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(54) Benævnelse: **GLYKOSYLERET VWF-FUSIONSPROTEINER MED FORBEDRET FARMAKOKINETIK**

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Doron Calo et al.: "Enhancing the longevity and in vivo potency of therapeutic proteins: The power of CTP", Precision Medicine , 30 September 2015 (2015-09-30), XP002771832, Retrieved from the Internet: URL:http://www.smartscitech.com/index.php/ pm/article/download/989/pdf_10 [retrieved on 2017-07-06]

DESCRIPTION

FIELD OF THE INVENTION

[0001] The invention relates to the half-life prolongation of proteins, in particular human coagulation factors such as von Willebrand factor (VWF) and factor VIII (FVIII).

BACKGROUND OF THE INVENTION

[0002] Hemophilia is a group of hereditary genetic disorders that impair the body's ability to control blood clotting or coagulation. In its most common form, Hemophilia A, clotting factor VIII (FVIII) is deficient. Hemophilia A occurs in about 1 in 5,000-10,000 male births. The FVIII protein is an essential cofactor in blood coagulation with multifunctional properties. The deficiency of FVIII can be treated with plasma-derived concentrates of FVIII or with recombinantly produced FVIII. The treatment with FVIII concentrates has led to a normalized life of the hemophilia patients.

[0003] Hemophilia A patients are treated with FVIII on demand or as a prophylactic therapy administered several times a week. For prophylactic treatment, 15-25 IU/kg bodyweight of FVIII is administered three times a week, which is necessary due to the constant need of FVIII and its short half-life in the blood system, which in humans is only about 11 hours (Ewenstein et al., 2004).

[0004] In the blood, under normal conditions, the FVIII molecule is always associated with its cofactor von Willebrand factor (VWF), which stabilizes the FVIII molecule from different forms of degeneration. The non-covalent complex of FVIII and VWF has a high binding affinity of 0.2-0.3 nM (Vlot et al., 1996).

[0005] Historically, Hemophilia A has been treated with FVIII originating from human blood plasma. However, since the 1990s, different recombinantly produced FVIII proteins were marketed. However, neither the plasma-derived nor the recombinant produced FVIII proteins have optimal pharmacokinetic properties. Like many other therapeutic proteins, they are subject to metabolic turnover by peptidases, which significantly limits their in vivo half-life.

[0006] As reviewed by Tiede et al. (2015), attempts for prolonging FVIII half-life include Fc fusion (Eloctate, Elocta, efmoroctocog alfa), addition of polyethylene glycol (turoctocog alfa pegol [N8-GP], BAY 94-9027, BAX 855), and a single-chain construct (CSL627). All these technologies change the FVIII molecule and result in approximate 1.5 times half-life prolonged FVIII.

[0007] Further half-life extension of FVIII is limited to the VWF half-life. As shown by Yee et al.,

the human VWF D'D3 domain is sufficient to stabilize FVIII in plasma. However, a D'D3-Fc fusion protein is able to extend FVIII half-life only in VWF-/- mice. In Hemophilia A mice, the D'D3-Fc construct does not result in FVIII half-life prolongation due to ineffective competition of the protein fragments with endogenous VWF for FVIII binding.

[0008] WO 2014/011819 A2 describes successful half-life prolongation of a FVIII construct containing the D'D3 domain of VWF, the Fc domain of IgG and XTEN. Since this construct does not bind to endogenous VWF, the same half-life prolonging effect is seen in both VWF/FVIII-double knock-out (DKO) and Hemophilia A mice. However, although fully functional *in vitro,* it exhibits markedly reduced activity *in vivo.*

[0009] Other approaches for increasing the half-life of therapeutic proteins include the genetic fusion of the therapeutic protein to a protein with naturally long half-life such as transferrin and albumin, or to protein domains such as the C-terminal peptide (CTP) of chorionic gonadotropin (CG).

[0010] CG belongs to the glycoprotein hormone family that includes luteinizing hormone (LH), follicle-stimulating hormone (FSH), and thyroid-stimulating hormone (TSH). These glycohormones are heterodimeric and consist of a common α-subunit and unique β-subunits that confer their different activities. The half-life of human CG (hCG) is significantly longer than the half-life of its counterparts LH, FSH and TSH. It was shown that the O-glycosylated CTP of hCG-β is responsible for this half-life prolongation. The CTP is described to consist of the sequence FQSSSS*KAPPPS*LPSPS*RLPGPS*DTPILPQ, which possesses four O-glycosylation sites (denoted by S*) (Birken et al., 1977).

[0011] As reviewed in Strohl et al (2015), different fusion proteins of a therapeutic protein and CTP have been developed and are presently in clinical trials. The therapeutic proteins include FSH (Elonva®), FVIIa, FIX, IFN-β and oxyntomodulin.

[0012] WO 93/15200 A1 is an international patent application relating to anti-thrombin polypeptides as antagonists of VWF binding to platelets or the subendothelium. It discloses different fusion proteins comprising VWF fragments. In particular, the fusion proteins of WO 93/15200 A1 comprise an adhesive part derived from the structure of the VWF and a part allowing its functional presentation and ensuring the stability and the *in vivo* distribution of the molecule.

[0013] WO 93/15199 A1 is based on the same basic principle as WO 93/15200 A1, i.e. fusion proteins of VWF and albumin in particular "sérumalbumine humaine" (SAH), but the application focuses on the albumin part.

[0014] Doron Calo et al. 2015 is a scientific article about the C-terminal peptide (CTP) of human chorionic gonadotropin (hCG) for use as a fusion to therapeutic proteins to enhance the longevity and in vivo potency.

SUMMARY OF THE INVENTION

[0015] The present invention is *inter alia* based on the finding that the addition of a cluster of O-glycosylated amino acids (which is present in full-length human VWF) to a fragment of VWF leads to a significant increase in its half-life. The half-life of the fusion protein is prolonged in comparison to the VWF fragment without the additional O-glycan cluster.

[0016] Thus, according to a first aspect, the invention relates to a fusion protein comprising a main protein and at least one extension peptide, wherein the amino acid sequence of the main protein is identical or similar to the amino acid sequence of a mammalian protein, such as VWF, or a fragment thereof, and said extension peptide(s) with a length of not more than 100 amino acids comprise(s) a cluster of O-glycosylated amino acids with at least two O-glycosylated amino acids and has/have a sequence identity of at least 90 % to SEQ ID NO: 1, and wherein the fusion protein has an increased half-life compared to the main protein without extension peptide(s).

[0017] The conclusion from the findings of the inventors is that the cluster of O-glycosylated amino acids of VWF identified by SEQ ID NO: 1 is useful as a half-life extension peptide.

[0018] According to a further preferred embodiment of the first aspect, the one or more extension peptides have a sequence identity of at least 95 %, preferably at least 98 %, more preferably 100 % to an O-glycosylated peptide of VWF, in particular to SEQ ID NO: 1.

[0019] In a second aspect, the invention relates to a polynucleotide encoding a fusion protein according to the first aspect.

[0020] According to the third aspect, the invention relates to a vector containing the polynucleotide according to the second aspect.

[0021] In a fourth aspect, the invention relates to a host cell containing the polynucleotide according to the second aspect or the vector according to the third aspect, wherein the host cell is a mammalian cell.

[0022] The inventors have found that not only the half-life of VWF is increased, but also the half-life of its binding partner FVIII. Thus, in the resulting complex or composition of the fusion protein and the second protein, the second protein also has an increased half-life.

[0023] Therefore, in a fifth aspect, the invention relates to a composition of a first protein and a second protein, wherein said first protein is a fusion protein according to the first aspect and is capable of binding said second protein, and said second protein is a therapeutic protein comprising an amino acid sequence that is identical or similar to the amino acid sequence of a second mammalian protein or fragment thereof, wherein the half-life of the second protein

bound to the first protein is increased as compared to the free form of said second protein.

FIGURES

[0024]

Fig. 1
shows schematic representations of A) a VWF fragment OCTA 11, and B) a fusion protein according to the invention with a VWF fragment as main protein: OCTA 12; C) a fusion protein according to the invention with a VWF fragment as main protein: OCTA14; D) a fusion protein according to the invention with a VWF fragment as main protein: OCTA15.

Fig. 2
shows a time-course of FVIII activity following intravenous administration of FVIII co-formulated with different VWF proteins or plasma-derived full-length VWF in FVIII/VWF double knock out (DKO) mice plasma. The data points and error bars represent the mean and standard deviation (SD) of 5 values. Due to the small size several of the error bars are not discernible.

Fig. 3
shows a time-course of OCTA 12 antigen concentration following subcutaneous administration of 100 U/kg FVIII co-formulated with OCTA 12 in minipig plasma.

Fig. 4
shows the time-course of FVIII antigen concentration following subcutaneous and intravenous injection of 100 U/kg FVIII or subcutaneous 100 U/kg FVIII co-formulated with VWF-protein OCTA 12 in minipig plasma.

DETAILED DESCRIPTION OF THE INVENTION

[0025] In order to provide a clear and consistent understanding of the specification and claims, and the scope to be given such terms, the following definitions are provided.

Definitions

[0026] A "peptide" as used herein may be composed of any number of amino acids of any type, preferably naturally occurring amino acids, which, preferably, are linked by peptide bonds. In particular, a peptide comprises at least 3 amino acids, preferably at least 5, at least 7, at least 9, at least 12, or at least 15 amino acids. Furthermore, there is no upper limit for the length of a peptide. However, preferably, a peptide according to the invention does not exceed a length of 500 amino acids, more preferably it does not exceed a length of 300 amino acids;

even more preferably it is not longer than 250 amino acids.

[0027] Thus, the term "peptide" includes "oligopeptides", which usually refer to peptides with a length of 2 to 10 amino acids, and "polypeptides" which usually refer to peptides with a length of more than 10 amino acids.

[0028] A "protein" as used herein may contain one or more polypeptide chains. Proteins with more than one polypeptide chain are often expressed as one polypeptide chain from one gene and cleaved post translationally. Thus, the terms "polypeptide" and "protein" are used interchangeably. The polypeptides and proteins as used herein include chemically synthesized proteins as well as naturally synthesized proteins which are encoded by genes. The polypeptides or proteins may be obtained from a natural source, such as human blood or produced in cell culture as recombinant proteins.

[0029] The term "therapeutic protein" as used herein relates to proteins or polypeptides with a therapeutic effect, i.e. proteins used as active pharmaceutical ingredient.

[0030] According to the invention the terms "protein precursor", "pro-protein" or "pro-peptide", relate to an inactive protein (or peptide) that can be turned into an active form by post-translational modification, enzymatic cleavage of a portion of the amino acid sequence.

[0031] The relatedness between two amino acid sequences or between two nucleotide sequences is described by the parameter "sequence identity". For purposes of the present invention, the degree of sequence identity between two amino acid sequences is determined using the Needleman-Wunsch algorithm (Needleman and Wunsch, 1970, J. Mol. Biol. 48: 443-453) as implemented in the Needle program of the EMBOSS package (EMBOSS: The European Molecular Biology Open Software Suite, Rice et a/., 2000, Trends Genet. 16: 276-277), preferably version 3.0.0 or later. The optional parameters used are gap open penalty of 10, gap extension penalty of 0.5, and the EBLOSUM62 (EMBOSS version of BLOSUM62) substitution matrix. The output of Needle labeled "longest identity" (obtained using the no brief option) is used as the percent identity and is calculated as follows:
(Identical Residues x 100)/(Length of Alignment - Total Number of Gaps in Alignment).

[0032] For purposes of the present invention, the degree of sequence identity between two nucleotide sequences is determined using the Needleman-Wunsch algorithm (Needleman and Wunsch, 1970, supra) as implemented in the Needle program of the EMBOSS package (EMBOSS: The European Molecular Biology Open Software Suite, Rice et a/., 2000, supra), preferably version 3.0.0 or later. The optional parameters used are gap open penalty of 10, gap extension penalty of 0.5, and the EDNAFULL (EMBOSS version of NCBI NUC4.4) substitution matrix. The output of Needle labeled "longest identity" (obtained using the -nobrief option) is used as the percent identity and is calculated as follows:
(Identical Desoxyribonucleotides x 100)/(Length of Alignment - Total Number of Gaps in Alignment)

Gaps in Alignment)

[0033] The terms "similarity" and "similar" as used herein with respect to the definition of a peptide or polynucleotide relate to a specified degree of sequence identity of the amino acid sequence or nucleotide sequence with a reference. A similar amino sequence is taken to include an amino acid sequence that is at least 80 %, 85 %, 86 %, 87 %, 88 %, 89 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 % or even 99% identical to the subject sequence. Typically, similar sequences will include the same residues in positions that are relevant for the function of the peptide or polynucleotide, such as active site residues or glycosylated amino acids, however, though may include any number of conservative amino acid substitutions. A similar nucleotide sequence is taken to include a nucleotide sequence that is at least 80 %, 85 %, 86 %, 87 %, 88 %, 89 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 % or even 99% identical to the subject sequence.

[0034] "Identical" as used herein refers to an amino acid or nucleotide sequence identity to a reference sequence of 100 %.

[0035] The term "recombinant" when used in reference to a cell, nucleic acid, protein or vector, indicates that the cell, nucleic acid, protein or vector has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found within the native (non-recombinant) form of the cell, or express native genes at different levels or under different conditions than found in nature.

[0036] The term "half-life" as used herein is the time required for plasma/blood concentration to decrease by 50% after pseudo-equilibrium of distribution has been reached (in accordance with the definition in Toutain et al., 2005). The term "half-life" is also referred to as "circulatory half-life", "terminal half-life" or "elimination half-life".

[0037] As used herein, the terms "transformed," "stably transformed," and "transgenic," used with reference to a cell means that the cell contains a non-native (e.g. heterologous) nucleic acid sequence integrated into its genome or carried as an episome that is maintained through multiple generations.

[0038] The term "fragment" as used herein refers to a polypeptide that has an amino-terminal and/or carboxy terminal deletion of one or more amino acids as compared to the native or wild-type protein but where the remaining amino acid sequence is identical to the corresponding positions in the amino acid sequence deduced from a full-length cDNA. Fragments are typically at least 50 amino acids in length.

[0039] The term "glycosylation" as used herein refers to the attachment of glycans to molecules, for example to proteins. Glycosylation may be an enzymatic reaction. The attachment formed may be through covalent bonds. Accordingly, a glycosylated polypeptide as used herein is a polypeptide to which one or multiple glycans are attached. The phrase "highly

glycosylated" refers to a molecule such as an enzyme which is glycosylated at all or nearly all of the available glycosylation sites, for instance O- linked or N-linked glycosylation sites.

[0040] The term "glycan" as used herein refers to a polysaccharide or oligosaccharide, or the carbohydrate section of a glycoprotein or glycosylated polypeptide. Glycans may be homo- or heteropolymers of monosaccharide residues. They may be linear or branched molecules. Glycans typically contain at least three sugars and can be linear or branched. A glycan may include natural sugar residues (e.g., glucose, N-acetylglucosamine, N-acetyl neuraminic acid, N-acetylgalactosamine, galactose, mannose, fucose, arabinose, ribose, xylose, etc.) and/or modified sugars (e.g., 2'-fluororibose, 2'-deoxyribose, phosphomannose, 6'-sulfo-N-acetylglucosamine, etc.).

[0041] The term "O-glycans" as used herein refers to glycans that are generally found covalently linked to serine and threonine residues of mammalian glycoproteins. O-glycans may be α-linked via an *N*-acetylgalactosamine (GalNAc) moiety to the - OH of serine or threonine by an O-glycosidic bond. Other linkages include α-linked O-fucose, β-linked O-xylose, α-linked O-mannose, β-linked O-GlcNAc (*N*-acetylglucosamine), α- or β-linked O-galactose, and α- or β-linked O-glucose glycans.

[0042] According to the invention, the terms "O-glycosylation cluster", "O-glycan cluster" and "cluster of O-glycosylated amino acids" are used interchangeably and related to two or more of O-glycosylated amino acids.

[0043] The term "sialylated" as used herein refers to molecules in particular glycans that have been reacted with sialic acid or its derivatives.

[0044] The transitional term "comprising", which is synonymous with "including," "containing," or "characterized by," is inclusive or open-ended and does not exclude additional, unrecited elements or method steps. The transitional phrase "consisting of" excludes any element, step, or ingredient not specified in the claim, except for impurities ordinarily associated therewith. When the phrase "consists of" appears in a clause of the body of a claim, rather than immediately following the preamble, it limits only the element set forth in that clause; other elements are not excluded from the claim as a whole. The transitional phrase "consisting essentially of" limits the scope of a claim to the specified materials or steps "and those that do not materially affect the basic and novel characteristic(s)" of the claimed invention. "A 'consisting essentially of' claim occupies a middle ground between closed claims that are written in a 'consisting of' format and fully open claims that are drafted in a 'comprising' format."

[0045] In the context of the invention for practical reasons the term "glycosylated protein" such as the fusion protein is used in the singular form. Generally, in praxis, proteins occur in a composition of protein molecules of the same type. However, in the case of glycosylated proteins, glycosylation will not be identical in every molecule of the composition. For example, not all of the individual molecules of the composition may be glycosylated to 100 %. Moreover,

differences in the glycans bound to a specific O-glycosylation site may arise. Accordingly, in the present application a reference to the "fusion protein" also relates to a composition of fusion protein molecules with identical amino acid sequences but variances in the O-glycan structure.

[0046] The terms "binding affinity" or "affinity" as used herein indicate the strength of the binding between two molecules, in particular a ligand and a protein target. Binding affinities are influenced by non-covalent intermolecular interactions between the two molecules such as hydrogen bonding, electrostatic interactions, hydrophobic interactions, and van der Waals forces.

[0047] An immune response as used herein relates to adaptive or innate immune response. The innate immune response refers to nonspecific defense mechanisms that are activated immediately or within hours of an antigen's appearance in the body. These mechanisms include physical barriers such as skin, chemicals in the blood, and immune system cells that attack foreign cells in the body. The innate immune response is activated by chemical properties of the antigen. The adaptive immune response refers to antigen-specific immune response. For this, the antigen first must be processed and recognized. Once an antigen has been recognized, the adaptive immune system creates a large number of immune cells specifically designed to attack that antigen.

Fusion Protein

[0048] According to a first aspect the invention provides a fusion protein comprising a main protein and at least one extension peptide, wherein the amino acid sequence of the main protein is identical or similar to the amino acid sequence of a mammalian protein or a fragment thereof, and said extension peptide(s) with a length of not more than 100 amino acids comprise(s) a cluster of O-glycosylated amino acids with at least two O-glycosylated amino acids and has/have a sequence identity of at least 90 % to SEQ ID NO: 1, and wherein the fusion protein has an increased half-life compared to the main protein without extension peptide(s).

[0049] The inventors have identified a modification of proteins leading to an increase in half-life, namely the addition of an extension peptide which contains a cluster of O-glycosylated amino acids. As shown in the examples, the fusion of O-glycosylation cluster 1 of human VWF as extension peptide to a fragment of VWF leads to a fusion protein (OCTA 12) with an increased half-life as compared to the VWF fragment (OCTA 11) alone.

[0050] The half-life ($t_{1/2}$) may be calculated by linear regression analysis of the log-linear portion of the individual plasma concentration-time curves or by non-linear regression using one-phase exponential decay model. Exemplary software programs for calculation are GraphPad Prism version 6.07 (La Jolla, CA 92037 USA) and WinNonlin, version 6.4 (Pharsight Corporation, Mountain View, CA, USA).

[0051] The calculations are based on the following equations:

$$t_{\frac{1}{2}} = \frac{\ln 2}{K_{el}} \quad [h]$$

$$\frac{dc}{dt} = K_{el} \cdot c \quad [h]$$

K_{el} = elimination rate constant

$t_{½}$ = elimination half-life

c = concentration

t = time

[0052] Thus, according to one embodiment, the fusion protein has an increased half-life compared to the main protein without extension peptide.

[0053] According to the present invention, two or more O-glycosylated amino acids in close proximity of the amino acid sequence are considered as a cluster. Thus, the cluster of O-glycosylated amino acids of the at least one extension peptide contains at least two O-glycosylated amino acids. The cluster may contain for example 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 O-glycosylated amino acids.

[0054] According to theory, the half-life extending effect is based on the negative charge of the O-glycans. Thus, the effect of half-life prolongation should increase with the number of O-glycosylated amino acids in the cluster. Thus, the cluster preferably contains at least three O-glycosylated amino acids. As shown in the Examples a significant half-life propagation effect was achieved with an extension peptide with a cluster of four O-glycosylated amino acids. Thus, according to a preferred embodiment the cluster contains at least four O-glycosylated amino acids.

[0055] In addition to the O-glycosylated amino acids of a cluster, also N-glycosylated amino acids may be present. Preferably, there are no N-glycosylated amino acids in the O-glycosylation cluster.

[0056] In case more than one extension peptide is present, the clusters of the extension peptides may have different numbers of O-glycosylated amino acids. For example, the fusion protein may contain one cluster with two and a second cluster with four O-glycosylated amino acids. Furthermore, one cluster may contain three O-glycosylation sites and the other four O-glycosylation sites.

[0057] The O-glycosylated amino acids of the extension peptide can be the mucin-type O-glycosylated amino acids serine (Ser) and threonine (Thr). However, also O-glycosylated

tyrosine (Tyr), hydroxlysine (Hydroxy-Lys) or hydroxyproline (Hydroxy-Pro) are known in the art. Thus, the one or more O-glycosylated amino acids in the fusion protein, in particular in the extension peptide, may be selected from Ser, Thr, Tyr, Hydroxy-Lys and Hydroxy-Pro.

[0058] The extension peptide fused to the VWF fragment in OCTA 12, which leads to a half-life prolongation of said fragment, contains both O-glycosylated threonine residues and serine residues. Thus, according to one embodiment of the first aspect, the cluster of O-glycosylated amino acids contains at least one O-glycosylated threonine. Preferably, said cluster contains both a threonine and a serine as O-glycosylated amino acids. Interestingly, the extension peptide of OCTA 12 contains two vicinal threonine residues that are O-glycosylated. Thus, in one embodiment the extension peptide contains at least two vicinal O-glycosylated threonine residues.

[0059] As explained above, it is believed that the negative charge of the protein surface generated by the O-glycans leads to the half-life prolongation. Without wanting to be bound to the theory, it is believed that for manifestation of the effect two or more O-glycans in close proximity are needed. Thus, according to a preferred embodiment the one or more clusters contain at least one glycosylation site in 8 amino acids.

[0060] The length of the extension peptide is defined by two different aspects. The extension peptide must be long enough to contain the recognition sites facilitating the glycosylation of the O-glycosylated amino acids. On the other hand, the shorter the extension peptide is, the less likely it is to interfere with the structural integrity or activity and thus the therapeutic effect of the main protein. Thus, the extension peptide does not exceed 100 amino acids. In order to allow four amino acids to be O-glycosylated within the extension peptide, the length is preferably in the range from 22 to 40 amino acids. Preferably, the length of the extension peptide is about the length of the extension peptides in OCTA 12, i.e. in the range from 26 to 36 amino acids. According to one embodiment the one or more extension peptides have a length of about 31 amino acids.

[0061] The presented results make it credible that the extension peptide - in analogy to the CTP - can increase the half-life of other proteins, i.e. of proteins in general.

[0062] The extension peptide(s) has/have a sequence identity to O-glycosylation cluster 2 of VWF (amino acids 1238-1268 of SEQ ID NO: 2): QEPGGLWPPTDAPVSPTTLYVEDISEPPLH (SEQ ID NO: 1) or a variant thereof of at least 90 %. The sequence identity to SEQ ID NO: 1 is preferably at least 95 %. More preferably, the sequence identity of the extension peptide to SEQ ID NO: 1 is at least 98 %. Most preferably, the one or more extension peptides have a sequence identity to SEQ ID NO: 1 of 100 %.

[0063] The main protein is based on a mammalian protein, i.e. contains an amino acid sequence similar or identical to a mammalian protein or fragment thereof. The mammalian protein is in particular a human protein.

[0064] The mammalian protein to which the amino acid sequence of the main protein is similar or identical to, may be a glycosylated protein. According to one embodiment of the fusion protein, the main protein comprises a glycosylated section of the mammalian protein. According to another embodiment, the main protein comprises at least one cluster of O-glycosylated amino acids. This cluster of O-glycosylated amino acids may be identical to the cluster of O-glycosylated amino acids in the extension peptide.

[0065] The mammalian protein, on which the main protein is based, is more preferably a blood protein. According to one embodiment, the mammalian protein is a human blood protein.

[0066] The mammalian blood protein may be a blood clotting factor, a transport protein, a protease inhibitor, an immunoglobulin, a cell related plasma protein, an apolipoprotein, a complement factor, a growth factor, an antiangiogenic protein, a highly glycosylated protein, a blood factor or another blood protein.

[0067] The blood clotting factor, in particular human blood clotting factor, is preferably selected from the group consisting of fibrinogen (FI), prothrombin (FII), tissue factor (FIII), FV, FVII, FVIII, FIX, FX, FXI, FXII, and FXIII, VWF, and ADAMTS13.

[0068] It is appreciated that the clotting factors FI, FII, FV, FVII, FVIII, FIX, FX, FXI, FXII, and FXIII can be in a non-active or an activated form. Thus, in the context of the invention, a reference to FI, FII, FV, FVII, FVIII, FIX, FX, FXI, FXII, and FXIII includes the activated forms FIa (fibrin), FIIa (thrombin), , FVa, FIXa, FVIIa, FVIIIa, FXa, FXIa, FXIIa, and FXIIIa, respectively unless explicitly stated otherwise or from the context, the activated form is logically excluded. Thus, e.g. in this context FI, FII, FV, FIX, FVII, FVIII, FX, FXI, FXII, and FXIII may be read as FI/FIa, FII/FIIa, , FV/FVa, FVII/FVIIa, FVIII/FVIIIa, FIX/FXIa, FX/FXa, FXI/FXIa, FXII/FXIIa, and FXIII/FXIIIa.

[0069] The transport protein, in particular human transport protein, may be selected from albumin, transferrin, ceruloplasmin, haptoglobin, hemoglobin, and hemopexin. According to one embodiment the mammalian protein is a protease inhibitor, in particular human protease inhibitor. Examples of such protease inhibitors are β-antithrombin, α-antithrombin, pre-latent-antithrombin, oxidized-antithrombin, 2-macroglobulin, C1-inhibitor, tissue factor pathway inhibitor (TFPI), heparin cofactor II, protein C inhibitor (PAI-3), Protein C, Protein S, and Protein Z.

[0070] Examples of immunoglobulins such as polyclonal antibodies (IgG), monoclonal antibodies, IgG1, IgG2, IgG3, IgG4, IgA, IgA1, IgA2, IgM, IgE, IgD, and Bence Jones protein.

[0071] The cell related plasma protein may be for example, fibronectin, thromboglobulin, or platelet factor 4. Examples of apolipoproteins are apo A-I, apo A-II, and apo E.

[0072] Complement factors according to the invention are e.g. Factor B, Factor D, Factor H, Factor I, C3b-Inactivator, properdin, C4-binding protein etc.

[0073] Examples of growth factors include Platelet derived growth factor (PDGF), Epidermal growth factor (EGF), Transforming growth factor alfa (TGF-α), Transforming growth factor beta (TGF-α), Fibroblast growth factor (FGF) and Hepatocyte growth factor (HGF).

[0074] Antiangionetic proteins include latent-antithrombin, prelatent-antithrombin, oxidized-antithrombin and plasminogen.

[0075] Examples of highly glycosylated proteins are alfa-1-acid glycoprotein, antichymotrypsin, inter-α-trypsin inhibitor, α-2-HS glycoprotein, C-reactive protein, Blood factors may be, e.g., erythropoeitin, interferon, tumor factors, tPA, or gCSF.

[0076] Other human blood proteins include histidine-rich glycoprotein, mannan binding lectin, C4-binding protein, fibronectin, GC-globulin, plasminogen/plasmin, α-1 microglobulin, C-reactive protein.

[0077] The mammalian protein is in particular selected from human VWF, fibrinogen, prothrombin, FiII, FV, FVII, FVIII, FIX, FX, FXI, FXII, FXIII, ADAMTS13, antithrombin, alpha-1 antitrypsin, C1-inhibitor, antichymotrypsin, PAI-1, PAI-3, 2-macroglobulin, TFPI, heparin cofactor II, Protein Z, Protein C, and Protein S.

[0078] Factor VIII in humans is coded by the F8 gene which comprises 187.000 base pairs in six exons. The transcribed mRNA has a length of 9.029 base pairs and is translated to a protein with 2.351 amino acids from which 19 amino acids are removed. The FVIII molecule in humans is glycosylated on 31 amino acids, with 25 N-glycosylations, and 6 O-glycosylations (see Kannicht et al., 2013).

[0079] After translation, the amino acid chain is cleaved by specific proteases in positions leading to the formation of a heavy chain with about 200 kDa and a light chain with about 80 kDa. The domain organization is typically characterized as A1-A2-B-A3-C1-C2. The light chain is a made-up of domains A3-C1-C2. The heavy chain is in principal composed of the domains A1-A2-B. Heavy chains found in plasma have a heterogeneous composition with molecular weights varying from 90 to 200 kDa. The reasons for this are the heterogeneity in its glycosylation, the existence of splice variants and the existence of proteolytic products such as the B domain depleted heavy chain A1-A2. The amino acid sequence of the full length FVIII is identified by amino acids 20 to 2.351 of P00451 of UniProtKB, sequence version 1 of July 21, 1986 (in the following UniProtKB P00451.1).

[0080] According to one embodiment the mammalian protein, to which the main protein is similar or identical, is human full length FVIII identified by amino acids 20 to 2.351 of UniProtKB P00451.1. According to another embodiment the main protein is FVIII, in which at least part of the B-domain is missing. In this regard the entire B-domain may be missing. The missing part of the B-domain is optionally replaced by a linker. The linker sequence has in particular the following amino acids sequence SFSQNSRHQAYRYRRG (SEQ ID NO: 12). An example of a

FVIII in which the B-domain is replaced by a linker, is Simoctocog alfa, the active ingredient of Nuwiq® or Vihuma®. Simoctocog alfa has the following sequence:

ATRRYYLGAVELSWDYMQSDLGELPVDARFPPRVPKSFPFNTSVVYKKTLFVEFTDHLFNIAKPRPPWMGLLGP
TIQAEVYDTVVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQREKEDDKVFPGGSHTYVWQVLKENGPMA
SDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDRDA
ASARAWPKMHTVNGYVNRSLPGLIGCHRKSVYWHVIGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTA
QTLLMDLGQFLLFCHISSHQHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRFDDDNSPSFIQ
IRSVAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGRKYKKVRFMAYTDETFKTREAIQH
ESGILGPLLYGEVGDTLLIIFKNQASRPYNIYPHGITDVRPLYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVE

DGPTKSDPRCLTRYYSSFVNMERDLASGLIGPLLICYKESVDQRGNQIMSDKRNVILFSVFDENRSWYLTENIQ
RFLPNPAGVQLEDPEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKHKMVYED
TLTLFPFSGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNTGDYYEDSYEDISAYLLSKNNAIEPR
SFSQNSRHQAYRYRRGEITRTTLQSDQEEIDYDDTISVEMKKEDFDIYDEDENQSPRSFQKKTRHYFIAAVERL
WDYGMSSSPHVLRNRAQSGSVPQFKKVVFQEFTDGSFTQPLYRGELNEHLGLLGPYIRAEVEDNIMVTFRNQAS
RPYSFYSSLISYEEDQRQGAEPRKNFVKPNETKTYFWKVQHHMAPTKDEFDCKAWAYFSDVDLEKDVHSGLIGP
LLVCHTNTLNPAHGRQVTVQEFALFFTIFDETKSWYFTENMERNCRAPCNIQMEDPTFKENYRFHAINGYIMDT
LPGLVMAQDQRIRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMALYNLYPGVFETVEMLPSKAGIWRVECLI
GEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDFQITASGQYGQWAPKLARLHYSGSINAWSTKEPFSWIKVDLL
APMIIHGIKTQGARQKFSSLYISQFIIMYSLDGKKWQTYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIR
LHPTHYSIRSTLRMELMGCDLNSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQGRSNAWRPQVN
NPKEWLQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLFFQNGKVKVFQGNQDSFTPVVNSLD
PPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY (SEQ ID NO: 13)

[0081] VWF is a multimeric adhesive glycoprotein present in the plasma of mammals, which has multiple physiological functions. During primary hemostasis, VWF acts as a mediator between specific receptors on the platelet surface and components of the extracellular matrix such as collagen. Moreover, VWF serves as a carrier and stabilizing protein for pro-coagulant Factor VIII. VWF is synthesized in endothelial cells and megakaryocytes as a 2813 amino acid precursor molecule.

[0082] The domain organization of VWF is typically characterized as Til3-D3-TIL4-A1-A2-A3-D4-C1-C2-C3-CK.

[0083] The precursor polypeptide, pre-pro-VWF, consists of a 22-residue signal peptide, a 741-residue pro-peptide (domains D1-D2) and the 2050-residue polypeptide found in mature plasma Von Willebrand Factor (Fischer et al., 1994). Full length VWF is identified by entry P04275 of UniprotKB (entry version 224 of April 12, 2017).

[0084] The human VWF according to the present invention has an amino acid sequence of any of the sequences said UniprotKB P04275, in particular SEQ ID NO: 2 (isoform 1). VWF contains two clusters of O-glycosylated amino acids. The first cluster of O-glycosylated amino acid is found between amino acids 1238 to 1268 of SEQ ID NO: 2. The second cluster includes amino acids 1468 to 1487 of SEQ ID NO: 2.

[0085] Upon secretion into plasma, VWF circulates in the form of various species with different molecular sizes. These VWF molecules consist of oligo- and multimers of the mature subunit of 2050 amino acid residues. VWF can be usually found in plasma as multimers ranging in size approximately from 500 to 20.000 kDa (Furlan et al., 1996).

[0086] According to one embodiment, the main protein has an amino acid sequence that is identical or similar to the sequence of human mature VWF.

[0087] According to another embodiment the main protein has an amino acid sequence that is similar or identical to the sequence of a fragment of human VWF.

[0088] For example, in the fragment of human VWF one or more of the domains A1, A2, A3, D4, C1, C2, C3, CK may be missing relative to the human mature VWF (Til3-D3-TIL4-A1-A2-A3-D4-C1-C2-C3-CK). The fragment VWF fragment may, for example, have a domain organization selected from the following group consisting of Til3-D3-TIL4-A1, Til3-D3-TIL4-A1-A2, Til3-D3-TIL4-A1-A2-A3, Til3-D3-TIL4-A1-A2-A3-D4, Til3-D3-TIL4-A1-A2-A3-D4-C1, Til3-D3-TIL4-A1-A2-A3-D4-C1-C2, and Til3-D3-TIL4-A1-A2-A3-D4-C1-C2-C3-CK.

[0089] In this regard the fragment of human VWF is in particular a fragment starting with amino acid 764 of SEQ ID NO: 2. Amino acids 764 to 1035 of SEQ ID NO: 2 comprise the FVIII binding domain of VWF.

[0090] The main protein may for example contain a fragment of VWF as defined in WO 2015/185758 A2. As shown in WO 2015/185758 A2, the complex of FVIII and the VWF fragments as defined therein exhibit a reduced binding to phospholipids membranes compared to FVIII alone as well as a reduced binding to collagen III and heparin compared to the complex of FVIII and full length VWF.

[0091] The fragment of VWF preferably starting with amino acid 764 of SEQ ID NO: 2 preferably ends with an amino acid of SEQ ID NO: 2 in the range from 1905 to 2153. According to one embodiment the VWF fragment ends with an amino acid of VWF in the range from 2030 to 2153 of SEQ ID NO: 2. According to a further embodiment the VWF fragment ends with an amino acid of SEQ ID NO: 2 in the range from 2100 to 2153.

[0092] According to one embodiment the main protein has an amino acid sequence that is similar or identical to amino acids 764 to 1268 of SEQ ID NO: 2. According to one embodiment the amino acid sequence of the main has an identity of at least 90 %, to amino acids 764 to 1268 of SEQ ID NO: 2. The amino acid sequence of the main protein may also have an identity of at least 95 % to amino acids 764 to 1268 of SEQ ID NO: 2. Furthermore, the identity to amino acids 764 to 1268 of SEQ ID NO: 2 of the amino acid sequence of the main protein may be at least 98 %. In particular, the amino acid sequence of the main protein may have an identity to amino acids 764 to 1268 of SEQ ID NO: 2 of 100 %.

[0093] According to one embodiment the main protein has an amino acid sequence that is similar or identical to amino acids 764 to 1905 of SEQ ID NO: 2. According to one embodiment the amino acid sequence of the main has an identity of at least 90 %, to amino acids 764 to 1905 of SEQ ID NO: 2. The amino acid sequence of the main protein may also have an identity of at least 95 % to amino acids 764 to 1905 of SEQ ID NO: 2. Furthermore, the identity to amino acids 764 to 1905 of SEQ ID NO: 2 of the amino acid sequence of the main protein may

be at least 98 %. In particular, the amino acid sequence of the main protein may have an identity to amino acids 764 to 1905 of SEQ ID NO: 2 of 100 %.

[0094] The fusion protein may contain any number of extension peptides, such as one, two, three, four, five, six, seven, eight, nine, or ten extension peptides. The fusion protein OCTA 12 contains two copies of the extension peptide and exhibits a significant increase in half-life as compared to the VWF fragment OCTA 11. Thus, according to one embodiment the fusion protein contains at least two extension peptides.

[0095] It is presently understood that the half-life prolongation effect is at least partially based on the negative charge of the O-glycans of the extension peptide. Thus, an increase in the copy number of the extension peptide leads to a further increase of the effect of half-life prolongation. This is confirmed by OCTA 14, which contains four copies of the extension peptide. Thus, according to one embodiment the fusion protein contains at least four extension peptides.

[0096] On the other hand, with the copy number of the extension peptide, the chance increases that the extension peptides interfere with the structural integrity or activity and, thus, the therapeutic effect of the main protein. Therefore, according to one embodiment the number of extension peptides is below 11.

[0097] The fusion protein may comprise further peptide components in addition to the main protein and the extension peptides. In particular, in addition to the extension peptide according to the invention the fusion protein may contain further peptides for half-life prolongation, such as CTP, XTEN, transferrin or fragments thereof, albumin or fragments thereof.

[0098] It is also possible that the main protein is a fragment of a mammalian protein and the fusion protein contains a further fragment of the same mammalian protein. In particular the two fragments are separated by one or more extension peptides. An example of such a protein is OCTA 15, which contains amino acids 764 to 1268 of VWF, two extension peptides with the sequence SEQ ID NO: 1 and the "cystein knot domain" of VWF consisting of amino acids 2721 to 2813 of SEQ ID NO: 2.

[0099] In the fusion protein, one or more extension peptides may be linked to the N-terminus or C-terminus of the main protein. Specifically, the fusion protein may contain one or more extension peptides linked to the N-terminus and one or more extension peptides linked to the C-terminus of the main protein.

[0100] As the fusion protein may contain further peptides in addition to the main protein and the one or more extension peptides. Accordingly, the extension peptides may be directly or indirectly linked to the main protein. In this regard, "directly linked" means that the amino acid sequences of the main protein and an extension peptide are directly adjacent. "Indirectly linked" means that between the main protein and the extension peptide a further peptide is located. In particular, a linker peptide could be located between the main protein and the

extension peptide. The linker may contain a cleavage site, making the extension peptide cleavable from the main protein.

[0101] The main protein, the one or more extension peptides and optionally the further peptides may be produced by joining of the genes, cDNAs, or sequences encoding them. Accordingly, the main protein, the one or more extension peptides and optionally the further peptides are linked by peptide bonds. According to the invention, the peptides of the fusion protein may instead be connected via other linkers such as chemical linkers or glycosidic bonds. Preferably, the peptides of the fusion protein are connected by peptide bonds.

[0102] According to one embodiment an extension peptide is directly linked to the C-terminus of the main protein. In particular, the fusion protein contains at least two consecutive extension peptides linked to the C-terminus of the main protein.

[0103] The fusion protein may be linked to two one or more affinity tags. Examples of affinity tags are polyhistidine, protein A, glutathione S transferase, substance P, FLAG, streptavidin, and an immunoglobulin heavy chain constant region. While the affinity tag generally forms part of the amino acid sequence of the full construct, the affinity tag is not considered as part of the fusion protein. The one or more affinity tags are preferably linked to the C-terminus or the N-terminus of the fusion protein. In case the fusion protein is linked to one or more affinity tags, the fusion protein preferably contains a cleavage site between the affinity tag and the rest of the protein making the affinity tag cleavable, e.g. by protease cleavage.

[0104] According to one embodiment, one extension peptide forms the N-terminus of the fusion protein. As explained above the N-terminal amino acid of said extension peptide is optionally linked to an affinity tag. According to one embodiment, one extension peptide forms the C-terminus of the fusion protein. As explained above the C-terminal amino acid of said extension peptide is optionally linked to an affinity tag.

[0105] According to one embodiment the fusion protein according to any of the preceding claims, wherein the fusion protein comprises at least 4, preferably at least 8, more preferably at least 12 additional O-glycans compared to the main protein.

[0106] According to one embodiment the fusion protein comprises a dimerization domain; in particular the main protein comprises a dimerization domain. In VWF, the dimers are formed by the binding of the CK-domains. Thus, in case the main protein is a VWF fragment, it preferably comprises the CK-domain.

[0107] A representative fusion protein according to the invention is OCTA 12. OCTA 12 has the following amino acid sequence (SEQ ID NO: 3):

SLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMSMGCVSGCLCPPGMVRHENRCVALERCPCFHQGKEYA
PGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLKYLFPGECQYVLVQDYCGSNPGTFRILVGN

KGCSHPSVKCKKRVTILVEGGEIELFDGEVNVKRPMKDETHFEVVESGRYIILLLGKALSVVWDRHLSISVVLK
QTYQEKVCGLCGNFDGIQNNDLTSSNLQVEEDPVDFGNSWKVSSQCADTRKVPLDSSPATCHNNIMKQTMVDSS
CRILTSDVFQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHGKVVTWRTATLCPQSCEER
NLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKILDELLQTCVDPEDCPVCEVAGRRFA

NLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKILDELLQTCVDPEDCPVCEVAGRRFA
SGKKVTLNPSDPEHCQICHCDVVNLTCEACQEPGGLVVPPTDAPVSPTTLYVEDISEPPLH**QEPGGLVVPPTDA**
PVSPTTLYVEDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLH

[0108] OCTA 12 is a fusion protein of the VWF fragment of amino acids 764 to 1268 of SEQ ID NO: 2 and two copies of an extension peptide (bold) bound to the C-terminus consisting of the amino acids 1238 to 1268 of SEQ ID NO: 2.

[0109] According to one embodiment the amino acid sequence of the fusion protein has an identity of at least 90 % to SEQ ID NO: 3. The amino acid sequence of the fusion protein may also have an identity of at least 95 % to SEQ ID NO: 3. Furthermore, the identity to SEQ ID NO: 3 of the amino acid sequence of the fusion protein may be at least 98 %. In particular, the amino acid sequence of the fusion protein may have an identity to SEQ ID NO: 3 of 100 %.

[0110] The following sequence (SEQ ID NO: 4) represents OCTA 12 with an additional 12 amino acid signal peptide (bold and underlined). An expression of this peptide provides a monomeric form of OCTA 12. The signal peptide is cleaved off.

MIPARFAGVLLALALILPGTLCSLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMSMGCVSGCLCPPGMV
RHENRCVALERCPCFHQGKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLKYLFPGEC
QYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKKRVTILVEGGEIELFDGEVNVKRPMKDETHFEVVESGRYII
LLLGKALSVVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQNNDLTSSNLQVEEDPVDFGNSWKVSSQCADTRKV
PLDSSPATCHNNIMKQTMVDSSCRILTSDVFQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVC
AQHGKVVTWRTATLCPQSCEERNLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKILDE
LLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQICHCDVVNLTCEACQEPGGLVVPPTDAPVSPTTLYV
EDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLH
(SEQ ID NO: 4)

[0111] According to one embodiment the amino acid sequence of the fusion protein has an identity of at least 90 % to SEQ ID NO: 4. The amino acid sequence of the fusion protein may also have an identity of at least 95 % to SEQ ID NO: 4. Furthermore, the identity to SEQ ID NO: 4 of the amino acid sequence of the fusion protein may be at least 98 %. In particular, the amino acid sequence of the fusion protein may have an identity to SEQ ID NO: 4 of 100 %.

[0112] A further representative fusion protein according to the invention is Pro-OCTA 12 including OCTA 12 and a propeptide (bold) with a signal peptide (bold and underlined). Pro-OCTA 12 is identified by SEQ ID NO: 5:

MIPARFAGVLLALALILPGTLCAEGTRGRSSTARCSLFGSDFVNTFDGSMYSFAGYCSYLLAGGCQKRSFSIIG
DFQNGKRVSLSVYLGEFFDIHLFVNGTVTQGDQRVSMPYASKGLYLETEAGYYKLSGEAYGFVARIDGSGNFQV
LLSDRYFNKTCGLCGNFNIFAEDDFMTQEGTLTSDPYDFANSWALSSGEQWCERASPPSSSCNISSGEMQKGLW
EQCQLLKSTSVFARCHPLVDPEPFVALCEKTLCECAGGLECACPALLEYARTCAQEGMVLYGWTDHSACSPVCP
AGMEYRQCVSPCARTCQSLHINEMCQERCVDGCSCPEGQLLDEGLCVESTECPCVHSGKRYPPGTSLSRDCNTC
ICRNSQWICSNEECPGECLVTGQSHFKSFDNRYFTFSGICQYLLARDCQDHSFSIVIETVQCADDRDAVCTRSV
TVRLPGLHNSLVKLKHGAGVAMDGQDVQLPLLKGDLRIQHTVTASVRLSYGEDLQMDWDGRGRLLVKLSPVYAG
KTCGLCGNYNGNQGDDFLTPSGLAEPRVEDFGNAWKLHGDCQDLQKQHSDPCALNPRMTRFSEEACAVLTSPTF
EACHRAVSPLPYLRNCRYDVCSCSDGRECLCGALASYAAACAGRGVRVAWREPGRCELNCPKGQVYLQCGTPCN
LTCRSLSYPDEECNEACLEGCFCPPGLYMDERGDCVPKAQCPCYYDGEIFQPEDIFSDHHTMCYCEDGFMHCTM
SGVPGSLLPDAVLSSPLSHRSKRSLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMSMGCVSGCLCPPGM
VRHENRCVALERCPCFHQGKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLKYLFPGE
CQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKKRVTILVEGGEIELFDGEVNVKRPMKDETHFEVVESGRYI
ILLLGKALSVVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQNNDLTSSNLQVEEDPVDFGNSWKVSSQCADTRK
VPLDSSPATCHNNIMKQTMVDSSCRILTSDVFQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHV
CAQHGKVVTWRTATLCPQSCEERNLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKILD
ELLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQICHCDVVNLTCEACQEPGGLVVPPTDAPVSPTTLY
VEDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLH

(SEQ ID NO: 5)

[0113] Expression of Pro-OCTA 12 results in the formation of dimers. The peptide dimers remain after cleavage of the propeptide.

[0114] According to one embodiment the amino acid sequence of the fusion protein has an identity of at least 90 %, to SEQ ID NO: 5. The amino acid sequence of the fusion protein may also have an identity of at least 95 % to SEQ ID NO: 5. Furthermore, the identity to SEQ ID NO: 5 of the amino acid sequence of the fusion protein may be at least 98 %. In particular, the amino acid sequence of the fusion protein may have an identity to SEQ ID NO: 5 of 100 %.

[0115] A further representative fusion protein according to the invention is OCTA 14. OCTA 14 has the following amino acid sequence:

SLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMSMGCVSGCLCPPGMVRHENRCVALERCPCFHQGKEYA
PGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLKYLFPGECQYVLVQDYCGSNPGTFRILVGN
KGCSHPSVKCKKRVTILVEGGEIELFDGEVNVKRPMKDETHFEVVESGRYIILLLGKALSVVWDRHLSISVVLK
QTYQEKVCGLCGNFDGIQNNDLTSSNLQVEEDPVDFGNSWKVSSQCADTRKVPLDSSPATCHNNIMKQTMVDSS
CRILTSDVFQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHGKVVTWRTATLCPQSCEER
NLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKILDELLQTCVDPEDCPVCEVAGRRFA
SGKKVTLNPSDPEHCQICHCDVVNLTCEACQEPGGLVVPPTDAPVSPTTLYVEDISEPPLH**QEPGGLVVPPTDA**

PVSPTTLYVEDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDI
SEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLH (SEQ ID NO: 6)

[0116] OCTA 14 is a fusion protein of the VWF fragment of amino acids 764 to 1268 of SEQ ID NO: 2 and four copies of an extension peptide (bold) bound to the C-terminus consisting of the amino acids 1238 to 1268 of SEQ ID NO: 2.

[0117] According to one embodiment the amino acid sequence of the fusion protein has an identity of at least 90 % to SEQ ID NO: 6. The amino acid sequence of the fusion protein may also have an identity of at least 95 % to SEQ ID NO: 6. Furthermore, the identity to SEQ ID NO: 6 of the amino acid sequence of the fusion protein may be at least 98 %. In particular, the amino acid sequence of the fusion protein may have an identity to SEQ ID NO: 6 of 100 %.

[0118] The following sequence (SEQ ID NO: 7) represents OCTA 14 with an additional 12 amino acid signal peptide (bold and underlined). An expression of this peptide provides a monomeric form of OCTA 14. The signal peptide is cleaved off.

MIPARFAGVLLALALILPGTLCSLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMSMGCVSGCLCPPGMV
RHENRCVALERCPCFHQGKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLKYLFPGEC
QYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKKRVTILVEGGEIELFDGEVNVKRPMKDETHFEVVESGRYII
LLLGKALSVVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQNNDLTSSNLQVEEDPVDFGNSWKVSSQCADTRKV
PLDSSPATCHNNIMKQTMVDSSCRILTSDVFQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVC
AQHGKVVTWRTATLCPQSCEERNLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKILDE
LLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQICHCDVVNLTCEACQEPGGLVVPPTDAPVSPTTLYV
EDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLHQEP
GGLVVPPTDAPVSPTTLYVEDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLH(SEQ ID NO: 7)

[0119] According to one embodiment the amino acid sequence of the fusion protein has an

identity of at least 90 % to SEQ ID NO: 7. The amino acid sequence of the fusion protein may also have an identity of at least 95 % to SEQ ID NO: 7. Furthermore, the identity to SEQ ID NO: 7 of the amino acid sequence of the fusion protein may be at least 98 %. In particular, the amino acid sequence of the fusion protein may have an identity to SEQ ID NO: 7 of 100 %.

[0120] A further representative fusion protein according to the invention is Pro-OCTA 14 including OCTA 14 and a propeptide (bold) with a signal peptide (bold and underlined). Pro-OCTA 14 is identified by SEQ ID NO: 8:

MIPARFAGVLLALALILPGTLCAEGTRGRSSTARCSLFGSDFVNTFDGSMYSFAGYCSYLLAGGCQKRSFSIIG
DFQNGKRVSLSVYLGEFFDIHLFVNGTVTQGDQRVSMPYASKGLYLETEAGYYKLSGEAYGFVARIDGSGNFQV

LLSDRYFNKTCGLCGNFNIFAEDDFMTQEGTLTSDPYDFANSWALSSGEQWCERASPPSSSCNISSGEMQKGLW
EQCQLLKSTSVFARCHPLVDPEPFVALCEKTLCECAGGLECACPALLEYARTCAQEGMVLYGWTDHSACSPVCP
AGMEYRQCVSPCARTCQSLHINEMCQERCVDGCSCPEGQLLDEGLCVESTECPCVHSGKRYPPGTSLSRDCNTC
ICRNSQWICSNEECPGECLVTGQSHFKSFDNRYFTFSGICQYLLARDCQDHSFSIVIETVQCADDRDAVCTRSV
TVRLPGLHNSLVKLKHGAGVAMDGQDVQLPLLKGDLRIQHTVTASVRLSYGEDLQMDWDGRGRLLVKLSPVYAG
KTCGLCGNYNGNQGDDFLTPSGLAEPRVEDFGNAWKLHGDCQDLQKQHSDPCALNPRMTRFSEEACAVLTSPTF
EACHRAVSPLPYLRNCRYDVCSCSDGRECLCGALASYAAACAGRGVRVAWREPGRCELNCPKGQVYLQCGTPCN
LTCRSLSYPDEECNEACLEGCFCPPGLYMDERGDCVPKAQCPCYYDGEIFQPEDIFSDHHTMCYCEDGFMHCTM
SGVPGSLLPDAVLSSPLSHRSKRSLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMSMGCVSGCLCPPGM
VRHENRCVALERCPCFHQGKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLKYLFPGE
CQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKKRVTILVEGGEIELFDGEVNVKRPMKDETHFEVVESGRYI
ILLLGKALSVVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQNNDLTSSNLQVEEDPVDFGNSWKVSSQCADTRK
VPLDSSPATCHNNIMKQTMVDSSCRILTSDVFQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHV
CAQHGKVVTWRTATLCPQSCEERNLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKILD
ELLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQICHCDVVNLTCEACQEPGGLVVPPTDAPVSPTTLY
VEDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLHQE
PGGLVVPPTDAPVSPTTLYVEDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLH (SEQ ID NO: 8)

[0121] According to one embodiment the amino acid sequence of the fusion protein has an identity of at least 90 % to SEQ ID NO: 8. The amino acid sequence of the fusion protein may also have an identity of at least 95 % to SEQ ID NO: 8. Furthermore, the identity to SEQ ID NO: 8 of the amino acid sequence of the fusion protein may be at least 98 %. In particular, the amino acid sequence of the fusion protein may have an identity to SEQ ID NO: 8 of 100 %.

[0122] A further representative fusion protein according to the invention is OCTA 15. OCTA 15 has the following amino acid sequence:

SLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMSMGCVSGCLCPPGMVRHENRCVALERCPCFHQGKEYA
PGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLKYLFPGECQYVLVQDYCGSNPGTFRILVGN
KGCSHPSVKCKKRVTILVEGGEIELFDGEVNVKRPMKDETHFEVVESGRYIILLLGKALSVVWDRHLSISVVLK
QTYQEKVCGLCGNFDGIQNNDLTSSNLQVEEDPVDFGNSWKVSSQCADTRKVPLDSSPATCHNNIMKQTMVDSS
CRILTSDVFQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHGKVVTWRTATLCPQSCEER
NLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKILDELLQTCVDPEDCPVCEVAGRRFA
SGKKVTLNPSDPEHCQICHCDVVNLTCEACQEPGGLVVPPTDAPVSPTTLYVEDISEPPLH**QEPGGLVVPPTDA**
PVSPTTLYVEDISEPPLHQEPGGLVVPPTDAPVPTTLYVEDISEPPLHEEPECNDITARLQYVKVGSCKSEVEV
DIHYCQGKCASKAMYSIDINDVQDQCSCCSPTRTEPMQVALHCTNGSVVYHEVLNAMECKCSPRKCSK (SEQ
ID NO: 9)

[0123] OCTA 15 is a fusion protein of the VWF fragment of amino acids 764 to 1268 of SEQ ID NO: 2, two copies of an extension peptide (bold) bound to the C-terminus consisting of the amino acids 1238 to 1268 of SEQ ID NO: 2 and the "cystein knot domain" of VWF consisting of amino acids 2721 to 2813 of SEQ ID NO: 2. According to one embodiment the amino acid

sequence of the fusion protein has an identity of at least 90 % to SEQ ID NO: 9. The amino acid sequence of the fusion protein may also have an identity of at least 95 % to SEQ ID NO: 9. Furthermore, the identity to SEQ ID NO: 9 of the amino acid sequence of the fusion protein may be at least 98 %. In particular, the amino acid sequence of the fusion protein may have an identity to SEQ ID NO: 9 of 100 %.

[0124] The following sequence (SEQ ID NO: 10) represents OCTA 15 with an additional 12 amino acid signal peptide (bold and underlined). An expression of this peptide provides a dimeric form of OCTA 15. The signal peptide is cleaved off.

MIPARFAGVLLALALILPGTLCSLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMSMGCVSGCLCPPGMV
RHENRCVALERCPCFHQGKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLKYLFPGEC
QYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKKRVTILVEGGEIELFDGEVNVKRPMKDETHFEVVESGRYII
LLLGKALSVVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQNNDLTSSNLQVEEDPVDFGNSWKVSSQCADTRKV
PLDSSPATCHNNIMKQTMVDSSCRILTSDVFQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVC
AQHGKVVTWRTATLCPQSCEERNLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKILDE
LLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQICHCDVVNLTCEACQEPGGLVVPPTDAPVSPTTLYV
EDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLHQEPGGLVVPPTDAPVPTTLYVEDISEPPLHEEPE
CNDITARLQYVKVGSCKSEVEVDIHYCQGKCASKAMYSIDINDVQDQCSCCSPTRTEPMQVALHCTNGSVVYHE
VLNAMECKCSPRKCSK (SEQ ID NO: 10)

[0125] According to one embodiment the amino acid sequence of the fusion protein has an identity of at least 90 % to SEQ ID NO: 10. The amino acid sequence of the fusion protein may also have an identity of at least 95 % to SEQ ID NO: 10. Furthermore, the identity to SEQ ID NO: 10 of the amino acid sequence of the fusion protein may be at least 98 %. In particular, the amino acid sequence of the fusion protein may have an identity to SEQ ID NO: 10 of 100 %.

[0126] A further representative fusion protein according to the invention is Pro-OCTA 15 including OCTA 15 and a propeptide (bold) with a signal peptide (bold and underlined). The expression of this sequence will result in formation of multimers. Pro-OCTA 15 is identified by SEQ ID NO: 11:

MIPARFAGVLLALALILPGTLCAEGTRGRSSTARCSLFGSDFVNTFDGSMYSFAGYCSYLLAGGCQKRSFSIIG
DFQNGKRVSLSVYLGEFFDIHLFVNGTVTQGDQRVSMPYASKGLYLETEAGYYKLSGEAYGFVARIDGSGNFQV
LLSDRYFNKTCGLCGNFNIFAEDDFMTQEGTLTSDPYDFANSWALSSGEQWCERASPPSSSCNISSGEMQKGLW
EQCQLLKSTSVFARCHPLVDPEPFVALCEKTLCECAGGLECACPALLEYARTCAQEGMVLYGWTDHSACSPVCP
AGMEYRQCVSPCARTCQSLHINEMCQERCVDGCSCPEGQLLDEGLCVESTECPCVHSGKRYPPGTSLSRDCNTC
ICRNSQWICSNEECPGECLVTGQSHFKSFDNRYFTFSGICQYLLARDCQDHSFSIVIETVQCADDRDAVCTRSV
TVRLPGLHNSLVKLKHGAGVAMDGQDVQLPLLKGDLRIQHTVTASVRLSYGEDLQMDWDGRGRLLVKLSPVYAG
KTCGLCGNYNGNQGDDFLTPSGLAEPRVEDFGNAWKLHGDCQDLQKQHSDPCALNPRMTRFSEEACAVLTSPTF

EACHRAVSPLPYLRNCRYDVCSCSDGRECLCGALASYAAACAGRGVRVAWREPGRCELNCPKGQVYLQCGTPCN
LTCRSLSYPDEECNEACLEGCFCPPGLYMDERGDCVPKAQCPCYYDGEIFQPEDIFSDHHTMCYCEDGFMHCTM
SGVPGSLLPDAVLSSPLSHRSKRSLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMSMGCVSGCLCPPGM
VRHENRCVALERCPCFHQGKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLKYLFPGE
CQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKKRVTILVEGGEIELFDGEVNVKRPMKDETHFEVVESGRYI
ILLLGKALSVVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQNNDLTSSNLQVEEDPVDFGNSWKVSSQCADTRK
VPLDSSPATCHNNIMKQTMVDSSCRILTSDVFQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHV
CAQHGKVVTWRTATLCPQSCEERNLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKILD
ELLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQICHCDVVNLTCEACQEPGGLVVPPTDAPVSPTTLY
VEDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLHQEPGGLVVPPTDAPVPTTLYVEDISEPPLHEEP
ECNDITARLQYVKVGSCKSEVEVDIHYCQGKCASKAMYSIDINDVQDQCSCCSPTRTEPMQVALHCTNGSVVYH
EVLNAMECKCSPRKCSK (SEQ ID NO: 11)

[0127] According to one embodiment the amino acid sequence of the fusion protein has an identity of at least 90 % to SEQ ID NO: 11. The amino acid sequence of the fusion protein may also have an identity of at least 95 % to SEQ ID NO: 11. Furthermore, the identity to SEQ ID NO: 11 of the amino acid sequence of the fusion protein may be at least 98 %. In particular, the amino acid sequence of the fusion protein may have an identity to SEQ ID NO: 11 of 100 %.

[0128] According to one embodiment of the invention the fusion protein is a modified FVIII protein based on Simoctocog alfa with two or more copies of the extension peptide.

[0129] In this embodiment, the main protein is preferably identical or similar to the heavy chain of FVIII, in particular to amino acids 20 to 759 of UniprotKB P00451.1. The fusion protein with a main protein identical or similar to the heavy chain of FVIII, in particular to amino acids 20 to 759 of UniprotKB P00451.1, preferably additionally contains a linker similar or identical to SEQ ID NO: 12 and a further amino acid sequence similar or identical to the light chain as identified by amino acids 1668 to 2351 of UniprotKB entry P0045.1.

[0130] The extension peptides may be fused to the C-terminus of the light chain. Alternatively, the extension peptides are located between the heavy chain and the light chain. In this regard the extension peptides may be connected to the C-terminus or the N-terminus of the linker. The extension peptides may also replace the linker. Moreover, the linker sequence may be interrupted by one or more extension peptides. It is also possible that extension peptides are located both between heavy and the light chain and on the C-terminus of the light chain. Preferably, the fusion protein based on Simoctocog alfa contains, from the N-terminus to the C-terminus, the heavy chain of FVIII, a first part of a linker, two or more, preferably three extension peptides (bold), a second part of a linker (underlined and bold) and the light chain. An example of such a protein is the protein identified by SEQ ID NO: 14:

ATRRYYLGAVELSWDYMQSDLGELPVDARFPPRVPKSFPFNTSVVYKKTLFVEFTDHLFNIAKPRPPWMGLLGP
TIQAEVYDTVVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQREKEDDKVFPGGSHTYVWQVLKENGPMA
SDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDRDA
ASARAWPKMHTVNGYVNRSLPGLIGCHRKSVYWHVIGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTA
QTLLMDLGQFLLFCHISSHQHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRFDDDNSPSFIQ
IRSVAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGRKYKKVRFMAYTDETFKTREAIQH
ESGILGPLLYGEVGDTLLIIFKNQASRPYNIYPHGITDVRPLYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVE
DGPTKSDPRCLTRYYSSFVNMERDLASGLIGPLLICYKESVDQRGNQIMSDKRNVILFSVFDENRSWYLTENIQ
RFLPNPAGVQLEDPEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKHKMVYED
TLTLFPFSGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNTGDYYEDSYEDISAYLLSKNNAIEPR
SFSQNSRHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLHQEPGGLVVPPTDAPVSPTTLYVEDISEPPLHQEPG
GLVVPPTDAPVSPTTLYVEDISEPPLHRYRRGEITRTTLQSDQEEIDYDDTISVEMKKEDFDIYDEDENQSPRS
FQKKTRHYFIAAVERLWDYGMSSSPHVLRNRAQSGSVPQFKKVVFQEFTDGSFTQPLYRGELNEHLGLLGPYIR
AEVEDNIMVTFRNQASRPYSFYSSLISYEEDQRQGAEPRKNFVKPNETKTYFWKVQHHMAPTKDEFDCKAWAYF
SDVDLEKDVHSGLIGPLLVCHTNTLNPAHGRQVTVQEFALFFTIFDETKSWYFTENMERNCRAPCNIQMEDPTF
KENYRFHAINGYIMDTLPGLVMAQDQRIRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMALYNLYPGVFETV
EMLPSKAGIWRVECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDFQITASGQYGQWAPKLARLHYSGSIN
AWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFSSLYISQFIIMYSLDGKKWQTYRGNSTGTLMVFFGNVDSSG
IKHNIFNPPIIARYIRLHPTHYSIRSTLRMELMGCDLNSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKA
RLHLQGRSNAWRPQVNNPKEWLQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLFFQNGKVKV
FQGNQDSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY (SEQ ID NO: 14)

[0131] According to one embodiment the amino acid sequence of the fusion protein has an identity of at least 90 % to SEQ ID NO: 14. The amino acid sequence of the fusion protein may also have an identity of at least 95 % to SEQ ID NO: 14. Furthermore, the identity to SEQ ID

NO: 14 of the amino acid sequence of the fusion protein may be at least 98 %. In particular, the amino acid sequence of the fusion protein may have an identity to SEQ ID NO: 14 of 100 %.

[0132] Alternatively, the fusion protein based on Simoctocog alfa contains two or more, preferably three extension peptides (bold) connected to the C-terminus of Simoctocog alfa. An example of such a protein is the protein identified by SEQ ID NO: 21. According to one embodiment the amino acid sequence of the fusion protein has an identity of at least 90 % to SEQ ID NO: 21. The amino acid sequence of the fusion protein may also have an identity of at least 95 % to SEQ ID NO: 21. Furthermore, the identity to SEQ ID NO: 21 of the amino acid sequence of the fusion protein may be at least 98 %. In particular, the amino acid sequence of the fusion protein may have an identity to SEQ ID NO: 21 of 100 %.

Polynucleotide

[0133] According to a second aspect, the invention provides an isolated polynucleotide that comprises a nucleic acid sequence encoding a fusion protein according to the first aspect of the invention.

[0134] The isolated polynucleotide may be a DNA molecule or an RNA molecule. The isolated polynucleotide is preferably a DNA molecule, in particular a cDNA molecule. The techniques used to isolate or clone a polynucleotide encoding a peptide are known in the art and include isolation from genomic DNA, preparation from cDNA, or a combination thereof. The cloning of the polynucleotides from such genomic DNA can be effected, e.g., by using the well-known polymerase chain reaction (PCR) or antibody screening of expression libraries to detect cloned DNA fragments with shared structural features (see, e.g., Innis et al, 1990) PCR: A Guide to Methods and Application, Academic Press, New York. Other nucleic acid amplification procedures such as ligase chain reaction (LCR), ligation activated transcription (LAT) and polynucleotide-based amplification (NASBA) may be used.

[0135] In particular, the sequence of the isolated polynucleotide may comprise a first part encoding the main protein and at least one second part sequence. The first part is preferably similar or identical to the SEQ ID NO: 15. The first part preferably has a degree of sequence identity SEQ ID NO: 15 of at least 80 %, at least 85 %, at least 90 %, at least 95 %, at least 96 %, at least 97 %, at least 98 %, at least 99 %, or 100 %.

[0136] The at least one second part is preferably similar or identical to SEQ ID NO: 16. The second part preferably has a degree of sequence identity SEQ ID NO: 16 of at least 80 %, at least 85 %, at least 90 %, at least 95 %, at least 96 %, at least 97 %, at least 98 %, at least 99 %, or 100 %.

[0137] The isolated polynucleotide may be a DNA molecule encoding a fusion protein with an amino acid sequence similar or identical to a sequence selected from the group consisting of

SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 14 and SEQ ID NO: 21.

[0138] In particular, the isolated polynucleotide may be a DNA molecule encoding a fusion protein having an amino acid sequence with an identity of at least 90 %, preferably at least 95 %, more preferably at least 98 %, most preferably 100 % to SEQ ID NO: 4. Alternatively, the isolated polynucleotide may be a DNA molecule encoding a fusion protein having an amino acid sequence with an identity of at least 90 %. Moreover, the isolated polynucleotide may be a DNA molecule encoding a fusion protein having an amino acid sequence with an identity of at least 90 %.preferably at least 95 %, more preferably at least 98 %, most preferably 100 % to SEQ ID NO: 5. According to one embodiment the isolated polynucleotide is a DNA molecule encoding a fusion protein having an amino acid sequence with an identity of at least 90 %.preferably at least 95 %, more preferably at least 98 %, most preferably 100 % to SEQ ID NO: 7. According to one embodiment, the isolated polynucleotide is a DNA molecule encoding a fusion protein having an amino acid sequence with an identity of at least 90 %.preferably at least 95 %, more preferably at least 98 %, most preferably 100 % to SEQ ID NO: 8. According to one embodiment the isolated polynucleotide is a DNA molecule encoding a fusion protein having an amino acid sequence with an identity of at least 90 %.preferably at least 95 %, more preferably at least 98 %, most preferably 100 % to SEQ ID NO: 10. According to one embodiment the isolated polynucleotide is a DNA molecule encoding a fusion protein having an amino acid sequence with an identity of at least 90 %.preferably at least 95 %, more preferably at least 98 %, most preferably 100 % to SEQ ID NO: 11. According to one embodiment the isolated polynucleotide is a DNA molecule encoding a fusion protein having an amino acid sequence with an identity of at least 90 %.preferably at least 95 %, more preferably at least 98 %, most preferably 100 % to and SEQ ID NO: 14. According to one embodiment the isolated polynucleotide is a DNA molecule encoding a fusion protein having an amino acid sequence with an identity of at least 90 %.preferably at least 95 %, more preferably at least 98 %, most preferably 100 % to and SEQ ID NO: 21.

[0139] The isolated polynucleotide may be a DNA molecule with a sequence similar or identical to a sequence selected from the group consisting of SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20 and SEQ ID NO: 22.

[0140] According to one embodiment, one strand of the isolated polynucleotide has a sequence identity to SEQ ID NO: 17 of at least 80 %, at least 85 %, at least 90 %, at least 95 %, at least 96 %, at least 97 %, at least 98 %, at least 99 %, or 100 %.

[0141] According to a further embodiment, the isolated polynucleotide has a sequence identity to SEQ ID NO: 18 of at least 80 %, at least 85 %, at least 90 %, at least 95 %, at least 96 %, at least 97 %, at least 98 %, at least 99 %, or 100 %. According to still another embodiment, the isolated polynucleotide has a sequence identity to SEQ ID NO: 19 of at least 80 %, at least 85 %, at least 90 %, at least 95 %, at least 96 %, at least 97 %, at least 98 %, at least 99 %, or 100 %. According to one embodiment, the isolated polynucleotide has a sequence identity to SEQ ID NO: 20 of at least 80 %, at least 85 %, at least 90 %, at least 95 %, at least 96 %, at least 97

%, at least 98 %, at least 99 %, or 100 %. According to one embodiment, the isolated polynucleotide has a sequence identity to SEQ ID NO: 20 of at least 80 %, at least 85 %, at least 90 %, at least 95 %, at least 96 %, at least 97 %, at least 98 %, at least 99 %, or 100 %.

List of the polynucleotide sequences:

[0142]

SEQ ID NO: 15	DNA encoding OCTA 11 (AA 1-1268 of SEQ ID NO: 2)
SEQ ID NO: 16	DNA encoding the extension peptide (SEQ ID NO: 1)
SEQ ID NO: 17	DNA encoding Pro-OCTA 12 (SEQ ID NO: 5)
SEQ ID NO: 18	DNA encoding Pro-OCTA 14 (SEQ ID NO: 8)
SEQ ID NO: 19	DNA encoding Pro-OCTA 15 (SEQ ID NO: 11)
SEQ ID NO: 20	DNA encoding Simoctocog alfa with three extension peptides in the linker region (SEQ ID NO 14)
SEQ ID NO: 22	DNA sequence encoding Simoctocog alfa with three C-terminal extension peptides (SEQ ID NO: 21)

Expression vector

[0143] In a third aspect the invention also relates to expression vectors comprising a polynucleotide according to the second aspect of the invention.

[0144] The expression vector further preferably comprises control elements such as a promoter, and transcriptional and translational stop signals. The polynucleotide according to the second aspect and of the control elements may be joined together to produce a recombinant expression vector that may include one or more restriction sites to allow for insertion or substitution of the polynucleotide encoding the polypeptide at such sites. The polynucleotide may be inserted into an appropriate expression vector for expression. In creating the expression vector, the coding sequence is located in the expression vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

[0145] The recombinant expression vector may be any vector (e.g., a plasmid or virus) that can be conveniently subjected to recombinant DNA procedures and can bring about expression of the polynucleotide of the fourth aspect of the invention. The choice of the expression vector will typically depend on the compatibility of the expression vector with the

host cell into which the expression vector is to be introduced. The expression vectors may be a linear or closed circular plasmid.

[0146] The expression vector is preferably adapted to expression in mammalian cells. The expression vector may be an autonomously replicating vector, i.e., a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. The origin of replication may be any plasmid replicator mediating autonomous replication that functions in a cell. The term "origin of replication" or "plasmid replicator" means a polynucleotide that enables a plasmid or vector to replicate in vivo.

[0147] The vector is preferably one that, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. For integration into the host cell genome, the expression vector may rely on any other element of the expression vector for integration into the genome by homologous or non-homologous recombination. Alternatively, the vector may contain additional polynucleotides for directing integration by homologous recombination into the genome of the host cell at a precise location in the chromosome.

[0148] The vectors of the present invention preferably contain one or more (e.g., several) selectable markers that permit easy selection of transformed, transfected, transduced, or the like cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

[0149] The procedures used to ligate the elements described above to construct the recombinant expression vectors of the present invention are well known to one skilled in the art (see, e.g., Sambrook et al., 1989, supra).

[0150] According to one embodiment the vector backbone of the vector according to the third aspect is selected from pCDNA3, pCDNA3.1, pCDNA4, pCDNA5, pCDNA6, pCEP4, pCEP-puro, pCET1019, pCMV, pEF1, pEF4, pEF5, pEF6, pExchange, pEXPR, pIRES, and pSCAS.

Host Cell

[0151] According to a fourth aspect the invention provides a host cell, comprising the expression vector according the third aspect of the invention. The expression vector according to the third aspect is introduced into a host cell so that the expression vector is maintained as a chromosomal integrant or as a self-replicating extrachromosomal vector as described earlier. The term "host cell" encompasses any progeny of a parent cell that is not identical to the parent cell due to mutations that occur during replication. The choice of a host cell will to a large extent depend upon the gene encoding the polypeptide and its source.

[0152] According to one embodiment the fusion protein is produced by expression in a mammalian host cell line. The fusion protein is preferably produced in a human host cell line. Generally, any human host cell line is suitable for expression of the fusion protein. A favourable glycosylation of the fusion protein is particularly obtained with human kidney cell lines. Preferred human kidney cell lines are HEK cell-lines, in particular HEK 293 cell lines.

[0153] Examples of HEK cell-lines for production of the glycosylated polypeptide are HEK 293 F, Flp-In™-293 (Invitrogen, R75007), 293 (ATCC® CRL-1573), 293 EBNA, 293 H (ThermoScientific 11631017), 293S, 293T (ATCC® CRL-3216™), 293T/17 (ATCC® CRL11268™), 293T/17 SF (ATCC® ACS4500™), HEK 293 STF (ATCC® CRL 3249™), HEK-293.2sus (ATCC® CRL-1573™). A preferred cell line for production of the polypeptide is the HEK 293 F cell line.

[0154] Other cell lines suitable as host cells for expression include cell lines derived from human myeloid leukemia cells. Specific examples of host cells are K562, NM-F9, NM-D4, NM-H9D8, NM-H9D8-E6, NM H9D8- E6Q12, GT-2X, GT-5s and cells derived from anyone of said host cells. K562 is a human myeloid leukemia cell line present in the American Type Culture Collection (ATCC CCL-243). The remaining cell lines are derived from K562 cells and have been selected for specific glycosylation features.

Use of the fusion protein

[0155] As shown in the examples, the extension peptides of SEQ ID NO: 1 in the fusion proteins OCTA 12 and OCTA 14 do not only lead to an increase of half-life of the fusion protein, i.e. as compared to the main protein, i.e. the VWF fragment. The fusion proteins OCTA 12 and OCTA 14, when administered together with FVIII, the binding partner of VWF, to a patient also lead to an increase in half-life of FVIII.

Composition and protein complex

[0156] Accordingly, the concept according to the invention, namely the half-life prolongation provided by the extension peptides is not limited to the fusion protein, but in addition the half-life of a second protein, which is bound by the fusion protein, can be extended.

[0157] Thus, according to a fifth aspect the invention provides a composition of a first protein and a second protein, wherein said first protein is a fusion protein according to the first aspect and is capable of binding said second protein, and said second protein is a therapeutic protein comprising an amino acid sequence which is identical or similar to the amino acid sequence of a second mammalian protein or fragment thereof.

[0158] The first protein may bind to the second protein covalently or non-covalently to form a complex. Accordingly, the present invention also relates to a complex of a first protein and a second protein, wherein said first protein is a fusion protein according to the first aspect, and said second protein has an amino acid sequence which is identical or similar to the amino acid sequence of a second mammalian protein or fragment thereof. Accordingly, the complexes are formed by non-covalent binding of the first protein to the second protein.

[0159] According to one embodiment the first protein binds to the second protein covalently. The linker facilitating the binding of the first and second protein may be selected from a disulfide bridge, peptide bond, a chemical linker, or a glycosidic bond.

[0160] Alternatively, the first protein binds to the second protein non-covalently. For the non-covalent binding, the first protein may, in particular, comprise a binding domain specific that renders it capable of binding to said second protein, i.e. a second protein binding domain. Depending on the location of the one or more extension peptides in the sequence of the first protein is may be located in different positions of the first protein. Preferably, the one or more extension peptides are located in a position that is exposed to the surface in the folded stated of the protein. The one or more extension peptides may be located in any position relative to the second protein binding site, e.g. the binding domain.

[0161] According to one embodiment of the composition, the one or more extension peptides are located in a position in the folded state of the first protein that does not interfere with the binding of the first protein to the second protein.

[0162] According to one embodiment, the half-life of the second protein, e.g. FVIII, bound to the first protein, e.g. a VWF fragment, is increased as compared to the free form of said second protein, e.g. a FVIII protein.

[0163] Preferably, the half-life of the second protein, e.g. a FVIII protein, bound to the first protein, e.g. OCTA 12, is increased as compared to said second protein bound to the native mammalian protein, e.g. mature VWF.

[0164] More preferably, the second protein, e.g. a FVIII protein, bound to the first protein, e.g. OCTA 12, is increased as compared to said second protein bound to the main protein without fusion peptide, e.g. OCTA 11.

[0165] The second mammalian protein may be selected from the same list as identified for the mammalian protein above. However, in the composition or complex, the second mammalian protein is not the same as the first mammalian protein.

[0166] According to one embodiment the second mammalian protein is a blood protein, in particular a human blood protein. Preferably the second mammalian protein is a coagulation factor, in particular a human coagulation factor.

[0167] According to one embodiment the second mammalian protein, to which the main protein is similar or identical, is human full length FVIII identified by amino acids 20 to 2,351 of UniProtKB P00451.1). According to another embodiment, the main protein is FVIII, in which at least part of the B-domain is missing. In this regard the entire B-domain may be missing. The missing part of the B-domain is optionally replaced by a linker. The linker sequence has in particular the following amino acids sequence SFSQNSRHQAYRYRRG (SEQ ID NO: 12). An example of a FVIII in which the B-domain is replaced by a linker, is Simoctocog alfa (SEQ ID NO: 13), the active ingredient of Nuwiq® or Vihuma®.

[0168] According to one embodiment, the FVIII protein is a human FVIII protein with a reduced immune response in patients.

[0169] The reduced immune response of the FVIII protein is preferably based on the binding to SIGLECs SIG-5, SIG-7, SIG-8 and SIG-9. Without wanting to be bound to theory, it is believed that the binding to SIGLECS on antigen presenting cells (like e.g. dendritic cells) lead to down-regulation of pro-inflammatory and upregulation of immunosuppressive receptor expression on the cell surface. Also, the binding leads to an enhanced production of anti-inflammatory cytokines, lowers the production of pro-inflammatory cytokines, and in consequence leads to the inhibition of T-cell proliferation and antibody production. Thus, binding of the SIGLECs SIG-5, SIG-7, SIG-8 and SIG-9 leads to a reduced immune response or increased immune tolerance when the glycosylated polypeptide is administered to a patient.

[0170] The SIGLEC binding, and consequently, the reduced immune response is based on an increased number or percentage of sialylated core 2 and/or extended core 1 O-glycans in the glycosylated protein as compared to the number of sialylated core 2 and/or extended core 1 O-glycans of the naturally occurring human FVIII.

[0171] Thus, according to one embodiment the FVIII protein exhibits an increased number or percentage of sialylated core 2 and/or extended core 1 O-glycans in the glycosylated protein as compared to the number of sialylated core 2 and/or extended core 1 O-glycans of the naturally occurring human FVIII.

[0172] For the case that the second protein is an FVIII protein, the main protein of the first protein is preferably a fragment of VWF comprising the FVIII binding domain to make it capable of binding to the FVIII protein.

[0173] According to one embodiment of the composition, the first protein has an amino acid sequence with an identity of at least 95 %, preferably at least 98 % more preferably 100 % to SEQ ID NO: 3 and the second protein has an amino acid with an identity of at least 95 %, preferably at least 98 % more preferably 100 % to SEQ ID NO: 13.

[0174] According to one embodiment of the composition, the first protein has an amino acid sequence with an identity of at least 95 %, preferably at least 98 % more preferably 100 % to SEQ ID NO: 6 and the second protein has an amino acid with an identity of at least 95 %,

preferably at least 98 % more preferably 100 % to SEQ ID NO: 13.

[0175] According to one embodiment of the composition, the first protein has an amino acid sequence with an identity of at least 95 %, preferably at least 98 % more preferably 100 % to SEQ ID NO: 9 and the second protein has an amino acid with an identity of at least 95 %, preferably at least 98 % more preferably 100 % to SEQ ID NO: 13.

[0176] Because in the blood of the patient the fusion protein containing the fragment of VWF, in particular OCTA 12, competes with endogenous VWF for binding to the FVIII protein, it is preferred that the composition comprises the fusion protein containing the fragment of VWF, in particular OCTA 12, in molar excess as compared to the FVIII protein.

[0177] Preferably, the molar ratio of the first protein to the second protein is in the range from 0.1 to 250, preferably in the range from 0.5 to 50 more preferably in the range from 1 to 25, most preferably in the range from 2 to 10.

[0178] To form a stable non-covalently bound complex and, therefore, allow the half-life prolongation of the second protein, the binding affinity of the first protein to the second protein defined by the equilibrium dissociation constant (K_D) should be below 10 µM. Preferably, the equilibrium dissociation constant of the VWF fragment in the first protein to the FVIII protein is in the range from 0.05 to 3 nM.

[0179] The first and second protein can be produced by separate recombinant expression and joined afterwards. Alternatively, the first and second protein are recombinantly expressed in the same cell. For this, the first and second protein may be encoded by the same vector or on two different vectors.

[0180] The VWF constructs used in the examples, i.e. OCTA 12, OCTA 14 and OCTA 15 were expressed in the form of their pro-proteins, leading to dimer formation or in case of OCTA 15 leading to multimer formation. These dimers remain intact even after cleavage of the pro-peptide and consequently each of the copies of the VWF construct in the dimer can bind to a FVIII protein. Thus, according to one embodiment, the complex contains two copies of the first and the second protein, wherein the two copies of the first protein form a dimer. This dimer of the first protein is preferably a non-covalently bound dimer.

Pharmaceutical composition and medical use

[0181] As described above, the fusion protein according to the first aspect and the composition according to the fifth aspect of the invention have the advantage of an increased half-life in the blood of patients and therefore increased therapeutic effect in patients. Therefore, the fusion protein according to the first aspect and the composition according to the fifth aspect are in particular useful as active ingredients for medical treatment. Preferably, they are useful for

treatment or prevention of a bleeding disorder. The fusion protein according to the first aspect and the composition according to the fifth aspect described herein can be administered alone or in the form of pharmaceutical compositions.

[0182] According to the invention, the pharmaceutical composition may comprise an effective amount of fusion protein according to the first aspect and the composition according to the fifth aspect formulated with at least one pharmaceutically acceptable carrier. Pharmaceutical compositions of the embodiments can be prepared and administered to a subject by any methods well known in the art of pharmacy. See, e. g, Goodman & Gilman's The Pharmacological Basis of Therapeutics, Hardman et al., eds., McGraw-Hill Professional (10th ed., 2001); Remington: The Science and Practice of Pharmacy, Gennaro, ed., Lippincott Williams & Wilkins (20th ed., 2003); and Pharmaceutical Dosage Forms and Drug Delivery Systems, Ansel et al. (eds), Lippincott Williams & Wilkins (7th ed., 1999). In addition, the pharmaceutical compositions of the embodiments may also be formulated to include other medically useful drugs or biological agents. The pharmaceutical composition typically comprises a therapeutically effective amount of the fusion protein or protein complex combined with a pharmaceutically acceptable carrier. The pharmaceutically acceptable carrier is any carrier known or established in the art. Exemplary pharmaceutically acceptable carriers include sterile pyrogen-free water and sterile pyrogen-free saline solution. Other forms of pharmaceutically acceptable carriers that can be utilized for the present embodiments include binders, disintegrants, surfactants, absorption accelerators, moisture retention agents, absorbers, lubricants, fillers, extenders, moisture imparting agents, preservatives, stabilizers, emulsifiers, solubilising agents, salts which control osmotic pressure, diluting agents such as buffers and excipients usually used depending on the use form of the formulation. These are optionally selected and used depending on the unit dosage of the resulting formulation.

[0183] As used herein "bleeding disorder" refers to a disease or condition that impairs normal hemostasis. The bleeding disorder can be, for example, Hemophilia A, Hemophilia B, Factor VIII deficiency, Factor XI deficiency, von Willebrand Disease, Glanzmann's Thrombasthenia, Bernard Soulier Syndrome, idiopathic thrombocytopenic purpura, intracerebral hemorrhage, trauma, traumatic brain injury, and the like.

[0184] As used herein, "hemophilia" refers to a group of bleeding disorders associated with increased blood clot formation time as compared to blood clot formation time in healthy individuals without hemophilia. Hemophilia includes Hemophilia A, which is a disorder that leads to the production of defective Factor VIII, Hemophilia B, which is a disorder that leads to the production of defective Factor IX and acquired Hemophilia A, a rare bleeding disorder caused by an autoantibody to coagulation factor (F) VIII.

[0185] The bleeding disorder is preferably Hemophilia A or B. The treatment may for example be the hemophilia treatment of PUPS (Previously untreated patients) or an immune tolerance induction (ITI) treatment and/or other related treatments of haemophilia disorders.

[0186] For *in vivo* applications, pharmaceutical compositions can be administered to the

patient by any customary administration route, e. g., orally, parenterally or by inhalation. Parenteral administration includes intravenous injection, subcutaneous injection, intraperitoneal injection, intramuscular injection, liquid agents, suspensions, emulsions and dripping agents. For parenteral administration the pharmaceutical composition should be an injectable agent such as a liquid agent or a suspension.

[0187] The pharmaceutical composition may be administered orally to a patient. In these embodiments, a form of the drug includes solid formulations such as tablets, coated tablets, powdered agents, granules, capsules and pills, liquid formulations such as liquid agents (e.g., eye drops, nose drops), suspension, emulsion and syrup, inhales such as aerosol agents, atomizers and nebulizers, and liposome inclusion agents. The glycosylated polypeptide, protein complex or pharmaceutical composition can be administered by inhalation to the respiratory tract of a patient to target the trachea and/or the lung of a subject.

[0188] The use may comprise an intravenous or non-intravenous injection. The non-intravenous injection preferably is a subcutaneous injection.

EXAMPLES

Example 1 - Recombinant expression of VWF proteins

[0189] The following recombinant VWF proteins were transiently expressed in HEK cell line 293 F with a C-terminal Strep-Tag and purified by StrepTactin affinity chromatography (IBA GmbH):

- OCTA 11
- OCTA 12

[0190] OCTA 12 is a fusion protein according to the invention. OCTA 11 is a comparative VWF fragment. The VWF proteins are schematically depicted in Fig. 1. Expression of Pro-proteins results in the formation of dimers. The peptide dimers remain also after cleavage of the propeptide.

Gene synthesis and cloning

[0191] As a first step, genes encoding the pro-proteins of the VWF proteins were synthesized by GeneArt (Thermo Fisher Scientific):

- Pro-OCTA 11

- Pro-OCTA 12

[0192] The genes encoding the pro-proteins were cloned into the pDSG expression vector (IBA GmbH), containing a Twin-Strep-tag. Individual cultures of TOP10 E. coli (IBA GmbH) were transformed with the vector constructs and single clones were selected following an overnight incubation at 37 °C on ampicillin-containing LB-agar plates.

[0193] Plasmid DNA preparations were performed using the QIAamp DNA Mini or Maxi kit (Qiagen) according to the manufacturer's recommendations. By sequencing, the integrity of the vectors was verified, in particular the correct orientation and integrity of the genes encoding Pro-OCTA 11, Pro- OCTA 12.

Protein Expression

[0194] For eukaryotic expression of the VWF proteins, MEXi-293 cells (IBA GmbH) grown in MEXi transfection-medium (IBA GmbH), were transfected with 1.5 mg/l of the constructs using 4.5 mg/ml 25 kDa linear polyethylenimine. After 2-4 hour incubation at 37 °C, 5 % CO_2 and 100-150 rpm, the culture was diluted 1:2 with MEXi transfection-medium and cultivation was continued until cell viability reached 75 %.

[0195] Subsequently, the supernatant was separated from cells by centrifugation at 4°C and 300 × g. In order to minimize the inhibitory effect of biotin in the cell culture medium and to adjust the pH, 0.1 volumes of buffer (1 M Tris-HCl, 1.5 mM NaCl, 10 mM EDTA, pH 8.0) and 0.09 % (v/v) BioLock solution (IBA GmbH) was added to the supernatant and incubated for 20 min at 4 °C.

Protein Purification

[0196] After centrifugation, the supernatant was applied on the Strep-Tactin XT column (IBA GmbH), washed five times with washing buffer (100 mM Tris-HCl, 150 mM NaCl, 1 mM EDTA, pH 8.0) and bound Strep-tag containing proteins were eluted with elution buffer (100 mM Tris-HCl, 150 mM NaCl, 1 mM EDTA, 10 mM desthiobiotin, pH 8.0).

Example 2 - Influence of full-length VWF or VWF proteins on FVIII half-life when co-administered with FVIII to FVIII/VWF double knock out (DKO) mice

2.1 Background

[0197] In this experiment, the influence of the VWF proteins produced according to Example 1 and full-length plasma derived VWF (pdVWF) on the half-life of FVIII was tested.

[0198] It is known that full-length VWF and FVIII are binding partners forming a non-covalent complex. The half-life of FVIII in circulation is determined mainly by the circulatory half-life of VWF.

[0199] As in serum endogenous VWF competes with administered VWF proteins (fragments) for FVIII binding, this competition would influence any effect of the administered VWF proteins on the half-life of FVIII.

[0200] Therefore, in the present experiment C57Bl/6 mice that are double knockouts for FVIII and VWF (FVIII/VWF-DKO) were used as model organisms for assessing the influence of the VWF on FVIII half-life.

2.2 Experimental procedure

2.2.1 FVIII-containing Products

[0201] The following FVIII-containing products were produced:

1. 1) FVIII alone
2. 2) FVIII and OCTA 11
3. 3) FVIII and OCTA 12
4. 4) FVIII and pdVWF

[0202] The VWF proteins OCTA 11 and OCTA 12 were produced as described in Example 1. The pdVWF was VWF concentrate Wilate (Octapharma). The FVIII was B-domain deleted human cell line FVIII (Nuwiq, Octapharma). The Nuwiq product contains the following buffer composition:

Arginine HCl	25.6 mM
Sucrose	15.8 mM
NaCl	308 mM
Pluronic F68	0.14 mM
Sodium citrate	3.6 mM
Calcium chloride	2.0 mM

[0203] The molar ratio of VWF protein to FVIII in the FVIII containing products 2)-4) was 5:1. The VWF proteins were added to the Nuwiq product (FVIII).

2.2.2 FVIII/VWF-DKO mouse strain

[0204] C57Bl/6 mice that are double knockouts for FVIII and VWF (FVIII/VWF-DKO) were used.

2.2.3 Administration of the products

[0205] The four FVIII containing products were administered to 20 FVIII/VWF-DKO mice by tail vein infusion with a dose of 240 IU FVIII/kg (~6 IU/mouse).

2.2.4 Sampling and Analysis

[0206] Blood samples of the mice were taken at 5 minutes and 1, 4, 8, 12, 24, 36 and 48 hours after treatment with the FVIII containing products. The blood samples were obtained from the retro-orbital plexus of the mice. For each time point, blood samples from 5 mice per FVIII containing product were obtained and analyzed individually. Each mouse was sampled at 5 min time point and maximally at two additional time points.

[0207] FVIII activity in each of the blood samples was analyzed using the chromogenic assay (CHROMOGENIX).

2.3 Results

[0208] With the FVIII activity values in the blood samples a time course of the FVIII activity for each of the FVIII containing products was determined as a shown in Fig. 2.

[0209] As for each time point and FVIII containing product, blood samples of five animals were measured, each data point in the diagram of Fig. 2 represents the mean of 5 values.

[0210] Moreover, FVIII activity for the individual time points is given as a percentage FVIII activity 5 minutes after treatment, which was defined as 100 % activity for each of the FVIII containing products.

[0211] The half-life of FVIII in five products was calculated after curve fitting using linear regression analysis of the log-linear portion of the individual plasma concentration-time curves or by non-linear regression using one-phase exponential decay model. Software programs

used for calculation were GraphPad Prism version 6.07 (La Jolla, CA 92037 USA) and WinNonlin, version 6.4 (Pharsight Corporation, Mountain View, CA, USA).

[0212] The calculations were based on the following equations:

$$t_{\frac{1}{2}} = \frac{\ln 2}{K_{el}} \quad [h]$$

$$\frac{dc}{dt} = K_{el} \cdot c \quad [h]$$

K_{el} = elimination rate constant

$t_{½}$ = elimination half-life

c = concentration

t = time

[0213] The results are summarized in Table 1.

Table 1. Terminal half-life of FVIII in the DKO mice

FVIII containing product		$t_{1/2}$ [h]
1)•	FVIII alone	0.07
2)	FVIII and OCTA 11	0.45
3)	FVIII and OCTA 12	1.03
4)	FVIII and flVWF	0.32

[0214] From these numbers it is apparent that co-administration of FVIII with any of the VWF proteins leads to an increase in half-life. Co-administration of FVIII with pdVWF leads to a ~4.6 fold increase of FVIII half-life (0.31).

[0215] The FVIII co-administered with the VWF protein OCTA 11 shows a comparable half-life of 0.45 h (about 1.4 fold increase).

[0216] Strikingly, co-administration with the VWF protein OCTA 12 gives a FVIII half-life of 1.03 h, which represents an increase of about 3.2 times in comparison to flVWF. The factor is 14.7-fold when compared to FVIII.

[0217] This result shows that the additional O-glycan repeats that are present in OCTA 12 lead to a significant half-life prolonging effect on the VWF-fragment and in turn on the VWF/FVIII complex. Moreover, this result shows that the addition of copies of an intrinsic O-glycan cluster may increase the half-life of a protein.

Example 3 - Pharmacokinetic profile of FVIII and VWF OCTA 12 following IV and subcutaneous (SQ) administration in minipigs

3.1 Background

[0218] SQ delivery of drugs is becoming more and more interesting in the field of coagulation factors. However, due to very low recovery this route was not yet applicable for the administration of FVIII. Minipig is the best-known animal model to test SQ administration of drugs due to close similarity to human structure of the epidermis. The aim of this experiment was the assessment of the half-life of VWF OCTA 12 and of FVIII when administered alone or with five-fold molar excess of OCTA 12 in minipig via the SQ route. Furthermore, the half-life of FVIII when administered alone via the conventional IV route was compared to FVIII administered SQ with or without VWF OCTA 12.

3.2 Experimental procedure

[0219] Nine female Aachener minipigs with an age of 10 to 14 months were used for this study. The body weight was between 13.7 and 19.5 kg. IV injection was performed in the lateral ear vein, SQ injection under the skin in the inguinal region. The dose was 100 U FVIII/kg BW, 3 animals per group were treated with each product:

- Group 1: FVIII alone SQ
- Group 2: FVIII with OCTA 12 SQ
- Group 3: FVIII alone IV

[0220] In order to obtain 2 × 200 µL Na-citrate plasma per animal and sampling time, sufficient blood was collected from the vena jugularis of all animals at the following time points: 0 (pre-dose), 0.5, 1, 2, 4, 8, 24, 32, 48, 72, 96 and 120 h after each administration.

[0221] The whole blood was sampled to tubes containing sodium citrate (0.15 M) as anticoagulant and cooled immediately using an IsoTherm-Rack system (Eppendorf). Plasma was separated by centrifugation within 30 minutes of blood withdrawal. Immediately after centrifugation, the plasma samples were frozen and stored at ≤-20°C until shipment.

[0222] Each sample was tested for FVIII antigen using the Asserachrom assay kit (Diagnostica Stago). OCTA 12 was quantified using an ELISA assay as follows; Strep-Tactin® XT coated microplate (IBA GmbH) was blocked with blocking buffer (1% BSA in PBS) for 2 h at RT. Plasma samples were diluted in blocking buffer 1:15 and applied on the plate. After 2h

incubation at 37 °C, the VWF fragment was detected with an anti VWF pAb (Dako P0226). After each incubation, the plate was washed 3 times with 0.1% Tween in PBS.

[0223] A pharmacokinetic evaluation of the analytical data was performed using WinNonlin, version 6.4 (Pharsight Corporation, Mountain View, CA, USA).

3.3 Results

[0224] Figure 3 shows the time course of VWF OCTA 12 concentration in minipig plasma after SQ administration of the FVIII/VWF OCTA 12 mixture. As summarized in Table 2, OCTA 12 circulates with a half-life of 219.31 h. The half-life was determined as described in Example 2.

Table 2. Pharmacokinetic parameters of VWF OCTA 12 antigen in minipigs. The values represent mean+- SD of three animals.

Pharmacokinetic parameters of OCTA 12 antigen			
Group / Dosage / Route	**C_{max} [nM]**	**t_{max} [h]**	**$t_{1/2}$ [h]**
Group 2: 100 U/ kg BW FVIII with OCTA 12 SQ.	0.93 ±0.38	8.00	219.31
C_{max} highest measured plasma concentration t_{max} time of Cmax $t_{1/2}$ terminal half-life			

[0225] In von Willebrand disease (VWD) pigs, the half-life of full length recombinant human (rhVWF) is ~10 to 16 hours, and the half-life of plasma derived porcine VWF is between 10 and 18 hours (Nichols *et al.*). The half-life of a VWF fragment containing the FVIII binding domains only is shorter than the half-life of flVWF as shown by Yee et al. in VWF deficient mice. Therefore, OCTA 12 half-life is approximately 14-22 times longer than the half-life of rhVWF in pig.

[0226] In addition, a significant prolonging effect on FVIII half-life was also observed. As shown in figure 4 and summarized in Table 3, FVIII when co-administered with OCTA 12 has a half-life of 25.3 h, which represents 6.7-fold increase in half-life when comparing with FVIII alone administered via the same route (SQ), and 3.9-fold improvement when comparing with FVIII administered alone via the conventional IV route.

Table 3. Pharmacokinetic parameters of FVIII antigen in minipigs. The values represent mean+- SD of three animals.

Pharmacokinetic parameters of FVIII Antigen			
Group / Dosage / Route	**C_{max} [U/mL]**	**t_{max} [h]**	**$t_{1/2}$ [h]**
Group 1: 100 U /kg BW FVIII alone SQ	0.03 ±0.015	8.00	3.78 ±1.31
Group 2: 100 U/kg BW	0.178 ±0.09	8.00	25.30 ±11.24

Pharmacokinetic parameters of FVIII Antigen			
Group / Dosage / Route	**C_{max} [U/mL]**	**t_{max} [h]**	**$t_{1/2}$ [h]**
FVIII with OCTA 12 SQ			
Group 3: FVIII alone IV	2.56 ±0.26	1.00	6.45 ±2.32

[0227] Many modifications and other embodiments of the invention set forth herein will come to the mind of the one skilled in the art to which the invention pertains having the benefit of the teachings presented in the foregoing description and the associated drawings. Therefore, it is to be understood that the invention is not to be limited to the specific embodiments disclosed and that modifications and other embodiments are intended to be included within the scope of the appended claims. Although specific terms are employed herein, they are used in a generic and descriptive sense only and not for purposes of limitation.

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P A T E N T K R A V

1. Fusionsprotein omfattende et hovedprotein og et eller flere forlængelsespeptider, hvor aminosyresekvensen af hovedproteinet er identisk med eller lignende aminosyresekvensen af et pattedyrsprotein eller et fragment deraf, og nævnte forlængelsespeptid(er) med en længde på ikke mere end 100 aminosyrer omfatter en klynge af O-glykosylerede aminosyrer med mindst to O-glykosylerede aminosyrer og har en sekvensidentitet på mindst 90 % med SEQ ID NO: 1, og hvor fusionsproteinet har en øget halveringstid sammenlignet med hovedproteinet uden forlængelsespeptid(er).

2. Fusionsprotein ifølge et hvilket som helst af de foregående krav, hvor det ene eller de flere forlængelsespeptider har en sekvensidentitet på mindst 95 %, fortrinsvis mindst 98 %, mere fortrinsvis 100 % med SEQ ID NO: 1.

3. Fusionsprotein ifølge et hvilket som helst af de foregående krav, hvor et forlængelsespeptid danner C-terminalen af fusionsproteinet, hvor den C-terminale aminosyre af nævnte forlængelsespeptid eventuelt er bundet til et affinitetsmærke-fusionspeptid.

4. Fusionsprotein ifølge et hvilket som helst af de foregående krav, hvor pattedyrsproteinet er et humant blodprotein, fortrinsvis en koagulationsfaktor eller en proteaseinhibitor, mere fortrinsvis valgt fra gruppen bestående af VWF, protrombin, fibrinogen, FIII, FV, FVII, FVIII, FIX, FX, FXI, FXII, FXIII, ADAMTS13, antitrombin, alfa-1-antitrypsin, C1-inhibitor, antichymotrypsin, PAI-1, PAI-3, 2-makroglobulin, TFPI, heparin cofaktor II Protein Z, Protein C og Protein S.

5. Fusionsprotein ifølge et hvilket som helst af de foregående krav, hvor hovedproteinet har en sekvensidentitet på mindst 90 %, fortrinsvis mindst 95 %, mere fortrinsvis mindst 98 %, mest fortrinsvis 100 % identitet med aminosyrerne 764 til 1268 af SEQ ID NO: 2.

6. Fusionsprotein ifølge et hvilket som helst af de foregående krav, hvor fusionsproteinet omfatter mindst 4, fortrinsvis mindst 8, mere fortrinsvis mindst 12 yderligere O-glykaner sammenlignet med hovedproteinet.

7. Fusionsprotein ifølge et hvilket som helst af de foregående krav, hvor aminosyresekvensen af fusionsproteinet har en identitet på mindst 90 %, fortrinsvis mindst 95 %, mere fortrinsvis mindst 98 %, mest fortrinsvis 100 % med en sekvens valgt blandt SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10 eller SEQ ID NO: 11.

8. Fusionsprotein ifølge et hvilket som helst af de foregående krav, hvor fusionsproteinet er frembragt ved ekspression i en pattedyrscellelinje, fortrinsvis en human cellelinje, mere fortrinsvis en human nyrecellelinje, mest fortrinsvis en human embryonal nyrecellelinje, især en HEK293-cellelinje, såsom HEK293F.

9. Sammensætning af et første protein og et andet protein, hvor det første protein er et fusionsprotein ifølge et hvilket som helst af krav 1 til 8 og er i stand til at binde nævnte andet protein, og nævnte andet protein er et terapeutisk protein omfattende en aminosyresekvens, som er identisk med eller lignende aminosyresekvensen af et andet pattedyrsprotein eller fragment deraf, hvor halveringstiden af det andet protein bundet til det første protein er øget sammenlignet med den frie form af det andet protein.

10. Sammensætning ifølge krav 9, hvor molforholdet mellem det første protein og det andet protein er i området fra 0,1 til 250, fortrinsvis i området fra 0,5 til 50, mere fortrinsvis i området fra 1 til 25, mest fortrinsvis i området fra 2 til 10.

11. Sammensætning ifølge krav 9 eller 10, hvor det andet pattedyrsprotein er et blodprotein, mere for-

trinsvis er nævnte andet pattedyrsprotein et plasmaprotein, mest fortrinsvis er nævnte andet protein en koagulationsfaktor, og/eller hvor det andet pattedyrsprotein er et humant protein.

12. Sammensætning ifølge krav 9 til 11, hvor det andet protein er et FVIII-protein, valgt blandt fuldlængde-FVIII, et FVIII-protein, hvori i det mindste en del af B-domænet mangler, og et FVIII-protein, hvori i det mindste en del af B-domænet er erstattet af et forlængelsespeptid, hvor forlængelsespeptidet er defineret ifølge krav 1 eller 2.

13. Polynukleotid, som koder for et fusionsprotein, ifølge et hvilket som helst af krav 1 til 8.

14. Vektor indeholdende polynukleotidet ifølge krav 13, hvor vektorrygraden fortrinsvis er valgt blandt pCDNA3, pCDNA3.1, pCDNA4, pCDNA5, pCDNA6, pCEP4, pCEP-puro, pCET1019, pCMV, pEF1, pEF4, pEF5, pEF6, pExchange, pEXPR, pIRES og pSCAS.

15. Værtscelle indeholdende polynukleotidet ifølge krav 13 eller vektoren ifølge krav 14, hvor værtscellen fortrinsvis er en pattedyrscelle, fortrinsvis en human celle, mere fortrinsvis en human nyrecelle, mest fortrinsvis en human embryonal nyrecellelinje, især en HEK293-cellelinje, såsom HEK293F.

DRAWINGS

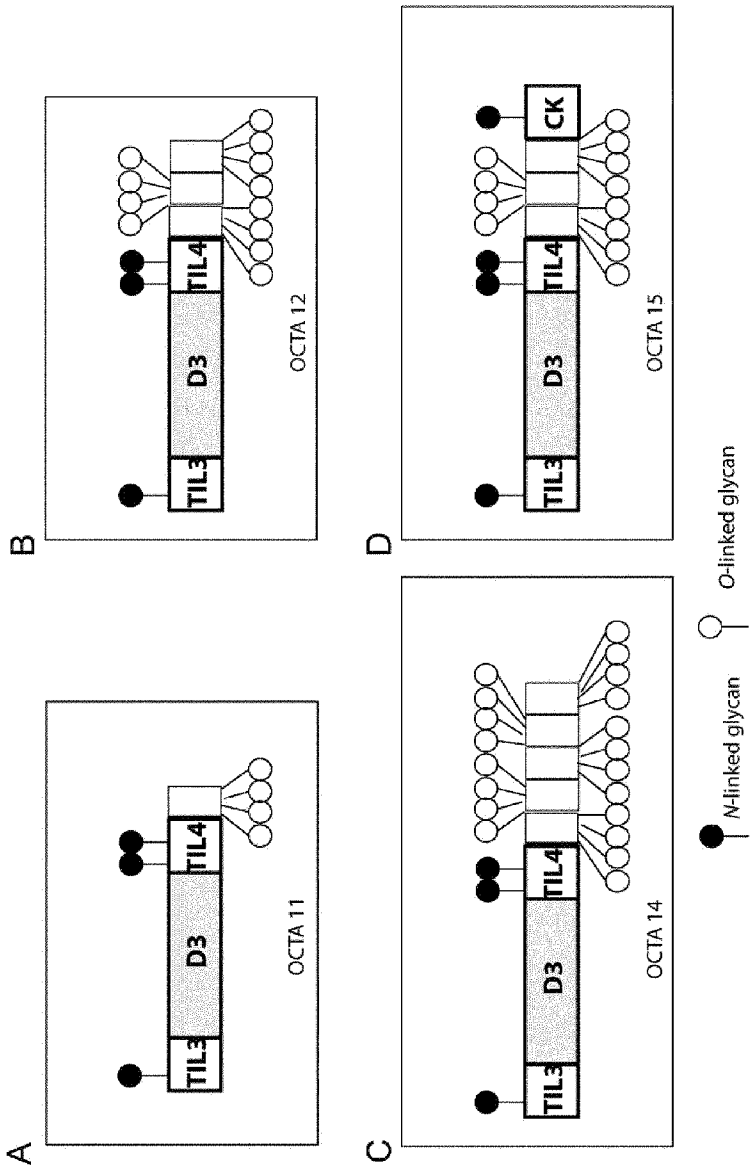

Fig. 1

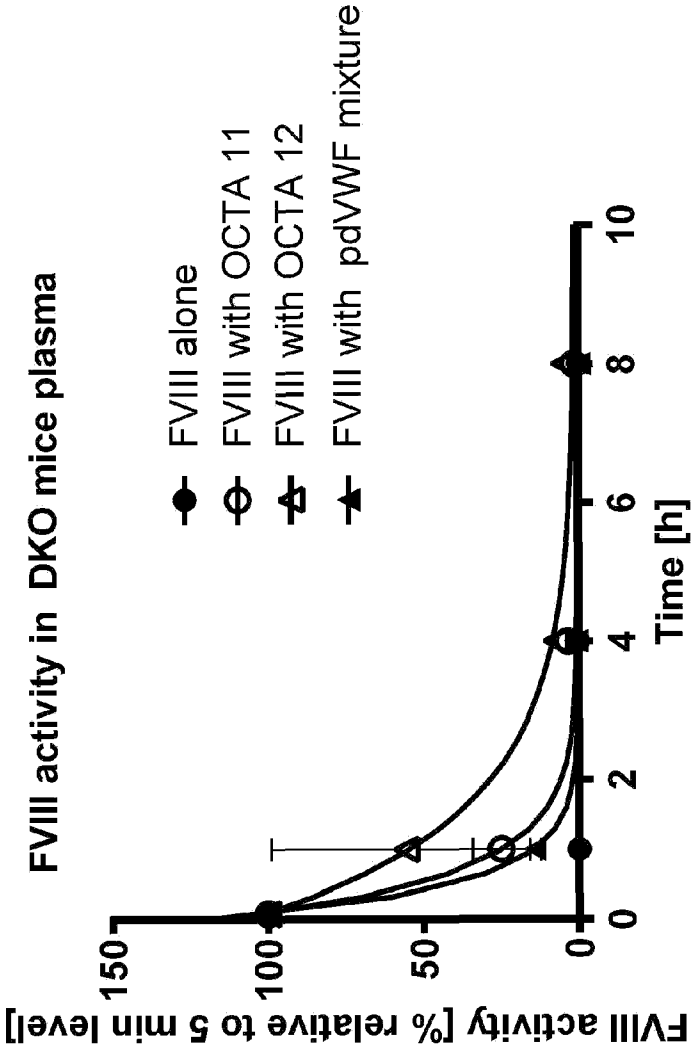
FVIII activity in DKO mice plasma
FVIII alone
FVIII with OCTA 11
FVIII with OCTA 12
FVIII with pdVWF mixture
FVIII activity [% relative to 5 min level]
150
100
50
0
0
2
4
6
8
10
Time [h]

Fig. 2

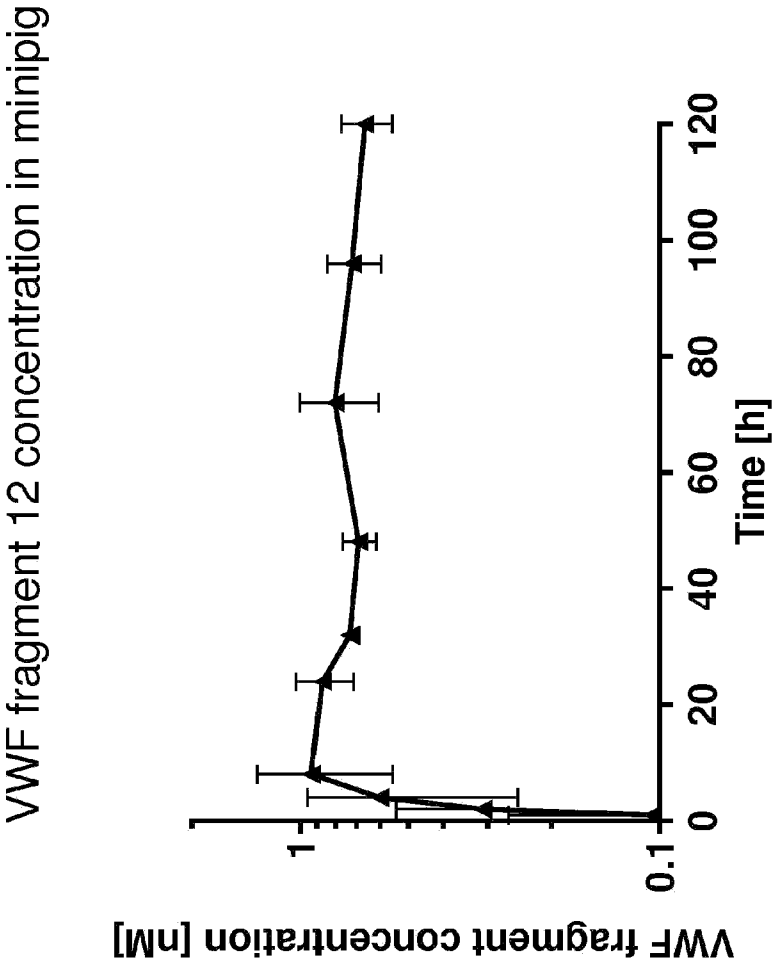
VWF fragment 12 concentration in minipig
VWF fragment concentration [nM]
1
0.1
0
20
40
60
80
100
120
Time [h]

Fig. 3

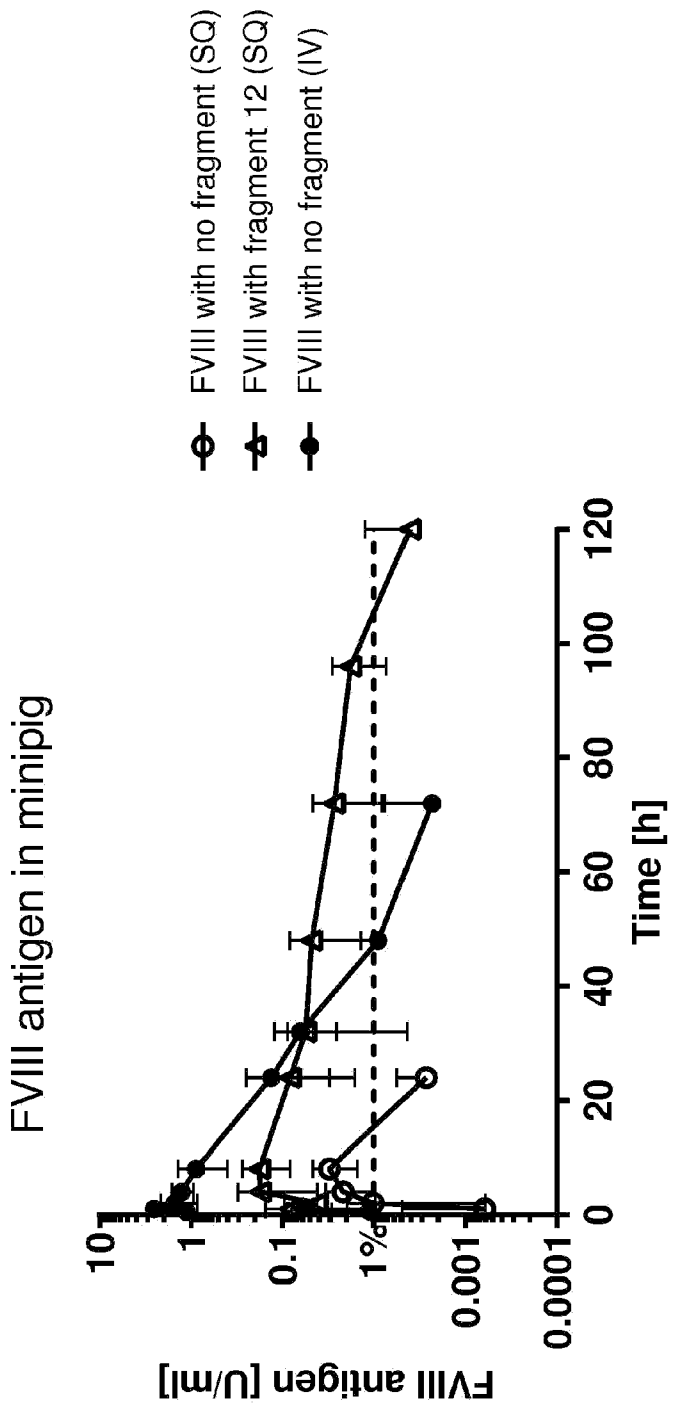
FVIII antigen in minipig
FVIII with no fragment (SQ)
FVIII with fragment 12 (SQ)
FVIII with no fragment (IV)
FVIII antigen [U/ml]
10
1
0.1
1%
0.001
0.0001
0
20
40
60
80
100
120
Time [h]

Fig. 4

SEKVENSLISTE

Sekvenslisten er udeladt af skriftet og kan hentes fra det Europæiske Patent Register.

The Sequence Listing was omitted from the document and can be downloaded from the European Patent Register.