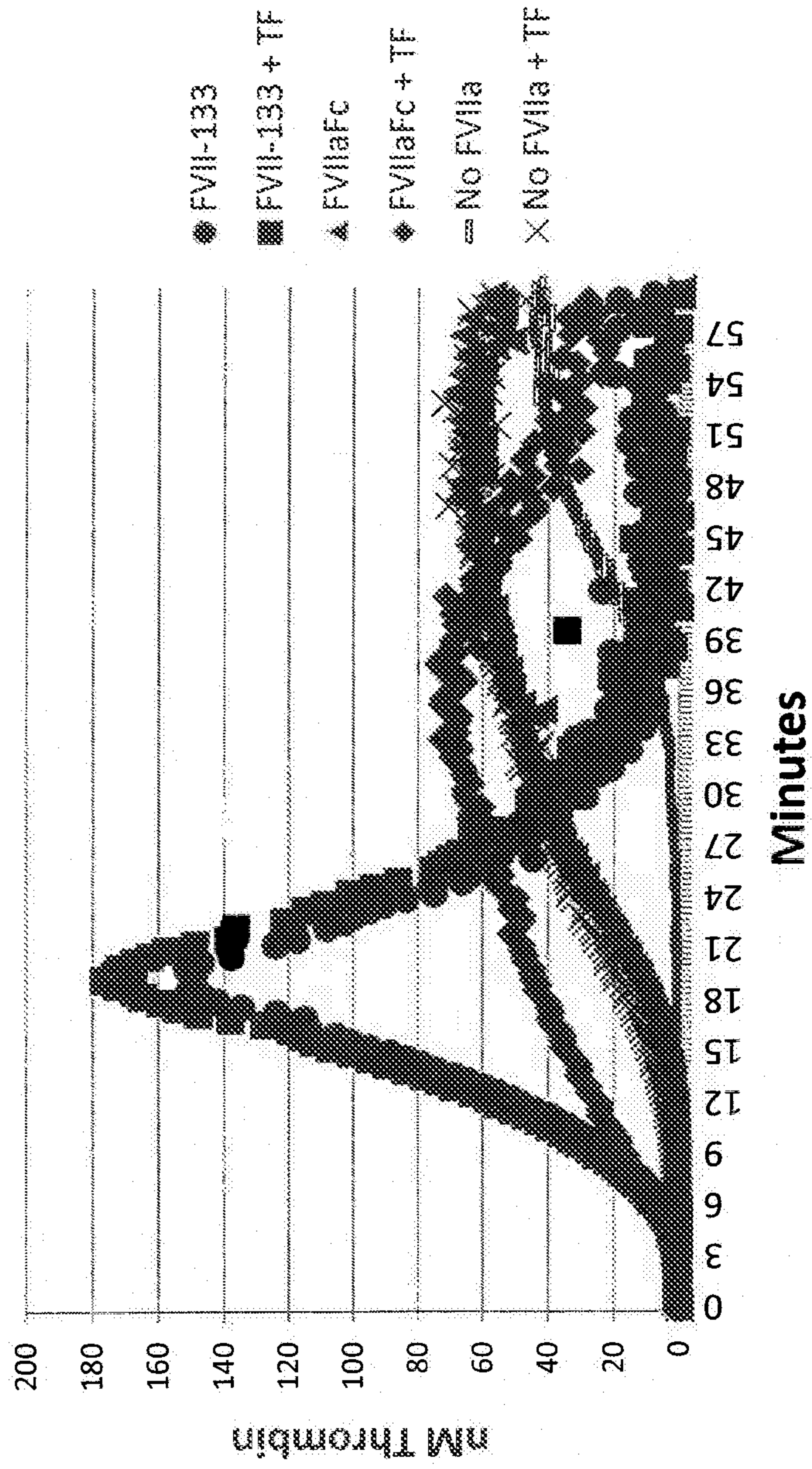
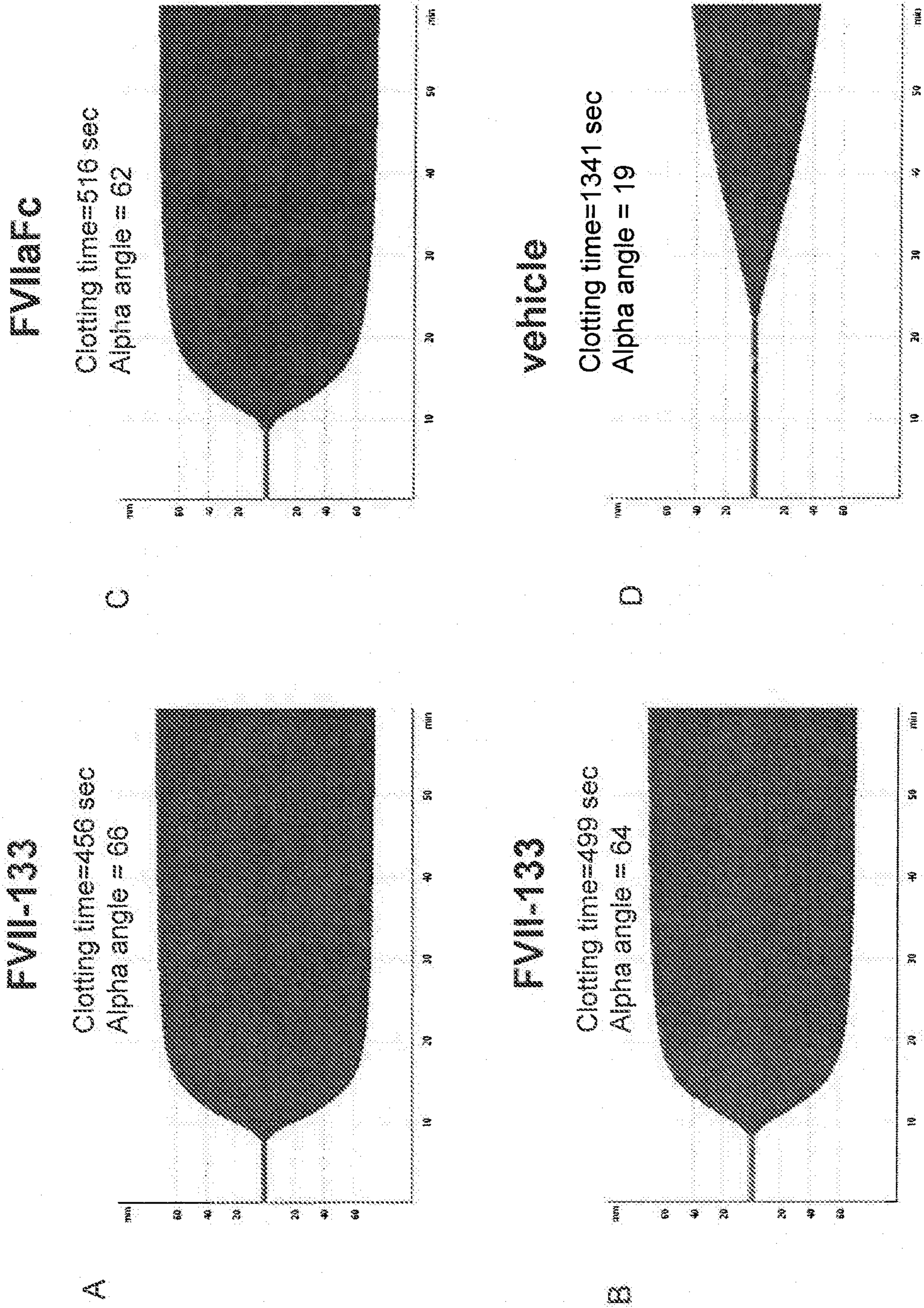


FIG. 6

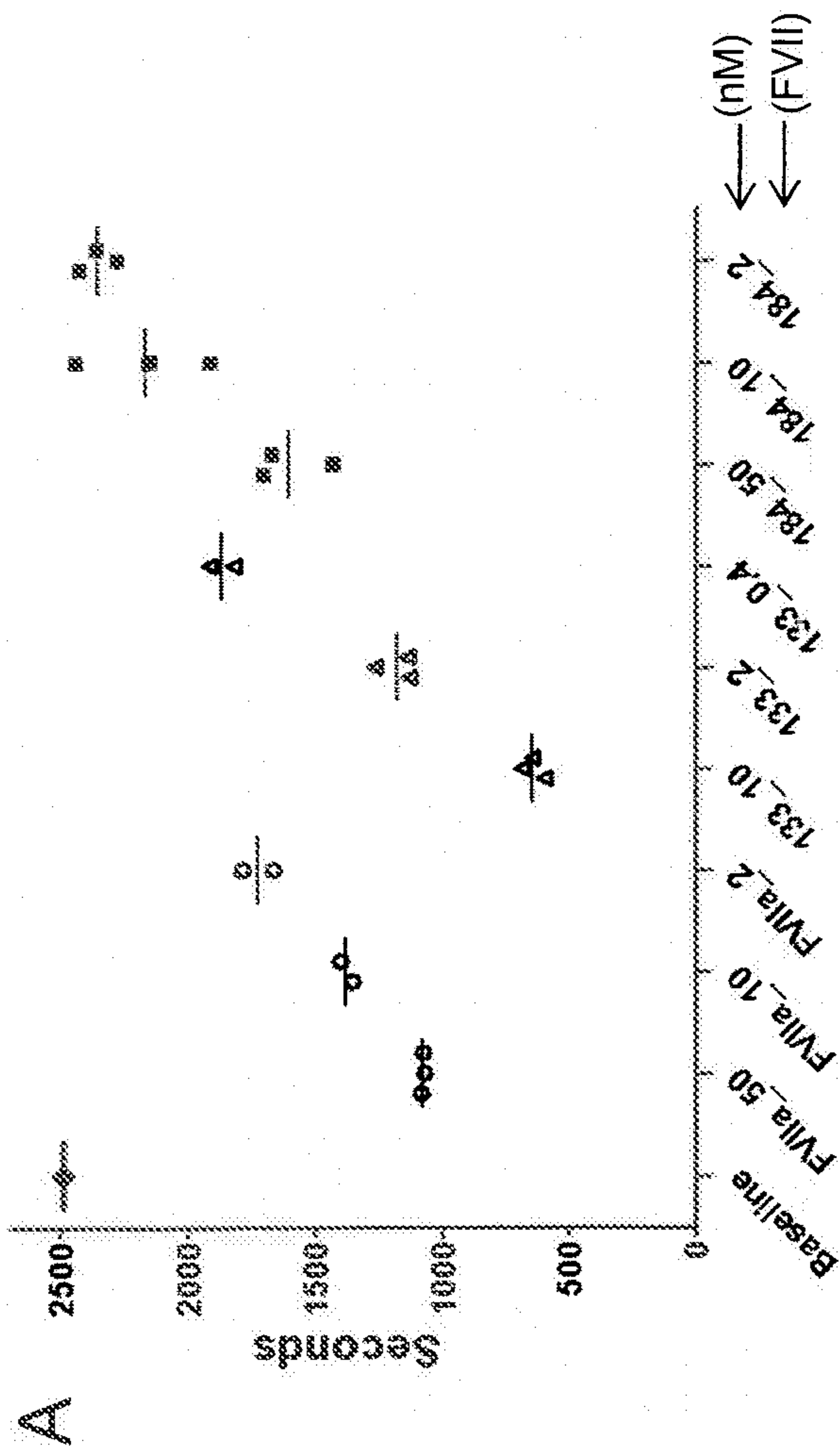
FIG. 7



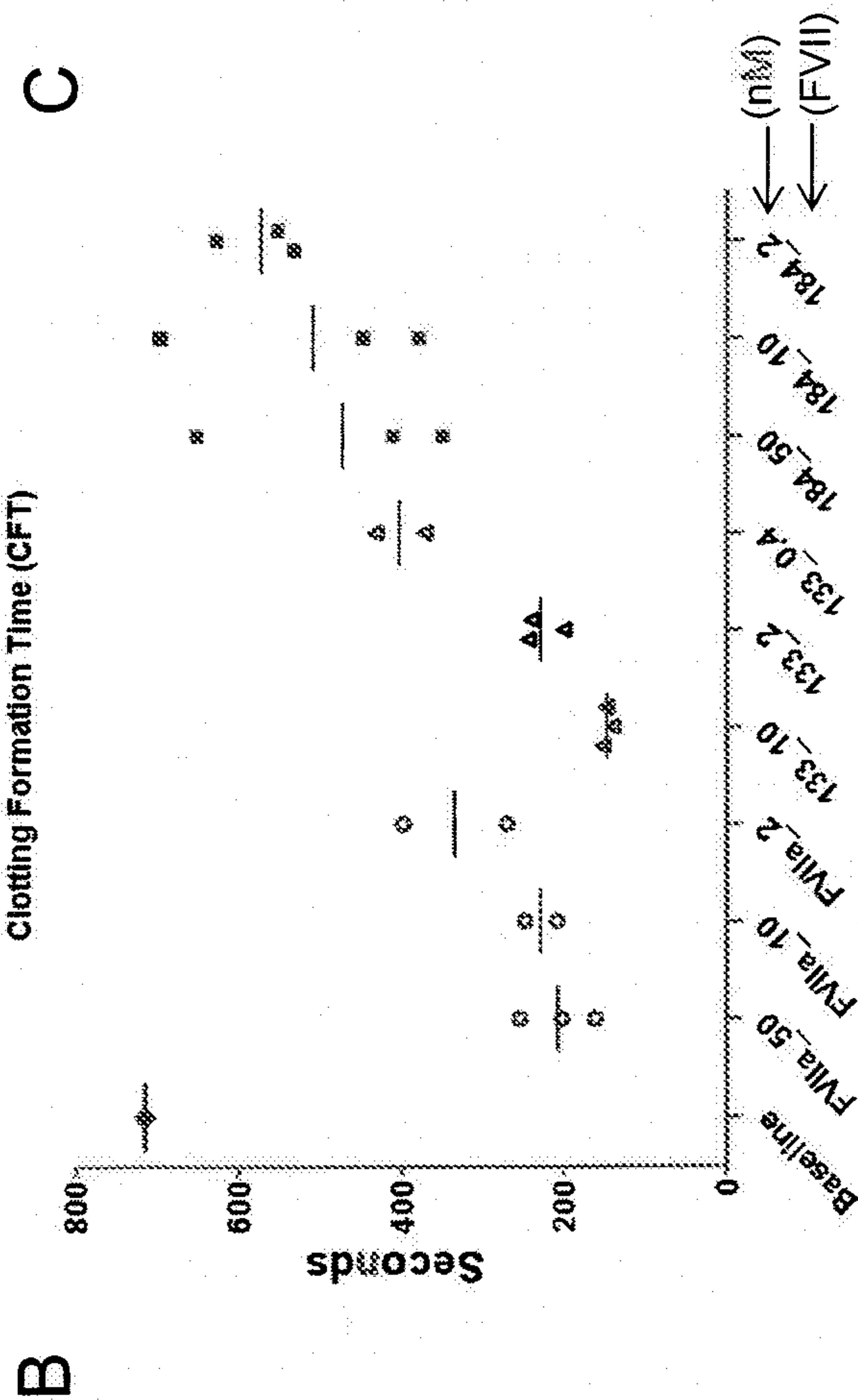
8/25

FIG. 8 FVII-133 activity in human hemophilia A blood by ROTEM assays

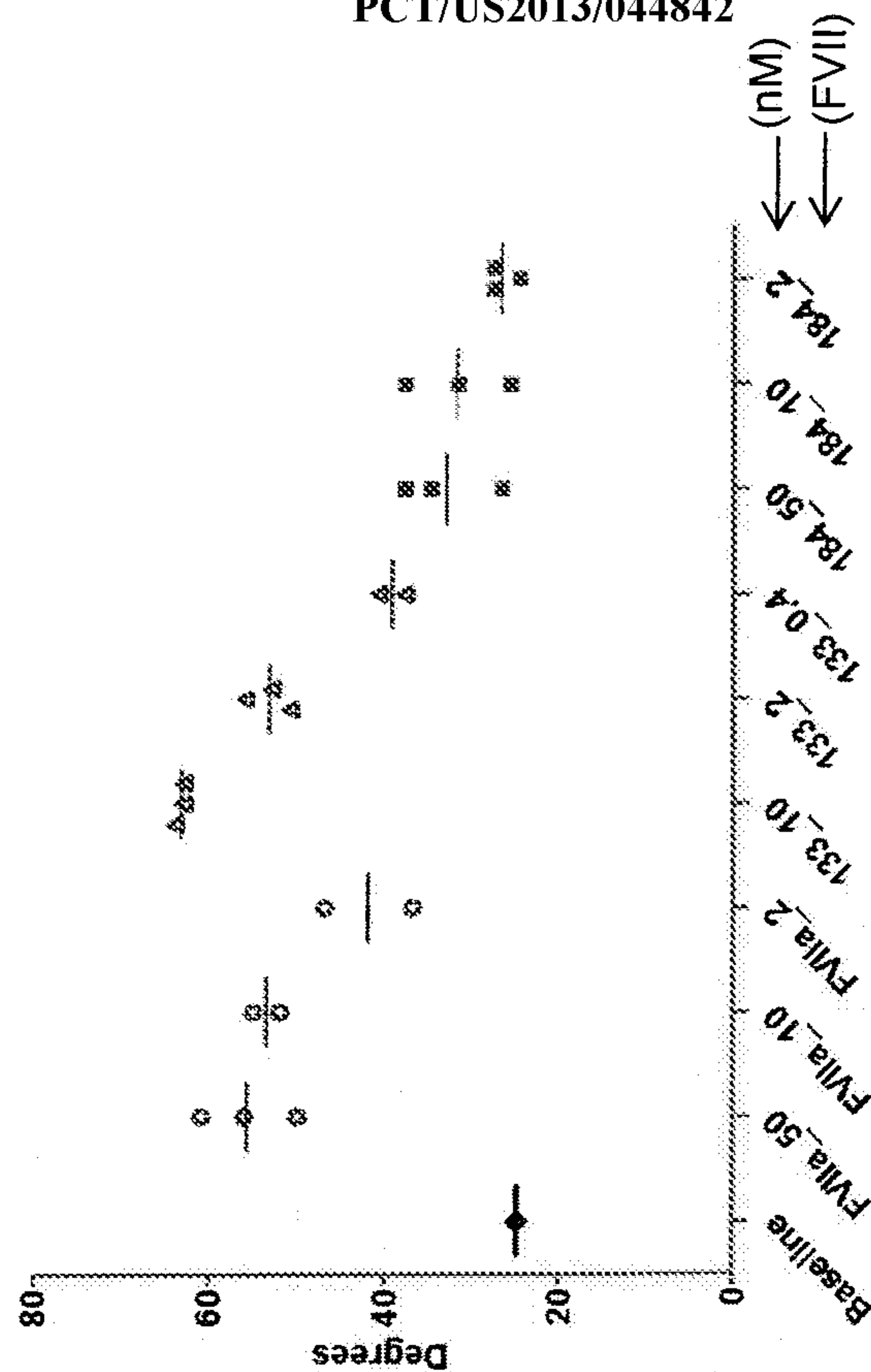
Clotting Time (CT)



Clotting Formation Time (CFT)



Alpha Angle



9/25

FVII-133 efficacy in hemB mice by Ex vivo Rotem Analysis

Clotting Time (CT)

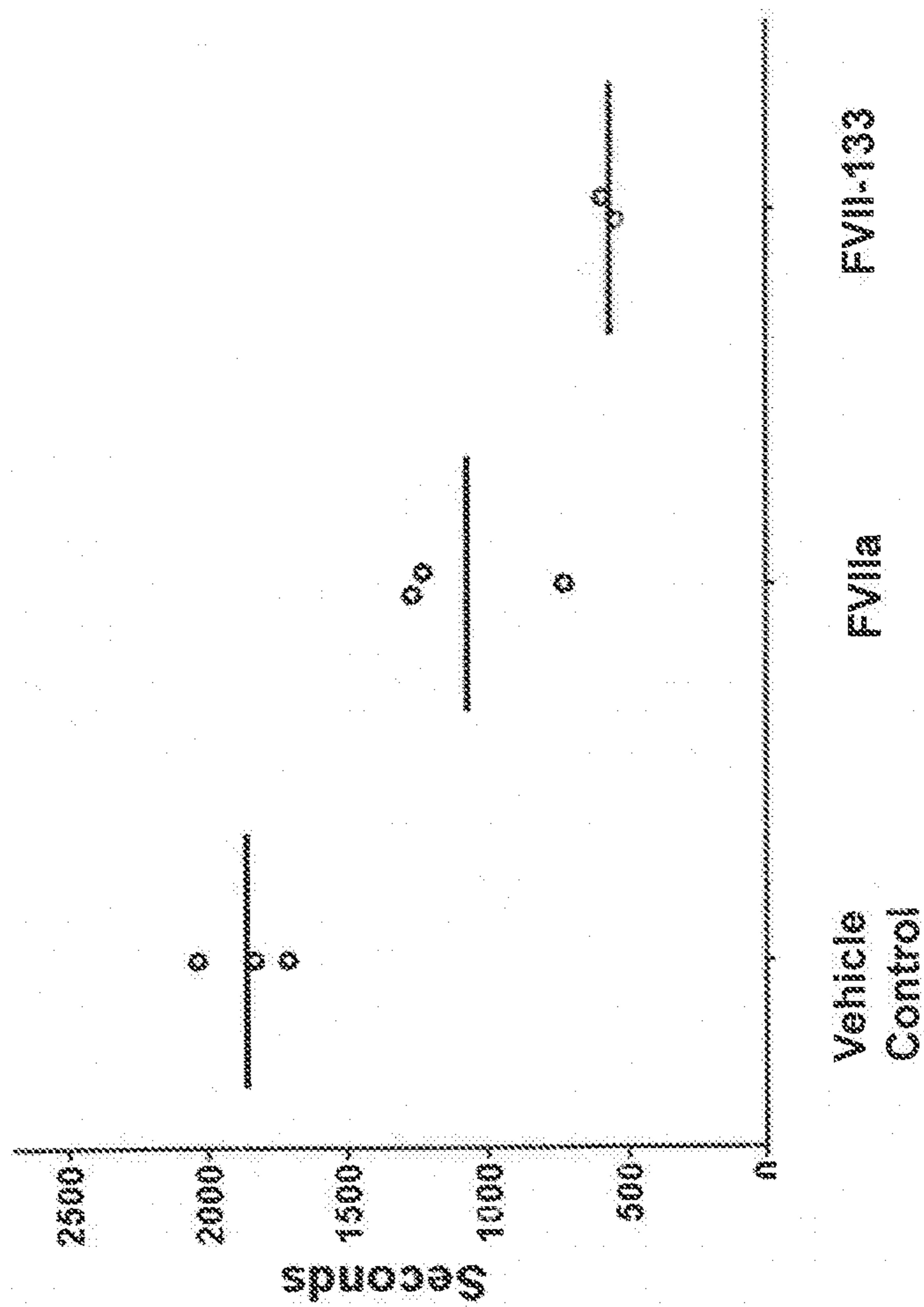


FIG. 9

10/25

Plasma protein concentration versus time curve

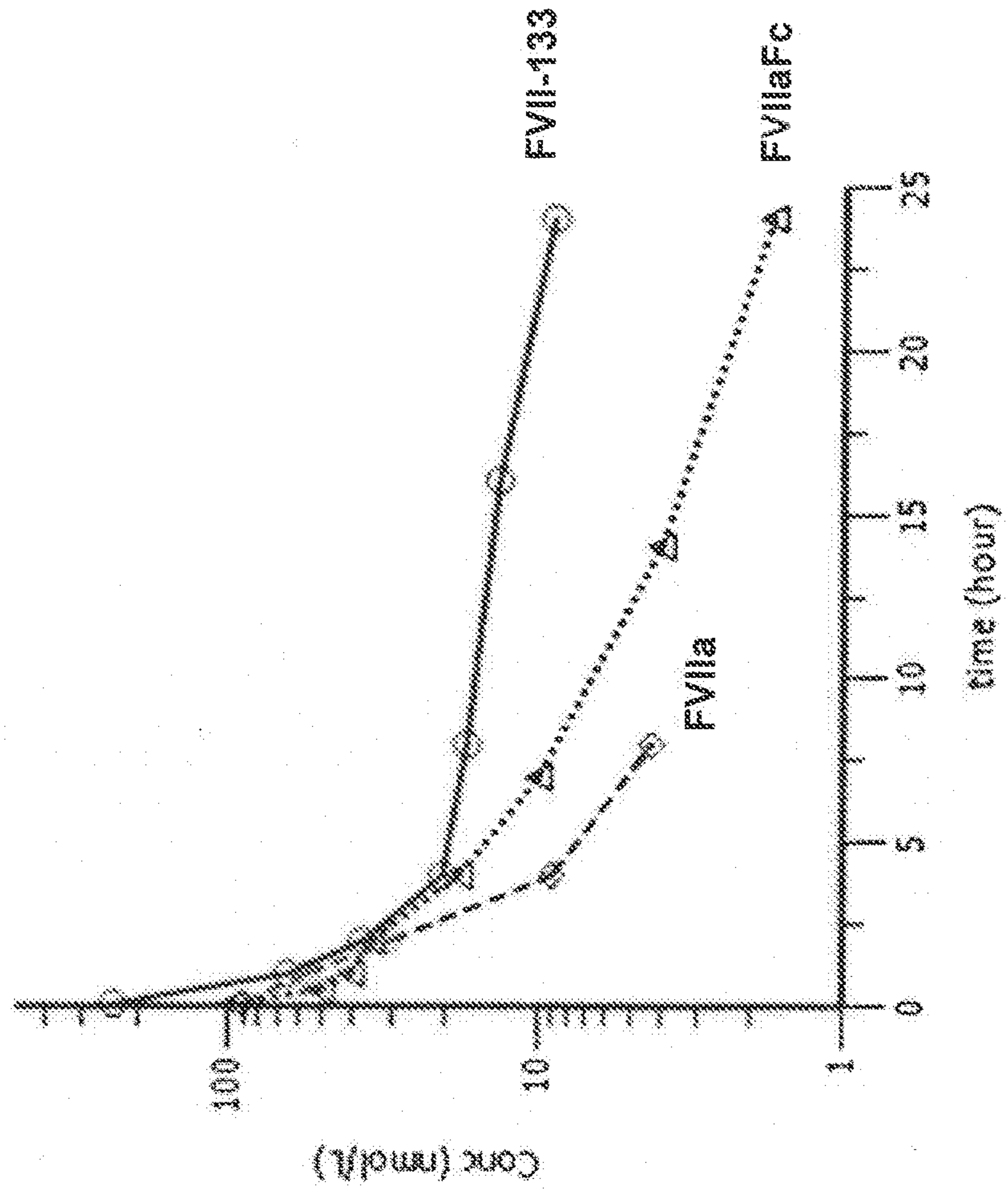


FIG. 10A

11/25

FVII-133 PK and FVII-133/ATIII complex formation in HemB mice

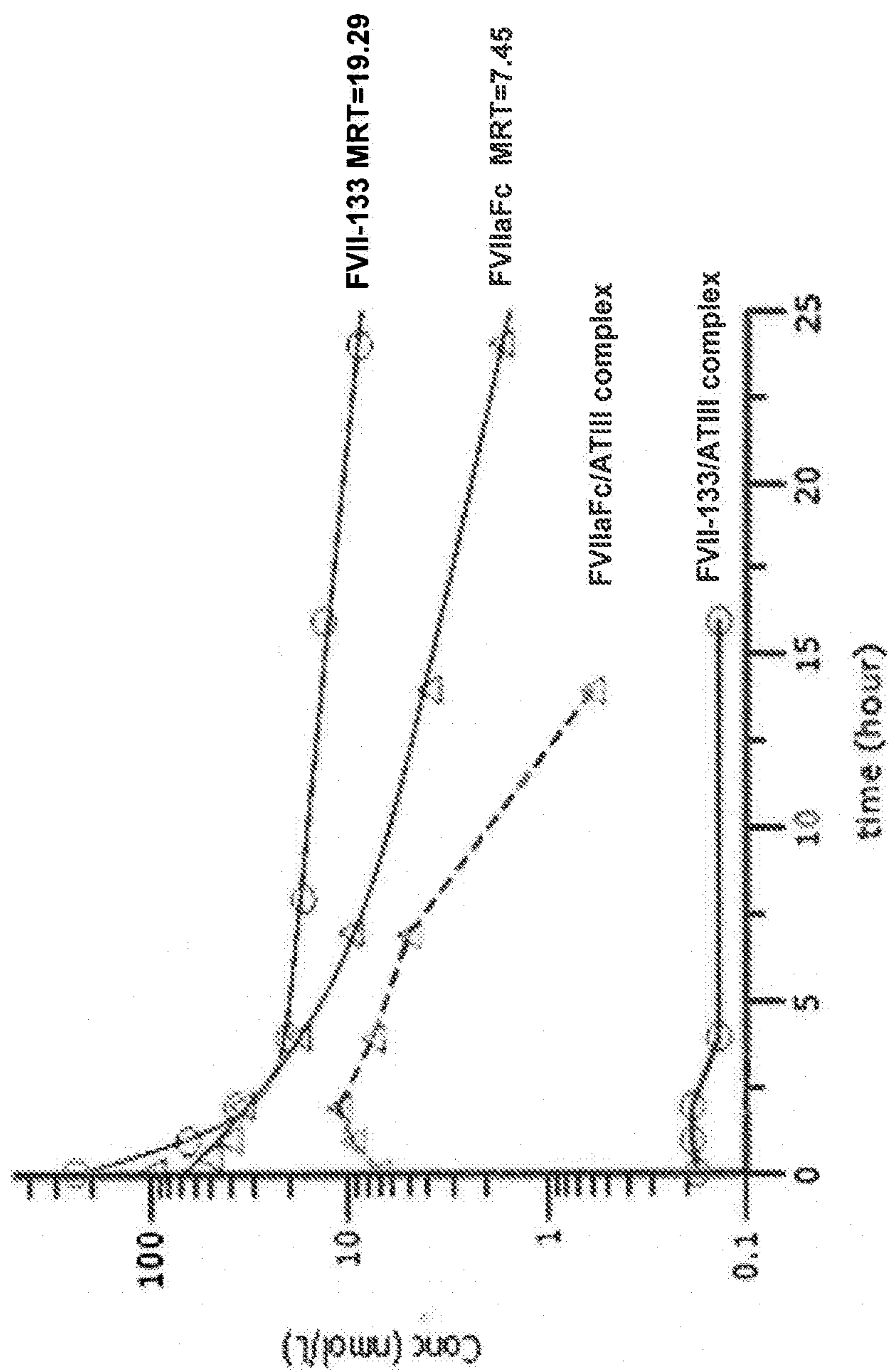


FIG. 10B

12/25

FVII-212 In Vitro ROTEM Activity in Human Hema Blood

NATEM CT

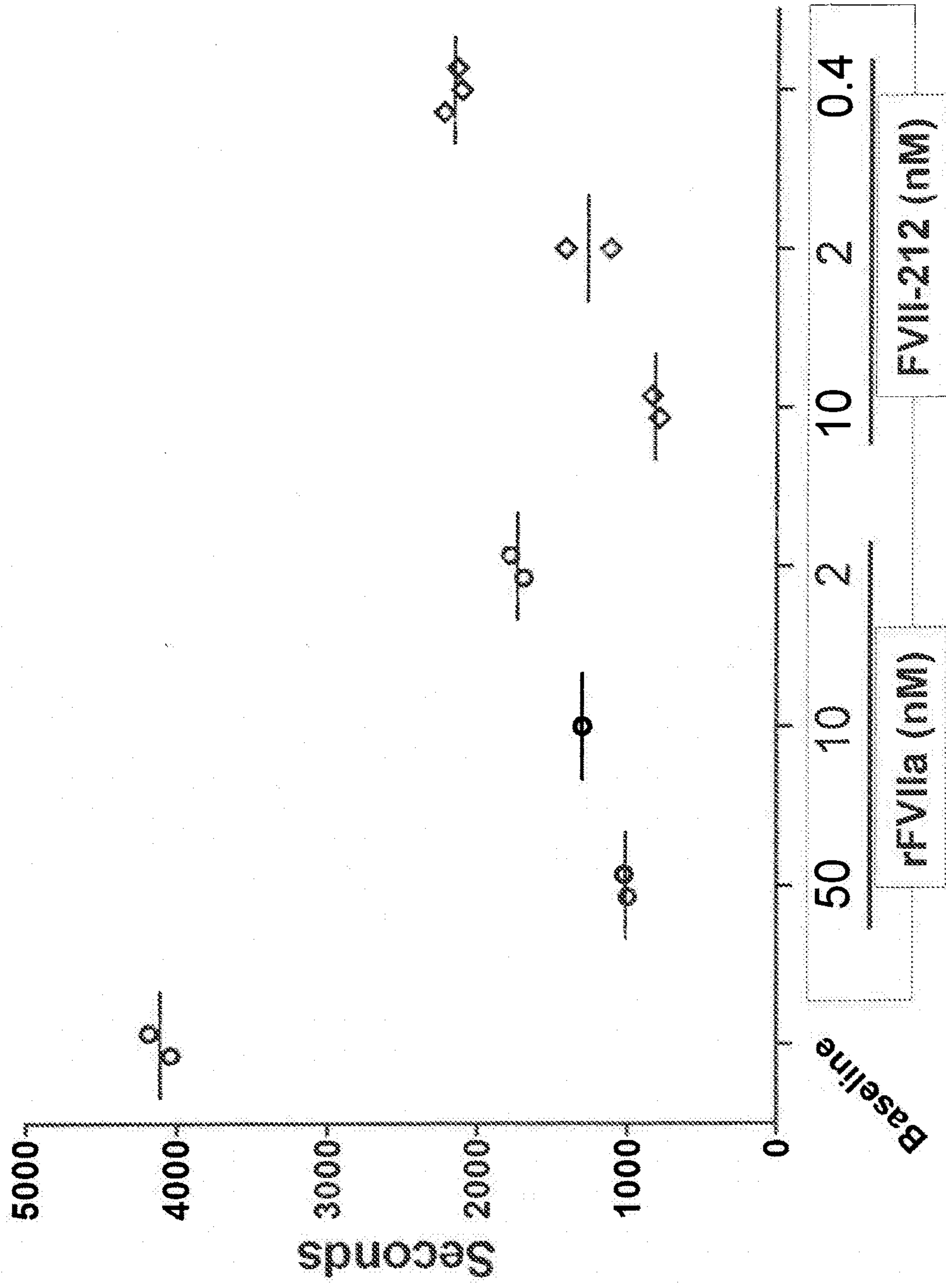


FIG. 11

13/25

FVII-212 In Vitro Rotem Activity in Mouse Hema Blood

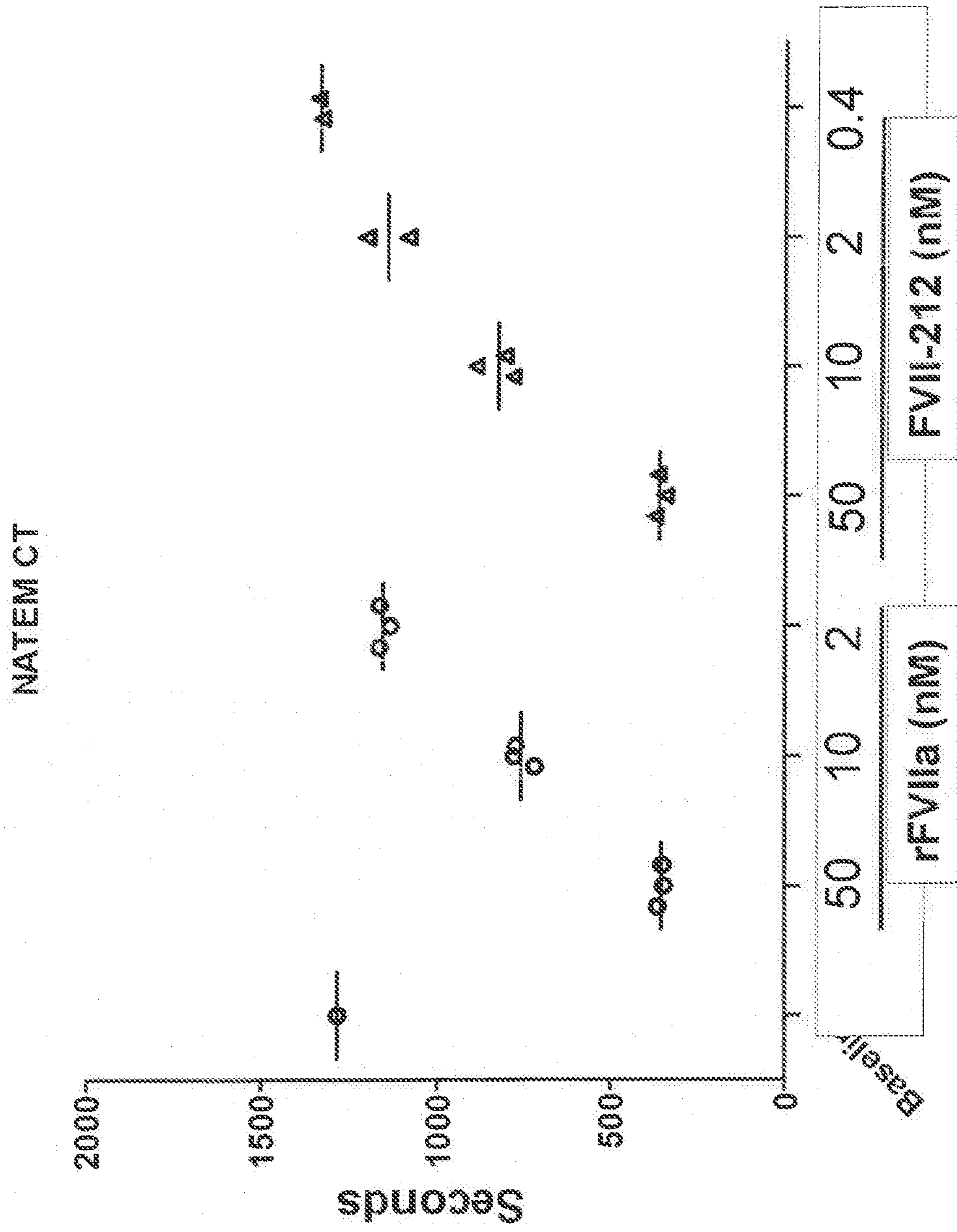


FIG. 12

14/25

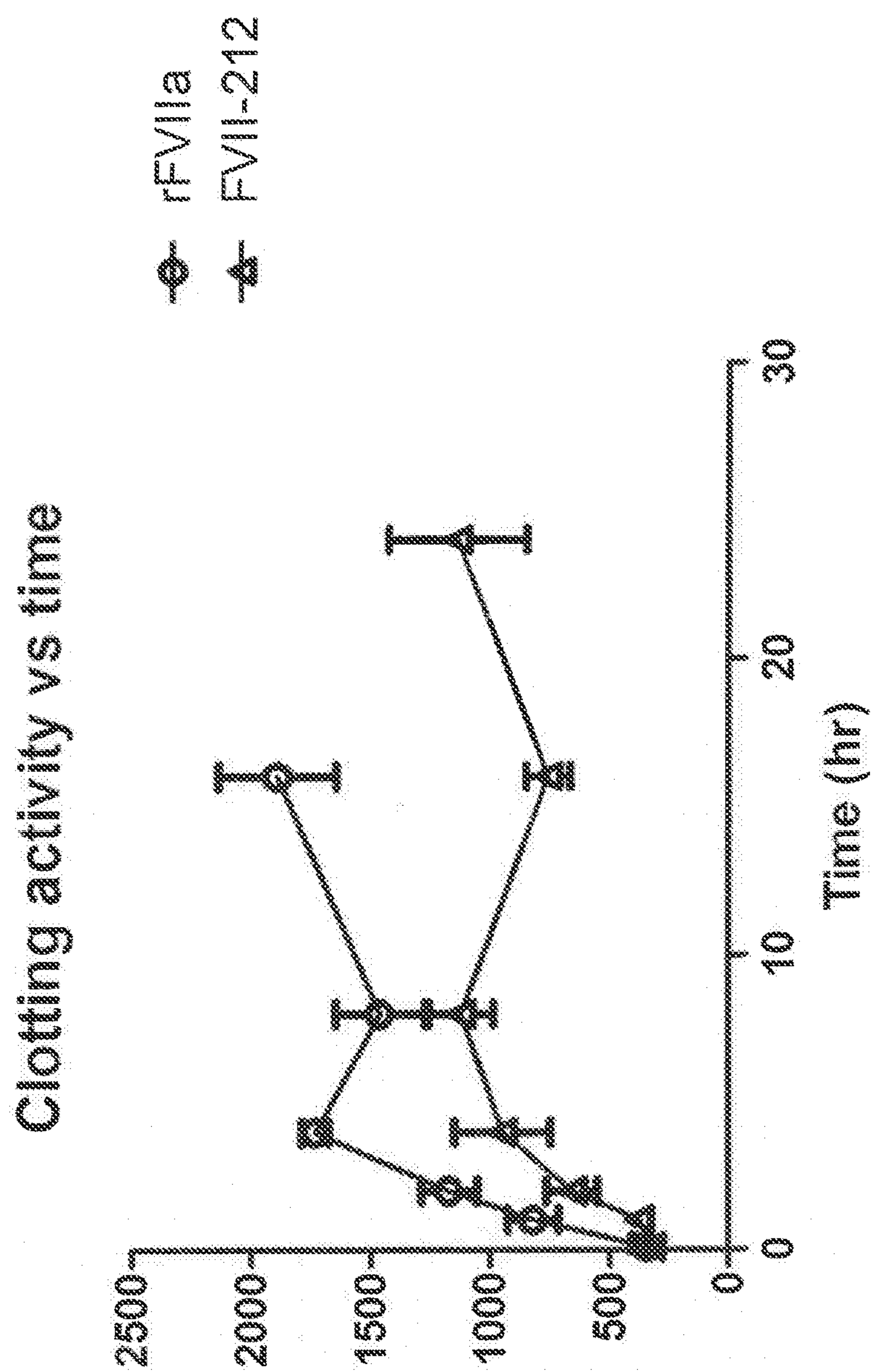


FIG. 13.

15/25

FVII-212 PK in mouse Hema

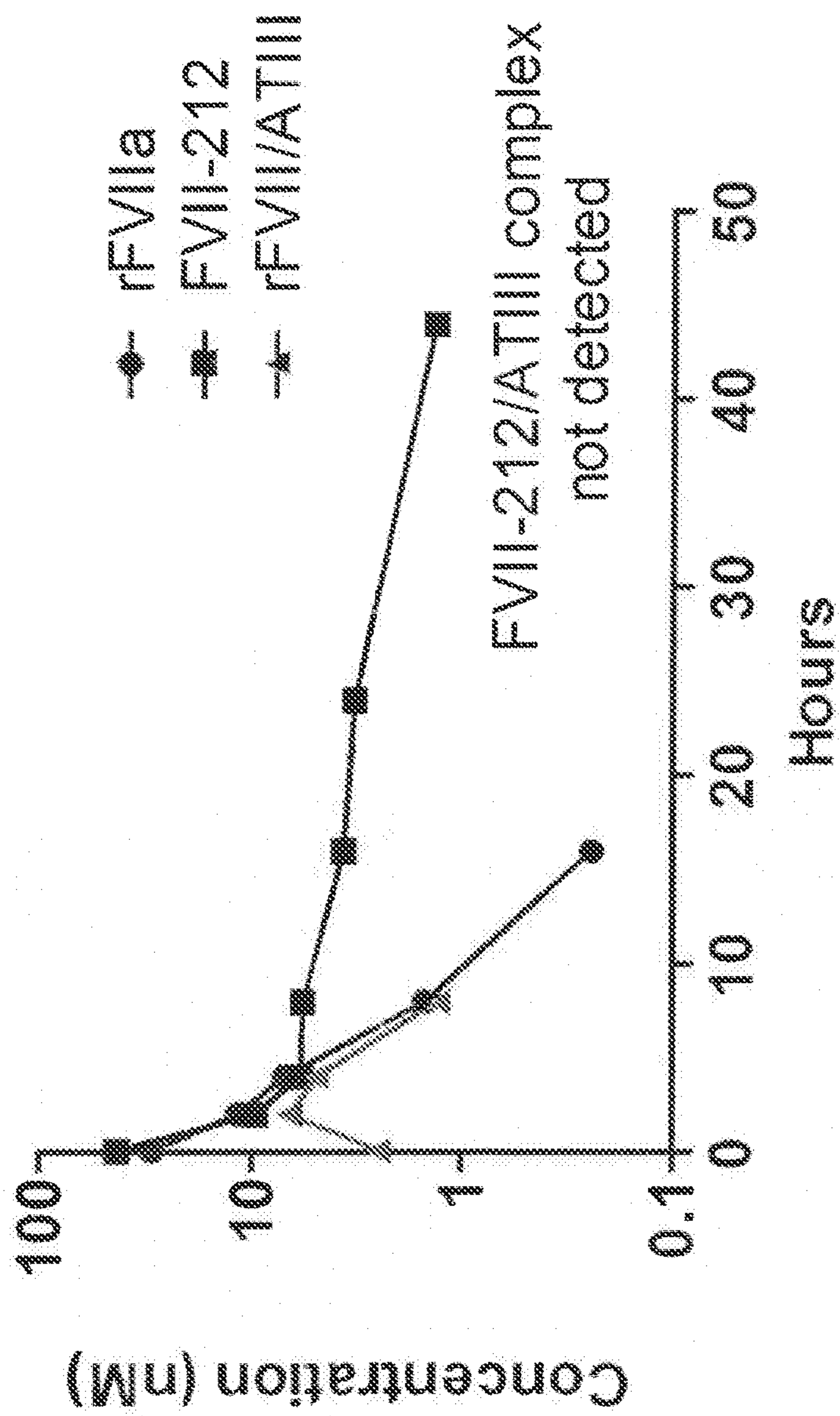


FIG. 14.

16/25

Amidolytic Activity of FVII-212

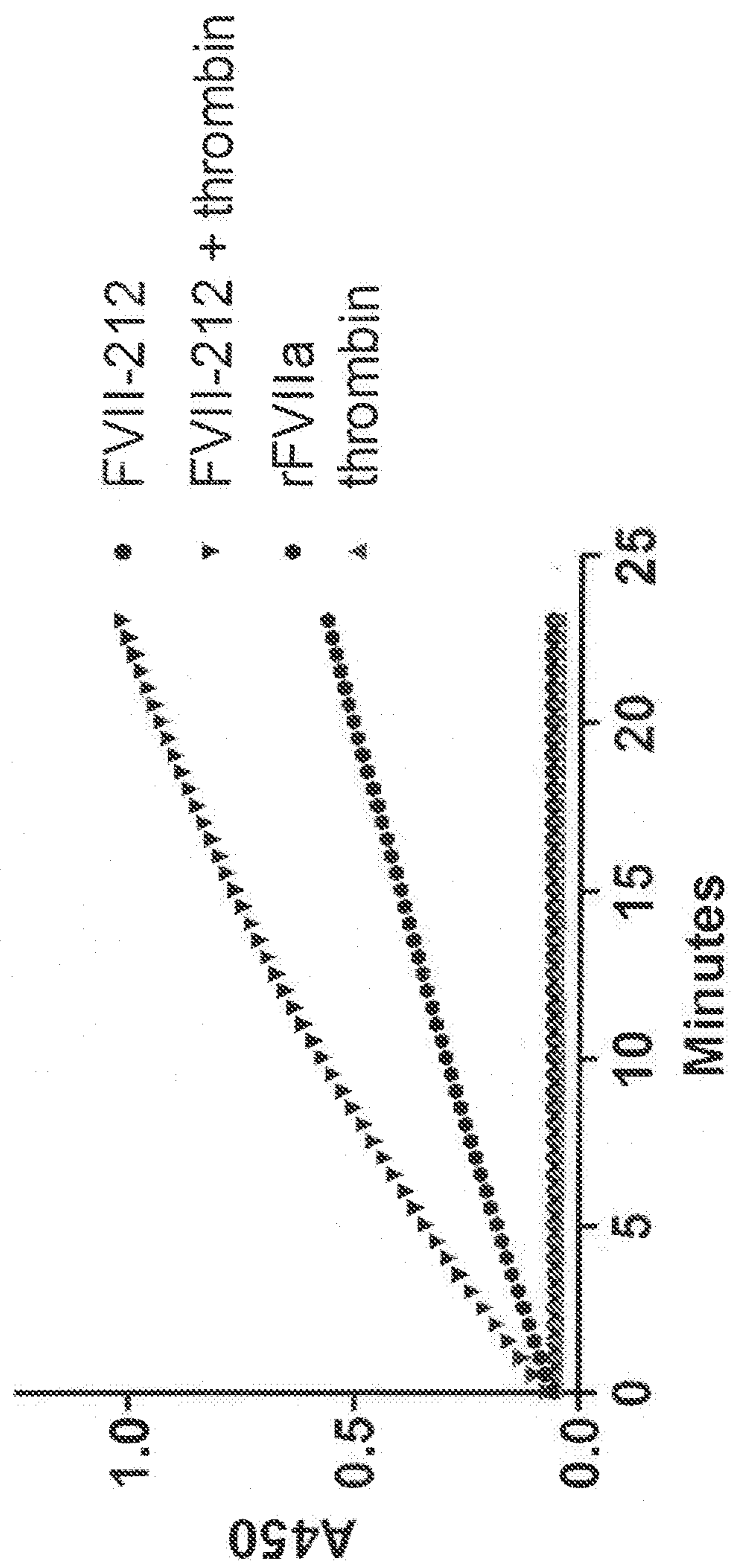
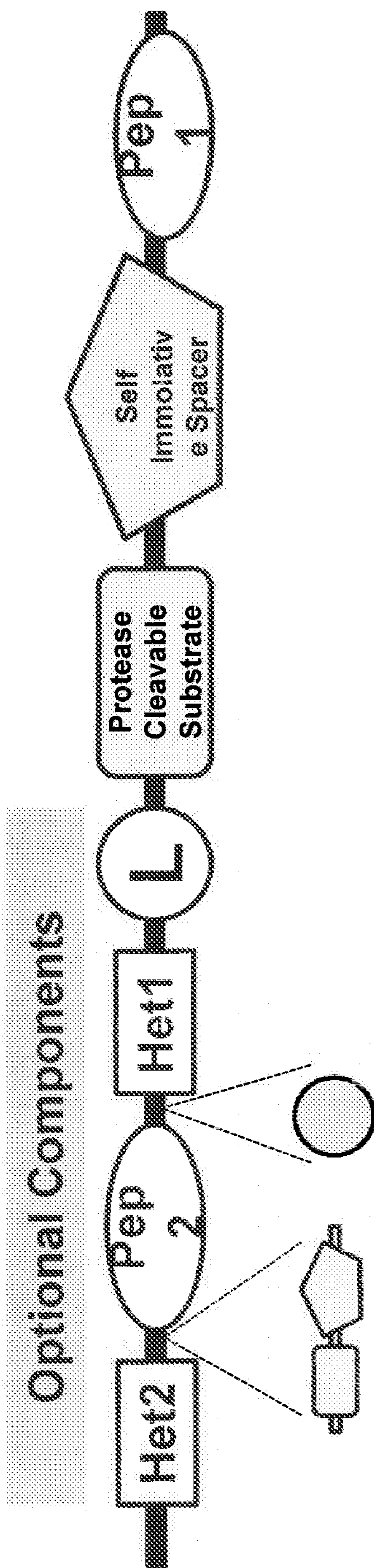


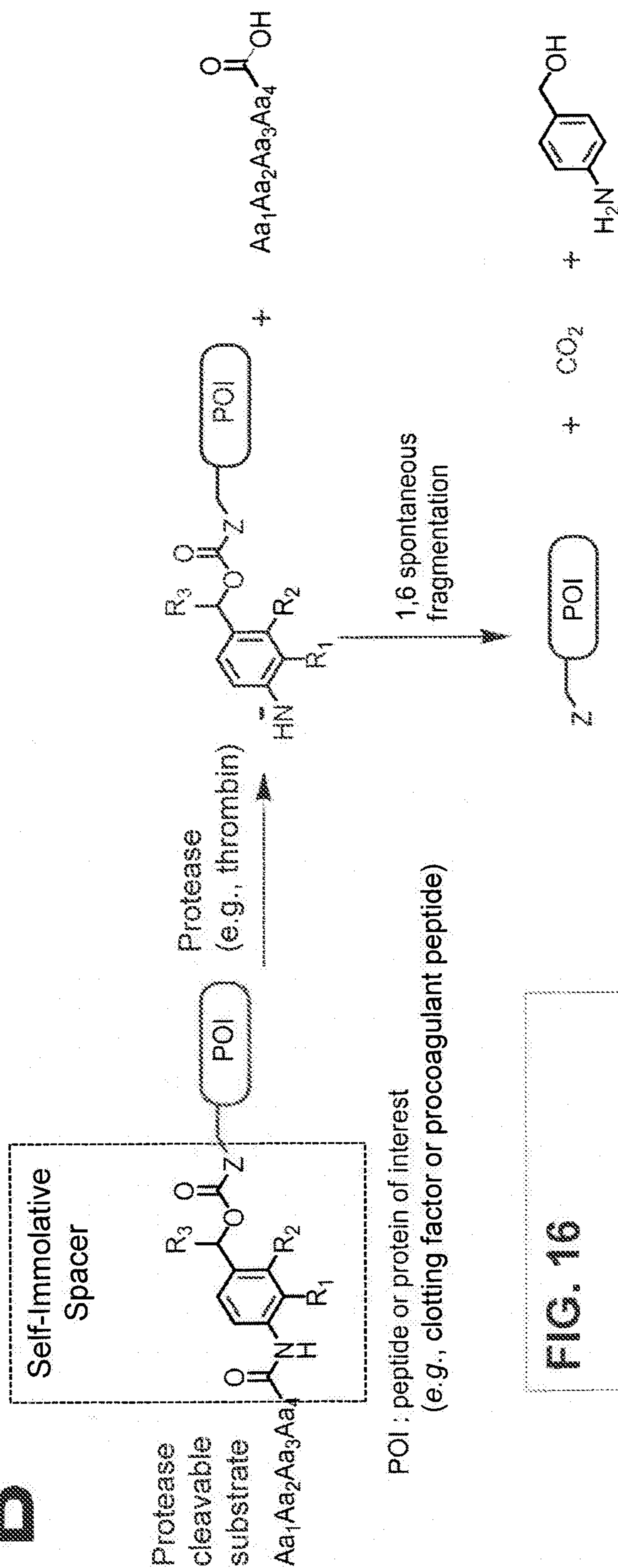
FIG. 15.

17/25

A



B



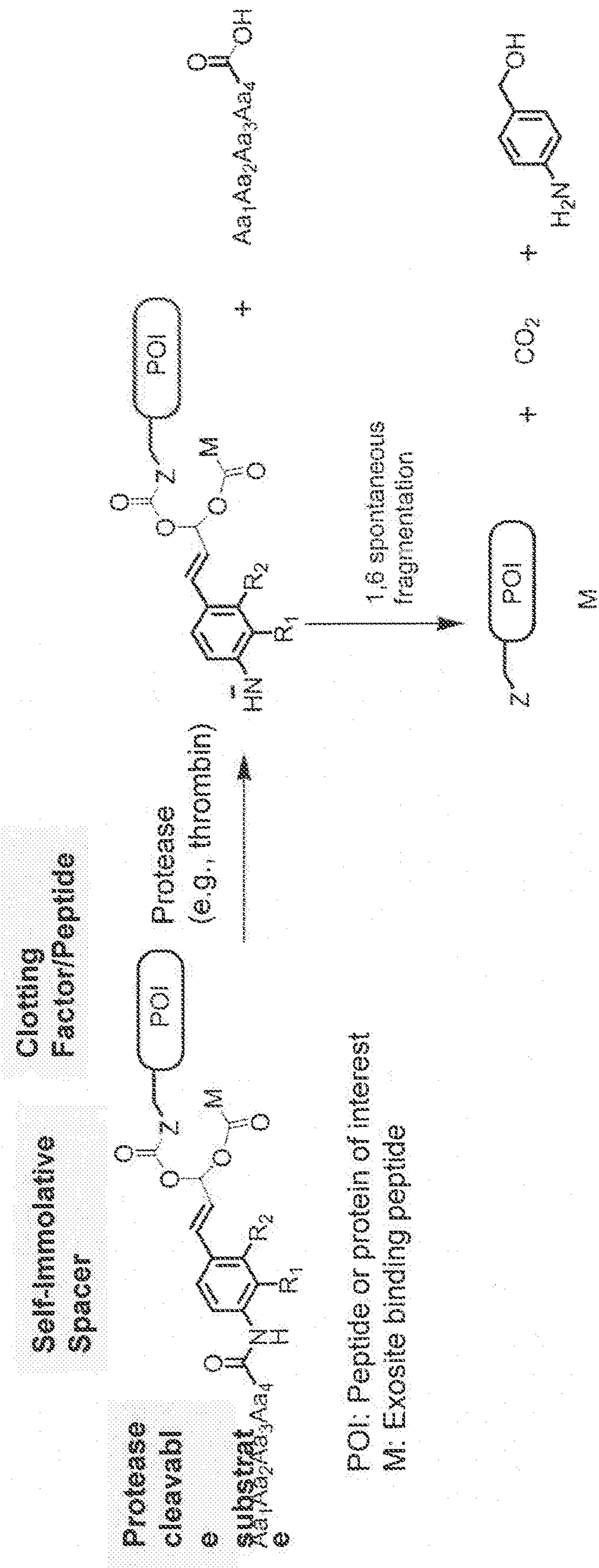
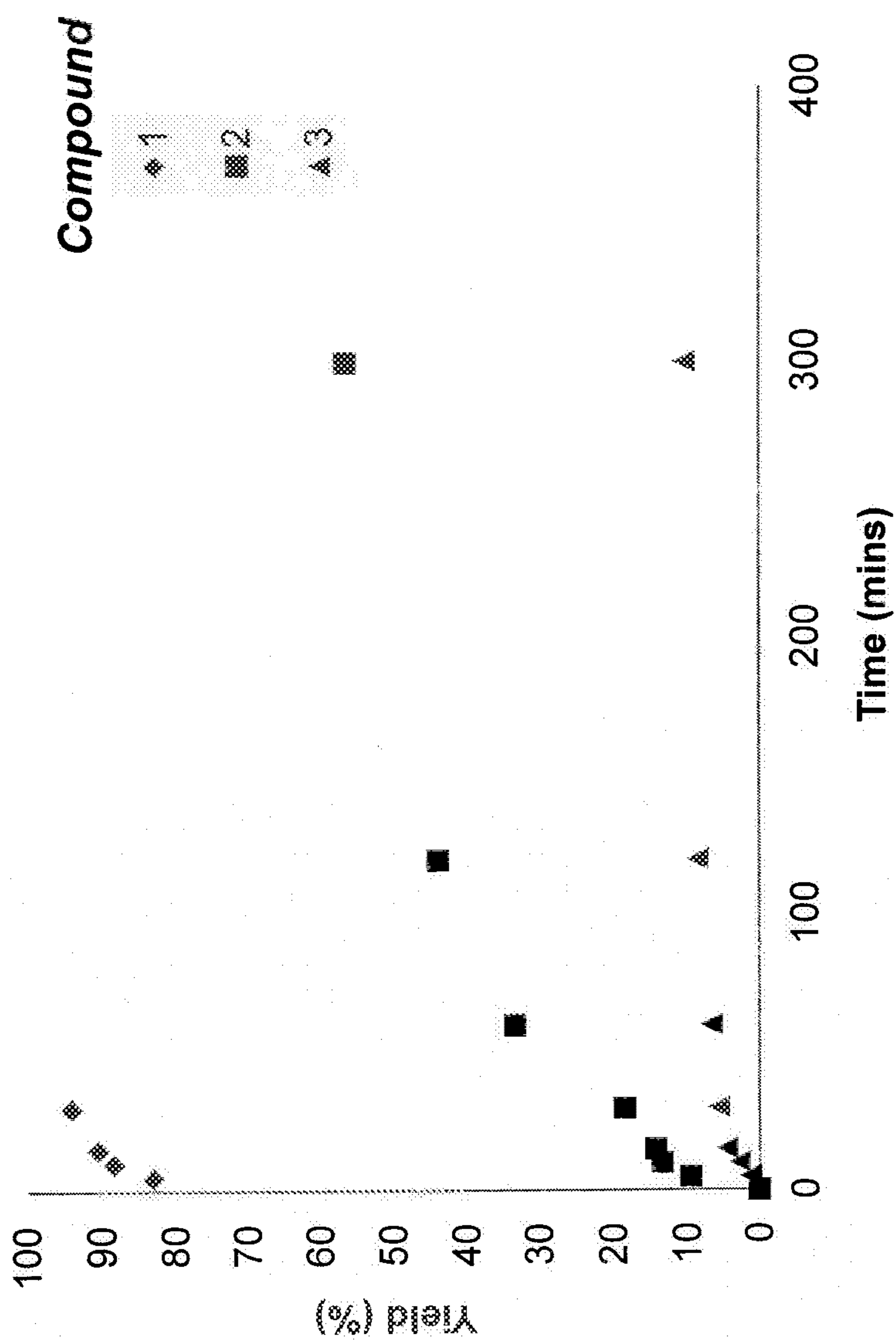


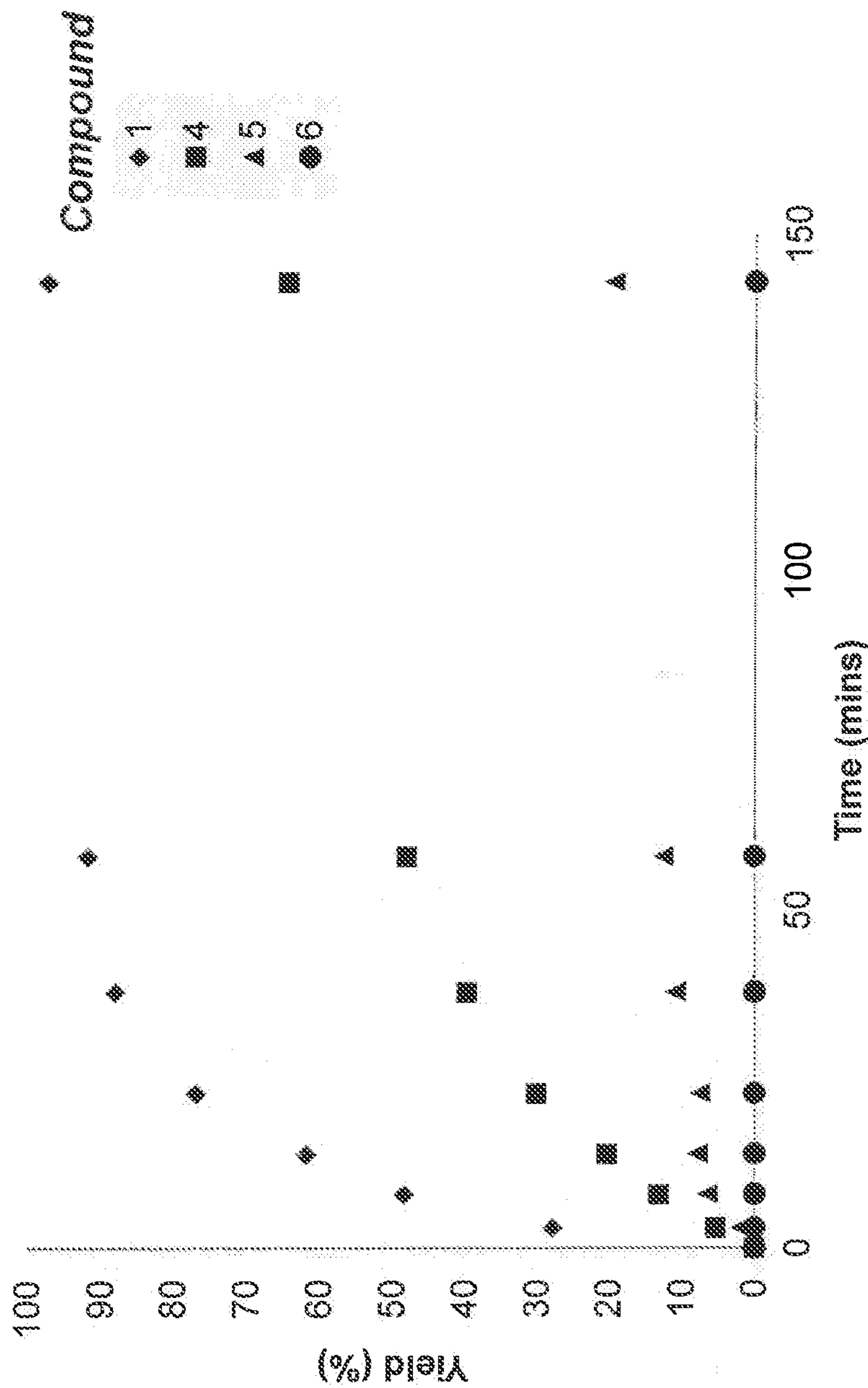
FIG. 17

19/25



Compound	Structure
1	D-Phe-Pip-R-PABC-IVGGQE
2	D-Phe-Pip-R-IVGGQE (Pip: pipecolic acid)
3	ALRPR-IVGGQE

FIG. 18



Compound	Structure
1	D-Phe-Pip-R-PABC-IVGGQE
4	D-Phe-P-R-PABC-IVGGQE
5	ALVPR-PABC-IVGGQE
6	ALVPR-IVGGQE

FIG. 19

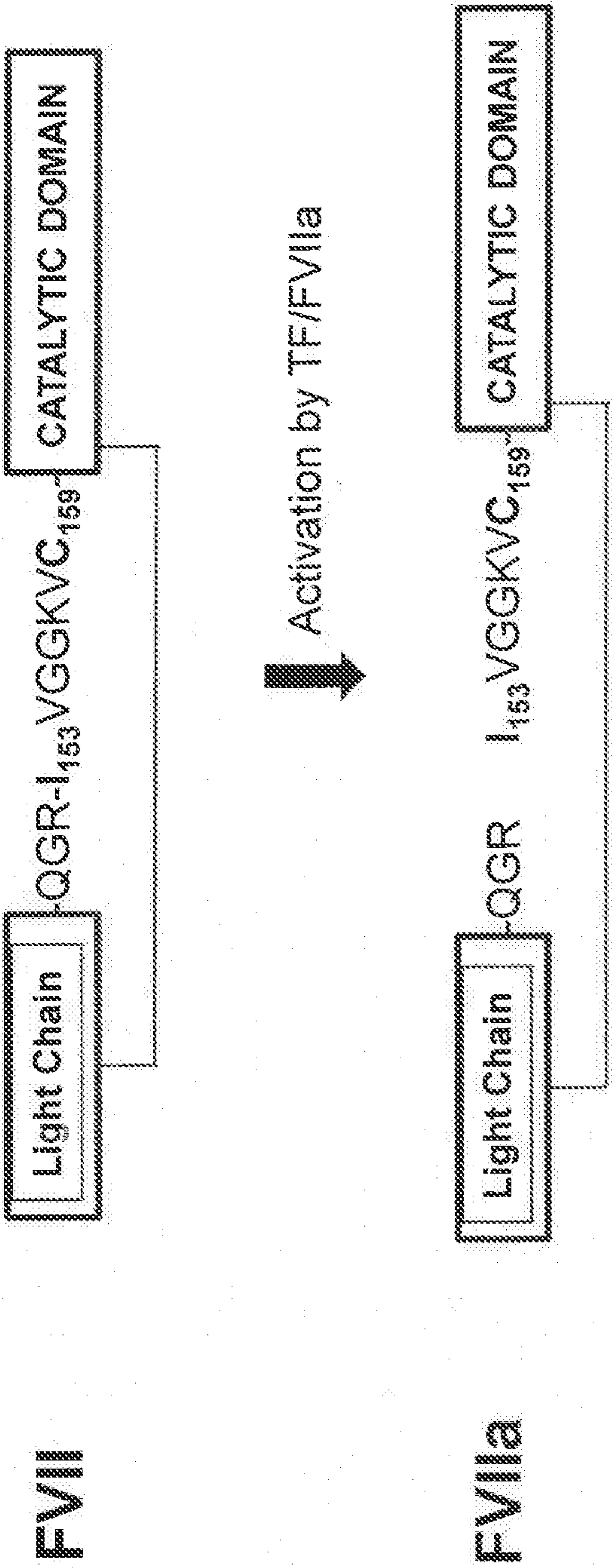


FIG. 20

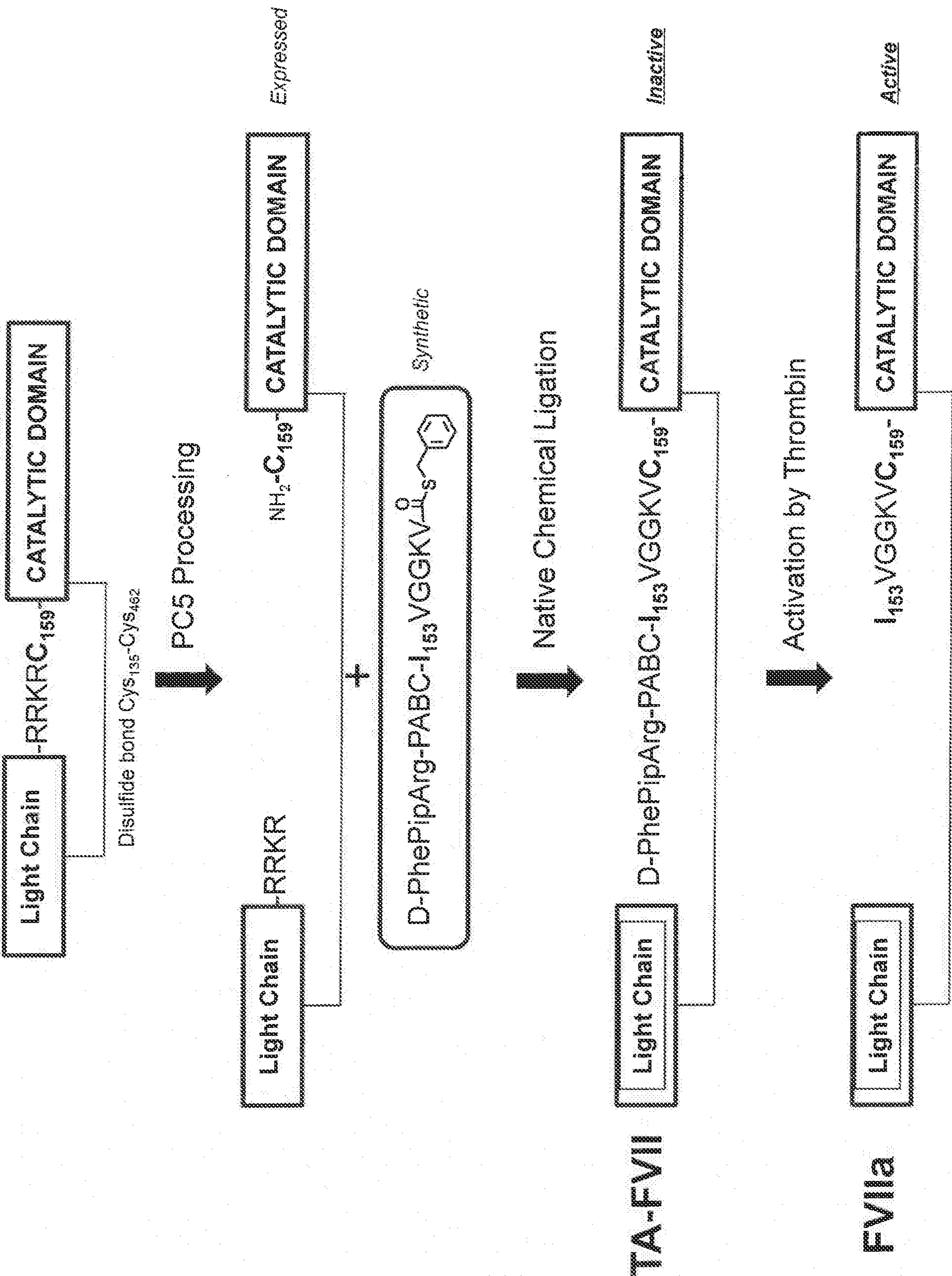
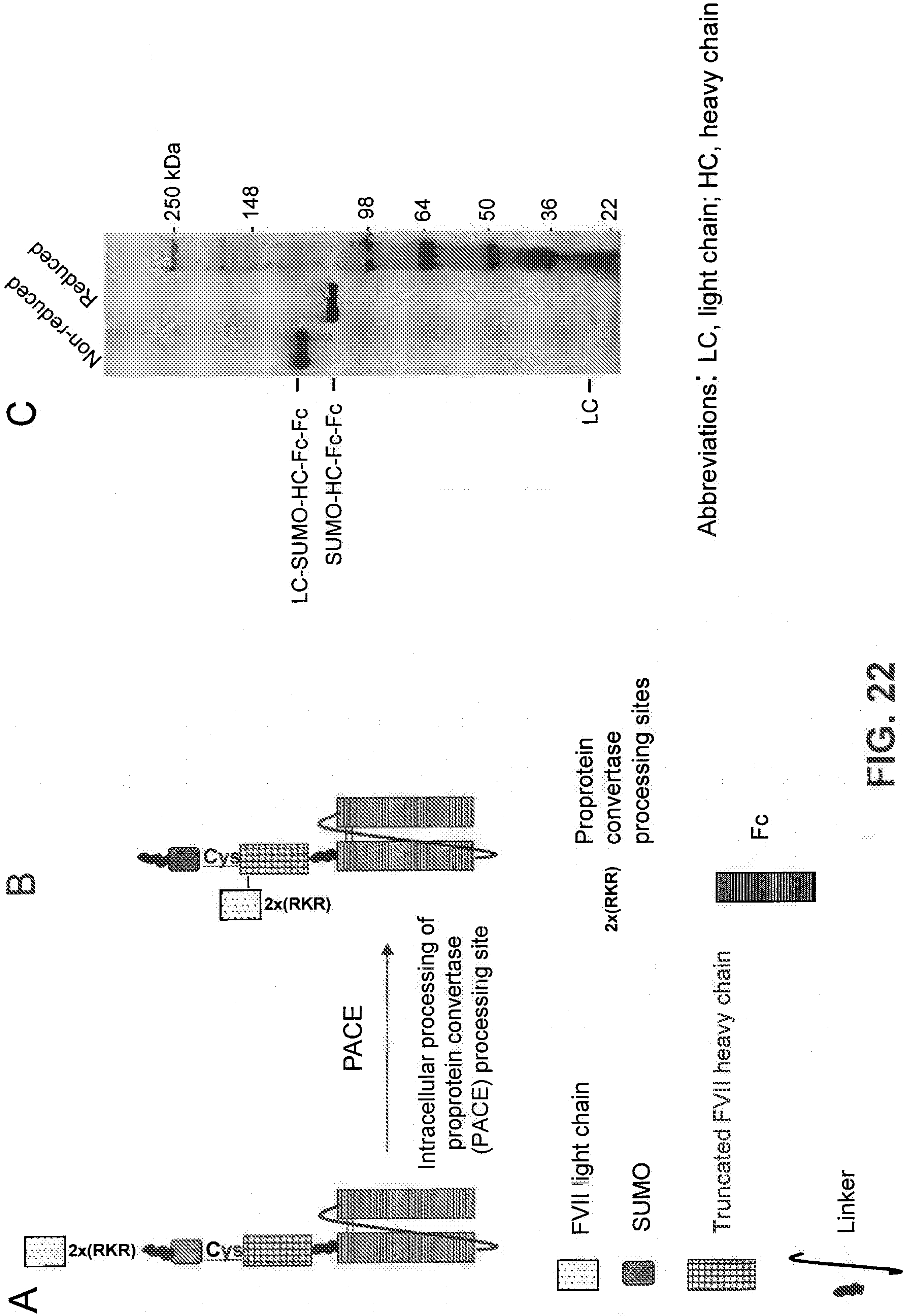


FIG. 21

FVII-186 Expression



FVII-186 SUMO Cleavage and TA-FVII-186 Semisynthesis by Native Chemical Ligation

WO 2013/185114
24/25

CA 02875247 2014-11-27

PCT/US2013/044842

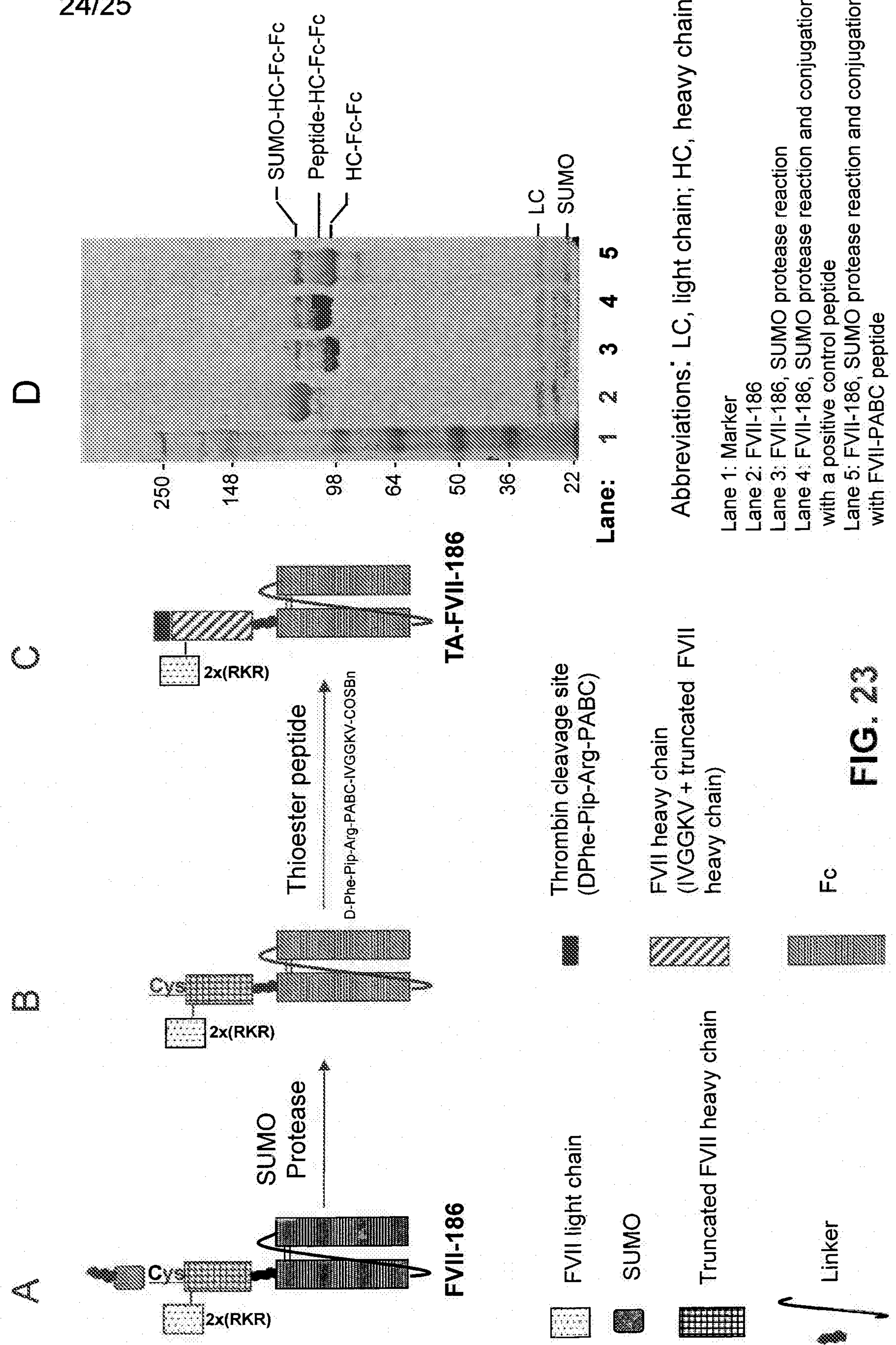


FIG. 23

FVIIa Chromogenic Assay after Thrombin Activation of TA-FVII-186

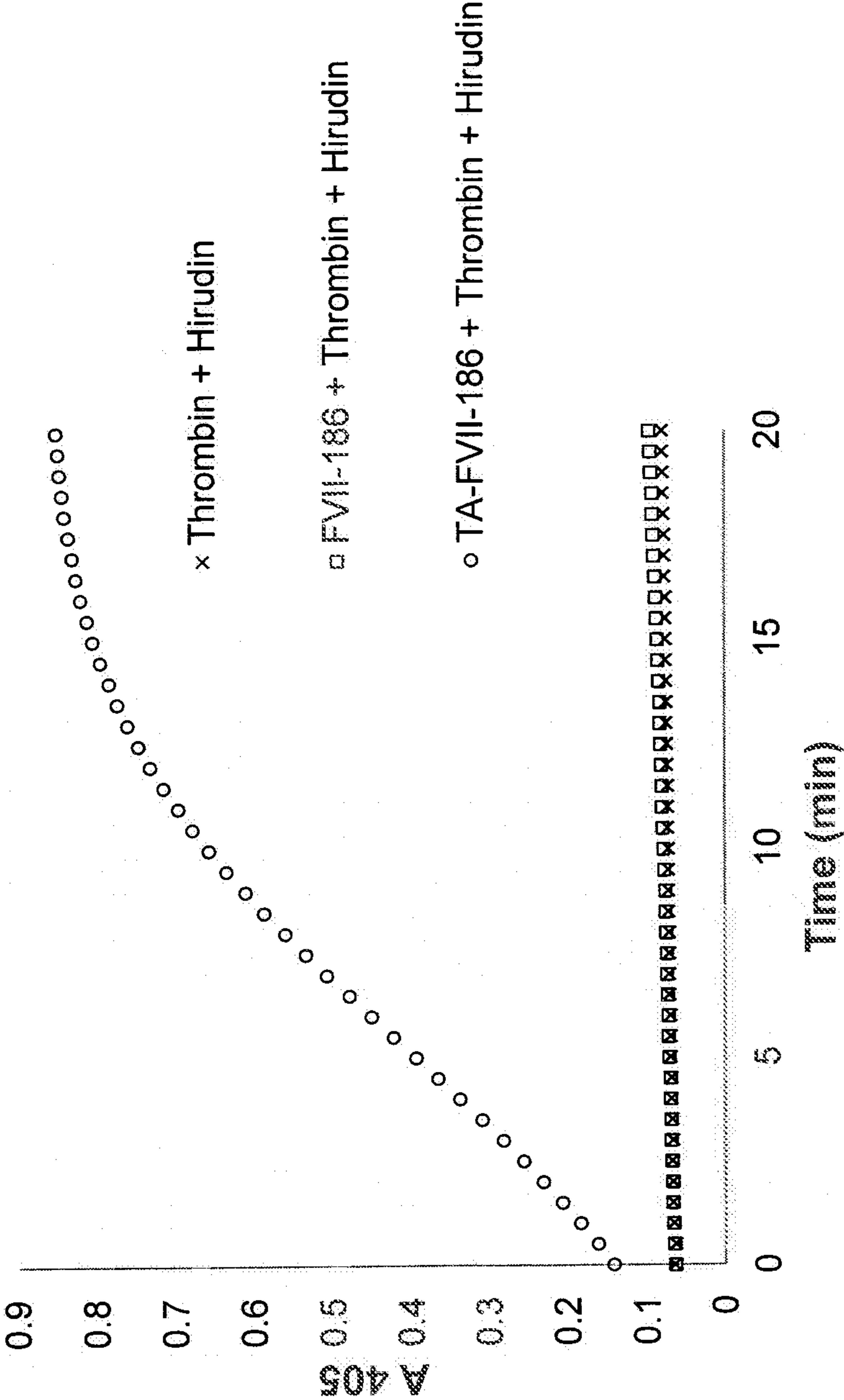


FIG. 24