

FVII OR FVIIa VARIANTS

FIELD OF THE INVENTION

The present invention relates to novel FVII or FVIIa variants comprising at least one amino acid modification in a position selected from the group consisting of 196, 237 and 341. The present invention also relates to use of such polypeptide variants in therapy, in particular for the treatment of a variety of coagulation-related disorders.

BACKGROUND OF THE INVENTION

Blood coagulation is a process consisting of a complex interaction of various blood components (or factors) that eventually results in a fibrin clot. Generally, the blood components participating in what is referred to as the "coagulation cascade" are proenzymes or zymogens, i.e. enzymatically inactive proteins that are converted into an active form by the action of an activator. One of these coagulation factors is factor VII (FVII).

FVII is a vitamin K-dependent plasma protein synthesized in the liver and secreted into the blood as a single-chain glycoprotein with a molecular weight of 53 kDa (Broze & Majerus, *J. Biol. Chem.* 1980; 255:1242-1247). The FVII zymogen is converted into an activated form (FVIIa) by proteolytic cleavage at a single site, R152-I153, resulting in two chains linked by a single disulfide bridge. FVIIa in complex with tissue factor (TF), the FVIIa complex, is able to convert both FIX and FX into their activated forms, followed by reactions leading to rapid thrombin production and fibrin formation (Østerud & Rapaport, *Proc Natl Acad Sci USA* 1977; 74:5260-5264).

FVII undergoes post-translational modifications, including vitamin K-dependent carboxylation resulting in ten γ -carboxyglutamic acid residues in the N-terminal region of the molecule. Thus, residues number 6, 7, 14, 16, 19, 20, 25, 26, 29 and 35 shown in SEQ ID NO:2 are γ -carboxyglutamic acids residues in the Gla domain important for FVII activity. Other post-translational modifications include sugar moiety attachment at two naturally occurring N-glycosylation sites at positions 145 and 322, respectively, and at two naturally occurring O-glycosylation sites at positions 52 and 60, respectively.

The gene coding for human FVII (hFVII) has been mapped to chromosome 13 at q34-qter 9 (de Grouchy et al., *Hum Genet* 1984; 66:230-233). It contains nine exons and spans 12.8 Kb (O'Hara et al., *Proc Natl Acad Sci USA* 1987; 84:5158-5162). The gene organisation and protein structure of FVII are similar to those of other vitamin K-dependent

procoagulant proteins, with exons 1a and 1b encoding for signal sequence; exon 2 the propeptide and Gla domain; exon 3 a short hydrophobic region; exons 4 and 5 the epidermal growth factor-like domains; and exon 6 through 8 the serine protease catalytic domain (Yoshitake et al., *Biochemistry* 1985; 24: 3736-3750).

5 Reports exist on experimental three-dimensional structures of hFVIIa (Pike et al., *Proc Natl Acad Sci USA* 1999; 96:8925-30 and Kemball-Cook et al., *J. Struct. Biol.* 1999; 127:213-223), of hFVIIa in complex with soluble tissue factor using X-ray crystallographic methods (Banner et al., *Nature*, 1996; 380:41 and Zhang et al., *J. Mol. Biol.*, 1999; 285: 2089), and of smaller fragments of hFVII (Muranyi et al., *Biochemistry*, 1998; 37:10605 and
10 Kao et al., *Biochemistry*, 1999; 38:7097).

Relatively few protein-engineered variants of FVII have been reported (Dickinson & Ruf, *J Biol Chem*, 1997;272:19875-19879, Kemball-Cook et al., *J Biol Chem*, 1998; 273:8516-8521, Bharadwaj et al., *J Biol Chem*, 1996; 271:30685-30691, Ruf et al., *Biochemistry*, 1999; 38:1957-1966).

15 Reports exist on expression of FVII in BHK or other mammalian cells (WO 92/15686, WO 91/11514 and WO 88/10295) and co-expression of FVII and kex2 endoprotease in eukaryotic cells (WO 00/28065).

Commercial preparations of recombinant human FVIIa (rhFVIIa) are sold under the tradename NovoSeven®. NovoSeven® is indicated for the treatment of bleeding episodes in
20 hemophilia A or B patients. NovoSeven® is the only rhFVIIa for effective and reliable treatment of bleeding episodes available on the market.

An inactive form of FVII in which arginine 152 and/or isoleucine 153 are modified has been reported in WO 91/11514. These amino acids are located at the activation site. WO 96/12800 describes inactivation of FVIIa by a serine proteinase inhibitor; inactivation by
25 carbamylation of FVIIa at the α -amino acid group I153 has been described by Petersen et al., *Eur J Biochem*, 1999;261:124-129. The inactivated form is capable of competing with hFVII or hFVIIa for binding to TF and inhibiting clotting activity. The inactivated form of FVIIa is suggested to be used for treatment of patients suffering from hypercoagulable states, such as patients with sepsis, at risk of myocardial infarction or of thrombotic stroke.

30 WO 98/32466 suggests that FVII, among many other proteins, may be PEGylated (i.e. attached to one or more polyethylene glycol molecules) but does not contain any further information in this respect.

WO 01/58935 discloses a new strategy for developing FVII or FVIIa molecules having *inter alia* an increased half-life by means of directed glycosylation or PEGylation.

WO 03/093465 discloses FVII or FVIIa variants having certain modifications in the Gla domain and having one or more N-glycosylation sites introduced outside the Gla domain.

5 A circulating rhFVIIa half-life of 2.3 hours was reported in "Summary Basis for Approval for NovoSeven®", FDA reference number 96-0597. Relatively high doses and frequent administration are necessary to reach and sustain the desired therapeutic or prophylactic effect. As a consequence, adequate dose regulation is difficult to obtain and the need for frequent intravenous administrations imposes restrictions on the patient's way of
10 living.

In normal hemostasis, the procoagulant system is in balance with anticoagulant systems involved in the termination of the hemostatic reaction and the fibrinolytic system, which dissolves clots once they are formed. The anticoagulant systems contain several protease inhibitors, e.g., the Tissue Factor Pathway Inhibitor (TFPI), antithrombin-III (AT-
15 III), heparin cofactor-II (HC-II), and the protein C pathway.

TFPI is a reversible, active site-directed inhibitor of FXa, which regulates coagulation by inhibiting FVIIa-TF in a FXa-dependent manner. The TFPI-FXa complex binds to the FVIIa-TF complex, resulting in the formation of a TF-FVIIa-TFPI-FXa complex.

The *in vivo* relevance of TFPI is supported by experiments showing a hemostatic
20 effect of a neutralizing anti-TFPI antibody in a hemophilia bleeding model (Erhardtsen et al. *Blood Coagul Fibrinolysis* 1995; 6:388-394). Furthermore, in biochemical reconstitution experiments, TFPI was shown to extend the initiation phase and reduce the rate of thrombin generation during the propagation phase (van't Veer and Mann; *J. Biol. Chem.* 1997; 272: 4367-4377).

25 An object of the present invention is to provide FVII or FVIIa variants which exhibit an increased clotting activity as compared to hFVIIa or rhFVIIa. It is contemplated that this may be obtained by way of FVII or FVIIa variants having an altered affinity to TFPI.

Another problem in current rhFVIIa treatment is the relative instability of the molecule with respect to proteolytic degradation. Proteolytic degradation is a major obstacle
30 for obtaining a preparation in solution as opposed to a lyophilized product. The advantage of obtaining a stable soluble preparation lies in easier handling for the patient, and, in the case of emergencies, quicker action, which potentially can become life saving. Attempts to prevent proteolytic degradation by site directed mutagenesis at major proteolytic sites have been disclosed in WO 88/10295.

Thus, a further object of the present invention is to provide FVII/FVIIa variants which, in addition to the above-mentioned improved properties, are more stable towards proteolytic degradation, i.e. possess reduced sensitivity to proteolytic degradation.

A molecule with a longer circulation half-life would decrease the number of necessary administrations. Given the association of current FVIIa product with frequent injections, and the potential for obtaining more optimal therapeutic FVIIa levels with concomitant enhanced therapeutic effect, there is a clear need for improved FVII- or FVIIa-like molecules. One way to increase the circulation half-life of a protein is to ensure that renal clearance of the protein is reduced. This may be achieved by conjugating the protein to a chemical moiety which is capable of conferring reduced renal clearance to the protein. Furthermore, attachment of a chemical moiety to the protein or substitution of amino acids exposed to proteolysis may effectively block a proteolytic enzyme from contact leading to proteolytic degradation of the protein. Polyethylene glycol (PEG) is one such chemical moiety that has been used in the preparation of therapeutic protein products.

Thus, a further objective of the present invention is to provide FVII/FVIIa variants which, in addition to the above-mentioned improved properties, possess an increased functional *in vivo* half-life and/or an increased serum half-life.

The improved FVII/FVIIa variants disclosed herein address these objectives.

BRIEF DISCLOSURE OF THE INVENTION

Disclosed are improved recombinant FVII or FVIIa variants comprising at least one amino acid modification in a position selected from the group consisting of 196, 237 and 341. These amino acid modifications result in an altered binding of FVIIa to TFPI. As indicated above, the resulting molecules have one or more improved properties as compared to commercially available rhFVIIa, such as NovoSeven®.

In interesting embodiments, the FVII or FVIIa variant has been further modified so that the resulting variant has an enhanced phospholipid membrane binding affinity, increased functional *in vivo* half-life, increased plasma half-life and/or an increased Area Under the Curve when administered intravenously (AUC_{IV}). Medical treatment with such a variant is contemplated to offer one or more advantages over the currently available rhFVIIa compound, such as lower dosage, faster action in uncontrolled bleedings and, optionally, longer duration between injections.

Accordingly, in a first aspect there is provided a variant of FVII or FVIIa, wherein said variant differs in 1-15 amino acid residues from

hFVII or hFVIIa with the sequence shown in SEQ ID NO:2 and comprises the substitution D196K.

In another aspect, there is provided a nucleotide sequence encoding the variant as defined above.

In a further aspect, there is provided an expression vector comprising the nucleotide sequence as defined above.

In a still further aspect, there is provided a host cell comprising the nucleotide sequence as defined above or the expression vector as defined above.

In an even further aspect, there is provided a composition comprising the variant as defined above and at least one pharmaceutically acceptable carrier or excipient.

In still another aspect, there is provided a variant as defined above for use as a medicament.

In a final aspect, there is provided the use of a variant as defined above for the manufacture of a medicament for the treatment of a disease or a disorder wherein clot formation is desirable.

Further aspects of the present invention will be apparent from the below description as well as from the appended claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows the clotting time vs. concentration for [G237GAA]rhFVIIa when assayed in the "Whole Blood Assay". For comparison, the result for rhFVIIa is included.

- rhFVIIa;
- [G237GAA]rhFVIIa.

DETAILED DISCLOSURE OF THE INVENTION

Definitions

In the context of the present application and invention the following definitions apply:

The term "conjugate" (or interchangeably "conjugated polypeptide variant") is intended to indicate a heterogeneous (in the sense of composite or chimeric) molecule formed by the covalent attachment of one or more polypeptide(s) to one or more non-polypeptide moieties such as polymer molecules, lipophilic compounds, sugar moieties or organic derivatizing agents. Preferably, the conjugate is soluble at relevant concentrations and

conditions, i.e. soluble in physiological fluids such as blood. Examples of conjugated polypeptide variants of the invention include glycosylated and/or PEGylated polypeptides.

The term "covalent attachment" or "covalently attached" means that the polypeptide variant and the non-polypeptide moiety are either directly covalently joined to one another, or
5 else are indirectly covalently joined to one another through an intervening moiety or moieties, such as a bridge, spacer, or linkage moiety or moieties.

When used herein, the term "non-polypeptide moiety" means a molecule that is capable of conjugating to an attachment group of the polypeptide variant of the invention. Preferred examples of such molecules include polymer molecules, sugar moieties, lipophilic
10 compounds, or organic derivatizing agents, in particular sugar moieties. When used in the context of a polypeptide variant of the invention it will be understood that the non-polypeptide moiety is linked to the polypeptide part of the polypeptide variant through an attachment group of the polypeptide variant. As explained above, the non-polypeptide moiety may be directly covalently joined to the attachment group or it may be indirectly covalently
15 joined to the attachment group through an intervening moiety or moieties, such as a bridge, spacer, or linkage moiety or moieties.

The "polymer molecule" is a molecule formed by covalent linkage of two or more monomers, wherein none of the monomers is an amino acid residue, except where the polymer is human albumin or another abundant plasma protein. The term "polymer" may be
20 used interchangeably with the term "polymer molecule". The term is also intended to cover carbohydrate molecules attached by *in vitro* glycosylation, i.e. a synthetic glycosylation performed *in vitro* normally involving covalently linking a carbohydrate molecule to an attachment group of the polypeptide variant, optionally using a cross-linking agent. *In vitro* glycosylation is discussed in detail further below.

The term "sugar moiety" is intended to indicate a carbohydrate-containing molecule comprising one or more monosaccharide residues, capable of being attached to the polypeptide variant (to produce a polypeptide variant conjugate in the form of a glycosylated polypeptide variant) by way of *in vivo* glycosylation. The term "*in vivo* glycosylation" is
25 intended to mean any attachment of a sugar moiety occurring *in vivo*, i.e. during posttranslational processing in a glycosylating cell used for expression of the polypeptide variant, e.g. by way of N-linked or O-linked glycosylation. The exact oligosaccharide structure depends, to a large extent, on the glycosylating organism in question.

An "N-glycosylation site" has the sequence N-X-S/T/C, wherein X is any amino acid residue except proline, N is asparagine and S/T/C is either serine, threonine or cysteine,

preferably serine or threonine, and most preferably threonine. Preferably, the amino acid residue in position +3 relative to the asparagine residue is not a proline residue.

An "O-glycosylation site" is the OH-group of a serine or threonine residue.

The term "attachment group" is intended to indicate a functional group of the
 5 polypeptide variant, in particular of an amino acid residue thereof or a carbohydrate moiety, capable of attaching a non-polypeptide moiety such as a polymer molecule, a lipophilic molecule, a sugar moiety or an organic derivatizing agent. Useful attachment groups and their matching non-polypeptide moieties are apparent from the table below.

Attachment group	Amino acid	Examples of non-polypeptide moiety	Conjugation method/- Activated PEG	Reference
-NH ₂	N-terminal, Lys	Polymer, e.g. PEG, with amide or imine group	mPEG-SPA Tresylated mPEG	Nektar Therapeutics Delgado et al, <i>Critical reviews in Therapeutic Drug Carrier Systems</i> 9(3,4):249-304 (1992)
-COOH	C-terminal, Asp, Glu	Polymer, e.g. PEG, with ester or amide group Carbohydrate moiety	mPEG-Hz <i>In vitro</i> coupling	Nektar Therapeutics
-SH	Cys	Polymer, e.g. PEG, with disulfide, maleimide or vinyl sulfone group Carbohydrate moiety	PEG-vinylsul- phone PEG-maleimide <i>In vitro</i> coupling	Nektar Therapeutics Delgado et al, <i>Critical reviews in Therapeutic Drug Carrier Systems</i> 9(3,4):249-304 (1992)
-OH	Ser, Thr, Lys, OH-	Sugar moiety PEG with ester, ether, carbamate, carbonate	<i>In vivo</i> O-linked glycosylation	
-CONH ₂	Asn as part of an N- glycosyla- tion site	Sugar moiety Polymer, e.g. PEG	<i>In vivo</i> N- glycosylation	
Aromatic residue	Phe, Tyr, Trp	Carbohydrate moiety	<i>In vitro</i> coupling	

-CONH ₂	Gln	Carbohydrate moiety	<i>In vitro</i> coupling	Yan and Wold, <i>Biochemistry</i> , 1984, Jul 31; 23(16): 3759-65
Aldehyde Ketone	Oxidized oligo-saccharide	Polymer, e.g. PEG, PEG-hydrazide	PEGylation	Andresz et al., 1978, <i>Macromol. Chem.</i> 179:301, WO 92/16555, WO 00/23114
Guanidino	Arg	Carbohydrate moiety	<i>In vitro</i> coupling	Lundblad and Noyes, <i>Chemical Reagents for Protein Modification</i> , CRC Press Inc., Florida, USA
Imidazole ring	His	Carbohydrate moiety	<i>In vitro</i> coupling	As for guanidine

For *in vivo* N-glycosylation, the term "attachment group" is used in an unconventional way to indicate the amino acid residues constituting a N-glycosylation site (with the sequence N-X-S/T/C, wherein X is any amino acid residue except proline, N is asparagine and S/T/C is either serine, threonine or cysteine, preferably serine or threonine, and most preferably threonine). Although the asparagine residue of the N-glycosylation site is the one to which the sugar moiety is attached during glycosylation, such attachment cannot be achieved unless the other amino acid residues of the N-glycosylation site are present. Accordingly, when the non-polypeptide moiety is a sugar moiety and the conjugation is to be achieved by *in vivo* N-glycosylation, the term "amino acid residue comprising an attachment group for the non-polypeptide moiety" as used in connection with alterations of the amino acid sequence of the polypeptide variant is to be understood as meaning that one or more amino acid residues constituting an *in vivo* N-glycosylation site are to be altered in such a manner that either a functional *in vivo* N-glycosylation site is introduced into the amino acid sequence or removed from said sequence.

In the present application, amino acid names and atom names (e.g. CA, CB, CD, CG, SG, NZ, N, O, C, etc) are used as defined by the Protein DataBank (PDB) (www.pdb.org) based on the IUPAC nomenclature (IUPAC Nomenclature and Symbolism for Amino Acids and Peptides (residue names, atom names, etc.), *Eur. J. Biochem.*, 138, 9-37 (1984) together with their corrections in *Eur. J. Biochem.*, 152, 1 (1985)).

The term "amino acid residue" is intended to include any natural or synthetic amino acid residue, and is primarily intended to indicate an amino acid residue contained in the

group consisting of the 20 naturally occurring amino acids, i.e. selected from the group consisting of alanine (Ala or A), cysteine (Cys or C), aspartic acid (Asp or D), glutamic acid (Glu or E), phenylalanine (Phe or F), glycine (Gly or G), histidine (His or H), isoleucine (Ile or I), lysine (Lys or K), leucine (Leu or L), methionine (Met or M), asparagine (Asn or N),
5 proline (Pro or P), glutamine (Gln or Q), arginine (Arg or R), serine (Ser or S), threonine (Thr or T), valine (Val or V), tryptophan (Trp or W), and tyrosine (Tyr or Y) residues.

The terminology used for identifying amino acid positions is illustrated as follows: G124 indicates that position 124 is occupied by a glycine residue in the amino acid sequence shown in SEQ ID NO:2. G124R indicates that the glycine residue of position 124 has been
10 substituted with an arginine residue. Alternative substitutions are indicated with a "/", e.g. N145S/T means an amino acid sequence in which asparagine in position 145 is substituted with either serine or threonine. Multiple substitutions are indicated with a "+", e.g. K143N+N145S/T means an amino acid sequence which comprises a substitution of the lysine residue in position 143 with an asparagine residue and a substitution of the asparagine residue
15 in position 145 with a serine or a threonine residue. Insertion of an additional amino acid residue, such as insertion of an alanine residue after G124 is indicated by G124GA. Insertion of two additional alanine residues after G124 is indicated by G124GAA, etc. When used herein, the term "inserted in position X" or "inserted at position X" means that the amino acid residue(s) is (are) inserted between amino acid residue X and X+1. A deletion of an
20 amino acid residue is indicated by an asterix. For example, deletion of the glycine residue in position 124 is indicated by G124*. Unless otherwise indicated, the numbering of amino acid residues made herein is made relative to the amino acid sequence of hFVII/hFVIIa (SEQ ID NO:2).

The term "differs from" as used in connection with specific mutations is intended to
25 allow for additional differences being present apart from the specified amino acid difference. For instance, in addition to the specified modifications in positions 196, 237 and 341, the FVII or FVIIa polypeptide variant may comprise other substitutions. Examples of such additional modifications or differences may include truncation of the N- and/or C-terminus by one or more amino acid residues (e.g. by 1-10 amino acid residues), or addition of one or
30 more extra residues at the N- and/or C-terminus, e.g. addition of a methionine residue at the N-terminus or addition of a cysteine residue near or at the C-terminus, as well as "conservative amino acid substitutions", i.e. substitutions performed within groups of amino acids with similar characteristics, e.g. small amino acids, acidic amino acids, polar amino acids, basic amino acids, hydrophobic amino acids and aromatic amino acids.

Examples of such conservative substitutions are shown in the below table.

1	Alanine (A)	Glycine (G)	Serine (S)	Threonine (T)
2	Aspartic acid (D)	Glutamic acid (E)		
3	Asparagine (N)	Glutamine (Q)		
4	Arginine (R)	Histidine (H)	Lysine (K)	
5	Isoleucine (I)	Leucine (L)	Methionine (M)	Valine (V)
6	Phenylalanine (F)	Tyrosine (Y)	Tryptophan (W)	

Still other examples of additional modifications include modifications giving rise to an increased functional *in vivo* half-life, an increased serum half-life or an increased AUC_{iv}. Specific examples of such modifications are given further below. Moreover, the polypeptide variant of the invention may contain additional modifications giving rise to an enhanced phospholipid membrane binding affinity. Specific examples of such modifications are also given further below.

The term “variant” or “polypeptide variant” (of hFVII or hFVIIa) is intended to cover a polypeptide which differs in one or more amino acid residues from SEQ ID NO:2, normally in 1-15 amino acid residues (for example in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues), e.g. in 1-10, 1-8, 1-6, 1-5, 1-4 or 1-3 amino acid residues, e.g. one or two amino acid residues. In the present context, the term “modification” encompasses insertions, deletions, substitutions and combinations thereof. It will be understood that a polypeptide variant according to the present invention will be modified in at least one of the following positions: 196, 237 and/or 314.

The term “nucleotide sequence” is intended to indicate a consecutive stretch of two or more nucleotide molecules. The nucleotide sequence may be of genomic, cDNA, RNA, semisynthetic, synthetic origin, or any combinations thereof.

“Cell”, “host cell”, “cell line” and “cell culture” are used interchangeably herein and all such terms should be understood to include progeny resulting from growth or culturing of a cell.

“Transformation” and “transfection” are used interchangeably to refer to the process of introducing DNA into a cell.

“Operably linked” refers to the covalent joining of two or more nucleotide sequences, by means of enzymatic ligation or otherwise, in a configuration relative to one another such that the normal function of the sequences can be performed. Generally,

“operably linked” means that the nucleotide sequences being linked are contiguous and, in the case of a secretory leader, contiguous and in reading phase.

The terms “mutation” and “substitution” are used interchangeably herein.

In the context of the present invention the terms “modification” or “amino acid
5 modification” are intended to cover replacement of an amino acid side chain, substitution of an amino acid residue, deletion of an amino acid residue and insertion of an amino acid residue.

The term “introduce” refers to introduction of an amino acid residue, in particular by substitution of an existing amino acid residue, or alternatively by insertion of an additional
10 amino acid residue.

The term “remove” refers to removal of an amino acid residue, in particular by substitution of the amino acid residue to be removed by another amino acid residue, or alternatively by deletion (without substitution) of the amino acid residue to be removed.

The term “FVII” or “FVII polypeptide” refers to a FVII molecule provided in single
15 chain form.

The term “FVIIa” or “FVIIa polypeptide” refers to a FVIIa molecule provided in its activated two-chain form. When the amino acid sequence of SEQ ID NO:2 is used to describe the amino acid sequence of FVIIa it will be understood that the peptide bond between R152 and I153 of the single-chain form has been cleaved, and that one of the chains
20 comprises amino acid residues 1-152, the other chain amino acid residues 153-406.

The terms “rFVII” and “rFVIIa” refer to FVII and FVIIa polypeptides produced by recombinant techniques.

The terms “hFVII” and “hFVIIa” refer to human wild-type FVII and FVIIa, respectively, having the amino acid sequence shown in SEQ ID NO:2

25 The terms “rhFVII” and “rhFVIIa” refer to human wild-type FVII and FVIIa, having the amino acid sequence shown in SEQ ID NO:2, produced by recombinant means. An example of rhFVIIa is NovoSeven®.

The term “TF” means Tissue Factor.

The term “TFPI” means Tissue Factor Pathway Inhibitor.

30 The term “FX” means Factor X.

The term “Gla domain” is used about the first about 45 amino acid residues counted from the N-terminus.

The term “protease domain” is used about residues 153-406 counted from the N-terminus.

The term "catalytic site" is used to mean the catalytic triad consisting of S344, D242 and H193 of the polypeptide variant.

The term "amidolytic activity" is intended to mean the activity measured in the "Amidolytic Assay" described herein. In order to exhibit "amidolytic activity" a variant of the invention, in its activated form, should have at least 10% of the amidolytic activity of rhFVIIa when assayed in the "Amidolytic Assay" described herein. In a preferred embodiment of the invention the variant, in its activated form, has at least 20% of the amidolytic activity of rhFVIIa, such as at least 30%, e.g. at least 40%, more preferably at least 50%, such as at least 60%, e.g. at least 70%, even more preferably at least 80%, such as at least 90% of the amidolytic activity of rhFVIIa when assayed in the "Amidolytic Assay" described herein. In an interesting embodiment the variant, in its activated form, has substantially the same amidolytic activity as rhFVIIa, such as an amidolytic activity of 75-125% of the amidolytic activity of rhFVIIa.

The term "clotting activity" is used to mean the activity measured in the "Whole Blood Assay" described herein. It will be understood that the activity measured in the "Whole Blood Assay" is the time needed to obtain clot formation. Thus, a lower clotting time corresponds to a higher clotting activity.

The term "increased clotting activity" is used to indicate that the clotting time of the polypeptide variant is statistically significantly decreased relative to that generated by rhFVIIa as determined under comparable conditions and when measured in the "Whole Blood Assay" described herein.

The term "immunogenicity" as used in connection with a given substance is intended to indicate the ability of the substance to induce a response from the immune system. The immune response may be a cell or antibody mediated response (see, e.g., Roitt: Essential Immunology (8th Edition, Blackwell) for further definition of immunogenicity). Normally, reduced antibody reactivity will be an indication of reduced immunogenicity. The reduced immunogenicity may be determined by use of any suitable method known in the art, e.g. *in vivo* or *in vitro*.

The term "functional *in vivo* half-life" is used in its normal meaning, i.e. the time at which 50% of the biological activity of the polypeptide variant is still present in the body/target organ, or the time at which the amidolytic or clotting activity of the polypeptide variant is 50% of the initial value.

As an alternative to determining functional *in vivo* half-life, "serum half-life" may be determined, i.e. the time at which 50% of the polypeptide variant circulates in the plasma

or bloodstream prior to being cleared. Determination of serum half-life is often more simple than determining the functional *in vivo* half-life and the magnitude of serum half-life is usually a good indication of the magnitude of functional *in vivo* half-life. Alternatively terms to serum half-life include "plasma half-life", "circulating half-life", "serum clearance",
5 "plasma clearance" and "clearance half-life". The polypeptide variant is cleared by the action of one or more of the reticuloendothelial systems (RES), kidney, spleen or liver, by tissue factor, SEC receptor or other receptor mediated elimination, or by specific or unspecific proteolysis. Normally, clearance depends on size (relative to the cutoff for glomerular filtration), charge, attached carbohydrate chains, and the presence of cellular receptors for the
10 protein. The functionality to be retained is normally selected from procoagulant, proteolytic or receptor binding activity. The functional *in vivo* half-life and the serum half-life may be determined by any suitable method known in the art.

The term "increased" as used about the functional *in vivo* half-life or serum half-life is used to indicate that the relevant half-life of the polypeptide variant is statistically
15 significantly increased relative to that of a reference molecule, such as a rhFVIIa as determined under comparable conditions (typically determined in an experimental animal, such as rats, rabbits, pigs or monkeys).

The term "AUC_{iv}" or "Area Under the Curve when administered intravenously" is used in its normal meaning, i.e. as the area under the activity in serum-time curve, where the
20 polypeptide variant has been administered intravenously, in particular when administered intravenously in rats. Once the experimental activity-time points have been determined, the AUC_{iv} may conveniently be calculated by a computer program, such as GraphPad Prism 3.01.

The term "reduced sensitivity to proteolytic degradation" is primarily intended to
25 mean that the polypeptide variant has reduced sensitivity to proteolytic degradation in comparison to rhFVIIa as determined under comparable conditions. Preferably, the proteolytic degradation is reduced by at least 10% (e.g. by 10-25% or by 10-50%), such as at least 25% (e.g. by 25-50%, by 25-75% or by 25-100%), more preferably by at least 35%, such as at least 50%, (e.g. by 50-75% or by 50-100%) even more preferably by at least 60%,
30 such as by at least 75% (e.g. by 75-100%) or even at least 90%. Most preferably, the proteolytic degradation is reduced by at least 99%.

The term "renal clearance" is used in its normal meaning to indicate any clearance taking place by the kidneys, e.g. by glomerular filtration, tubular excretion or degradation in the tubular cells. Renal clearance depends on physical characteristics of the polypeptide,

including size (diameter), hydrodynamic volume, symmetry, shape/rigidity, and charge. A molecular weight of about 67 kDa is often considered to be a cut-off-value for renal clearance. Renal clearance may be established by any suitable assay, e.g. an established *in vivo* assay. Typically, renal clearance is determined by administering a labelled (e.g.

5 radiolabelled or fluorescence labelled) polypeptide to a patient and measuring the label activity in urine collected from the patient. Reduced renal clearance is determined relative to a corresponding reference polypeptide, e.g. rh FVIIa, under comparable conditions. Preferably, the renal clearance rate of the polypeptide variant is reduced by at least 50%, e.g. at least 75% or at least 90% compared to rhFVIIa.

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Polypeptide variants of the invention

In its broadest aspect the present invention relates to a variant of FVII or FVIIa, wherein said variant comprises at least one amino acid modification in a position selected from the group consisting of 196, 237 and 341 as compared to hFVII or hFVIIa, preferably as
15 compared to hFVIIa. Although the variant will typically contain a modification in one of these positions, it may also contain a modification in two of these positions, i.e. modifications in 196+237, 196+341 or 237+341, or in all three positions.

In the following sections preferred modifications in the above-mentioned positions are given.

20

Position 196

In one embodiment of the invention, the present invention relates to a variant of FVII or FVIIa, wherein said variant comprises at least one modification in position 196 as compared to hFVII or hFVIIa (SEQ ID NO:2).

25 In a preferred embodiment of the invention the modification in position 196 is a substitution, in particular D196N or D196K.

The variant will generally comprise a total of 1-15 amino acid modifications (e.g. substitutions), such as 1-10 amino acid modifications (e.g. substitutions), e.g. 1-5 amino acid modifications (e.g. substitutions) or 1-3 amino acid modifications (e.g. substitutions).

30 For example, the variant may contain at least one further amino acid modification made in the Gla domain as explained in the section entitled "Modifications in the Gla domain" below, and/or at least one further amino acid modification which leads to introduction of an *in vivo* N-glycosylation site as explained in the section entitled "Introduction of additional sugar moieties" below, and/or at least one further amino acid

modification capable of increasing the intrinsic activity and/or at least one further amino acid modification which increases the TF-binding affinity. Examples of the latter modifications are described in the section entitled "Other modifications" below.

5 Position 237

In a further embodiment of the invention, the present invention relates to a variant of FVII or FVIIa, wherein said variant comprises at least one modification in position 237 as compared to hFVII or hFVIIa (SEQ ID NO:2).

10 In a preferred embodiment of the invention the modification in position 237 is a substitution, in particular G237L.

The variant will generally comprise a total of 1-15 amino acid modifications (e.g. substitutions), such as 1-10 amino acid modifications (e.g. substitutions), e.g. 1-5 amino acid modifications (e.g. substitutions) or 1-3 amino acid modifications (e.g. substitutions).

For example, the variant may contain at least one further amino acid modification
15 made in the Gla domain as explained in the section entitled "Modifications in the Gla domain" below, and/or at least one further amino acid modification which leads to introduction of an in vivo N-glycosylation site as explained in the section entitled "Introduction of additional sugar moieties" below, and/or at least one further amino acid modification capable of increasing the intrinsic activity and/or at least one further amino acid
20 modification which increases the TF-binding affinity. Examples of the latter modifications are described in the section entitled "Other modifications" below.

In still another embodiment of the invention the modification in position 237 is an insertion. In an interesting embodiment the insertion is selected from the group consisting of G237GXX, G237GXXX and G237GXXXX, wherein X is any amino acid residue.

25 Preferably, X is selected from the group consisting of Ala, Val, Leu, Ile, Gly, Ser and Thr, in particular Ala. Specific examples of preferred insertions include G237GAA, G237GAAA and G237GAAAA. Most preferably, the insertions are G237GAA.

Position 341

30 In a still further embodiment of the invention, the present invention relates to a variant of FVII or FVIIa, wherein said variant comprises at least one modification in position 341 as compared to hFVII or hFVIIa (SEQ ID NO:2).

In a preferred embodiment of the invention the modification in position 341 is a substitution, such as K341N or K341Q, in particular K341Q.

The variant will generally comprise a total of 1-15 amino acid modifications (e.g. substitutions), such as 1-10 amino acid modifications (e.g. substitutions), e.g. 1-5 amino acid modifications (e.g. substitutions) or 1-3 amino acid modifications (e.g. substitutions).

For example, the variant may contain at least one further amino acid modification
5 made in the Gla domain as explained in the section entitled "Modifications in the Gla domain" below, and/or at least one further amino acid modification which leads to introduction of an in vivo N-glycosylation site as explained in the section entitled "Introduction of additional sugar moieties" below, and/or at least one further amino acid
10 modification capable of increasing the intrinsic activity and/or at least one further amino acid modification which increases the TF-binding affinity. Examples of the latter modifications are described in the section entitled "Other modifications" below.

Properties of the variants of the invention

The variants disclosed may have an altered affinity for TFPI, which may be assessed
15 using the BIAcore® Assays described herein. Using the BIAcore® assays it is possible to estimate various kinetic binding constants, such as the equilibrium dissociation constant, K_D , where $K_D = k_d/k_a$, where k_a is the association rate constant and k_d is the dissociation rate constant. It will be understood that a higher value of K_D corresponds to a decreased affinity for TFPI.

20 The variants of the invention possess an increased clotting activity (or a reduced clotting time) as compared to hFVIIa or rhFVIIa. In a preferred embodiment of the invention the ratio between the time to reach clot formation for the variant (t_{variant}) and the time to reach clot formation for hFVIIa or rhFVIIa (t_{wt}) is at the most 0.9 when assayed in the "Whole Blood Assay" described herein. More preferably the ratio ($t_{\text{variant}}/t_{\text{wt}}$) is at the most 0.75, such
25 as 0.7, even more preferably the ratio ($t_{\text{variant}}/t_{\text{wt}}$) is at the most 0.6, most preferably the ratio ($t_{\text{variant}}/t_{\text{wt}}$) is at the most 0.5 when assayed in the "Whole Blood Assay" described herein.

Further modifications

As indicated above the FVII or FVIIa variant of the invention may comprise further
30 modifications aimed at conferring additional advantageous properties to the FVII or FVIIa molecule, e.g. at least one further amino acid substitution.

In order to avoid too much disruption of the structure and function of the FVII or FVIIa polypeptide, the FVII or FVIIa polypeptide variant of the invention will typically have an amino acid sequence having more than 95% identity with SEQ ID NO:2, preferably more

than 96% identity with SEQ ID NO:2, such as more than 97% identity with SEQ ID NO:2, more preferably at least 98% identity with SEQ ID NO:2, such as more than 99% identity with SEQ ID NO:2. Amino acid sequence homology/identity is conveniently determined from aligned sequences, using e.g. the ClustalW program, version 1.8, June 1999, using
5 default parameters (Thompson et al., 1994, ClustalW: Improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice, *Nucleic Acids Res.*, 22: 4673-4680) or from the PFAM families database version 4.0 (<http://pfam.wustl.edu/>) (*Nucleic Acids Res.* 1999 Jan 1; 27(1):260-2) by use of GENEDOC version 2.5 (Nicholas et al., 1997 GeneDoc: Analysis and
10 Visualization of Genetic Variation, EMBNEW.NEWS 4:14; Nicholas, K.B. and Nicholas H.B. Jr. 1997 GeneDoc: Analysis and Visualization of Genetic Variation).

Modifications in the Gla domain

In an interesting embodiment of the invention, at least one further amino acid
15 modification is made in the Gla domain, i.e. within the first about 45 amino acid residues counted from the N-terminus of the FVII or FVIIa molecule. Preferably, no modifications are made in residues 6, 7, 14, 16, 19, 20, 25, 26, 29 and 35.

Without being limited by any particular theory, it is presently believed that an increased clotting activity may be achieved by an enhanced binding affinity of the FVIIa
20 molecule to the phospholipid membranes present on the surface of activated platelets. This enhanced affinity is believed to result in a higher local concentration of the activated FVIIa polypeptide in close proximity to the other coagulation factors, particularly FX. Thus, the rate of activation of FX to FXa will be higher, simply due to a higher molar ratio of the activated FVII polypeptide to FX. The increased activation rate of FX then results in a higher amount
25 of active thrombin, and thus a higher rate of cross-linking of fibrin.

Thus, in a preferred embodiment according to this aspect of the invention, the polypeptide variant has, in its activated form, an enhanced phospholipid membrane binding affinity relative to the rhFVIIa polypeptide. Phospholipid membrane binding affinity may be measured by methods known in the art, such as by the BIAcore® assays described in K.
30 Nagata and H. Handa (Ads.), Real-Time Analysis of Biomolecular Interactions, Springer-Verlag, Tokyo, 2000, Chapter 6 entitled "Lipid-Protein Interactions".

A number of modifications in the FVII Gla domain leading to an increased membrane binding affinity have been described in the art (see, for example, WO 99/20767 and WO 00/66753). Particular interesting positions in the Gla domain to be modified are

positions P10, K32, D33, A34 as well as insertion of an amino acid residue between A3 and F4. Thus, in a preferred embodiment of the invention, the variant comprises, in addition to one or more of the modifications mentioned above a substitution in a position selected from the group consisting of P10, K32, D33 and A34 and combinations thereof as well as an
5 insertion between A3 and F4. Particularly preferred positions are P10 and K32.

Preferably, the substitution to be made in position 32 is K32E, the substitution to be made in position 10 is P10Q, the substitution to be made in position 33 is D33F, the substitution to be made in position 34 is A34E and the insertion between A3 and F4 is preferably A3AY. In an interesting embodiment of the invention the variant comprises at
10 least one of the following further modifications: A3AY, P10Q, K32E, D33F, A34E or combinations thereof. Most preferably, the variant comprises one of the following further modifications: K32E, P10Q+K32E, A3AY+P10Q+K32E+D33F+A34E.

Introduction of non-polypeptide moieties

15 In another embodiment, the FVII or FVIIa variant has been further modified so that the resulting polypeptide variant has increased functional *in vivo* half-life and/or increased plasma half-life and/or increased increased Area Under the Curve when administered intravenously (AUC_{iv}), in particular when administered intravenously in rats, and/or increased bioavailability and/or reduced sensitivity to proteolytic degradation. Medical
20 treatment with a polypeptide variant according to this aspect of the invention may offer a number of advantages over the currently available rFVIIa compound, such as lower dosage and, optionally, longer duration between injections. Numerous examples of relevant amino acid substitutions are given in WO 01/58935.

The variants disclosed in WO 01/58935 are the result of a generally new strategy for
25 developing improved FVII or FVIIa molecules. This strategy, in which non-polypeptide moieties are attached to FVII/FVIIa variants, may also be used for the FVII or FVIIa variants of the present invention. More specifically, by removing and/or introducing an amino acid residue comprising an attachment group for a non-polypeptide moiety in the FVII or FVIIa polypeptide variant of the invention, it is possible to specifically adapt the polypeptide
30 variant so as to make the molecule more susceptible to conjugation to a non-polypeptide moiety of choice, to optimize the conjugation pattern (e.g. to ensure an optimal distribution and number of non-polypeptide moieties on the surface of the FVII or FVIIa polypeptide variant and to ensure that only the attachment groups intended to be conjugated are present in the molecule) and thereby obtain a new conjugate molecule, which has activity and in

addition one or more improved properties as compared to the FVII and FVIIa molecules available today. For instance, when the total number of amino acid residues comprising an attachment group for the non-polypeptide of choice is increased or decreased to an optimized level, the renal clearance of the conjugate is typically significantly reduced due to the altered
5 shape, size and/or charge of the molecule achieved by the conjugation.

Thus, interesting polypeptide variants according to this aspect of the present invention are such polypeptides wherein at least one amino acid residue comprising an attachment group for a non-polypeptide moiety has been introduced or removed in a FVII or FVIIa polypeptide variant as described elsewhere herein.

10 In interesting embodiments of the present invention more than one amino acid residue of the FVII or FVIIa polypeptide variant is altered, e.g. the alteration embraces removal as well as introduction of amino acid residues comprising an attachment group for the non-polypeptide moiety of choice. In addition to the removal and/or introduction of amino acid residues the polypeptide variant may comprise other substitutions or
15 glycosylations that are not related to introduction and/or removal of amino acid residues comprising an attachment group for the non-polypeptide moiety. Also, the polypeptide variant may be attached, e.g., to a serine proteinase inhibitor to inhibit the catalytic site of the polypeptide.

The amino acid residue comprising an attachment group for a non-polypeptide
20 moiety, whether it be removed or introduced, is selected on the basis of the nature of the non-polypeptide moiety of choice and, in most instances, on the basis of the method in which conjugation between the polypeptide variant and the non-polypeptide moiety is to be achieved. For instance, when the non-polypeptide moiety is a polymer molecule such as a polyethylene glycol or polyalkylene oxide derived molecule, amino acid residues comprising
25 an attachment group may be selected from the group consisting of lysine, cysteine, aspartic acid, glutamic acid, histidine, and tyrosine, preferably lysine, cysteine, aspartic acid and glutamic acid, more preferably lysine and cysteine, in particular cysteine.

Whenever an attachment group for a non-polypeptide moiety is to be introduced into or removed from the FVII or FVIIa polypeptide variant, the position of the amino acid
30 residue to be modified is preferably located at the surface of the FVII or FVIIa polypeptide, and more preferably occupied by an amino acid residue which has more than 25% of its side chain exposed to the surface (as defined in WO 01/58935 and in Example 1 herein), preferably more than 50% of its side chain exposed to the surface (as defined in WO 01/58935 and in Example 1 herein).

Furthermore, the position is preferably selected from a part of the FVII molecule that is located outside the tissue factor binding site, the Gla domain, the active site region and/or the ridge of the active site binding cleft. These sites/regions are identified in Example 1 herein.

5 The polypeptide variant of the invention may contain 1-10 non-polypeptide moieties, typically 1-8 or 2-8 non-polypeptide moieties, preferably 1-5 or 2-5 non-polypeptide moieties, such as 1-4 or 1-3 non-polypeptide moieties, e.g. 1, 2 or 3 non-polypeptide moieties, in particular PEG, such as mPEG or sugar moieties.

Further details regarding introduction of non-polypeptide moieties may be found in
10 WO 01/58935, incorporated by reference.

Introduction of additional sugar moieties

In an interesting embodiment of the invention the non-polypeptide moiety is a sugar moiety, i.e., the polypeptide variant of the invention is one which, in addition to one or more
15 of the modifications described elsewhere herein comprises at least one sugar moiety covalently attached to an introduced glycosylation site. Preferably said glycosylation site is an *in vivo* glycosylation site, in particular an *in vivo* N-glycosylation site, which has been introduced by substitution. Preferably, said glycosylation site is introduced in a position located outside the Gla domain, the tissue factor binding site, the active site region and the
20 ridge of the active site binding cleft.

When used in the present context, the term "naturally occurring glycosylation site" covers the glycosylation sites at positions N145, N322, S52 and S60. In a similar way, the term "naturally occurring *in vivo* O-glycosylation site" includes the positions S52 and S60, whereas the term "naturally occurring *in vivo* N-glycosylation site" includes positions N145
25 and N322.

Thus, in a very interesting embodiment of the invention, the non-polypeptide moiety is a sugar moiety and the introduced attachment group is a glycosylation site, preferably an *in vivo* glycosylation site, such as an *in vivo* O-glycosylation site or an *in vivo* N-glycosylation site, in particular an *in vivo* N-glycosylation site. Typically, 1-10 glycosylation sites, in
30 particular *in vivo* N-glycosylation sites, have been introduced, preferably 1-8, 1-6, 1-4 or 1-3 glycosylation sites. In particular, 1, 2 or 3 *in vivo* N-glycosylation sites have been introduced, preferably by substitution.

It will be understood that in order to prepare a polypeptide variant wherein the FVII or FVII polypeptide variant comprises one or more glycosylation sites, the polypeptide

variant must be expressed in a host cell capable of attaching sugar (oligosaccharide) moieties at the glycosylation site(s). Examples of glycosylating host cells are given in the section further below entitled "Coupling to a sugar moiety".

Examples of positions wherein the glycosylation sites may be introduced include, but are not limited to, positions comprising an amino acid residue having an amino acid residue having at least 25% of its side chain exposed to the surface (as defined in Example 1 herein), such as in a position comprising an amino acid residue having at least 50% of its side chain exposed to the surface (as defined in Example 1 herein). It should be understood that when the term "at least 25% (or at least 50%) of its side chain exposed to the surface" is used in connection with introduction of an *in vivo* N-glycosylation site this term refers to the surface accessibility of the amino acid side chain in the position where the sugar moiety is actually attached. In many cases it will be necessary to introduce a serine or a threonine residue in position +2 relative to the asparagine residue to which the sugar moiety is actually attached (unless, of course, this position is already occupied by a serine or a threonine residue) and these positions, where the serine or threonine residues are introduced, are allowed to be buried, i.e. to have less than 25% (or 50%) of their side chains exposed to the surface.

Specific examples of such substitutions creating an *in vivo* N-glycosylation site include a substitution selected from the group consisting of A51N, G58N, T106N, K109N, G124N, K143N+N145T, A175T, I205S, I205T, V253N, T267N, T267N+S269T, S314N+K316S, S314N+K316T, R315N+V317S, R315N+V317T, K316N+G318S, K316N+G318T, G318N, D334N and combinations thereof. In a preferred embodiment of the invention the *in vivo* N-glycosylation site is created by performing a substitution selected from the group consisting of A51N, G58N, T106N, K109N, G124N, K143N+N145T, A175T, I205T, V253N, T267N+S269T, S314N+K316T, R315N+V317T, K316N+G318T, G318N, D334N and combinations thereof, more preferably by a substitution selected from the group consisting of T106N, A175T, I205T, V253N, T267N+S269T and combinations thereof, in particular I205T.

In one embodiment of the invention, one *in vivo* N-glycosylation site has been introduced by substitution. In another embodiment of the invention at least two *in vivo* N-glycosylation site sites, such as two *in vivo* N-glycosylation sites, have been introduced by substitution. Specific examples of substitutions creating two *in vivo* N-glycosylation sites include A51N+G58N, A51N+T106N, A51N+K109N, A51N+G124N, A51N+K143N+N145T, A51N+A175T, A51N+I205T, A51N+V253N,

- A51N+T267N+S269T, A51N+S314N+K316T, A51N+R315N+V317T,
 A51N+K316N+G318T, A51N+G318N, A51N+D334N, G58N+T106N, G58N+K109N,
 G58N+G124N, G58N+K143N+N145T, G58N+A175T, G58N+I205T, G58N+V253N,
 G58N+T267N+S269T, G58N+S314N+K316T, G58N+R315N+V317T,
- 5 G58N+K316N+G318T, G58N+G318N, G58N+D334N, T106N+K109N, T106N+G124N,
 T106N+K143N+N145T, T106N+A175T, T106N+I205T, T106N+V253N,
 T106N+T267N+S269T, T106N+S314N+K316T, T106N+R315N+V317T,
 T106N+K316N+G318T, T106N+G318N, T106N+D334N, K109N+G124N,
 K109N+K143N+N145T, K109N+A175T, K109N+I205T, K109N+V253N,
- 10 K109N+T267N+S269T, K109N+S314N+K316T, K109N+R315N+V317T,
 K109N+K316N+G318T, K109N+G318N, K109N+D334N, G124N+K143N+N145T,
 G124N+A175T, G124N+I205T, G124N+V253N, G124N+T267N+S269T,
 G124N+S314N+K316T, G124N+R315N+V317T, G124N+K316N+G318T, G124N+G318N,
 G124N+D334N, K143N+N145T+A175T, K143N+N145T+I205T, K143N+N145T+V253N,
- 15 K143N+N145T+T267N+S269T, K143N+N145T+S314N+K316T,
 K143N+N145T+R315N+V317T, K143N+N145T+K316N+G318T, K143N+N145T+G318N,
 K143N+N145T+D334N, A175T+I205T, A175T+V253N, A175T+T267N+S269T,
 A175T+S314N+K316T, A175T+R315N+V317T, A175T+K316N+G318T, A175T+G318N,
 A175T+D334N, I205T+V253N, I205T+T267N+S269T, I205T+S314N+K316T,
- 20 I205T+R315N+V317T, I205T+K316N+G318T, I205T+G318N, I205T+D334N,
 V253N+T267N+S269T, V253N+S314N+K316T, V253N+R315N+V317T,
 V253N+K316N+G318T, V253N+G318N, V253N+D334N, T267N+S269T+S314N+K316T,
 T267N+S269T+R315N+V317T, T267N+S269T+K316N+G318T, T267N+S269T+G318N,
 T267N+S269T+D334N, S314N+K316T+R315N+V317T, S314N+K316T+G318N,
- 25 S314N+K316T+D334N, R315N+V317T+K316N+G318T, R315N+V317T+G318N,
 R315N+V317T+D334N or G318N+D334N, preferably T106N+A175T, T106N+I205T,
 T106N+V253N, T106N+T267N+S269T, A175T+I205T, A175T+V253N,
 A175T+T267N+S269T, I205T+V253N, I205T+T267N+S269T or V253N+T267N+S269T,
 more preferably T106N+I205T, T106N+V253N or I205T+T267N+S269T.
- 30 In a still further embodiment of the invention at least three *in vivo* N-glycosylation
 site sites, such as three *in vivo* N-glycosylation sites, have been introduced by substitution.
 Specific examples of substitutions creating three *in vivo* N-glycosylation sites include
 I205T+V253N+T267N+S269T and T106N+I205T+V253N.

In addition to a sugar moiety, the polypeptide variant according to the aspect of the invention described in the present section may contain additional non-polypeptide moieties, in particular a polymer molecule, as described in the present application, conjugated to one or more attachment groups present in the FVII or FVIIa variant.

5 It will be understood that any of the amino acid changes, in particular substitutions, specified in this section can be combined with any of the amino acid changes, in particular substitutions, specified in the other sections herein disclosing specific amino acid changes. For instance, any of the glycosylated polypeptides variants disclosed in the present section having introduced and/or removed at least one glycosylation site may further be conjugated
10 to a polymer molecule, such as PEG, or any other non-polypeptide moiety.

Further information on introduction of glycosylation sites may be found in WO 01/58935 and WO 03/093465, incorporated by reference.

Introduction of non-polypeptide moieties that have cysteine as an attachment group

15 In a further interesting embodiment of the invention the non-polypeptide moiety has cysteine as an attachment group, i.e., the polypeptide variant of the invention is one which, in addition to one or more of the modifications described above comprises at least one non-polypeptide moiety covalently attached to an introduced cysteine. Preferably said cysteine residue is introduced by substitution. Preferably, said cysteine residue is introduced in a
20 position located outside the TF binding site, the Gla domain, the active site region, and the ridge of the active site binding cleft.

FVII/FVIIa contains 22 cysteine residues located outside the Gla domain and disulfide bridges are established between the following cysteine residues: C50 and C61, C55 and C70, C72 and C81, C91 and C102, C98 and C112, C114 and C127, C135 and C262,
25 C159 and C164, C178 and C194, C310 and C329, and between C340 and C368.

Thus, in an interesting embodiment of the invention at least one cysteine residue has been introduced, preferably by substitution, in the FVII or FVIIa polypeptide variant. Typically 1-10 cysteine residues have been introduced, preferably 1-8, 1-6, 1-4 or 1-3 cysteine residues have been introduced. In particular 1, 2 or 3 cysteine residues have been
30 introduced, preferably by substitution.

Examples of positions where the cysteine residues may be introduced include, but are not limited to, positions comprising an amino acid residue having an amino acid residue having at least 25% of its side chain exposed to the surface (as defined in Example 1 herein),

such as in a position comprising an amino acid residue having at least 50% of its side chain exposed to the surface (as defined in Example 1 herein).

In an interesting embodiment of the invention, a cysteine residue is introduced near or at the C-terminus. For example, a cysteine residue may be introduced, either by
5 substitution or insertion, in position 400-406. Specific examples of substitutions include: L400C, L401C, R402C, A403C, P404C, F405C and P406C, in particular P406C. Specific examples of insertions include L400LC, L401LC, R402RC, A403AC, P404PC, F405FC and P406PC, in particular P406PC.

While the non-polypeptide moiety according to this aspect of the invention
10 may be any molecule which when using the given conjugation method has cysteine as an attachment group, it is preferred that the non-polypeptide moiety is a polymer molecule. The polymer molecule may be any of the molecules mentioned in the section entitled "Conjugation to a polymer molecule", but is preferably selected from the group consisting of linear or branched polyethylene glycol or another polyalkylene oxide. In a particular
15 interesting embodiment the polymer molecule is PEG, such as VS-PEG.

The conjugation between the polypeptide variant and the polymer may be achieved in any suitable manner, e.g. as described WO 01/58935.

When the FVII or FVIIa polypeptide variant comprises only one conjugatable cysteine residue, this residue is preferably conjugated to a non-polypeptide moiety with a
20 molecular weight of from about 5 kDa to about 20 kDa, e.g. from about 10 kDa to about 20 kDa, such as a molecular weight of about 5 kDa, about 10 kDa, about 12 kDa, about 15 kDa or about 20 kDa, either directly conjugated or indirectly through a low molecular weight polymer (as disclosed in WO 99/55377). When the FVII or FVIIa polypeptide variant comprises two or more conjugatable cysteine residues, normally each of the non-polypeptide
25 moieties has a molecular weight of from about 5 to about 10 kDa, such as about 5 kDa or about 10 kDa.

It will be understood that any of the amino acid changes, in particular substitutions, specified in this section can be combined with any of the amino acid modifications specified in the other sections herein.

30

Other modifications

In a further embodiment of the present invention, the FVII or FVIIa variant may, in addition to the modifications described in the sections above, also contain mutations which

are already known to increase the intrinsic activity of the polypeptide, e.g. those described in WO 02/22776.

Examples of preferred substitutions include substitutions selected from the group consisting of V158D, E296D, M298Q, L305V and K337A. More preferably, said

5 substitutions are selected from the group consisting of

V158D+E296D+M298Q+L305V+K337A,

V158D+E296D+M298Q+K337A, V158D+E296D+M298Q+L305V,

V158D+E296D+M298Q,

M298Q, L305V+K337A, L305V and K337A.

10 Moreover, the variant may contain modifications which increase the TF binding affinity. Examples of such modifications include substitutions selected from the group consisting of L39E, L39Q, L39H, I42R, S43H, S43Q, K62E, K62R, L65Q, L65S, F71D, F71Y, F71E, F71Q, F71N, E82Q, E82N, E82K, F275H and combinations thereof, in particular L65Q, F71Y, K62E, S43Q and combinations thereof.

15 As already indicated above, the variant may also contain conservative amino acid substitutions.

The non-polypeptide moiety

As indicated further above the non-polypeptide moiety of the polypeptide variant of
20 the invention is preferably selected from the group consisting of a polymer molecule, a lipophilic compound, a sugar moiety (by way of *in vivo* glycosylation) and an organic derivatizing agent. All of these agents may confer desirable properties to the polypeptide variant, in particular increased functional *in vivo* half-life and/or increased plasma half-life.

The polypeptide variant is normally conjugated to only one type of non-polypeptide
25 moiety, but may also be conjugated to two or more different types of non-polypeptide moieties, e.g. to a polymer molecule and a sugar moiety, to a lipophilic group and a sugar moiety, to an organic derivatizing agent and a sugar moiety, to a lipophilic group and a polymer molecule, etc. The conjugation to two or more different non-polypeptide moieties may be done simultaneously or sequentially. Further information on conjugation to non-
30 polypeptide moieties is found in WO 01/58935 and WO 03/093465, incorporated by reference.

Methods of preparing a conjugated polypeptide variant of the invention

In general, a conjugated polypeptide variant according to the invention may be produced by culturing an appropriate host cell under conditions conducive for the expression of the polypeptide, and recovering the polypeptide variant, wherein a) the polypeptide variant
5 comprises at least one N- or O-glycosylation site and the host cell is a eukaryotic host cell capable of *in vivo* glycosylation, and/or b) the polypeptide variant is subjected to conjugation to a non-polypeptide moiety *in vitro*. See e.g. WO 01/58935 and WO 03/093465 for further information on preparation of conjugated variants of FVII.

10 Conjugation to a polymer molecule

The polymer molecule to be coupled to the polypeptide variant may be any suitable polymer molecule, such as a natural or synthetic homo-polymer or hetero-polymer, typically with a molecular weight in the range of about 300-100,000 Da, such as about 500-20,000 Da, more preferably in the range of about 500-15,000 Da, even more preferably in the range of
15 about 2-12 kDa, such as in the range of about 3-10 kDa. When the term "about" is used herein in connection with a certain molecular weight, the word "about" indicates an approximate average molecular weight and reflects the fact that there will normally be a certain molecular weight distribution in a given polymer preparation.

Examples of homo-polymers include a polyol (i.e. poly-OH), a polyamine (i.e. poly-
20 NH₂) and a polycarboxylic acid (i.e. poly-COOH). A hetero-polymer is a polymer comprising different coupling groups, such as a hydroxyl group and an amine group.

Examples of suitable polymer molecules include polymer molecules selected from the group consisting of polyalkylene oxide (PAO), including polyalkylene glycol (PAG), such as polyethylene glycol (PEG) and polypropylene glycol (PPG), branched PEGs, poly-
25 vinyl alcohol (PVA), poly-carboxylate, poly-(vinylpyrrolidone), polyethylene-co-maleic acid anhydride, polystyrene-co-maleic acid anhydride, dextran, including carboxymethyl-dextran, or any other biopolymer suitable for reducing immunogenicity and/or increasing functional *in vivo* half-life and/or serum half-life. Another example of a polymer molecule is human albumin or another abundant plasma protein. Generally, polyalkylene glycol-derived
30 polymers are biocompatible, non-toxic, non-antigenic, non-immunogenic, have various water solubility properties, and are easily excreted from living organisms.

PEG is the preferred polymer molecule, since it has only few reactive groups capable of cross-linking compared to, e.g., polysaccharides such as dextran. In particular, monofunctional PEG, e.g. methoxypolyethylene glycol (mPEG), is of interest since its

coupling chemistry is relatively simple (only one reactive group is available for conjugating with attachment groups on the polypeptide). Consequently, the risk of cross-linking is eliminated, the resulting conjugated polypeptide variants are more homogeneous and the reaction of the polymer molecules with the polypeptide variant is easier to control.

5 To effect covalent attachment of the polymer molecule(s) to the polypeptide variant, the hydroxyl end groups of the polymer molecule must be provided in an activated form, i.e. with reactive functional groups (examples of which include primary amino groups, hydrazide (HZ), thiol, succinate (SUC), succinimidyl succinate (SS), succinimidyl succinamide (SSA), succinimidyl propionate (SPA), succinimidyl carboxymethylate (SCM), benzotriazole
10 carbonate (BTC), N-hydroxysuccinimide (NHS), aldehyde, nitrophenylcarbonate (NPC), and tresylate (TRES)). Suitable activated polymer molecules are commercially available, e.g. from Nektar Therapeutics, Huntsville, AL, USA, or from PolyMASC Pharmaceuticals plc, UK. Specific examples of activated linear or branched polymer molecules for use in the present invention are described in the Nektar Molecule Engineering Catalog 2003 (Nektar
15 Therapeutics), incorporated herein by reference.

In a particular interesting embodiment PEGylation is achieved by conjugating the PEG group(s) to introduced cysteine residues. Specific examples of activated PEG polymers particularly preferred for coupling to cysteine residues, include the following linear PEGs: vinylsulfone-PEG (VS-PEG), preferably vinylsulfone-mPEG (VS-mPEG); maleimide-PEG
20 (MAL-PEG), preferably maleimide-mPEG (MAL-mPEG) and orthopyridyl-disulfide-PEG (OPSS-PEG), preferably orthopyridyl-disulfide-mPEG (OPSS-mPEG). Typically, such PEG or mPEG polymers will have a size of about 5 kDa, about 10 kDa, about 12 kDa or about 20 kDa.

In another embodiment, a suitable PEG molecule may be attached to the N-terminal.

25 Detailed information on methods and polymers that may be used for PEGylation of FVII is found in WO 01/58935, incorporated herein by reference.

Coupling to a sugar moiety

In order to achieve *in vivo* glycosylation of the polypeptide variant of the invention,
30 the nucleotide sequence encoding the polypeptide variant must be inserted in a glycosylating, eukaryotic expression host. The expression host cell may be selected from fungal (filamentous fungal or yeast), insect or animal cells or from transgenic plant cells. In one embodiment the host cell is a mammalian cell, such as a CHO cell, a COS cell, a BHK cell or a HEK cell, e.g. a HEK 293 cell, or an insect cell, such as an SF9 cell, or a yeast cell, such as

S. cerevisiae or *Pichia pastoris*, or any of the host cells mentioned hereinafter. Further information on *in vivo* glycosylation of FVII and FVIIa is found in WO 01/58935 and WO 03/093465, incorporated by reference.

5 Methods of preparing a polypeptide variant of the invention

The polypeptide variants of the present invention, optionally in glycosylated form, may be produced by any suitable method known in the art. Such methods include constructing a nucleotide sequence encoding the polypeptide variant and expressing the sequence in a suitable transformed or transfected host. Preferably, the host cell is a gamma-
10 carboxylating host cell such as a mammalian cell. However, polypeptide variants of the invention may be produced, albeit less efficiently, by chemical synthesis or a combination of chemical synthesis or a combination of chemical synthesis and recombinant DNA technology.

A nucleotide sequence encoding a polypeptide variant of the invention may be
15 constructed by isolating or synthesizing a nucleotide sequence encoding hFVII and then changing the nucleotide sequence so as to effect introduction (i.e. insertion or substitution) or removal (i.e. deletion or substitution) of the relevant amino acid residue(s).

The nucleotide sequence is conveniently modified by site-directed mutagenesis in accordance with conventional methods. Alternatively, the nucleotide sequence is prepared by
20 chemical synthesis, e.g. by using an oligonucleotide synthesizer, wherein oligonucleotides are designed based on the amino acid sequence of the desired polypeptide variant, and preferably selecting those codons that are favored in the host cell in which the recombinant polypeptide variant will be produced. For example, several small oligonucleotides coding for portions of the desired polypeptide variant may be synthesized and assembled by PCR
25 (polymerase chain reaction), ligation or ligation chain reaction (LCR) (Barany, *Proc Natl Acad Sci USA* 88:189-193, 1991). The individual oligonucleotides typically contain 5' or 3' overhangs for complementary assembly.

Once assembled (by synthesis, site-directed mutagenesis or another method), the nucleotide sequence encoding the polypeptide is inserted into a recombinant vector and
30 operably linked to control sequences necessary for expression of the FVII in the desired transformed host cell.

Persons skilled will be capable of selecting suitable vectors, expression control sequences and hosts for expressing the polypeptide

The recombinant vector may be an autonomously replicating vector, i.e. a vector, which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g. a plasmid. Alternatively, the vector is one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with
5 the chromosome(s) into which it has been integrated.

The vector is preferably an expression vector in which the nucleotide sequence encoding the polypeptide variant of the invention is operably linked to additional segments required for transcription of the nucleotide sequence. The vector is typically derived from plasmid or viral DNA. A number of suitable expression vectors for expression in the host
10 cells mentioned herein are commercially available or described in the literature. Detailed information on suitable vectors for expressing FVII may be found in WO 01/58935, incorporated by reference.

The term "control sequences" is defined herein to include all components which are necessary or advantageous for the expression of the polypeptide variant of the invention.
15 Each control sequence may be native or foreign to the nucleic acid sequence encoding the polypeptide variant. Such control sequences include, but are not limited to, a leader sequence, polyadenylation sequence, propeptide sequence, promoter, enhancer or upstream activating sequence, signal peptide sequence, and transcription terminator. At a minimum, the control sequences include a promoter. A wide variety of expression control sequences may be used
20 in the present invention, e.g. any of the control sequences disclosed in WO 01/58935, incorporated by reference.

The nucleotide sequence of the invention encoding a polypeptide variant, whether prepared by site-directed mutagenesis, synthesis, PCR or other methods, may optionally include a nucleotide sequence that encodes a signal peptide. The signal peptide is present
25 when the polypeptide variant is to be secreted from the cells in which it is expressed. Such signal peptide, if present, should be one recognized by the cell chosen for expression of the polypeptide variant. The signal peptide may be homologous (i.e. normally associated with hFVII) or heterologous (i.e. originating from another source than hFVII) to the polypeptide or may be homologous or heterologous to the host cell, i.e. be a signal peptide normally
30 expressed from the host cell or one which is not normally expressed from the host cell. For further information on suitable signal peptides, see WO 01/58935.

Any suitable host may be used to produce the polypeptide variant, including bacteria (although not particularly preferred), fungi (including yeasts), plant, insect, mammal, or other appropriate animal cells or cell lines, as well as transgenic animals or plants. Mammalian

cells are preferred. Examples of bacterial host cells include gram-positive bacteria such as strains of *Bacillus*, e.g. *B. brevis* or *B. subtilis*, or *Streptomyces*, or gram-negative bacteria, such as strains of *E. coli*. Examples of suitable filamentous fungal host cells include strains of *Aspergillus*, e.g. *A. oryzae*, *A. niger*, or *A. nidulans*, *Fusarium* or *Trichoderma*. Examples of
5 suitable yeast host cells include strains of *Saccharomyces*, e.g. *S. cerevisiae*, *Schizosaccharomyces*, *Kluyveromyces*, *Pichia*, such as *P. pastoris* or *P. methanolica*, *Hansenula*, such as *H. Polymorpha* or *Yarrowia*. Examples of suitable insect host cells include a *Lepidoptera* cell line, such as *Spodoptera frugiperda* (Sf9 or Sf21) or *Trichoplusia ni* cells (High Five) (US 5,077,214). Examples of suitable mammalian host cells include
10 Chinese hamster ovary (CHO) cell lines, (e.g. CHO-K1; ATCC CCL-61), Green Monkey cell lines (COS) (e.g. COS 1 (ATCC CRL-1650), COS 7 (ATCC CRL-1651)); mouse cells (e.g. NS/O), Baby Hamster Kidney (BHK) cell lines (e.g. ATCC CRL-1632 or ATCC CCL-10), and human cells (e.g. HEK 293 (ATCC CRL-1573)). Additional suitable cell lines are known in the art and available from public depositories such as the American Type Culture
15 Collection, Rockville, Maryland. Also, mammalian cells, such as a CHO cell, may be modified to express sialyltransferase, e.g. 1,6-sialyltransferase, e.g. as described in US 5,047,335, in order to provide improved glycosylation of the polypeptide variant.

Methods for introducing exogeneous DNA into the above cell types, as well as other information regarding expression, production and purification of FVII variants, is found in
20 WO 01/58935, incorporated herein by reference.

Pharmaceutical composition of the invention and its use

In a further aspect, the present invention relates to a composition, in particular to a pharmaceutical composition, comprising a polypeptide variant of the invention and a
25 pharmaceutically acceptable carrier or excipient.

The polypeptide variant or the pharmaceutical composition according to the invention may be used as a medicament.

Due to the high clotting efficiency, the polypeptide variant of the invention, or the pharmaceutical composition of the invention, is particular useful for the treatment of
30 uncontrollable bleeding events in trauma patients, thrombocytopenic patients, patients in anticoagulant treatment, and cirrhosis patients with variceal bleeding, or other upper gastrointestinal bleedings, in patients undergoing orthotopic liver transplantation or liver resection (allowing for transfusion free surgery), or in hemophilia patients.

Trauma is defined as an injury to living tissue caused by an extrinsic agent. It is the 4th leading cause of death in the US and places a large financial burden on the economy.

Trauma is classified as either blunt or penetrative. Blunt trauma results in internal compression, organ damage and internal haemorrhage whereas penetrative trauma (as the
5 consequence of an agent penetrating the body and destroying tissue, vessels and organs) results in external haemorrhage.

Trauma may be caused by numerous events, e.g. traffic accidents, gunshot wounds, falls, machinery accidents, and stab wounds.

Cirrhosis of the liver may be caused by direct liver injury, including chronic
10 alcoholism, chronic viral hepatitis (types B, C, and D), and autoimmune hepatitis as well as by indirect injury by way of bile duct damage, including primary biliary cirrhosis, primary sclerosing cholangitis and biliary atresia. Less common causes of cirrhosis include direct liver injury from inherited disease such as cystic fibrosis, alpha-1-antitrypsin deficiency, hemochromatosis, Wilson's disease, galactosemia, and glycogen storage disease.

15 Transplantation is the key intervention for treating late stage cirrhotic patients.

Thus, in a further aspect the present invention relates to a polypeptide variant of the invention for the manufacture of a medicament for the treatment of diseases or disorder wherein clot formation is desirable. A still further aspect of the present invention relates to a method for treating a mammal having a disease or disorder wherein clot formation is
20 desirable, comprising administering to a mammal in need thereof an effective amount of the polypeptide variant or the pharmaceutical composition of the invention.

Examples of diseases/disorders wherein increased clot formation is desirable include, but is not limited to, hemorrhages, including brain hemorrhages, as well as patient with severe uncontrolled bleedings, such as trauma. Further examples include patients
25 undergoing transplantations, patients undergoing resection and patients with variceal bleedings. Another widespread disease/disorder in which it is contemplated that the polypeptides of the invention will be useful for increased clot formation is hemophilia, e.g. von Willebrand disease, hemophilia A, hemophilia B or hemophilia C.

The polypeptide variant of the invention is administered to patients in a
30 therapeutically effective dose, normally one approximately paralleling that employed in therapy with rhFVII such as NovoSeven®, or at lower dosage. By "therapeutically effective dose" herein is meant a dose that is sufficient to produce the desired effects in relation to the condition for which it is administered. The exact dose will depend on the circumstances, and

will be ascertainable by one skilled in the art using known techniques. Normally, the dose should be capable of preventing or lessening the severity or spread of the condition or indication being treated. It will be apparent to those of skill in the art that an effective amount of a polypeptide variant or composition of the invention depends, *inter alia*, upon the disease, the dose, the administration schedule, whether the polypeptide variant or composition is administered alone or in conjunction with other therapeutic agents, the plasma half-life of the compositions, and the general health of the patient.

The polypeptide variant of the invention is preferably administered in a composition including a pharmaceutically acceptable carrier or excipient. "Pharmaceutically acceptable" means a carrier or excipient that does not cause any untoward effects in patients to whom it is administered. Such pharmaceutically acceptable carriers and excipients are well known in the art (see, for example, Remington's Pharmaceutical Sciences, 18th edition, A. R. Gennaro, Ed., Mack Publishing Company [1990]; Pharmaceutical Formulation Development of Peptides and Proteins, S. Frokjaer and L. Hovgaard, Eds., Taylor & Francis [2000]; and Handbook of Pharmaceutical Excipients, 3rd edition, A. Kibbe, Ed., Pharmaceutical Press [2000]).

The polypeptide variants of the invention can be used "as is" and/or in a salt form thereof. Suitable salts include, but are not limited to, salts with alkali metals or alkaline earth metals, such as sodium, potassium, calcium and magnesium, as well as e.g. zinc salts. These salts or complexes may be present as a crystalline and/or amorphous structure.

The pharmaceutical composition of the invention may be administered alone or in conjunction with other therapeutic agents. These agents may be incorporated as part of the same pharmaceutical composition or may be administered separately from the polypeptide variant of the invention, either concurrently or in accordance with another treatment schedule. In addition, the polypeptide variant or pharmaceutical composition of the invention may be used as an adjuvant to other therapies.

A "patient" for the purposes of the present invention includes both humans and other mammals. Thus, the methods are applicable to both human therapy and veterinary applications.

The pharmaceutical composition comprising the polypeptide variant of the invention may be formulated in a variety of forms, e.g. as a liquid, gel, lyophilized, or as a compressed solid. The preferred form will depend upon the particular indication being treated and will be apparent to one skilled in the art.

In particular, the pharmaceutical composition comprising the polypeptide variant of the invention may be formulated in lyophilized or stable soluble form. The polypeptide variant may be lyophilised by a variety of procedures known in the art. The polypeptide variant may be in a stable soluble form by the removal or shielding of proteolytic degradation sites as described herein. The advantage of obtaining a stable soluble preparation lies in easier handling for the patient and, in the case of emergencies, quicker action, which potentially can become life saving. The preferred form will depend upon the particular indication being treated and will be apparent to one of skill in the art.

The administration of the formulations of the present invention can be performed in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intracerebrally, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, intraocularly, or in any other acceptable manner. The formulations can be administered continuously by infusion, although bolus injection is acceptable, using techniques well known in the art, such as pumps or implantation. In some instances the formulations may be directly applied as a solution or spray.

Parenterals

A preferred example of a pharmaceutical composition is a solution, in particular an aqueous solution, designed for parenteral administration. Although in many cases pharmaceutical solution formulations are provided in liquid form, appropriate for immediate use, such parenteral formulations may also be provided in frozen or in lyophilized form. In the former case, the composition must be thawed prior to use. The latter form is often used to enhance the stability of the active compound contained in the composition under a wider variety of storage conditions, as it is recognized by those skilled in the art that lyophilized preparations are generally more stable than their liquid counterparts. Such lyophilized preparations are reconstituted prior to use by the addition of one or more suitable pharmaceutically acceptable diluents such as sterile water for injection or sterile physiological saline solution.

In case of parenterals, they are prepared for storage as lyophilized formulations or aqueous solutions by mixing, as appropriate, the polypeptide variant having the desired degree of purity with one or more pharmaceutically acceptable carriers, excipients or stabilizers typically employed in the art (all of which are termed "excipients"), for example buffering agents, stabilizing agents, preservatives, isotonifiers, non-ionic surfactants or detergents, antioxidants and/or other miscellaneous additives.

Detailed information on parental formulations suitable for administration of FVII variants, as well as sustained release preparations, is found in WO 01/58935 and WO 03/093465, incorporated herein by reference.

5 The invention is further described in the following non-limiting examples.

MATERIALS AND METHODS

Active Site Region

10 The active site region is defined as any residues having at least one atom within 10 Å of any atom in the catalytic triad (residues H193, D242, S344).

Measurement of Reduced Sensitivity to Proteolytic Degradation

Proteolytic degradation can be measured using the assay described in US 5,580,560,
15 Example 5, where proteolysis is autoprolysis.

Furthermore, reduced proteolysis can be tested in an *in vivo* model using radiolabelled samples and comparing proteolysis of rhFVIIa and the polypeptide variant of the invention by withdrawing blood samples and subjecting these to SDS-PAGE and autoradiography.

20 Irrespectively of the assay used for determining proteolytic degradation, "reduced proteolytic degradation" is intended to mean a measurable reduction in cleavage compared to that obtained by rhFVIIa as measured by gel scanning of Coomassie stained SDS-PAGE gels, HPLC or as measured by conserved catalytic activity in comparison to wild type using the tissue factor independent activity assay described below.

25

Determination of the Molecular Weight of Polypeptide Variants

The molecular weight of polypeptide variants is determined by either SDS-PAGE, gel filtration, Western Blots, matrix assisted laser desorption mass spectrometry or equilibrium centrifugation, e.g. SDS-PAGE according to Laemmli, U.K., *Nature* Vol 227 (1970), pp. 680-
30 85.

Determination of TFPI Inhibition

FVII inhibition by TFPI can be monitored in the amidolytic assay described in Chang et al. *Biochemistry* 1999, 38: 10940-10948.

Determination of TFPI Affinity

The capacity of variants to bind to TFPI is evaluated using one or more of the three BIAcore® assays described in Dickinson et al. *Proc. Natl. Acad. Sci. USA* 1996, 93: 14379-14384; Roberge et al. *Biochemistry* 2001, 40: 9522-9531; and Ruf et al. *Biochemistry* 1999, 38(7): 1957-1966.

TF-independent Factor X Activation Assay

This assay has been described in detail on page 39826 in Nelsestuen et al., *J Biol Chem*, 2001; 276:39825-39831.

Briefly, the molecule to be assayed (either hFVIIa, rhFVIIa or the polypeptide variant of the invention in its activated form) is mixed with a source of phospholipid (preferably phosphatidylcholine and phosphatidylserine in a ratio of 8:2) and relipidated Factor X in Tris buffer containing BSA. After a specified incubation time the reaction is stopped by addition of excess EDTA. The concentration of factor Xa is then measured from absorbance change at 405 nm after addition of a chromogenic substrate (S-2222, Chromogenix). After correction from background the tissue factor independent activity of rhFVIIa (a_{wt}) is determined as the absorbance change after 10 minutes and the tissue factor independent activity of the polypeptide variant of the invention ($a_{variant}$) is also determined as the absorbance change after 10 minutes. The ratio between the activity of the polypeptide variant, in its activated form, and the activity of rhFVIIa is defined as $a_{variant}/a_{wt}$.

Clotting Assay

The clotting activity of the FVIIa and variants thereof were measured in one-stage assays and the clotting times were recorded on a Thrombotrack IV coagulometer (Medinor). Factor VII-depleted human plasma (American Diagnostica) was reconstituted and equilibrated at room temperature for 15-20 minutes. 50 microliters of plasma was then transferred to the coagulometer cups.

FVIIa and variants thereof were diluted in Glyoxaline Buffer (5.7 mM barbiturate, 4.3 mM sodium citrate, 117 mM NaCl, 1 mg/ml BSA, pH 7.35). The samples were added to the cup in 50 ul and incubated at 37°C for 2 minutes.

Technoplastin His (Medinor) was reconstituted with water and CaCl_2 was added to a final concentration of 4.5 mM. The mixture was equilibrated at 37°C for 15-20 min. The reaction was initiated by adding 100 μl Technoplastin His.

To measure the clotting activity in the absence of TF the same assay was used
5 without addition of Technoplastin His. Data was analysed using PRISM software.

Whole Blood Assay

The clotting activity of FVIIa and variants thereof were measured in one-stage assays and the clotting times were recorded on a Thrombotrack IV coagulometer (Medinor).
10 100 μl of FVIIa or variants thereof were diluted in a buffer containing 10 mM glycylglycine, 50 mM NaCl, 37.5 mM CaCl_2 , pH 7.35 and transferred to the reaction cup. The clotting reaction was initiated by addition of 50 μl blood containing 10% 0.13 M tri-sodium citrate as anticoagulant. Data was analysed using Excel or PRISM software.

15 *Amidolytic Assay*

The ability of the variants to cleave small peptide substrates can be measured using the chromogenic substrate S-2288 (D-Ile-Pro-Arg-p-nitroanilide). FVIIa is diluted to about 10-90 nM in assay buffer (50 mM Na-Hepes pH 7.5, 150 mM NaCl, 5 mM CaCl_2 , 0.1% BSA, 1U/ml Heparin). Furthermore, soluble TF (sTF) is diluted to 50-450 nM in assay
20 buffer. 120 μl of assay buffer is mixed with 20 μl of the FVIIa sample and 20 μl sTF. After 5 min incubation at room temperature with gentle shaking, followed by 10 min incubation at 37°C, the reaction is started by addition of the S-2288 substrate to 1 mM and the absorption at 405 nm is determined at several time points.

25 *ELISA Assay*

FVII/FVIIa (or variant) concentrations are determined by ELISA. Wells of a microtiter plate are coated with an antibody directed against the protease domain using a solution of 2 $\mu\text{g/ml}$ in PBS (100 μl per well). After overnight coating at R.T. (room temperature), the wells are washed 4 times with THT buffer (100 mM NaCl, 50 mM Tris-HCl pH 7.2 0.05% Tween-20). Subsequently, 200 μl of 1% Casein (diluted from 2.5% stock
30 using 100 mM NaCl, 50 mM Tris-HCl pH 7.2) is added per well for blocking. After 1 hr incubation at R.T., the wells are emptied, and 100 μl of sample (optionally diluted in dilution buffer (THT + 0.1% Casein)) is added. After another incubation of 1 hr at room temperature,

the wells are washed 4 times with THT buffer, and 100 µl of a biotin-labelled antibody directed against the EGF-like domain (1 µg/ml) is added. After another 1 hr incubation at R.T., followed by 4 more washes with THT buffer, 100 µl of streptavidin-horse radish peroxidase (DAKO A/S, Glostrup, Denmark, diluted 1/10000) is added. After another 1 hr
5 incubation at R.T., followed by 4 more washes with THT buffer, 100 µl of TMB (3,3',5,5'-tetramethylbenzidine, Kem-en-Tech A/S, Denmark) is added. After 30 min incubation at R.T. in the dark, 100 µl of 1 M H₂SO₄ is added and OD_{450nm} is determined. A standard curve is prepared using rhFVIIa (NovoSeven®).

Alternatively, FVII/FVIIa or variants may be quantified through the Gla domain
10 rather than through the protease domain. In this ELISA set-up, wells are coated overnight with an antibody directed against the EGF-like domain and for detection, a calcium-dependent biotin-labelled monoclonal anti-Gla domain antibody is used (2 µg/ml, 100 µl per well). In this set-up, 5 mM CaCl₂ is added to the THT and dilution buffers.

15 EXAMPLES

Example 1

The X-ray structure of hFVIIa in complex with soluble tissue factor by Banner et al., *J Mol Biol*, 1996; 285:2089 is used for this example. It is noted that the numbering of
20 residues in the reference does not follow the sequence. Here, we have used the sequential numbering according to SEQ ID NO:2. The gamma-carboxy glutamic acids at positions 6, 7, 14, 16, 19, 20, 25, 26, 29 and 35 are all here named Glu (three letter abbreviation) or E (one letter abbreviation). Residues 143-152 are not present in the structure. For further information on the calculations in this example, see WO 01/58935.

25

Surface Exposure

Performing fractional ASA calculations resulted in the following residues being determined to have more than 25% of their side chain exposed to the surface: A1, N2, A3, F4, L5, E6, E7, L8, R9, P10, S12, L13, E14, E16, K18, E19, E20, Q21, S23, F24, E25, E26,
30 R28, E29, F31, K32, D33, A34, E35, R36, K38, L39, W41, I42, S43, S45, G47, D48, Q49, A51, S52, S53, Q56, G58, S60, K62, D63, Q64, L65, Q66, S67, I69, F71, L73, P74, A75, E77, G78, R79, E82, T83, H84, K85, D86, D87, Q88, L89, I90, V92, N93, E94, G97, E99, S103, D104, H105, T106, G107, T108, K109, S111, R113, E116, G117, S119, L120, L121,

A122, D123, G124, V125, S126, T128, P129, T130, V131, E132, I140, L141, E142, K143, R144, N145, A146, S147, K148, P149, Q150, G151, R152, G155, K157, V158, P160, K161, E163, L171, N173, G174, A175, N184, T185, I186, H193, K197, K199, N200, R202, N203, I205, S214, E215, H216, D217, G218, D219, S222, R224, S232, T233, V235, P236, G237, T238, T239, N240, H249, Q250, P251, V253, T255, D256, E265, R266, T267, E270, R271, F275, V276, R277, F278, L280, L287, L288, D289, R290, G291, A292, T293, L295, E296, N301, M306, T307, Q308, D309, L311, Q312, Q313, R315, K316, V317, G318, D319, S320, P321, N322, T324, E325, Y326, Y332, S333, D334, S336, K337, K341, G342, H351, R353, G354, Q366, G367, T370, V371, G372, R379, E385, Q388, K389, R392, S393, E394, P395, R396, P397, G398, V399, L400, L401, R402, P404 and P406.

The following residues were determined to have more than 50% of their side chain exposed to the surface: A1, A3, F4, L5, E6, E7, L8, R9, P10, E14, E16, K18, E19, E20, Q21, S23, E25, E26, E29, K32, A34, E35, R36, K38, L39, I42, S43, G47, D48, A51, S52, S53, Q56, G58, S60, K62, L65, Q66, S67, I69, F71, L73, P74, A75, E77, G78, R79, E82, H84, K85, D86, D87, Q88, L89, I90, V92, N93, E94, G97, T106, G107, T108, K109, S111, E116, S119, L121, A122, D123, G124, V131, E132, L141, E142, K143, R144, N145, A146, S147, K148, P149, Q150, G151, R152, G155, K157, P160, N173, G174, A175, K197, K199, N200, R202, S214, E215, H216, G218, R224, V235, P236, G237, T238, H249, Q250, V253, D256, T267, F275, R277, F278, L288, D289, R290, G291, A292, T293, L295, N301, M306, Q308, D309, L311, Q312, Q313, R315, K316, G318, D319, N322, E325, D334, K341, G354, G367, V371, E385, K389, R392, E394, R396, P397, G398, R402, P404 and P406.

Tissue Factor Binding Site

It was determined using ASA calculations that the following residues in hFVII change their ASA in the complex. These residues were defined as constituting the tissue factor binding site: L13, K18, F31, E35, R36, L39, F40, I42, S43, S60, K62, D63, Q64, L65, I69, C70, F71, C72, L73, P74, F76, E77, G78, R79, E82, K85, Q88, I90, V92, N93, E94, R271, A274, F275, V276, R277, F278, R304, L305, M306, T307, Q308, D309, Q312, Q313, E325 and R379.

Active Site Region

The active site region is defined as any residue having at least one atom within a distance of 10 Å from any atom in the catalytic triad (residues H193, D242, S344): I153, Q167, V168, L169, L170, L171, Q176, L177, C178, G179, G180, T181, V188, V189, S190,

A191, A192, H193, C194, F195, D196, K197, I198, W201, V228, I229, I230, P231, S232, T233, Y234, V235, P236, G237, T238, T239, N240, H241, D242, I243, A244, L245, L246, V281, S282, G283, W284, G285, Q286, T293, T324, E325, Y326, M327, F328, D338, S339, C340, K341, G342, D343, S344, G345, G346, P347, H348, L358, T359, G360, I361, V362,
 5 S363, W364, G365, C368, V376, Y377, T378, R379, V380, Q382, Y383, W386, L387, L400
 and F405.

The Ridge of the Active Site Binding Cleft

The ridge of the active site binding cleft region was defined by visual inspection of
 10 the FVIIa structure 1FAK.pdb as: N173, A175, K199, N200, N203, D289, R290, G291,
 A292, P321 and T370.

Example 2

Design of an expression cassette for expression of hFVII in mammalian cells

15 The DNA sequence shown in SEQ ID NO:1, encompassing the short form of the full
 length cDNA encoding hFVII with its native short signal peptide (Hagen et al., 1986. *Proc
 Natl Acad Sci USA* 83:2412), was synthesized in order to facilitate high expression in
 mammalian cells. First the ATG start codon context was modified according to the Kozak
 consensus sequence (Kozak, M. *J Mol Biol* 1987 Aug 20;196(4):947-50), so that there is a
 20 perfect match to the consensus sequence upstream of the ATG start codon. Secondly the open
 reading frame of the native cDNA was modified by making a bias in the codon usage towards
 the codons frequently used in highly expressed human genes. Further, two translational stop
 codons were inserted at the end of the open reading frame in order to facilitate efficient
 translational stop. The fully synthetic and expression optimized hFVII gene was assembled
 25 from 70-mer DNA oligonucleotides and finally amplified using end primers inserting *Bam*HI
 and *Hind*III sites at the 5' and 3' ends respectively using standard PCR techniques, which
 resulted in the following sequence (SEQ ID NO:3):

ggatcccgccaccatggtcagccaggccctccgcctcctgtgcctgctcctggggctgcagggtgcctggctgccgtcttcgtcacc
 30 caggaggaagcccatggcgtcctgcacgcggcgccgggccaatgcctttctggaagagctccgccctggctccctggaacgcg
 aatgcaaagaggaacagtgcagctttgaggaagcccgaggagattttcaaagacgctgagcggaccaaactgtttggattagctatag
 cgatggcgatcagtgcgcctccagcccttgccagaacgggggctcctgcaaagaccagctgcagagctatatctgcttgcctgcct
 gcctttgagggggcgcaattgcgaaaccataaggatgaccagctgatttgcgtcaacgaaaacgggggctgcgagcagtactgcag
 cgatcacacgggcacgaagcggagctgccgctgccacgaaggctatagcctcctggctgacgggggtgcctgcagcccacgggtg

gaatacccttgcggaagattccattctagaaaagcggaacgctagcaaaccaggcgccggtcgtcgccgggaaggctgtccc
 taagggggagtgccctggcaggtcctgctcctggtaacggggccagctgtgcggcgggaccctcatcaataccatttgggtcgt
 gtccgccgctcactgctcgataagattaagaattggcggaacctcatcgctgtgctcggcgaacacgatctgtccgagcatgacggg
 gacgaacagtgcccgccgggtgggtcagggtcatcctccctccacatgtgcctggcagcacaatcacgatatcgtctgctccgct
 5 ccaccagcccgtcgtgctcaccgatcacgtcgtgcctctgtgcctgagcggaccttagcgaacgcacgtggcttctgctccgt
 ttagcctcgtgtccgggtggggccagctgctgacggggcgctaccgctctcgagctgatgggtcctcaacgtccccgggtgatga
 ccaggactgcctgcagcagtgccgcaaagtgggggactccccaatatcacggagtatatgtttgcgtggctatagcgatggctc
 caaggatagctgcaaggggggactccggcgggccccatgccacgcactatcgcgggacctggtacctcaccgggatcgtcagctgg
 ggccagggtgctgccacgggtggggcacttggcgtctacacgcgcgtcagccagtacattgagtggtgcagaagctcatgcggag
 10 cgaaccccgcccggggtgctcctgcgggcccccttcccttgataaaagctt

A vector for the cloning of the generated PCR product encompassing the expression cassette for hFVII was prepared by cloning the intron from pCINeo (Promega). The synthetic intron from pCI-Neo was amplified using standard PCR conditions and the primers:

15

CBProFpr174: 5'- AGCTGGCTAGCCACTGGGCAGGTAAGTATCA -3' (SEQ ID NO:4)
 and
CBProFpr175: 5'- TGGCGGGATCCTTAAGAGCTGTAATTGAACT -3' (SEQ ID NO:5)

20 resulting in a 332 bp PCR fragment. The fragment was cut with *NheI* and *BamHI* before cloning into pCDNA3.1/HygR (obtained from Invitrogen) resulting in PF#34.

The expression cassette for hFVII was cloned between the *BamHI* and *HindIII* sites of PF#34, resulting in plasmid PF#226.

25 Example 3

Construction of expression vectors encoding polypeptide variants of the invention

Sequence overhang extension (SOE) PCR was used for generating constructs having variant FVII open reading frames with substituted codons. In the SOE-PCR both the N-terminal part and the C-terminal part of the FVII open reading frame was first amplified in
 30 individual primary PCRs.

In order to change the codon for D196 to the codon for N196 the following primers were used pairwise for the primary PCRs:

CB499: 5'- CCCATTCTAGAAAAGCGGAACGCCAGCAAACCCCAGGG -3' (SEQ ID NO:6) and

CB562: 5'- CCAATTCTTAATCTTGTGAAGCAGTGAGCGGCG -3', (SEQ ID NO:7) and

5 CB256: 5'- CTCCGTGATATTGGGGGAGTC -3' (SEQ ID NO:8) and

CB561: 5'- CGCCGCTCACTGCTTCAACAAGATTAAGAATTGG -3' (SEQ ID NO:9).

The primary PCR products were then combined and the terminal primers (CB499 and CB256) were added, allowing for the secondary full-length product encoding the mutated
10 fragment of the desired D196N variant to be made. This PCR product was restricted with *Xba*I and *Xho*I and used to substitute the equivalent fragment of the FVII coding region of expression vector PF226 resulting in the expression vector pB0014 encoding the D196N variant.

With the exception of the constructs for position 341 variants, the constructs were
15 made in the same way as for D196N. Constructs for position 341 variants were made using the end primers

CB220: 5'- CGCTCTCGAGCTGATGGTGCTC - 3' (SEQ ID NO:10) and

CB362: 5'- CAAACAACAGATGGCTGGCAAC - 3' (SEQ ID NO:11)

20

allowing for directional cloning between *Xho*I and *Hind*III. The central primer used in the SOE-PCR reactions for the substitution variants were:

D196K

25 CB563: CGCCGCTCACTGCTTCAAGAAGATTAAGAATTGG (SEQ ID NO:12)

CB564: CCAATTCTTAATCTTCTTGAAGCAGTGAGCGGCG (SEQ ID NO:13)

G237L

CB565: CTCCACCTATGTGCCTCTGACGACCAATCACGA (SEQ ID NO:14)

30 CB566: TCGTGATTGGTCGTCAGAGGCACATAGGTGGAG (SEQ ID NO:15)

K341Q

CB569: CCAAGGATGCCAGGGGGACTCCGGCGGGC (SEQ ID NO:16)

CB570: GCCCGCCGGAGTCCCCCTGGCAGCTATCCTTGG (SEQ ID NO:17)

For the insertion variant the central primers were:

G237GAA

5 CB597: ACCTATGTGCCTGGCGCTGCCACGACCAATCACGAT (SEQ ID NO:18)

CB598: ATCGTGATTGGTCGTGGCAGCGCCAGGCACATAGGT (SEQ ID NO:19)

Example 4

Expression of FVII or FVII variants in CHO K1 cells

10 The cell line CHO K1 (ATCC # CCL-61) is seeded at 50% confluence in T-25 flasks using MEM α , 10% FCS (Gibco/BRL Cat # 10091), P/S and 5 μ g/ml phyloquinone and allowed to grow until confluent. The confluent mono cell layer is transfected with 5 μ g of the relevant plasmid described above using the Lipofectamine 2000 transfection agent (Life Technologies) according to the manufacturer's instructions. Twenty four hours post
15 transfection a sample is drawn and quantified using e.g. an ELISA recognizing the EGF1 domain of hFVII. At this time point relevant selection (e.g. Hygromycin B) may be applied to the cells for the purpose of generating a pool of stable transfectants. When using CHO K1 cells and the Hygromycin B resistance gene as a selectable marker on the plasmid, this is usually achieved within one week.

20

Example 5

Generation of CHO-K1 cells stably expressing polypeptide variants

A vial of CHO-K1 transfectant pool is thawed and the cells seeded in a 175 cm² tissue flask containing 25 ml of MEM α , 10% FCS, phyloquinone (5 μ g/ml), 100 U/l
25 penicillin, 100 μ g/l streptomycin and grown for 24 hours. The cells are harvested, diluted and plated in 96 well microtiter plates at a cell density of 1/2-1 cell/well. After a week of growth, colonies of 20-100 cells are present in the wells and those wells containing only one colony are labelled. After a further two weeks, the media in all wells containing only one colony is substituted with 200 μ l fresh medium. After 24 hours, a medium sample is withdrawn and
30 analysed by e.g. ELISA. High producing clones are selected and used to produce FVII or variant on large scale.

Example 6*Purification of polypeptide variants and subsequent activation*

FVII and FVII variants are purified as follows: The procedure is performed at 4°C. The harvested culture media from large-scale production is ultrafiltered using a Millipore
5 TFF system with 30 KDa cut-off Pellicon membranes. After concentration of the medium, citrate is added to 5 mM and the pH is adjusted to 8.6. If necessary, the conductivity is lowered to below 10 mS/cm. Subsequently, the sample is applied to a Q-sepharose FF column, equilibrated with 50 mM NaCl, 10 mM Tris pH 8.6. After washing the column with 100 mM NaCl, 10 mM Tris pH 8.6, followed by 150 mM NaCl, 10 mM Tris pH 8.6, FVII is
10 eluted using 10 mM Tris, 25 mM NaCl, 35 mM CaCl₂, pH 8.6.

For the second chromatographic step, an affinity column is prepared by coupling of a monoclonal Calcium-dependent antiGla-domain antibody to CNBr-activated Sepharose FF. About 5.5 mg antibody is coupled per ml resin. The column is equilibrated with 10 mM Tris, 100 mM NaCl, 35 mM CaCl₂, pH 7.5. NaCl is added to the sample to a concentration of 100
15 mM NaCl and the pH is adjusted to 7.4 -7.6. After O/N application of the sample, the column is washed with 100 mM NaCl, 35 mM CaCl₂, 10 mM Tris pH 7.5, and the FVII protein is eluted with 100 mM NaCl, 50 mM citrate, 75 mM Tris pH 7.5.

For the third chromatographic, the conductivity of the sample is lowered to below 10 mS/cm, if necessary, and the pH is adjusted to 8.6. The sample is then applied to a Q-
20 sepharose column (equilibrated with 50 mM NaCl, 10 mM Tris pH 8.6) at a density around 3-5 mg protein per ml gel to obtain efficient activation. After application, the column is washed with 50 mM NaCl, 10 mM Tris pH 8.6 for about 4 hours with a flow of 3-4 column volumes (cv) per hour. The FVII protein is eluted using a gradient of 0-100% of 500 mM NaCl, 10 mM Tris pH 8.6 over 40 cv. FVII containing fractions are pooled.

25 For the final chromatographic step, the conductivity is lowered to below 10 mS/cm. Subsequently, the sample is applied to a Q-sepharose column (equilibrated with 140 mM NaCl, 10 mM glycylglycine pH 8.6) at a concentration of 3-5 mg protein per ml gel. The column is then washed with 140 mM NaCl, 10 mM glycylglycine pH 8.6 and FVII is eluted with 140 mM NaCl, 15 mM CaCl₂, 10 mM glycylglycine pH 8.6. The eluate is diluted to 10
30 mM CaCl₂ and the pH is adjusted 6.8-7.2. Finally, Tween-80 is added to 0.01% and the pH is adjusted to 5.5 for storage at -80°C.

Example 7*Experimental results*

Subjecting the variants of the invention to the "Whole Blood Assay" revealed that the variants exhibit a significantly increased clotting activity (reduced clotting time) as compared to rhFVIIa. The experimental results are compiled in Table 1 below. The results are in addition illustrated in the appended Fig. 1, which shows the clotting time vs. concentration for the G237GAA variant versus rhFVIIa.

10	Variant	Clotting time (Whole Blood Assay)
		$t_{\text{variant}}/t_{\text{wt}}$
	rhFVIIa (reference)	1
	D196K	0.4
	D196N	0.4
15	K341Q	0.4
	G237L	0.3
	G237GAA	0.3

Table 1

CLAIMS

1. A variant of FVII or FVIIa, wherein said variant differs in 1-15 amino acid residues from hFVII or hFVIIa with the sequence shown in SEQ ID NO:2 and comprises the substitution D196K.
2. The variant of claim 1, wherein said variant is a variant of hFVIIa.
3. The variant of claim 1 or 2, wherein said variant further comprises a modification in position 237 as compared to hFVII or hFVIIa with the sequence shown in SEQ ID NO:2.
4. The variant of claim 3, wherein said modification is a substitution.
5. The variant of claim 4, wherein said substitution is G237L.
6. The variant of claim 3, wherein said modification is an insertion.
7. The variant of claim 6, wherein said insertion is selected from the group consisting of G237GXX, G237GXXX and G237GXXXX, wherein X is any amino acid residue.
8. The variant of claim 7, wherein X is selected from the group consisting of Ala, Val, Leu, Ile, Gly, Ser and Thr.
9. The variant of claim 8, wherein X is Ala.

10. The variant of claim 9, wherein said insertions are G237GAA.
11. The variant of claim 1 or 2, wherein said variant further comprises a modification in position 341 as compared to hFVH or hFVIIa with the sequence shown in SEQ ID NO:2.
12. The variant of claim 11, wherein said modification is a substitution.
13. The variant of claim 12, wherein said substitution is K341Q.
14. The variant of any of claims 1-13, wherein said variant comprises 1-10 further amino acid modifications.
15. The variant of claim 14, wherein said further modifications are substitutions.
16. The variant of claim 14 or 15, wherein at least one of said further amino acid substitutions is made in the Gla domain.
17. The variant of claim 16, comprising at least one further substitution in a position selected from the group consisting of P10, K32, D33 and A34, and an insertion between A3 and F4.
18. The variant of claim 17, comprising a further substitution in position K32.
19. The variant of claim 18, wherein said further substitution is K32E.
20. The variant of any of claims 16-19, comprising a further substitution in position P10.
21. The variant of claim 20, wherein said further substitution is P10Q.
22. The variant of any of claims 16-21, comprising further substitutions in P10+K32+D33+A34 as well as insertion of an amino acid residue between A3 and F4.

23. The variant of claim 22, comprising the modifications A3AY+P10Q+K32E+D33F+A34E.
24. The variant of any of claims 16-23, wherein no modifications are made in residues 6,7, 14,16, 19, 20, 25, 26, 29 and 35.
25. The variant of any of claims 1-24, wherein at least one amino acid residue comprising an attachment group for a non-polypeptide moiety has been introduced or removed.
26. The variant of claim 25, wherein at least one amino acid residue comprising an attachment group for a non-polypeptide moiety has been introduced.
27. The variant of claim 26, wherein at least one non-polypeptide moiety is covalently attached to at least one of said attachment groups.
28. The variant of claim 27, wherein said attachment group is a glycosylation site.
29. The variant of claim 28, wherein said non-polypeptide moiety is a sugar moiety.
30. The variant of claim 28 or 29, wherein the introduced glycosylation site is an *in vivo* glycosylation site.
31. The variant of claim 30, wherein the *in vivo* glycosylation site is an *in vivo* O-glycosylation site.
32. The variant of claim 30, wherein the *in vivo* glycosylation site is an *in vivo* N-glycosylation site.
33. The variant of claim 32, wherein said *in vivo* N-glycosylation site is introduced into a position comprising an amino acid residue having at least 25% of its side chain exposed to the surface (as defined in Example 1 herein).

34. The variant of claim 33, wherein said *in vivo* N-glycosylation site is introduced into a position comprising an amino acid residue having at least 50% of its side chain exposed to the surface (as defined in Example 1 herein).
35. The variant of any of claims 32-24, wherein said *in vivo* N-glycosylation site is introduced by at least one substitution selected from the group consisting of A51N, G58N, T106N, K109N, G124N, K143N+N145T, A175T, I205S, I205T, V253N, T267N, T267N+S269T, S314N+K316S, S314N+K316T, R315N+V317S, R315N+V317T, K316N+G318S, K316N+G318T, G318N and D334N.
36. The variant of claim 35, wherein said *in vivo* N-glycosylation site is introduced by at least one substitution selected from the group consisting of A51N, G58N, T106N, K109N, G124N, K143N+N145T, A175T, I205T, V253N, T267N+S269T, S314N+K316T, R315N+V317T, K316N+G318T, G318N and D334N.
37. The variant of claim 36, wherein said *in vivo* N-glycosylation site is introduced by at least one substitution selected from the group consisting of T106N, A175T, I205T, V253N and T267N+S269T.
38. The variant of any of claims 32-37, wherein one *in vivo* N-glycosylation site has been introduced by substitution.
39. The variant of any of claims 32-37, wherein two or more *in vivo* N-glycosylation sites have been introduced by substitution.
40. The variant of claim 39, wherein two *in vivo* N-glycosylation sites have been introduced by substitution.
41. The variant of claim 39 or 40, wherein said *in vivo* N-glycosylation sites have been introduced by substitutions selected from the group consisting of A51N+G58N, A51N+T106N, A51N+K109N, A51N+G124N, A51N+K143N+N145T, A51N+A175T, A51N+I205T, A51N+V253N, A51N+T267N+S269T, A51N+S314N+K316T, A51N+R315N+V317T, A51N+K316N+G318T, A51N+G318N, A51N+D334N, G58N+T106N, G58N+K109N, G58N+G124N, G58N+K143N+N145T, G58N+A175T,

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42. The variant of claim 41, wherein said *in vivo* N-glycosylation sites have been introduced by substitutions selected from the group consisting of T106N+A175T, T106N+I205T, T106N+V253N, T106N+T267N+S269T, A175T+I205T, A175T+V253N, A175T+T267N+S269T, I205T+V253N, I205T+T267N+S269T and V253N+T267N+S269T.

43. The variant of claim 42, wherein said *in vivo* N-glycosylation sites have been introduced by substitutions selected from the group consisting of T106N+I205T, T106N+V253N and I205T+T267N+S269T.

44. The variant of any of claims 32-37, wherein three or more *in vivo* N-glycosylation sites have been introduced by substitution.
45. The variant of claim 44, wherein three *in vivo* N-glycosylation sites have been introduced by substitution.
46. The variant of claim 44 or 45, wherein said *in vivo* N-glycosylation sites have been introduced by substitutions selected from the group consisting of I205T+V253N+T267N+S269T and T106N+I205T+V253N.
47. The variant of any of the preceding claims, wherein said variant further comprises at least one modification in a position selected from the group consisting of 157, 158, 296, 298, 305, 334, 336, 337 and 374.
48. The variant of claim 47, wherein said modification is at least one substitution selected from the group consisting of V158D, E296D, M298Q, L305V and K337A.
49. The variant of claim 48, wherein said substitutions are selected from the group consisting of V158D+E296D+M298Q+L305V+K337A, V158D+E296D+M298Q+K337A, V158D+E296D+M298Q+L305V, V158D+E296D+M298Q, M298Q, L305V+K337A, L305V and K337A.
50. The variant of any of the preceding claims, wherein said variant further comprises at least one modification selected from the group consisting of L39E, L39Q, L39H, I42R, S43H, S43Q, K62E, K62R, L65Q, L65S, F71D, F71Y, F71E, F71Q, F71N, E82Q, E82N, E82K and F275H.
51. The variant of any of the preceding claims, wherein said variant is in its activated form.
52. A nucleotide sequence encoding a variant as defined in any of claims 1-51.
53. An expression vector comprising a nucleotide sequence as defined in claim 52.

54. A host cell comprising a nucleotide sequence as defined in claim 52 or an expression vector as defined in claim 53.
55. The host cell of claim 54, wherein said host cell is a gamma-carboxylating cell capable of *in vivo* glycosylation.
56. A composition comprising a variant as defined in any of claims 1-51 and at least one pharmaceutically acceptable carrier or excipient.
57. A variant as defined in any of claims 1-51 for use as a medicament.
58. Use of a variant as defined in any of claims 1-51 for the manufacture of a medicament for the treatment of a disease or a disorder wherein clot formation is desirable.
59. Use according to claim 58, wherein said disease or disorder is selected from the group consisting of hemorrhages, including brain hemorrhages, severe uncontrolled bleedings, such as trauma, bleedings in patients undergoing transplantations or resection, variceal bleedings, and hemophilia.
60. Use according to claim 59, wherein said disease or disorder is trauma.
61. Use according to claim 59, wherein said disease or disorder is hemophilia.

SEQUENCE LISTING

<110> Maxygen ApS
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<120> FVII or FVIIa Variants

<130> 0272wo310

<150> US 60/456,547

<151> 2003-03-20

<150> US 60/479,708

<151> 2003-06-19

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                                     Ala
                                     1

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Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
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aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac      213
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp
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gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag      261
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cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc      357
Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys
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gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc      405
Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly
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tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc      453
Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg
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tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc      501

```

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gct Ala	agc Ser	aaa Lys	ccc Pro	cag Gln 150	ggc Gly	cgg Arg	atc Ile	gtc Val	ggc Gly 155	ggg Gly	aag Lys	gtc Val	tgc Cys	cct Pro 160	aag Lys	597
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gct Ala	cag Gln	gtc Val	atc Ile 230	att Ile	ccc Pro	tcc Ser	acc Thr	tat Tyr	gtg Val 235	cct Pro	ggc Gly	acg Thr	acc Thr	aat Asn 240	cac His	837
gat Asp	atc Ile	gct Ala	ctg Leu 245	ctc Leu	cgc Arg	ctc Leu	cac His	cag Gln 250	ccc Pro	gtc Val	gtg Val	ctc Leu	acc Thr 255	gat Asp	cac His	885
gtc Val	gtg Val	cct Pro 260	ctg Leu	tgc Cys	ctg Leu	cct Pro	gag Glu 265	cgg Arg	acc Thr	ttt Phe	agc Ser	gaa Glu 270	cgc Arg	acg Thr	ctg Leu	933
gct Ala	ttc Phe 275	gtc Val	cgc Arg	ttt Phe	agc Ser	ctc Leu 280	gtg Val	tcc Ser	ggc Gly	tgg Trp	ggc Gly 285	cag Gln	ctg Leu	ctc Leu	gac Asp	981
cgg Arg 290	ggc Gly	gct Ala	acc Thr	gct Ala	ctc Leu 295	gag Glu	ctg Leu	atg Met	gtg Val	ctc Leu 300	aac Asn	gtc Val	ccc Pro	cgg Arg	ctg Leu 305	1029
atg Met	acc Thr	cag Gln	gac Asp	tgc Cys 310	ctg Leu	cag Gln	cag Gln	tcc Ser	cgc Arg 315	aaa Lys	gtg Val	ggg Gly	gac Asp	tcc Ser 320	ccc Pro	1077
aat Asn	atc Ile	acg Thr	gag Glu 325	tat Tyr	atg Met	ttt Phe	tgc Cys	gct Ala 330	ggc Gly	tat Tyr	agc Ser	gat Asp	ggc Gly 335	tcc Ser	aag Lys	1125
gat Asp	agc Ser	tgc Cys 340	aag Lys	ggg Gly	gac Asp	tcc Ser	ggc Gly 345	ggg Gly	ccc Pro	cat His	gcc Ala	acg Thr 350	cac His	tat Tyr	cgc Arg	1173
ggg Gly	acc Thr 355	tgg Trp	tac Tyr	ctc Leu	acc Thr	ggg Gly 360	atc Ile	gtc Val	agc Ser	tgg Trp	ggc Gly 365	cag Gln	ggc Gly	tgc Cys	gcc Ala	1221
acg Thr 370	gtg Val	ggg Gly	cac His	ttt Phe	ggc Gly 375	gtc Val	tac Tyr	acg Thr	cgc Arg	gtc Val 380	agc Ser	cag Gln	tac Tyr	att Ile	gag Glu 385	1269
tgg Trp	ctg Leu	cag Gln	aag Lys	ctc Leu	atg Met	cgg Arg	agc Ser	gaa Glu	ccc Pro	cgg Arg	ccc Pro	ggg Gly	gtg Val	ctc Leu	ctg Leu	1317

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 Arg Ala Pro Phe Pro
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 <212> PRT
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Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys
 20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
 225 230 235 240
 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
 245 250 255
 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
 260 265 270
 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
 275 280 285
 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
 290 295 300
 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
 305 310 315 320
 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
 325 330 335
 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
 340 345 350
 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
 355 360 365
 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
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 Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
 385 390 395 400
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<220>
 <223> Synthetic gene for optimized expression of hFVII

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 gcgccggggcc aatgcctttc tggaagagct ccgccctggc tccctggaac gcgaatgcaa 180
 agaggaacag tgcagctttg aggaagcccg ggagattttc aaagacgctg agcggaccaa 240
 actgttttgg attagctata gcgatggcga tcagtgcgcc tccagccctt gccagaacgg 300
 gggctcctgc aaagaccagc tgcagagcta tatctgcttc tgcctgcctg cctttgaggg 360

gcgcaattgc gaaacccata aggatgacca gctgatttgc gtcaacgaaa acgggggctg 420
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 cggcgggacc ctcatcaata ccatttgggt cgtgtccgcc gctcactgct tcgataagat 720
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<220>
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<210> 5
 <211> 31
 <212> DNA
 <213> Artificial

<220>
 <223> Primer

<400> 5
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<210> 6
 <211> 38
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<220>
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<400> 11
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<210> 19

<211> 36

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<220>

<223> Primer

<400> 19

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36