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(54) Title: FACTOR X BINDERS ENHANCING FX ACTIVATION

(57) Abstract: The application relates to unique FX binding molecules, such as antibodies and fragments thereof which are useful in the treatment of haemophilia.

FACTOR X BINDERS ENHANCING FX ACTIVATION**TECHNICAL FIELD OF THE INVENTION**

The invention relates to coagulation Factor X binders and their use in the treatment of

5 coagulopathy, such as haemophilia.

INCORPORATION-BY-REFERENCE OF THE SEQUENCE LISTING

The present application is filed with a Sequence Listing in electronic form. The entire contents of the sequence listing are hereby incorporated by reference.

10

BACKGROUND

In patients with a coagulopathy, such as in human beings with haemophilia A and B, various steps of the coagulation cascade are rendered dysfunctional due to, for example, the absence or insufficient presence of a coagulation factor. Such dysfunction of one part of the coagulation 15 cascade results in insufficient blood coagulation and potentially life-threatening bleeding, or damage to internal organs, such as the joints.

Coagulation Factor VIII (FVIII) deficiency, commonly referred to as haemophilia A, is a congenital bleeding disorder affecting approximately 420,000 people worldwide, of which around 105,000 are currently diagnosed.

20 Patients with haemophilia A may receive coagulation factor replacement therapy such as exogenous FVIII. Conventional treatment consists of replacement therapy, provided as prophylaxis or on demand treatment of bleeding episodes. The current standard of care for a patient with severe haemophilia A is up to three prophylactic intravenous injections/week with either plasma-derived FVIII or recombinant FVIII or long-acting variants thereof.

25 However, such patients are at risk of developing neutralizing antibodies, so-called "inhibitors", to such exogenous factors, rendering formerly efficient therapy ineffective. Haemophilia A patients with "inhibitors" (that is, allo-antibodies against FVIII) is a non-limiting example of a coagulopathy that is partly congenital and partly acquired. Patients that have developed "inhibitors" to FVIII are unable to receive conventional replacement therapy, either as 30 prophylaxis or on demand.

Furthermore, exogenous coagulation factors may only be administered intravenously, which is of considerable inconvenience and discomfort to patients. For example, infants and toddlers may have to have intravenous catheters surgically inserted into a chest vein, in order for venous access to be guaranteed. This leaves them at great risk of developing bacterial 35 infections.

In a bleeding individual, coagulation is initiated by the Tissue Factor/Factor VIIa (TF/FVIIa) complex when extravascular TF is exposed to activated FVII (FVIIa) in the blood. TF/FVIIa complex formation leads to the activation of Factor X (FX) to activated Factor Xa (FXa) which, together with activated Factor V (FVa), generates a limited amount of thrombin.

5 Small amounts of thrombin activate platelets. Activated platelets support the assembly and binding of the tenase complex composed of activated Factor VIII (FVIIIa) and activated Factor IX (FIXa). The tenase complex is a very efficient catalyst of FX activation and FXa generated in this second step serves as the active protease in the FVa/FXa pro-thrombinase complex which is responsible for the final thrombin burst. Thrombin cleaves fibrinogen to generate fibrin

10 monomers, which polymerise to form a fibrin network which seals the leaking vessel and stops the bleeding. The rapid and extensive thrombin burst is a prerequisite for the formation of a solid and stable fibrin clot.

An inadequate FXa formation and decreased thrombin generation caused by absence of coagulation Factor VIII activity is the reason underlying the bleeding diathesis in haemophilia

15 A patients.

As mentioned, proteolytic conversion of FX into its enzymatically active form FXa can be achieved by the intrinsic FX-activating complex comprising FIXa and its cofactor FVIIIa. Cofactor binding increases the enzymatic activity of FIXa by about five orders of magnitude and is believed to result through multiple mechanisms as outlined by Scheiflinger *et al.* (2008) *J Thromb Haemost*, 6:315-322. Notably, FVIIIa has been found to stabilize a conformation of FIXa that has increased proteolytic activity towards FX (Kolkman JA, Mertens K (2000) *Biochemistry*, 39:7398-7405, Zögg T, Brandstetter H (2009) *Biol Chem*, 390:391-400). Based on this observation and realizing that antibodies are versatile binding proteins capable of mimicking a variety of protein-protein interactions, Scheiflinger *et al.* performed a screen for

20 agonistic anti-FIXa antibodies characterized by an ability to enhance FX activation by FIXa in the presence of a phospholipid surface and calcium, but the absence of the natural cofactor FVIIIa. From a screen of 5280 hybridoma supernatants, 88 antibodies were found to exhibit different degrees of FIXa agonistic activity.

25 Antibodies binding to Factor X/Xa have previously been characterized (US 8,062,635) and emicizumab also known as ACE910 (US 9,334,331) is approved as a by-passing agent mimicking the action of FVIIIa by binding to Factor IX/IXa with one arm and factor X/Xa with the other. The anti-FX arm of emicizumab binds the light chain of FX and is not specific for the zymogen form but rather binds FX and FXa with comparable affinities. The anti-FX arm is believed mainly to recruit FX and bring it close to FIXa.

Thus, while mimicking the overall activity of FVIIIa, the FVIII mimetic compound emicizumab appears to lack some of the inherent specificity and functions of FVIIIa. Specifically, FVIIIa works by binding FIXa and zymogen FX on a phospholipid surface, enhancing FX-activation by stimulating FIXa activity by approximately 200,000-fold and subsequently releasing FXa.

5 Variants of ACE910 stated to have functional improvements are disclosed in WO2018/021450. Further bispecific anti-FIX/anti-FX FVIII mimetic compounds are disclosed in WO2018/098363. The present invention relates to FX binders stimulating the generation of FXa. Such molecules are thus of potential therapeutic use either as individual compounds or as a component of a FVIII mimicking compound.

10

SUMMARY

The present invention relates to a group of FX binders, such as FX antibodies or fragments thereof which are capable of stimulating FX activation, i.e. the generation of FXa from FX, as well as the identification of such FX binders.

15 The present invention further relates to a group of FX binders, including antibodies and antigen-binding fragments thereof, including immunoglobulin single variable domains, such as Nanobodies®, capable of binding to zymogen FX and not the activated FX (FXa). The binding of FX by the FX binders disclosed herein stimulates subsequent activation of FX by FIXa. In one aspect, the binding occurs via a peptide stretch in activating peptide of FX. It has 20 thus been observed that the FX binders disclosed herein stimulate FX activation by making FX more prone to FIXa-mediated activation.

In one aspect, specific binding of the zymogen form of FX relative to the activated form (FXa) prevent sequestering of the FX binder on generated FXa, thereby increasing the amount of FX binder available for interaction with zymogen FX. Furthermore, specific binding to zymogen FX 25 avoids potential inhibitory effects on FXa activity (such as interference with assembly of the prothrombinase complex).

The FX binders disclosed herein display unexpected functional properties by binding to FX in a manner that makes FX more prone to proteolysis by FIXa. It is a surprising finding by the 30 inventors that increased proteolysis of FX by FIXa can be accomplished by binding of FX in a manner that makes it more prone to proteolysis and consequent activation by FIXa. There are examples in the art of anti-FIXa compounds stimulating FIXa proteolytic activity for conversion of FX into FXa. However, there are to our knowledge, no prior knowledge of compounds capable of binding to FX and stimulating FX activation by making FX more prone to proteolysis 35 by FIXa.

An aspect of the invention relates to a FX binder, such as an antibody or antigen-binding fragment thereof, binding to FX, wherein the antibody or antigen-binding fragment thereof is capable of stimulating FX activation. Another aspect of the invention relates to the identification of such compounds.

5 Further aspects of the invention relates to the use of such FX binders, possibly, but not exclusively as part of a FVIII mimetic compound, in methods of treatment. Stimulation of FX activation is useful for stimulation of coagulation, and such molecules are thus suitable for treatment of coagulopathies such as haemophilia, including haemophilia A and B.

10 **OVERVIEW OF SEQUENCE LISTING**

SEQ ID NO:1 – human Factor IX zymogen

YNSGKLEEFV	QGNLERECME	EKCSFEEARE	VFENTERTTE	FWKQYVDGDQ	CESNPCLNGG	60
SCKDDINSYE	CWCPFGFEVK	NCELDVTNCI	KNGRCEQFCK	NSADNKVVCS	CTEGYRLAEN	120
QKSCEPAVPF	PCGRVSVSQT	SKLTRAEEAVF	PDVDYVNSTE	AETILDNITQ	STQSFNDFTR	180
15 VVGGEDAKPG	QFPWQVVLNG	KVDAFCGGSI	VNEKWIVTAA	HCVETGVKIT	VVAGEHNIEE	240
TEHTEQKRVN	IRIIPHNNYN	AAINKYNHDI	ALLELDEPLV	LNSYVTPICI	ADKEYTNIFL	300
KFGSGYVSGW	GRVFHKGRSA	LVLQYLRVPL	VDRATCLRST	KFTIYNNMFC	AGFHEGGRDS	360
CQGDGGPHV	TEVEGTSFLT	GIISWGEECA	MKGKYGIYTK	VSRYVNWIKE	KTKLT	

20 SEQ ID NO:2 – human Factor X zymogen

ANSFLEEMKK	GHLERECMEE	TCSYEEAREV	FEDSDKTNEF	WNKYKDGDC	ETSPCQNQGK	60
CKDGLGEYTC	TCLEGFEGKN	CELFTRKLCS	LDNGDCDQFC	HEEQNSVVCS	CARGYTLADN	120
GKACIPTGPY	PCGKQTLERR	<u>KRSVAQATSS</u>	SGEAPDSITW	KPYDAADLDP	TENPDF LLDF	180
<u>NQTQPERGDN</u>	<u>NLTRIVGGQE</u>	CKDGECPWQA	LLINEENEGF	CGGTILSEFY	ILTAAHCLYQ	240
25 AKRFKVRVGD	RNTEQEEGGE	AVHEVEVVIK	HNRFKETYD	FDIAVRLKT	PITFRMNVAP	300
ACLPERDWAE	STLMTQKTGI	VSGFGRTHEK	GRQSTRLKML	EVPYVDRNSC	KLSSFIITQ	360
NMFCAGYDTK	QEDACQGDG	GPHVTRFKDT	YFVTGIVSWG	EGCARKGKYG	IYTKVTAFLK	420
WIDRSMKTRG	LPKAKSHAPE	VITSSPLK				

Underlined: activation peptide (aa 143-194). **Bold**: “Common minimal epitope” (aa 177-178)

30

SEQ ID NO:3 - “Common minimal epitope” on FX (shown in bold in SEQ ID NO:2 above)

LL

SEQ ID NO:4 – heavy chain variable domain mAb 00916

35 QSVEESGGRL	VTPGTPLTLT	CTVSGFSLSS	<u>YAMSWVRQAP</u>	<u>GKGLEWIGII</u>	<u>STSGSTFYAT</u>	60
WAKGRFTISK	TSTTVDLKII	SPTIEDTATY	FCARDMWAGS	RYDFNIWPGP	TLTVSS	117

SEQ ID NO:5 – light chain variable domain mAb 00916

ADIVMTQTPA SVEAAVGGTV TIKC <u>QASQSI</u> SSYLA <u>WYQQK</u> PGQRPKLLIY <u>RASTLES</u> GVP	60
SRFKGSGSGT QFTLTISDLE CADAATYY <u>CQ</u> TYY <u>YSGGGSY</u> ASA <u>FGGGTEV</u> VVK	113

5

SEQ ID NO:6 – heavy chain variable domain mAb 13F62

EVQLVESGGG QVKPGGSLRL SCAASGFTFS TSS <u>IYWVRQA</u> PGKGLEWVSS <u>ISSGSSYIFY</u>	60
<u>ADSVKGRFTI</u> SRD <u>NAKNSLF</u> LQ <u>MNSLRAED</u> TAVYY <u>CVSGY</u> SR <u>LLDYWGQG</u> TL <u>TVSS</u>	117

10 SEQ ID NO:7 – light chain variable domain mAb 13F62

DVVM <u>TQSPLS</u> LPV <u>TLGQPAS</u> IS <u>CRSSQSLV</u> YSDGNTYLNW FQQRPGQSPR RLIYKVS <u>NRD</u>	60
<u>SGVPDRFSGS</u> GSG <u>TDFTLKI</u> SRVEAEDVGF YY <u>CMQGTHWP</u> LT <u>FGGGTKVE</u> IK	112

SEQ ID NO:8 – Nb 701B09

EVQLVESGGVVQ <u>PGGSLRLSCAASGRTF</u> STYAMGWF <u>RQAPGK</u> ERFVAA <u>ISWSGSRTYY</u> A <u>DSVKG</u> RFTI	
SRD <u>NSKNTVY</u> LQ <u>MNSLRP</u> E <u>DTALYY</u> CA <u>ADATPANGELD</u> YWG <u>QGTL</u> VSS	

SEQ ID NO:9 – Nb 701C06

EVQLVESGGVVQ <u>PGGSLRLSCAASGRTF</u> STYAMGWF <u>RQAPGK</u> ERFVAA <u>ISRRGGRTYY</u> A <u>DSVKG</u> RFTI	
SRD <u>NSKNTVY</u> LQ <u>MNSLRP</u> E <u>DTALYY</u> CA <u>ADATARDGL</u> LDYWG <u>QGTL</u> VSS	

SEQ ID NO:10 – Nb 702C12

EVQLVESGGVVQ <u>PGGSLRLSCAASGRTF</u> SRYAMGWF <u>RQAPGK</u> ERFVAA <u>ISRRGGSTNY</u> A <u>DSVKG</u> RFTI	
SRD <u>NSKNTVY</u> LQ <u>MNSLRP</u> E <u>DTALYY</u> CA <u>ADYSSGD</u> GYLDYWG <u>QGTL</u> VSS	

25

SEQ ID NO:11 – Nb 701D07

EVQLVESGGVVQ <u>PGGSLRLSCAASGGT</u> LSRYAMGWF <u>RQAPGK</u> ERFVAA <u>ITRRGSRTYY</u> A <u>DSVKG</u> RFTI	
SRD <u>NSKNTVY</u> LQ <u>MNSLRP</u> E <u>DTALYY</u> CA <u>ADLAPGDY</u> ALDYWG <u>QGTL</u> VSS	

30 SEQ ID NO:12 – Nb 501A02

EVQLVESGGGLVQ <u>PGGSLRLSCAASGFT</u> FSNYEMSWVRQAPGKGLEWVSDIGGGVSTYY A <u>DSVKG</u> RFTI	
ISRDNAKNTLYLQ <u>MNSLK</u> P <u>EDTAMYY</u> C <u>ARGWTY</u> G <u>SDGMDY</u> WG <u>KGT</u> L <u>TVSS</u>	

SEQ ID NOs 13-53 correspond to the sequences recited in table 5 of Example 5.

35

SEQ ID NO:54 – Nb 721E08

EVQLVESGGVVQPGGSLRLSCAASGRTFSTYSMGWFRQAPGKEREVAAITRRGSRTYYADSVKGRFTI
SRDNSKNTVYLQMNSLRPEDTALYYCAADRRPADSYLDYWGQGTLVTVSS

5 SEQ ID NO:55 – Nb 729A04

EVQLVESGGVVQPGGSLRLSCAASGFTFSDYAMSWVRQAPGKGLEWVSGITSGGRTYYADSVKGRFTI
SRDNSKNTLYLQMNSLRPEDTALYYCAAVRTLGLRGSYDYWGQGTLVTVSS

SEQ ID NO:56 – Nb 729C08

10 EVQLVESGGVVQPGGSLRLSCAASGFTFSDYAMSWVRQAPGKGLEWVSGITGGGRTYYADSVKGRFTIS
RDNSKNTLYLQMNSLRPEDTALYYCAAAILTRTRRTYDYWGQGTLVTVSS

SEQ ID NO:57 – Nb 730C03

15 EVQLVESGGVVQPGGSLRLSCVASGFTFSDYAMSWVRQAPGKGLEWVSGITSGSGRTYYADSVKGRFTISRDNSKN
TVYLMNSLRPEDTALYYCAAAILRGYRKTYDYWGQGTLVTVSS

The underlined sequences represent the CDRs of the mAbs using Kabat numbering and definition whereas the CDRs of Nanobodies®(Nbs) are determined using Kabat numbering and AbM definition as described in Kontermann and Dübel (2010, Eds., Antibody Engineering, vol 2, Springer Verlag

20 Heidelberg Berlin, Martin, Chapter 3, pp. 33-51).

DESCRIPTION

FIX is a vitamin K-dependent coagulation factor with structural similarities to Factor VII,

prothrombin, FX, and Protein C. The circulating zymogen form consists of 415 amino acids

25 divided into four distinct domains comprising an N-terminal γ -carboxyglutamic acid-rich (Gla) domain, two EGF domains and a C-terminal trypsin-like serine protease domain. FIX circulates in plasma as a single-chain zymogen (SEQ ID NO:1). Activation of FIX occurs by limited proteolysis at Arg145 and Arg180 to release the activation peptide (residues 146 to 180 of SEQ ID NO:1). Thus, activated FIX (FIXa) is composed of residues 1-145 of SEQ ID NO:1 (light chain) and residues 181-415 of SEQ ID NO:1 (heavy chain).

30 FIXa is a trypsin-like serine protease that serves a key role in haemostasis by generating, as part of the tenase complex, most of the FXa required to support proper thrombin formation during coagulation.

FX is a vitamin K-dependent coagulation factor with structural similarities to Factor VII, prothrombin, FIX, and protein C. It is synthesised with a pre-pro-sequence containing a hydrophobic signal sequence that targets the protein for secretion. The pro-peptide is important for directing γ -carboxylation to the light chain of FX. Human FX zymogen comprises four distinct

5 domains comprising an N-terminal gamma-carboxyglutamic acid rich (Gla) domain, two EGF domains; EGF1 (residues 46-82) and EGF2 (residues 85-125), respectively, and a C-terminal trypsin-like serine protease domain (residues 195-448). FX circulates in plasma as a two-chain zymogen including residues 1-139 of SEQ ID NO:2 (light chain) and residues 143-448 of SEQ ID NO:2 (heavy chain). Activation of FX occurs by limited proteolysis at Arg194, which results in

10 the release of the activation peptide (residues 143-194). Thus, activated FX (FXa) is composed of residues 1-139 of SEQ ID NO:2 (light chain) and residues 195-448 of SEQ ID NO:2 (activated heavy chain).

The term "binder" as used herein is to be understood in its broadest sense and comprises, for

15 example, lectins, proteins, polypeptides and peptides and all FX-binding molecules or substances. A FX binding molecule comprises, for example, antibodies and antigen-binding fragments thereof (such as – but not limited to - single variable domain antibodies, Nanobodies[®], Fabs, Fab'₂, Fvs and scFvs), affibodies, adnectins, anticalins, DARPins, avimers. The term "antibody" as used herein refers to a protein, derived from an immunoglobulin

20 sequence, which is capable of binding to an antigen or a portion thereof. The term antibody includes, but is not limited to, full-length antibodies of any class (or isotype), that is, IgA, IgD, IgE, IgG, IgM and/or IgY. An antibody that specifically binds to an antigen, or a fragment thereof, may bind exclusively to that antigen, or a portion or fragment thereof, or it may bind to a limited number of homologous antigens. Usually the simple term "binding" or "binding to" is

25 used and it is generally understood that the binding of an antibody or fragment thereof is a "specific" binding. If the epitope is shared between homologous antigens, it is logical that an antibody may bind further such highly homologous antigens. The term antibody includes antibodies that are multivalent, e.g. bivalent such as bi-specific antibodies.

Natural full-length antibodies comprise at least four polypeptide chains: two heavy chains (HC)

30 and two light chains (LC) that are connected by disulfide bonds. In some cases, natural antibodies comprise less than four chains, as in the case of the IgNARs found in Chondrichthyes. One class of immunoglobulins of particular pharmaceutical interest is the IgGs. In humans, the IgG class may be divided into four sub-classes IgG1, IgG2, IgG3 and IgG4, based on the sequence of their heavy chain constant regions. The light chains can be divided

35 into two types, kappa and lambda chains based on differences in their sequence composition.

IgG molecules are composed of two heavy chains, interlinked by two or more disulfide bonds, and two light chains, each attached to a heavy chain by a disulfide bond. An IgG heavy chain may comprise a heavy chain variable domain (V_H) and up to three heavy chain constant (C_H) domains: C_H1 , C_H2 and C_H3 . A light chain may comprise a light chain variable domain (V_L) and

5 a light chain constant domain (C_L). V_H and V_L domains can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDRs) or hypervariable regions (HVRs), interspersed with regions that are more conserved, termed framework regions (FR). V_H and V_L domains are typically composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4.

10 The heavy and light chain variable domains containing the hypervariable regions (CDRs) form a structure that is capable of interacting with an antigen, whilst the constant region of an antibody may mediate binding of the immunoglobulin to host tissues or factors, including, but not limited to various cells of the immune system (effector cells), Fc receptors and the first component, C1q, of the C1 complex of the classical complement system.

15 Antibodies of the invention may be monoclonal antibodies (mAbs), in the sense that they represent a set of unique heavy and light chain variable domain sequences as expressed from a single B-cell or by a clonal population of B cells. Antibodies of the invention may be produced and purified using various methods that are known to the person skilled in the art. For example, antibodies may be produced from hybridoma cells. Antibodies may be produced by B-cell

20 expansion. Antibodies or fragments thereof may be recombinantly expressed in mammalian or microbial expression systems, or by *in vitro* translation. Antibodies or fragments thereof may also be recombinantly expressed as cell surface bound molecules, by means of e.g. phage display, bacterial display, yeast display, mammalian cell display or ribosome or mRNA display. Antibodies of the current invention may be isolated. The term "isolated antibody" refers to an

25 antibody that has been separated and/or recovered from (an)other component(s) in the environment in which it was produced and/or that has been purified from a mixture of components present in the environment in which it was produced.

Certain antigen-binding fragments of antibodies may be suitable in the context of the current invention, as it has been shown that the antigen-binding function of an antibody can be

30 performed by fragments of a full-length antibody. The term "antigen-binding fragment" of an antibody refers to one or more fragment(s) of an antibody that retain(s) the ability to bind to or recognise an antigen, such as FX or another target molecule, as described herein. Examples of antigen-binding fragments include (but is not limited to) Fab, Fab', Fab₂, Fab'₂, Fv (typically the combination of V_L and V_H domains of a single arm of an antibody), single-chain Fv (scFv); see e.g. Bird *et al.* Science 1988; 242:423-426; and Huston *et al.* PNAS 1988; 85:5879-5883), dsFv,

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Fd (typically the V_H and C_H1 domain), monovalent molecules comprising a single V_H and a single V_L chain; minibodies, diabodies, triabodies, tetrabodies, and kappa bodies (see, e.g. III et al (1997) *Protein Eng* 10: 949-57); as well as one or more isolated CDRs or a functional paratope, where the isolated CDRs or antigen-binding residues or polypeptides can be

5 associated or linked together so as to form a functional antibody fragment. These antibody fragments may be obtained using conventional techniques known to those of skill in the art, and the fragments may be screened for utility in the same manner as intact antibodies.

“Fab fragments” of an antibody, including “Fab” and “ Fab'_2 ” fragments, can be derived from said antibody by cleavage of the heavy chain in the hinge region on the N-terminal or C-terminal

10 side of the hinge cysteine residues connecting the heavy chains of the antibody. A “Fab” fragment includes the variable and constant domains of the light chain and the variable domain and C_H1 domain of the heavy chain. “ Fab'_2 ” fragments comprise a pair of “Fab” fragments that are generally covalently linked by their hinge cysteines. A Fab' is formally derived from a Fab'_2 fragment by cleavage of the hinge disulfide bonds connecting the heavy chains in the Fab'_2 .

15 Other chemical couplings than disulfide linkages of antibody fragments are also known in the art. A Fab fragment retains the ability of the parent antibody to bind to its antigen, potentially with a lower affinity. Fab'_2 fragments are capable of divalent binding, whereas Fab and Fab' fragments can bind monovalently. Generally, Fab fragments lack the constant C_H2 and C_H3 domains, i.e. the Fc part, where interaction with the Fc receptors and C1q would occur. Thus,

20 Fab fragments are in general devoid of effector functions. Fab fragments may be produced by methods known in the art, either by enzymatic cleavage of an antibody, e.g. using papain to obtain the Fab or pepsin to obtain the Fab'_2 . Fab fragments including Fab, Fab' , Fab'_2 may be produced recombinantly using techniques that are well known to the person skilled in the art. A “Fv” (fragment variable) fragment is an antibody fragment that contains a complete antigen

25 recognition and binding site, and generally comprises a dimer of one heavy and one light chain variable domain in association that can be covalent in nature, for example in a single chain variable domain fragment (scFv). It is in this configuration that the three hypervariable regions of each variable domain interact to define an antigen-binding site on the surface of the V_H - V_L dimer. Collectively, the six hypervariable regions or a subset thereof confer antigen binding

30 specificity to the antibody.

“Single-chain Fv” or “scFv” antibody comprise the V_H and V_L domains of antibody, where these domains are present in a single polypeptide chain. Generally, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains that enables the scFv to form the desired structure for antigen binding. For a review of scFv, see Pluckthun, 1994, In: *The*

Pharmacology of Monoclonal Antibodies, Vol. 113, Rosenburg and Moore eds. Springer-Verlag, New York, pp. 269-315.

“Single-chain Fab” or “scFab” antibody comprise the V_H , C_{H1} , V_L and C_L domains of antibody, where these domains are present in a single polypeptide chain. Generally, the Fab polypeptide further comprises a polypeptide linker between either V_H and C_L or V_L and C_{H1} domains that enables the scFab to form the desired structure for antigen binding (Koerber *et al.* (2015) *J Mol Biol.* 427:576-86).

The term “diabodies” refers to small antibody fragments with two antigen-binding sites, in which fragments comprise a heavy chain variable domain (V_H) connected to a light chain variable

domain (V_L) in the same polypeptide chain (V_H and V_L). By using a linker that is too short to allow pairing between the two variable domains on the same chain, the variable domains are forced to pair with complementary domains of another chain, creating two antigen-binding sites. The expression “linear antibodies” refers to antibodies as described in Zapata *et al.* (1995) *Protein Eng.* 8: 1057-1062. Briefly, these antibodies contain a pair of tandem Fd segments ($V_H-C_{H1}-V_H-C_{H1}$) that, together with complementary light chain polypeptides, form a pair of antigen binding regions. Linear antibodies can be bi-specific or monospecific.

Antibody fragments may be obtained using conventional recombinant or protein engineering techniques and the fragments can be screened for binding to an antigen, such as FX in the same manner as intact antibodies.

Antibody fragments of the invention may be made by truncation, e.g. by removal of one or more amino acids from the N and/or C-terminal ends of a polypeptide. Fragments may also be generated by one or more internal deletions.

An antibody of the invention may be, or may comprise, a fragment of the antibody, or a variant of any one of the antibodies disclosed herein. An antibody of the invention may be, or may

comprise, an antigen-binding portion of one of these antibodies, or variants thereof. For example, an antibody of the invention may be a Fab fragment of one of these antibodies or variants thereof, or it may be a single chain antibody derived from one of these antibodies, or a variant thereof. Also, an antibody of the invention may be a combination of a full length antibody and fragment thereof.

However, even a single variable domain comprising only three hypervariable regions specific for an antigen can retain the ability to recognize and bind antigen with high affinity, although usually at a lower affinity than the entire binding site (Cai & Garen (1996) *PNAS* 93: 6280-6285). Naturally occurring camelid antibodies that only have a heavy chain variable domain (V_HH) can bind antigen (Desmyter *et al.* (2002) *J. Biol. Chem.* 277: 23645-23650; Bond *et al.* (2003) *J. Mol. Biol.* 332: 643-655). Likewise IgNAR (or V_{NAR}), from Cartilaginous fishes provides

a single domain antibody binding region. An alternative is provided by Creative Biolabs which uses human tenth fibronectin FN3 domain (10FN3 domain) as scaffold. Such antibody molecules are referred to as single variable domains, immunoglobulin single variable domains or single variable domain fragments. The molecules are monomeric and typically 12-15 kDa in 5 size.

In particular, an immunoglobulin single variable domain or single variable domain may be a Nanobody® (as defined herein) or a suitable fragment thereof. For a general description of Nanobodies®, reference is made to such as WO2008/020079 (page 16).

The term "immunoglobulin single variable domain", interchangeably used with "single variable 10 domain", defines molecules wherein the antigen-binding site is present on, and formed by, a single immunoglobulin domain. This sets immunoglobulin single variable domains apart from "conventional" immunoglobulins or their fragments (such as Fabs, scFvs, etc.), wherein as described above two immunoglobulin domains, in particular two variable domains (a heavy chain variable domain (V_H) and a light chain variable domain (V_L)) interact to form an antigen- 15 binding site. In contrast, the binding site of an immunoglobulin single variable domain is formed by a single V_H or V_L domain. Hence, the antigen-binding site of an immunoglobulin single variable domain is formed by no more than three CDRs.

The term "immunoglobulin single variable domain" and "single variable domain" hence does not 20 comprise conventional immunoglobulins or their fragments which require interaction of at least two variable domains for the formation of an antigen-binding site. However, these terms do comprise fragments of conventional immunoglobulins wherein the antigen-binding site is formed by a single variable domain.

Generally, single variable domains will be polypeptide sequences essentially consisting of 4 25 framework regions (FR1 to FR4 respectively) and 3 complementarity determining regions (CDR1 to CDR3 respectively); or any suitable fragment of such an polypeptide sequence (which will then usually contain at least some of the amino acid residues that form at least one of the CDR's). The amino acid sequence and structure of an immunoglobulin sequence, in particular an immunoglobulin single variable domain such as a Nanobody® can be considered - without however being limited thereto - to be comprised of four framework regions or "FR's", 30 which are referred to in the art and herein as "Framework region 1" or "FR1"; as "Framework region 2" or "FR2"; as "Framework region 3" or "FR3"; and as "Framework region 4" or "FR4", respectively; which framework regions are interrupted by three complementary determining regions or "CDR's", which are referred to in the art as "Complementarity Determining Region 1" or "CDR1"; as "Complementarity Determining Region 2" or "CDR2"; and as "Complementarity 35 Determining Region 3" or "CDR3", respectively.

The total length of an immunoglobulin single variable domain is usually, such as for a Nanobody® in the region of 110-120 amino acid residues, is preferably 112-115, and is most preferably 113 amino residues.

Such single variable domains and fragments are most preferably such that they comprise an immunoglobulin fold or are capable for forming, under suitable conditions, an immunoglobulin fold. As such, the single variable domain may for example comprise a light chain variable domain sequence (e.g. a V_L -sequence) or a suitable fragment thereof; or a heavy chain variable domain sequence (e.g. a V_H -sequence or V_HH sequence) or a suitable fragment thereof; as long as it is capable of forming a single antigen-binding unit (i.e. a functional antigen-binding unit that essentially consists of the single variable domain, such that the single antigen-binding domain does not need to interact with another variable domain to form a functional antigen-binding unit, as is for example the case for the variable domains that are present in for example conventional antibodies and scFv fragments that need to interact with another variable domain – e.g. through a V_H/V_L interaction – to form a functional antigen-binding domain).

In one embodiment of the invention, the immunoglobulin single variable domains are light chain variable domain sequences (e.g. a V_L -sequence), or heavy chain variable domain sequences (e.g. a V_H -sequence); more specifically, the immunoglobulin single variable domains can be heavy chain variable domain sequences that are derived from a conventional four-chain antibody or heavy chain variable domain sequences that are derived from a heavy chain antibody.

For example, the single variable domain or immunoglobulin single variable domain (or an amino acid sequence that is suitable for use as an immunoglobulin single variable domain) may be referred to as a (single) domain antibody; a “dAb” or “sdAb” or a Nanobody® (including but not limited to a V_HH , a humanized V_HH or a camelized V_H domain); other single variable domains, or any suitable fragment of any one thereof. For a general description of (single) domain antibodies, reference is also made to such as EP0368684. For the term “dAb”, reference is made to for example Ward *et al.* 1989 (Nature 341: 544), to Holt *et al.* 2003 (Trends Biotechnol. 21: 484); as well as for example WO2004/068820, WO2006/030220, WO2006/003388 and other published patent applications of Domantis Ltd.

Thus, in the meaning of the present invention, the term “immunoglobulin single variable domain” or “single variable domain” comprises polypeptides which are derived from a non-human source, preferably a camelid, preferably a camelid heavy chain antibody (e.g. V_HHs). They may be humanized (e.g. humanized V_HHs). Moreover, the term comprises polypeptides derived from non-camelid sources, e.g. mouse or human, which have been “camelized” (e.g. camelized V_H domains), as e.g. described in Davies and Riechmann 1994 (FEBS 339: 285),

1995 (Biotechonol. 13: 475) and 1996 (Prot. Eng. 9: 531) and Riechmann and Muyldermans 1999 (J. Immunol. Methods 231: 25).

The term “mono-specific” antibody, as used herein, refers to an antibody which is capable of binding to one particular epitope (including but not limited to bivalent antibodies).

5 The term “bi-specific” antibody, as used herein, refers to an antibody which is capable of binding to two different antigens or two different epitopes on the same antigen.

The term “tri-specific” antibody, as used herein, refers to an antibody which is capable of binding to three different antigens or three different epitopes on the same antigen or three different epitopes present on two different antigens.

10 The term “multi-specific” antibody, as used herein, refers to an antibody which is capable of binding to two or more different antigens or two or more different epitopes on the same antigen. Multispecific antibodies thus comprise bi- and tri-specific antibodies.

Bi-specific antibodies in full length IgG format can be generated by fusion of two individual hybridomas to form a hybrid quadroma which produces a mixture of antibodies including a

15 fraction of bi-specific heterodimerising antibodies (Chelius D. *et al.*; *MAbs*. 2010 May-Jun; 2(3): 309–319). Bi-specific heterodimerising antibodies may alternatively be produced by using recombinant technologies. Heterodimerisation can be also be achieved by engineering the dimerisation interface of the Fc region to promote heterodimerisation. One example hereof is the so-called knob-in-hole mutations where sterically bulky side chains (knobs) are introduced 20 in one Fc matched by sterically small side chains (holes) on the opposite Fc thereby creating steric complementarity promoting heterodimerisation. Other methods for engineered heterodimerisation Fc interfaces are electrostatic complementarity, fusion to non-IgG heterodimerisation domains or utilising the natural Fab-arm exchange phenomenon of human IgG4 to control heterodimerisation. Examples of heterodimerised bi-specific antibodies are well

25 described in the literature, e.g. (Klein C, *et al.*; *MAbs*. 2012 Nov-Dec; 4(6): 653–663). Special attention has to be paid to the light chains in heterodimeric antibodies. Correct pairing of LCs and HCs can be accomplished by the use of a common light chain. Again engineering of the LC/HC interface can be used to promote heterodimerisation or light chain cross-over engineering as in CrossMabs. *In vitro* re-assembly under mildly reducing conditions of

30 antibodies from two individual IgGs containing appropriate mutations can also be used to generate bi-specifics (e.g. Labrijn *et al.*, *PNAS*, 110, 5145-5150 (2013)). Also the natural Fab-arm exchange method is reported to ensure correct light chains paring.

Multispecific antibody-based molecules may also be expressed recombinantly as fusion proteins combining the natural modules of IgGs to form multi-specific and multivalent antibody derivatives as described in the literature. Examples of fusion antibodies are DVD-Igs, IgG-scFV,

Diabodies, DARTs etc. Specific detection or purification tags, half-life extension moieties or other components can be incorporated in the fusion proteins. Additional non-IgG modalities may also be incorporated in the fusion proteins. Bi-specific full length antibodies based on Fc heterodimerisation are commonly referred to as asymmetric IgGs, irrespective of the LC paring

5 methodology. Generally, bispecific antibodies may be produced in a variety of molecular formats as reviewed by Brinkmann *et al.* (Brinkmann *et al.* The making of bispecific antibodies. *Mabs* 9, 182-212 (2017)).

Multi-specific antibody-based molecules may also be produced by chemical conjugation or coupling of individual full length IgGs or coupling of fragments of IgGs to form multi-specific and

10 multivalent antibody derivatives as described in the literature. Examples of fusion antibodies are chemical coupled Fab'2, IgG-dimer etc.. Specific detection or purification tags, half-life extension molecules or other components can be incorporated in the conjugate proteins. Additional non-IgG polypeptide may also be incorporated in the fusion proteins. Multi-specific molecules may also be produced by combining recombinant and chemical methods including those described

15 above.

Anti-FX antibodies or antigen-binding fragments thereof as disclosed herein can be used as part of a multispecific procoagulant antibody. Thus, one aspect the invention relates to individual component (intermediate) anti-FX antibodies or antigen-binding fragments thereof that are suitable for use in a multispecific procoagulant antibody, such as a bispecific

20 procoagulant antibody. In one aspect such a bispecific (or multispecific) antibody is capable of binding to FIX and/or the activated form thereof FIXa, and FX.

In one aspect, an antibody of the invention is a chimeric antibody, a human antibody or a humanised antibody. Such antibody can be generated by using, for example, suitable antibody display or immunization platforms or other suitable platforms or methods known in the field).

25 The term "human antibody", as used herein, is intended to include antibodies having variable domains in which at least a portion of a framework region and/or at least a portion of a CDR are derived from human germline immunoglobulin sequences. (For example, a human antibody may have variable domains in which both the framework and CDRs are derived from human germline immunoglobulin sequences.) Furthermore, if the antibody contains a constant region,

30 the constant region or a portion thereof is also derived from human germline immunoglobulin sequences. The human antibodies of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*).

In one aspect, such a human antibody is a human monoclonal antibody. Such a human

35 monoclonal antibody may be produced by a hybridoma which includes a B cell obtained from a

transgenic nonhuman animal, e.g., a transgenic mouse, having a genome comprising human immunoglobulin heavy and light chain gene segments repertoires, fused to an immortalised cell. Human antibodies may be isolated from sequence libraries built on selections of human germline sequences, further diversified with natural and synthetic sequence diversity.

5 Human antibodies may be prepared by *in vitro* immunisation of human lymphocytes followed by transformation of the lymphocytes with Epstein-Barr virus.

The term “human antibody derivative” refers to any modified form of a human antibody, such as a conjugate of the antibody and another compound or antibody.

The term “humanised antibody”, as used herein, refers to a human/non-human chimeric

10 antibody that contains a sequence (CDRs or parts thereof) derived from a non-human immunoglobulin. A humanised antibody is, thus, a human immunoglobulin (recipient antibody) in which at least residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of an antibody from a non-human species (donor antibody) such as from a mouse, rat, rabbit or non-human primate, which have the desired specificity, affinity,

15 sequence composition and functionality. In some instances, framework (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. An example of such a modification is the introduction of one or more so-called back-mutations, which are typically amino acid residues derived from the donor antibody. Humanisation of an antibody may be carried out using recombinant techniques known to the person skilled in the art (see,

20 e.g., Antibody Engineering, Methods in Molecular Biology, vol. 248, edited by Benny K. Lo). A suitable human recipient framework for both the light and heavy chain variable domains may be identified by, for example, sequence or structural homology. Alternatively, fixed recipient frameworks may be used, e.g., based on knowledge of structure, biophysical and biochemical properties. The recipient frameworks can be germline derived or derived from a mature

25 antibody sequence. CDRs from the donor antibody can be transferred by CDR grafting. The CDR grafted humanised antibody can be further optimised for e.g. affinity, functionality and biophysical properties by identification of critical framework positions where re-introduction (back-mutation) of the amino acid residue from the donor antibody has beneficial impact on the properties of the humanised antibody. In addition to donor antibody derived back-mutations, the

30 humanised antibody can be engineered by introduction of germline residues in the CDR or framework regions, elimination of immunogenic epitopes, site-directed mutagenesis, or affinity maturation, etc.

In further aspects, a humanised antibody comprises residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody

35 performance. In general, a humanised antibody comprises at least one – typically two – variable

domains, in which all or substantially all of the CDRs correspond to those of a non-human immunoglobulin and in which all or substantially all of the FR residues are those of a human immunoglobulin sequence. The humanised antibody can, optionally, also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin.

5 The term “humanised antibody derivative” refers to any modified form of the humanised antibody, such as a conjugate of the antibody and a chemical compound or a conjugate of the antibody with another antibody.

The term “chimeric antibody”, as used herein, refers to an antibody comprising portions of antibodies derived from two or more species. For example, the genes encoding such antibody

10 comprise genes encoding variable domains and genes encoding constant regions which originates from two different species. For example, the genes encoding variable segments of a mouse monoclonal antibody may be joined to the genes encoding the constant regions of an antibody of human origin.

The fragment crystallisable region (“Fc region”/“Fc domain”) of an antibody is the C-terminal

15 region of an antibody, which comprises the hinge and the constant C_H2 and C_H3 domains. The Fc domain may interact with cell surface receptors called Fc receptors, as well as some proteins of the complement system. The Fc region enables antibodies to interact with the immune system. In one aspect of the invention, antibodies may be engineered to include modifications within the Fc region, typically to alter one or more of its functional properties, such 20 as serum half-life, complement fixation, Fc-receptor binding, protein stability and/or antigen-dependent cellular cytotoxicity, or lack thereof, among others. Furthermore, an antibody of the invention may be chemically modified (e.g., one or more chemical moieties can be attached to the antibody) or be modified to alter its glycosylation, again to alter one or more functional properties of the antibody. An IgG1 antibody may carry a modified Fc domain comprising one or 25 more, and perhaps all of the following mutations that will result in decreased affinity to certain Fc-gamma receptors (L234A, L235E, and G237A) and in reduced C1q-mediated complement fixation (A330S and P331S), respectively (residue numbering according to the EU index).

The isotype of an antibody of the invention may be IgG, such as IgG1, such as IgG2, such as IgG4. If desired, the class of an antibody may be “switched” by known techniques. For example,

30 an antibody that was originally produced as an IgM molecule may be class switched to an IgG antibody. Class switching techniques also may be used to convert one IgG subclass to another, for example: from IgG1 to IgG2 or IgG4; from IgG2 to IgG1 or IgG4; or from IgG4 to IgG1 or IgG2. Engineering of antibodies to generate constant region chimeric molecules, by combination of regions from different IgG subclasses, can also be performed.

In one embodiment, the hinge region of C_H1 is modified such that the number of cysteine residues in the hinge region is altered, e.g., increased or decreased. This approach is described further for instance in U.S. Patent No. 5,677,425 by Bodmer *et al.*

The constant region may be modified to stabilise the antibody, e.g., to reduce the risk of a

5 bivalent antibody separating into two monovalent VH-VL fragments. For example, in an IgG4 constant region, residue S228 (according to the EU numbering index and S241 according to Kabat) may be mutated to a proline (P) residue to stabilise inter heavy chain disulphide bridge formation at the hinge (see, e.g., Angal *et al.* Mol Immunol. 1993; 30:105-8).

Antibodies or fragments thereof may be defined in terms of their complementarity-determining

10 regions (CDRs). The term "complementarity-determining region" or "hypervariable region", when used herein, refers to the regions of an antibody in which amino acid residues involved in antigen-binding are situated. The region of hypervariability or CDRs can be identified as the regions with the highest variability in amino acid alignments of antibody variable domains.

Databases can be used for CDR identification such as the Kabat database, the CDRs e.g.

15 being defined as comprising amino acid residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) of the light-chain variable domain and 31-35 (H1), 50-65 (H2) and 95-102 (H3) in the heavy-chain variable domain; (Kabat *et al.* 1991; Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242)

Alternatively CDRs can be defined as those residues from a "hypervariable loop" (residues 26-

20 33 (L1), 50-52 (L2) and 91-96 (L3) in the light-chain variable domain and 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the heavy-chain variable domain; Chothia and Lesk, J. Mol. Biol. 1987; 196:901-917). Typically, the numbering of amino acid residues in this region is performed by the method described in Kabat *et al. supra*. Phrases such as "Kabat position", "Kabat residue", and "according to Kabat" herein refer to this numbering system for heavy chain variable

25 domains or light chain variable domains. Using the Kabat numbering system, the actual linear amino acid sequence of a peptide may contain fewer or additional amino acids corresponding to a shortening of, or insertion into, a framework (FR) or CDR of the variable domain. For example, a heavy chain variable domain may include amino acid insertions (residue 52a, 52b and 52c according to Kabat) after residue 52 of CDR H2 and inserted residues (e.g. residues 30 82a, 82b, and 82c, etc. according to Kabat) after heavy chain FR residue 82. The Kabat numbering of residues may be determined for a given antibody by alignment at regions of homology of the sequence of the antibody with a "standard" Kabat numbered sequence.

The amino acid residues of a V_HH domain may be numbered according to the general numbering for V_H domains given by Kabat *et al.* as applied to V_HH domains from Camelids, as shown e.g., in Figure 2 of Riechmann and Muyldermans (1999, J. Immunol. Methods 231: 25-

38). Alternative methods for numbering the amino acid residues of VH domains, which methods can also be applied in an analogous manner to V_HH domains, are known in the art.

Determination of CDRs may also be done according to different methods. In the CDR determination according to Kabat, FR1 of a V_HH comprises the amino acid residues at positions

5 1-30, CDR1 of a V_HH comprises the amino acid residues at positions 31-35, FR2 of a V_HH comprises the amino acids at positions 36-49, CDR2 of a V_HH comprises the amino acid residues at positions 50-65, FR3 of a V_HH comprises the amino acid residues at positions 66-94, CDR3 of a V_HH comprises the amino acid residues at positions 95-102, and FR4 of a V_HH comprises the amino acid residues at positions 103-113.

10 In the present document, CDR sequences of single variable domain antibodies (Nanobodies[®]) are determined using the AbM definition according to Kontermann and Dübel (2010, Eds., Antibody Engineering, vol 2, Springer Verlag Heidelberg Berlin, Martin, Chapter 3, pp. 33-51). According to this method, FR1 comprises the amino acid residues at positions 1-25, CDR1 comprises the amino acid residues at positions 26-35, FR2 comprises the amino acids at 15 positions 36-49, CDR2 comprises the amino acid residues at positions 50-58, FR3 comprises the amino acid residues at positions 59-94, CDR3 comprises the amino acid residues at positions 95-102, and FR4 comprises the amino acid residues at positions 103-113 (according to Kabat numbering).

20 In the present document, CDR sequences of IgG antibodies (including full-length IgG antibodies and Fab fragments thereof) are determined using the Kabat definition according to Kontermann and Dübel (2010, Eds., Antibody Engineering, vol 2, Springer Verlag Heidelberg Berlin, Martin, Chapter 3, pp. 33-51). According to this method, the CDRs of the light chain variable domain is defined as position 24-34 (CDR1), position 50-56 (CDR2) and position 89-97 (CDR3), while the CDRs of the heavy chain variable domain is defined as position 31-35 (CDR1), position 50-65 25 (CDR2) and position 95-102 (CDR3).

The term “framework region” or “FR” residues refer to those V_H or V_L amino acid residues that are not within the CDRs, as defined herein.

30 In one embodiment an antibody or antigen-binding fragment thereof of the invention may comprise a CDR from one or more of the specific antibodies disclosed herein.

The term “procoagulant antibody” refers to an antibody which potentiates blood coagulation for example by accelerating the process of blood coagulation and/or increasing the enzymatic activity of one or more coagulation factors.

The term “procoagulant activity” refers to the ability of a compound, such as an antibody, to potentiate blood coagulation for example by accelerating the process of blood coagulation and/or increasing the enzymatic activity of one or more coagulation factors.

5 It should be noted that - as is well known in the art for V_H domains and for V_{HH} domains - the total number of amino acid residues in each of the CDRs may vary and may not correspond to the total number of amino acid residues indicated by the Kabat numbering (that is, one or more positions according to the Kabat numbering may not be occupied in the actual sequence, or the actual sequence may contain more amino acid residues than the number allowed for by the

10 Kabat numbering). This means that, generally, the numbering according to Kabat may or may not correspond to the actual numbering of the amino acid residues in the actual sequence. The total number of amino acid residues in a V_H domain and a V_{HH} domain will usually be in the range of from 110 to 120, often between 112 and 115. It should however be noted that smaller and longer sequences may also be suitable for the purposes described herein. An antibody of

15 the invention may comprise a CDR from one or more of the specific antibodies disclosed herein.

The term “antigen” (Ag) refers to the molecular entity used for immunisation of an immunocompetent vertebrate to produce the antibody (Ab) that recognizes the Ag. Herein, Ag is termed more broadly and is generally intended to include target molecules that are

20 specifically recognized by the Ab, thus including fragments or mimics of the molecule used in the immunisation process, or other process, e.g. phage display, used for generating the Ab.

The term “epitope”, as used herein, is defined in the context of a molecular interaction between an “antigen-binding polypeptide”, such as an antibody (Ab), and its corresponding antigen (Ag). Generally, “epitope” refers to the area or region on an Ag to which an Ab specifically binds, i.e.

25 the area or region in physical contact with the Ab. Physical contact may be defined using various criteria (e.g. a distance cut-off of 2-6 Å, such as 3 Å, such as 3.5 Å such as 4 Å, such as 4.5 Å, such as 5 Å; or solvent accessibility) for atoms in the Ab and Ag molecules.

FX/FXa may comprise a number of different epitopes, which may include, without limitation, (1) linear peptide epitopes (2) conformational epitopes which consist of one or more non-

30 contiguous amino acids located near each other in the mature FX/FXa conformation; and (3) epitopes which consist, either in whole or part, of molecular structures covalently attached to FX/FXa, such as carbohydrate groups.

The epitope for a given antibody (Ab)/antigen (Ag) pair can be described and characterized at different levels of detail using a variety of experimental and computational epitope mapping methods. The experimental methods include mutagenesis, X-ray crystallography, Nuclear

Magnetic Resonance (NMR) spectroscopy, Hydrogen Deuterium eXchange Mass Spectrometry (HDX-MS) and various competition binding methods; methods that are known in the art. As each method relies on a unique principle, the description of an epitope is intimately linked to the method by which it has been determined. Thus, depending on the epitope mapping method

5 employed, the epitope for a given Ab/Ag pair may be described differently.

The epitope and paratope for a given antibody (Ab)/antigen (Ag) pair may be identified by routine methods. For example, the general location of an epitope may be determined by assessing the ability of an antibody to bind to different fragments or variants of FX. The specific amino acids within FX that make contact with an antibody (epitope) and the specific amino

10 acids in an antibody that make contact with FX (paratope) may also be determined using routine methods. An antibody according to the current invention may be able to compete with another molecule, such as a naturally occurring ligand or receptor or another antibody, for binding to FX.

A competitive binding assay can be conducted in which the binding of the antibody to the target

15 is compared to the binding of the target by another ligand of that target, such as another antibody.

Antibodies that bind to the same antigen can be characterised with respect to their ability to bind to their common antigen simultaneously and may be subject to "competition binding"/"binning". In the present context, the term "binning" refers to a method of grouping

20 antibodies that bind to the same antigen. "Binning" of antibodies may be based on competition binding of two antibodies to their common antigen in assays based on standard techniques.

An antibody's "bin" is defined using a reference antibody. If a second antibody is unable to bind to an antigen at the same time as the reference antibody, the second antibody is said to belong to the same "bin" as the reference antibody. In this case, the reference and the second antibody

25 competitively bind the same part of an antigen and are considered "competing antibodies". If a second antibody is capable of binding to an antigen at the same time as the reference antibody, the second antibody is said to belong to a separate "bin". In this case, the reference and the second antibody do not competitively bind the same part of an antigen and are considered "non-competing antibodies".

30 Antibody "binning" does not provide direct information about the epitope.

Competing antibodies, i.e. antibodies belonging to the same "bin" may have identical epitopes, overlapping epitopes or even separate epitopes. The latter is the case if the reference antibody bound to its epitope on the antigen takes up the space required for the second antibody to contact its epitope on the antigen ("steric hindrance"). Non-competing antibodies generally have

separate epitopes. Thus, in some embodiments antibodies of the invention will bind to the same epitope as at least one of the antibodies specifically disclosed herein.

Competition assays for determining whether an antibody binds to the same epitope as, or competes for binding with, an anti-FX antibody disclosed herein are known in the art.

- 5 Exemplary competition assays include immunoassays (e.g., ELISA assays, RIA assays), Surface Plasmon Resonance analysis (e.g., using a BIACore™ instrument), biolayer interferometry and flow cytometry. Typically, a competition assay involves the use of an antigen bound to a solid surface or expressed on a cell surface, a test FX binding antibody and a reference antibody. The reference antibody is labelled and the test antibody is unlabelled.
- 10 Competitive inhibition is measured by determining the amount of labelled reference antibody bound to the solid surface or cells in the presence of the test antibody. Usually the test antibody is present in excess (e.g. 1, 5, 10, 20, 100, 1000, 10000 or 100000-fold) of the reference antibody. Antibodies identified as being competitive in the competition assay (i.e., competing antibodies) include antibodies binding to the same epitope, or overlapping epitopes, as the reference antibody, and antibodies binding to an adjacent epitope sufficiently proximal to the epitope bound by the reference antibody for steric hindrance to occur.
- 15 In an exemplary competition assay, a reference anti-FX or anti-FXa antibody is biotinylated using commercially available reagents. The biotinylated reference antibody is mixed with serial dilutions of the test antibody or unlabelled reference antibody (self-competition control) resulting in a mixture of various molar ratios (e.g. 1, 5, 10, 20, 100, 1000, 10000 or 100000-fold) of test antibody (or unlabelled reference antibody) to labelled reference antibody. The antibody mixture is added to a FX or FXa polypeptide coated-ELISA plate. The plate is then washed, and horseradish peroxidase (HRP)-streavidin is added to the plate as the detection reagent. The amount of labelled reference antibody bound to the target antigen is detected following addition 20 of a chromogenic substrate (e.g., TMB (3,3',5,5'-tetramethylbenzidine) or ABTS (2,2"-azino-di-(3-ethylbenzthiazoline-6- sulfonate)), which are known in the art. Optical density readings (OD units) are measured using a Spectrometer (e.g. a SpectraMax® M2 spectrometer (Molecular Devices)). The response (OD units) corresponding to zero percent inhibition is determined from wells without any competing antibody. The response (OD units) corresponding to 100% 25 inhibition, i.e. the assay background is determined from wells without any labelled reference antibody or test antibody. Percent inhibition of labelled reference antibody to FX or FXa by the test antibody (or the unlabelled reference antibody) at each concentration is calculated as follows: % inhibition = (1- (OD units - 100% inhibition)/(0% inhibition - 100% inhibition))* 100. A person skilled in the art understands that similar assays may be performed to determine if two 30 or more anti-FX/FXa antibodies share a binding region, a bin and/or competitively bind the 35

antigen. A person skilled in the art also appreciates that the competition assay can be performed by using various detection systems known in the art.

A test antibody competes with a reference antibody for binding to the antigen if an excess of one antibody (e.g., 1, 5, 10, 20, 100, 1000, 10000 or 100000-fold) inhibits binding of the other antibody, e.g., by at least 50%, 75%, 90%, 95% or 99%, as measured in a competitive binding assay. An example of a competition assay is provided in the method section 5.

The term "binding affinity" is herein used as a measure of the strength of a non-covalent interaction between two molecules, e.g. an antibody, or fragment thereof, and an antigen. The term "binding affinity" is used to describe monovalent interactions.

Binding affinity between two molecules, e.g. an antibody, or fragment thereof, and an antigen, through a monovalent interaction may be quantified by determining the equilibrium dissociation constant (K_D). K_D can be determined by measurement of the kinetics of complex formation and dissociation, e.g. by the SPR method. The rate constants corresponding to the association and the dissociation of a monovalent complex are referred to as the association rate constant k_a (or k_{on}) and dissociation rate constant k_d (or k_{off}), respectively. K_D is related to k_a and k_d through the equation $K_D = k_d / k_a$.

Following the above definition, binding affinities associated with different molecular interactions, such as comparison of the binding affinity of different antibodies for a given antigen, may be compared by comparison of the K_D values for the individual antibody/antigen complexes.

The value of the dissociation constant can be determined directly by well-known methods. Standard assays to evaluate the binding ability of ligands such as antibodies towards targets are known in the art and include, for example, ELISAs, Western blots, RIAs, and flow cytometry analysis. The binding kinetics and binding affinity of the antibody also can be assessed by standard assays known in the art, such as SPR. An example of an SPR binding assay is provided in Example 2 herein.

A FX binder, such as an antibody or a fragment thereof according to the invention may have a K_D for its target of $1 \times 10^{-4} M$ or less, $1 \times 10^{-5} M$ or less, $1 \times 10^{-6} M$ or less, $1 \times 10^{-7} M$ or less, $1 \times 10^{-8} M$ or less, or $1 \times 10^{-9} M$ or less, or $1 \times 10^{-10} M$ or less, $1 \times 10^{-11} M$ or less, $1 \times 10^{-12} M$ or less, $1 \times 10^{-13} M$ or less or $1 \times 10^{-14} M$ or less. In an embodiment the K_D of an antibody according to the invention may be less than $100 \mu M$ such as less than $50 \mu M$, such as less than $10 \mu M$. In one embodiment the K_D is less than $9 \mu M$, such as less than $8 \mu M$, such as less than $7 \mu M$, such as less than $6 \mu M$, such as less than $5 \mu M$. In one embodiment the K_D is less than $4 \mu M$, such as less than $3 \mu M$, such as less than $2 \mu M$, such as less than $1 \mu M$.

Identity

The term "identity" as known in the art, refers to a relationship between the sequences of two or more polypeptides, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptides, as determined by the

5 number of matches between strings of two or more amino acid residues. "Identity" measures the percent of identical matches between the smaller of two or more sequences with gap alignments (if any) addressed by a particular mathematical model or computer program (i.e., "algorithms"). Identity of related polypeptides can be readily calculated by known methods.

In the present invention similarity and identity were determined using Needleman (Needleman 10 et al. J. Mol. Biol. 1970; 48:443-453) from EMBOSS-6.6.0 using the parameters 10 and 0.5 for gaps opening and extensions, respectively (gapopen=10, gapextend=0.5).

Pharmaceutical formulations

In another aspect, the present invention provides compositions and formulations comprising 15 compounds of the invention, such as the antibodies described herein. For example, the invention provides a pharmaceutical composition that comprises antibodies or antigen-binding fragment thereof of the invention, formulated together with a pharmaceutically acceptable carrier.

Accordingly, one object of the invention is to provide a pharmaceutical formulation comprising 20 such an antibody or antigen-binding fragment thereof which is present in a concentration from 0.1 mg/ml to 500 mg/ml, and wherein said formulation has a pH from 2.0 to 10.0. The formulation may further comprise one or more of a buffer system, a preservative, a tonicity agent, a chelating agent, a stabilizer, or a surfactant, as well as various combinations thereof. The use of preservatives, isotonic agents, chelating agents, stabilizers and surfactants in 25 pharmaceutical compositions is well-known to the skilled person. Reference may be made to Remington: The Science and Practice of Pharmacy, 19th edition, 1995.

In one embodiment, the pharmaceutical formulation is an aqueous formulation. Such a formulation is typically a solution or a suspension, but may also include colloids, dispersions, emulsions, and multi-phase materials. The term "aqueous formulation" is defined as a 30 formulation comprising at least 50% w/w water. Likewise, the term "aqueous solution" is defined as a solution comprising at least 50% w/w water, and the term "aqueous suspension" is defined as a suspension comprising at least 50% w/w water.

In another embodiment, the pharmaceutical formulation is a freeze-dried formulation, to which a solvent and/or a diluent is added prior to use.

In a further aspect, the pharmaceutical formulation comprises an aqueous solution of such an antibody, and a buffer, wherein the antibody is present in a concentration from 0.1 mg/ml or above, and wherein said formulation has a pH from about 2.0 to about 10.0.

In one embodiment, the present invention relates to an injection device with content of said

5 composition. In some embodiments, the pharmaceutical composition of the invention is intended for use and/or contained in an injection device. In some embodiments, the injection device is a disposable, pre-filled, multi-dose pen of the FlexTouch® type (supplier Novo Nordisk A/S, Denmark). In some embodiments the injection device is a single shot device.

In some embodiments the injection device is a fixed dose device, such as one configured to

10 deliver multiple predetermined doses of drug, sometimes referred to as a multiple fixed dose device or a fixed dose, multi-shot device.

Administration

A compound of the invention, such as an antibody or antigen-binding fragment thereof, or

15 compositions comprising such compound, may be administered parenterally, such as intravenously, such as intramuscularly, such as subcutaneously. Alternatively, a compound of the invention, such as an antibody or antigen-binding fragment thereof, or compositions comprising such compound, may be administered via a non-parenteral route, such as periorally or topically. The compound or composition may be administered prophylactically. Alternatively, 20 the compound or composition may be administered therapeutically (on demand).

Dosages

The dose of the compounds to be delivered may be from about 0.01 mg to 500 mg of the

compound per day, preferably from about 0.1 mg to 250 mg per day, and more preferably from

25 about 0.5 mg to about 250 mg per day, per week, per second week or per month as loading and maintenance doses, depending on the severity of the condition. A suitable dose may also be adjusted for a particular compound based on the properties of that compound, including its *in vivo* half-life or mean residence time and its biological activity. For example, compounds to be delivered could in one embodiment be administered once weekly, or in another embodiment 30 once every second week or in another embodiment one monthly and in either of said embodiments in a dose of for example 0.1, 0.25, 0.5, 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5 or 10 mg per kg body weight.

Compositions containing the compounds as disclosed herein can be administered for

prophylactic and/or in some embodiments therapeutic treatments. In therapeutic applications,

35 compositions are administered to a subject already suffering from a disease, such as any

bleeding disorder as described above, in an amount sufficient to cure, alleviate or partially arrest the disease and its complications. An amount adequate to accomplish this is defined as "therapeutically effective amount". As will be understood by the person skilled in the art amounts effective for this purpose will depend on the severity of the disease or injury as well as 5 the weight and general state of the subject.

In one aspect, the invention relates to FX binding molecules with the capability of stimulating the activation of FX to generate FXa. As described above, such functionality is desirable in the quest for new and improved treatment to improve the coagulation function in particular 10 haemophilia patients.

In one embodiment, the invention relates to a FX binder, such as an antibody or antigen-binding fragment thereof which binds human FX and stimulates FX activation.

In one embodiment, the invention relates to a FX binder, such as an antibody or antigen-binding fragment thereof, wherein the FX binder, antibody or antigen-binding fragment thereof is 15 binding human FX and capable of stimulating FX activation.

It is of special interest that the activation observed occurs also in the absence of a FIX binding moiety, such as FVIII or a FVIII mimetic compound comprising a FIXa binder which can bring FX and FIXa together. In one embodiment, the FX binder, such as an antibody or antigen-binding fragment thereof binds human FX and thereby stimulates proteolysis of FX by FIXa 20 generating FXa.

In one embodiment the antibody or antigen-binding fragment thereof stimulates FXa generation independently of the presence of a FIXa binding moiety. In one embodiment the antibody or antigen-binding fragment thereof is capable of stimulating FXa generation independently of the presence of a FIXa binding moiety.

25 In one embodiment, the FX binder, such as an antibody or antigen-binding fragment thereof capable of binding FX, is capable of making FX more prone to proteolysis independently of the presence of a FIXa binding moiety. In one embodiment, the FX binder, such as an antibody or antigen-binding fragment thereof capable of binding FX, is capable of making FX more prone to proteolysis by FIXa. In one embodiment, the FX binder, such as an antibody or antigen-binding 30 fragment thereof capable of binding FX, is capable of making FX more prone to proteolysis independently of the presence of a FIXa binding moiety.

The ability of a FX binder to stimulate FXa generation may be tested by a suitable assay known to the person skilled in the art. References is made to example 3 herein providing an *in vitro* assay suitable for testing the activating function of a given FX binder. In one embodiment, the 35 FX binder, such as an antibody or antigen-binding fragment thereof capable of binding FX,

stimulates FX activation as determined by Example 3. A FX binder is stimulatory or capable of stimulating FX activation when an increase in FXa is measured in the presence of said FX binder compared to the equivalent assay performed with no FX binder or a non-activating FX binder.

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The ability of a FX binder to promote FIXa-mediated FX-activation is considered present when an increase in FX activation rate - as described in the assay according to Example 3 herein - is observed for a given FX binder relative to absence of FX binder, i.e. when a fold increase in FX activation above 1 is observed, such as above 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8 or 1.9. In

10 preferred embodiments the fold increase in FX activation observed is more than 2 fold such as 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 fold or above. In one embodiment the fold increase in FX activation is 2-100,000 fold. In one such embodiment the fold increase in FX activation is 2-500 fold. In one such embodiment the fold increase in FX activation is 3-500 fold. In another such embodiment the fold increase in FX activation is 4-500 fold. In another such

15 embodiment the increase in FX activation is 5-100 fold. In another embodiment the increase in FX activation is 10-100 fold, such as 10-83 fold.

20 In order to avoid that the avidity of a FX-binder influences the measurements in an assay such as that described in Example 3 herein, the assay should preferably be performed by using a monovalent FX binder. In case the FX binder is a bi- or multi-valent FX binder, the activation assay should thus be performed using a monovalent antigen-binding fragment thereof.

An aspect of the invention relates to a FX binder, such as an antibody or antigen-binding fragment thereof which binds human FX stronger than FXa. In one embodiment, the FX binder does not bind FXa. In another embodiment, the FX binder preferentially binds FX relative to FXa. In one such embodiment, the FX binder binds FXa with a lower affinity. As FX is distinguished from FXa by the presence of the activation peptide, the invention in an aspect relates to a FX binder such as an antibody or antigen-binding fragment thereof which binds the activation peptide of human FX. The activation peptide of human FX is defined by amino acid residues 143-194 of SEQ ID NO:2.

30 In one embodiment, the antibody or antigen-binding fragment thereof binds the activation peptide of FX identified by amino acid residues 143-194 of SEQ ID NO:2. In a further embodiment, the antibody or antigen-binding fragment thereof binds amino acid residues 170-185 within the activation peptide of FX as identified by SEQ ID NO:2.

35 Based on the peptide array performed as described in Example 5, a shared binding site for the identified FX activating FX binders was identified. A common minimal peptide epitope was

determined and found to comprise the peptide “LL” within the activation peptide of FX corresponding to amino acid residues 177-178 of human FX as identified by SEQ ID NO:2. In an embodiment, the invention relates to a FX binder, such as an antibody or antigen-binding fragment thereof, capable of binding “LL” within the activation peptide of FX corresponding to 5 amino acid residues 177-178 of human FX as identified by SEQ ID NO:2.

In an embodiment, the invention relates to a FX binder, such as an antibody or antigen-binding fragment thereof capable of binding the activation peptide of FX, and wherein the common minimal epitope as determined by peptide array, is comprised by “LL” (amino acid residues 177-178 of SEQ ID NO:2).

10 In an embodiment, the FX binder, such as an antibody or antigen-binding fragment thereof binds the activation peptide of FX identified by amino acid residues 143-194 of SEQ ID NO:2 and wherein the common minimal epitope as determined by peptide array is comprised by “LL” (amino acid residues 177-178 of SEQ ID NO:2).

It is well known in the art that antigen-binding molecules may take various forms. A series of 15 well-known types of molecular formats are described herein, while it is also noted that it is not to be considered an exhaustive list, and that the skilled artisan will be able to apply the teaching of the present application to their preferred molecular format without difficulties.

In one embodiment, the FX binder is a monovalent. In one such embodiment the FX binder is an immunoglobulin single variable domain, such as a (single) domain antibody or antibody 20 fragment thereof or a Nanobody®, a V_HH, a humanized V_HH or a camelized V_H domain. In one embodiment the FX binder is Fab. In one embodiment the FX binder is bi-valent. In one embodiment the FX binder is a monoclonal whole antibody (mAb) or an antigen-binding fragment of a mAb.

An aspect of the invention relates to the identification of a FX binder which is capable of 25 stimulating FX activation. In one such embodiment, a method is provided comprising the following steps a) providing a FX binder b) testing the FX binder in an *in vitro* assay suitable for testing the FX activating function of a given FX binder and c) selecting a FX binder capable of stimulating FX activation.

As mentioned above, a FX binder capable of stimulating FX activation may be a desired 30 element to include in a bi-specific molecule, or tri-specific molecule or even a multi-specific molecule.

An aspect of the invention thus relates to bi-, tri and multi-specific molecules, such as antibody molecules (or antigen-binding fragments thereof) comprising at least one FX binding moiety providing FX stimulation.

An aspect of the invention relates to the use of a molecule, such as an antibody or an antigen-binding fragment thereof as described herein for the manufacture of a medicament.

An aspect of the invention relates a molecule, such as an antibody or an antigen-binding fragment thereof as described herein for use in a method of treatment.

- 5 An aspect of the invention relates use of a molecule, such as an antibody or an antigen-binding fragment thereof as described herein for the treatment of a coagulopathy, such as haemophilia. An aspect of the invention relates to a method of treatment comprising the step of administering to an individual in need thereof, a therapeutically effective dose of a molecule, such as an antibody or an antigen-binding fragment thereof as described herein. In one embodiment the
- 10 method is for treatment a patient suffering from a coagulopathy, such as haemophilia and in particular haemophilia A with or without inhibitors. In one embodiment the method is for treatment a patient suffering from haemophilia B with or without inhibitors.

15 EMBODIMENTS

1. An antibody or antigen-binding fragment thereof capable of binding to the activation peptide of FX identified by amino acid residues 143-194 of SEQ ID NO:2.
2. An antibody or antigen-binding fragment thereof capable of binding to one or more of amino acid residues 170-185 within the activation peptide of FX as identified by SEQ ID NO:2.
3. An antibody or antigen-binding fragment thereof capable of binding to "LL" within the activation peptide of FX corresponding to amino acid residues in position 177-178 of human FX as identified by SEQ ID NO:2.
- 25 4. An antibody or antigen-binding fragment thereof capable of binding to the activation peptide of FX, wherein the common minimal epitope as determined by peptide array, comprises "LL" (AA 177-178 of SEQ ID NO:2).
- 30 5. An antibody or antigen-binding fragment thereof capable of binding FX, wherein the antibody or antigen-binding fragment is capable of stimulating FX activation.
6. An antibody or antigen-binding fragment thereof capable of binding FX, wherein the antibody or antigen-binding fragment is capable of stimulating FX activation by FIXa.

7. An antibody or antigen-binding fragment thereof capable of binding FX, wherein the antibody or antigen-binding fragment is capable of stimulating FX activation by FIXa independently of the presence of a FIXa binder.
- 5 8. An antibody or antigen-binding fragment thereof capable of binding FX according to any of embodiments 1-4, wherein the antibody or antigen-binding fragment thereof is capable of stimulating FX activation.
- 10 9. The antibody or antigen-binding fragment thereof capable of binding FX according to any of the embodiments 5-8, wherein the capability of the antibody or antigen-binding fragment thereof to stimulate FX activation is determined as described in Example 3 herein.
- 15 10. An antibody or antigen-binding fragment thereof capable of binding FX, wherein the antibody or antigen-binding fragment thereof stimulates FX activation by FIXa independently of the presence of a FIXa binding moiety.
- 20 11. The antibody or antigen-binding fragment thereof capable of binding FX according to any of the embodiments 5-10, wherein the stimulation of FX activation is determined as described in Example 3 herein.
12. An antibody or antigen-binding fragment thereof capable of binding FX, wherein the antibody or antigen-binding fragment is capable of making FX more prone to activation.
- 25 13. An antibody or antigen-binding fragment thereof capable of binding FX, wherein the antibody or antigen-binding fragment is capable of making FX more prone to proteolysis by FIXa.
14. An antibody or antigen-binding fragment thereof capable of binding FX, wherein the antibody or antigen-binding fragment is capable of making FX more prone to proteolysis by FIXa independently on the presence of a FIXa binding moiety.
- 30 15. The antibody or antigen-binding fragment thereof capable of binding FX according to any of the embodiments 12-14, wherein the capability of the antibody or antigen-binding fragment to make FX more prone to proteolysis is determined as described in Example 3 herein.

16. The antibody or antigen-binding fragment thereof capable of binding FX according to any of the embodiments 1-4, wherein the antibody or antigen-binding fragment is capable of stimulating FX activation according to any of the embodiments 5-11.
- 5 17. The antibody or antigen-binding fragment thereof according to any of the embodiments 1-4, wherein the antibody or antigen-binding fragment thereof is a single variable domain antibody which stimulates FX activation according to any of the embodiments 5-11.
- 10 18. The antibody or antigen-binding fragment thereof capable of binding FX according to any of the embodiments 1-4, wherein the antibody or antigen-binding fragment thereof is a single variable domain antibody which is capable of making FX more prone to proteolysis according to any of the embodiments 12-15.
- 15 19. The antibody or antigen-binding fragment thereof capable of binding FX according to any of the embodiments 5-18, wherein a monovalent antigen-binding fragment thereof
 - a. stimulates FX activation;
 - b. stimulates FX activation by FIXa;
 - c. is capable of stimulating FX activation;
 - d. is capable of stimulating FX activation by FIXa;
 - 20 e. is capable of making FX more prone to proteolysis; or
 - f. is capable of making FX more prone to proteolysis by FIXa.
- 25 20. The antibody or antigen-binding fragment thereof capable of binding FX according to any of the previous embodiments, wherein the antibody or antigen-binding fragment has a binding affinity determined as the equilibrium dissociation constant (K_D) is less than 10 μM , such as less than 9 μM , such as less than 8 μM , such as less than 7 μM , such as less than 6 μM , such as less than 5 μM , such as less than 4 μM , such as less than 3 μM or such as less than 2 μM .
- 30 21. The antibody or antigen-binding fragment thereof according to any of the previous embodiments, wherein the antibody or antigen-binding fragment is monovalent.
22. The antibody or antigen-binding fragment thereof according to any of the previous embodiments, wherein the antibody or antigen-binding fragment thereof is an

immunoglobulin single variable domain or antibody fragment thereof, such as a domain antibody, a Nanobody®, a V_HH, a humanized V_HH or a camelized V_H domain.

23. The antibody or antigen-binding fragment thereof according to any of the previous

5 embodiments wherein the antibody or antigen-binding fragment thereof is a Fab, scFab, Fv or scFv.

24. The antibody or antigen-binding fragment thereof according to any of the previous

embodiments 1-15, wherein the antibody or antigen-binding fragment thereof is bivalent.

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25. The antibody or antigen-binding fragment thereof according to embodiment 24, wherein the antibody or antigen-binding fragment is a mAb of a Fab'₂.

26. The antibody or antigen-binding fragment thereof according to any of the previous

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embodiments wherein the heavy chain variable domain is at least 90, 91, 92, 93, 94, 95, 96, 97, 98 or 99% identical to the sequence identified by SEQ ID NO:8, 9, 10, 11, 54, 55, 56 or 57, respectively.

27. The antibody or antigen-binding fragment thereof according to any of embodiments 1-25,

20

wherein the antibody or antigen-binding fragment thereof comprises

a. three heavy chain CDR sequences with at most 10 amino acid residue changes compared to the three CDR sequences of the heavy chain variable domain identified by SEQ ID NO:8;

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b. three heavy chain CDR sequences with at most 10 amino acid residue changes compared to the three CDR sequences of the heavy chain variable domain identified by SEQ ID NO:9;

c. three heavy chain CDR sequences with at most 10 amino acid residue changes compared to the three CDR sequences of the heavy chain variable domain identified by SEQ ID NO:10;

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d. three heavy chain three CDR sequences with at most 10 amino acid residue changes compared to the three CDR sequences of the heavy chain variable domain identified by SEQ ID NO:11;

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e. three heavy chain CDR sequences with at most 10 amino acid residue changes compared to the three CDR sequences of the heavy chain variable domain identified by SEQ ID NO:54;

- f. three heavy chain CDR sequences with at most 10 amino acid residue changes compared to the three CDR sequences of the heavy chain variable domain identified by SEQ ID NO:55;
- 5 g. three heavy chain CDR sequences with at most 10 amino acid residue changes compared to the three CDR sequences of the heavy chain variable domain identified by SEQ ID NO:56; or
 - three heavy chain CDR sequences with at most 10 amino acid residue changes compared to the three CDR sequences of the heavy chain variable domain identified by SEQ ID NO:57.
- 10 28. The antibody or antigen-binding fragment thereof according to embodiment 27, wherein the three heavy chain CDR sequences have at most 9, such as 8, such as 7 or such as 6 amino acid changes compared to the three CDRs of the identified SEQ ID NOs.
- 15 29. The antibody or antigen-binding fragment thereof according to embodiment 28, wherein the three heavy chain CDR sequences have at most 5, such as 4, such as 3, such as 2 or at most 1 amino acid changes compared to the three CDRs of the identified SEQ ID NOs.
- 20 30. An antibody or antigen-binding fragment thereof comprising or consisting of SEQ ID NO:8, 9, 10, 11, 54, 55, 56, or 57.
- 31. An antibody or antigen-binding fragment thereof comprising the three CDRs of SEQ ID NO:8, 9, 10, 11, 54, 55, 56, or 57.
- 25 32. An antibody or antigen-binding fragment thereof, wherein the antibody or antigen-binding fragment competes with a reference antibody or antigen-binding fragment comprising or consisting of SEQ ID NO:8, 9, 10, 11, 54, 55, 56, or 57.
- 33. An antibody or antigen-binding fragment thereof comprising the heavy chain variable domain (SEQ ID NO:4) and light chain variable domain (SEQ ID NO:5) of mAb 00916.
- 30 34. An antibody or antigen-binding fragment thereof comprising the heavy chain variable domain (SEQ ID NO:6) and light chain variable domain (SEQ ID NO:7) of mAb 13F62.

35. An antibody or antigen-binding fragment thereof comprising the three CDRs of the heavy chain variable domain (SEQ ID NO:4) and the three CDRs of the light chain variable domain (SEQ ID NO:5) of mAb 00916.
- 5 36. An antibody or antigen-binding fragment thereof comprising the three CDRs of the heavy chain variable domain (SEQ ID NO:6) and the three CDRs of the light chain variable domain (SEQ ID NO:7) of mAb 13F62.
- 10 37. An antibody or antigen-binding fragment thereof, wherein the antibody or antigen-binding fragment competes with a reference antibody or antigen-binding fragment comprising the heavy chain variable domain (SEQ ID NO:4) and light chain variable domain (SEQ ID NO:5) of mAb 00916.
- 15 38. An antibody or antigen-binding fragment thereof, wherein the antibody or antigen-binding fragment competes with a reference antibody or antigen-binding fragment comprising the heavy chain variable domain (SEQ ID NO:6) and light chain variable domain (SEQ ID NO:7) of mAb 13F62.
- 20 39. The antibody or antigen-binding fragment thereof according to any of the embodiments 26-38 wherein the antibody or antigen-binding fragment is capable of stimulating FX activation according to any of the embodiments 5-9.
- 25 40. The antibody or antigen-binding fragment thereof according to any of the embodiments 26-38 wherein the antibody or antigen-binding fragment stimulates FX activation according to any of the embodiments 9-11.
- 30 41. The antibody or antigen-binding fragment thereof according to any of the embodiments 26-38 wherein the antibody or antigen-binding fragment is capable of making FX more prone to proteolysis according to any of the embodiments 12-15.
42. A bi-, tri- or multi-specific molecule comprising an antibody or antigen-binding fragment, according to any of the previous embodiments.

43. The bi-, tri- or multi-specific molecule comprising an antibody or antigen-binding fragment thereof, according to any of the previous embodiments, wherein said antibody or antigen-binding fragment thereof is a single variable domain antibody.
- 5 44. A pharmaceutical composition comprising the antibody or antigen-binding fragment thereof according to any of the previous embodiments and optionally one or more pharmaceutically acceptable carrier(s).
- 10 45. Use of the antibody or antigen-binding fragment thereof or composition according to any of the previous embodiments for the manufacture of a medicament for use in the treatment of a coagulopathy, such as haemophilia A with or without inhibitors, or such as haemophilia B with or without inhibitors.
- 15 46. The antibody or antigen-binding fragment thereof or composition according to any of the embodiments 1-44 for use in the treatment of a coagulopathy, such as haemophilia A with or without inhibitors or such as haemophilia B with or without inhibitors.
- 20 47. A method of treating a subject suffering from a blood coagulation disorder such as haemophilia, comprising administering to said subject an antibody or antigen-binding fragment thereof or composition according to any of the previous embodiments.
48. A method according to embodiment 47 wherein the coagulopathy or blood coagulation disorder is haemophilia A or B with inhibitors or without inhibitors.
- 25 49. A method for identifying an antibody according to any of the embodiments 1-25 comprising the steps of a) providing a FX binder, b) testing the FX binder in an *in vitro* assay suitable for testing the FX activating function of the FX binder provided in step a and c) selecting a FX binder capable of stimulating FX activation.
- 30 50. A method for identifying an antibody according to any of the embodiments 5-23 comprising the steps of a) providing a FX binder, b) testing the FX binder in an *in vitro* assay suitable for testing the FX activating function of the FX binder provided in step a and c) selecting a FX binder capable of making FX more prone to proteolysis, for example by FIXa.
- 35 51. A eukaryotic cell which expresses the antibody or antigen-binding fragment thereof, according to any of the embodiments 1-43.

52. A kit comprising the antibody or antigen-binding fragment thereof or composition according to any of the embodiments 1-44 and instructions for use.

EXAMPLES AND METHODS

General methods

5 **Preparation of FX-binding Nanobodies**

General molecular biology

For general molecular biology techniques, please see Molecular Cloning: A Laboratory Manual (Third Edition, 2001, Sambrook, Fritsch and Maniatis eds., CSHL Press, Cold Spring Harbor,

10 NY).

1. Immunizations and libraries

After approval of the Ethical Committee of the Ablynx Camelid Facility (LA1400575), one llama and one alpaca were immunized with FX (Haemotologic Technologies, VT USA).

15 Cloning of heavy chain-only antibody fragment repertoires and preparation of phage immune libraries was performed as follows.

Following the final immunogen injection, blood samples were collected. From these blood samples, peripheral blood mononuclear cells (PBMCs) were prepared using Ficoll-Hypaque according to the manufacturer's instructions (Amersham Biosciences, Piscataway, NJ, US).

20 From the PBMCs, total RNA was extracted and used as starting material for RT-PCR to amplify the V_H/Nanobody[®]-encoding DNA segments, essentially as described in WO2005/044858. In short, the Nanobody[®]-encoding DNA segments were cloned into phagemid vector pAX212 enabling production of phage particles displaying Nanobodies[®] fused with His₆- and FLAG₃-tags. Subsequently, phages were prepared and stored according to standard protocols.

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Synthetic libraries

Synthetic libraries were generated by cloning synthetic Nanobody[®] gene fragments into phagemid vector pAX190, which has the same features as the above described pAX212, but with differences in the multiple cloning site.

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Library screening of Nanobodies binding to FX

Nanobody[®] Phage Display selections were performed with the generated immune and synthetic libraries. The libraries were subjected to one to four successive rounds of enrichment against different combinations of immobilized human FX (Haemotologic Technologies, VT USA) and cynomolgus FX (Novo Nordisk in house production).

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In order to specifically enrich for Nanobodies that were selective for FX versus FXa, in certain experiments excess soluble FXa was used for competition during the incubation of the libraries with the immobilized FX.

In order to specifically enrich for Nanobodies that were selective for FX versus other structurally related coagulation factors, in certain experiments excess soluble FIX was used for competition during the incubation of the libraries with the immobilized FX.

Approximately 4500 individual clones from the selection outputs were screened for binding in ELISA (using periplasmic extracts from *E.coli* cells expressing the Nanobodies) against human and cynomolgus FX, FXa or FIX. Approximately 1500 clones that showed specific binding to

10 human FX/FXa were identified, of which the majority showed cross-binding to cynomolgus FX.

Some clones showed preferential binding to FX versus FXa. Sequence analysis of the ELISA positive clones identified approximately 700 unique sequences of Nanobodies binding to FX/FXa.

15 **2. Generation of Nanobody® expression constructs**

Sequence analysis of Nanobodies from phage display selection outputs was done according to commonly known procedures (Pardon et al. (2014) *Nat Protoc* 9: 674).

Nanobody®-containing DNA fragments, obtained by PCR with specific combinations of forward FR1 and reverse FR4 primers each carrying a unique restriction site, were digested with the

20 appropriate restriction enzymes and ligated into the matching cloning cassettes of Nanobody® expression vectors (described below). The ligation mixtures were then transformed to

electrocompetent *Escherichia coli* TG1 (60502, Lucigen, Middleton, WI) or TOP10 (C404052,

ThermoFisher Scientific, Waltham, MA) cells which were then grown under the appropriate

antibiotic selection pressure (kanamycin or Zeocin). Resistant clones were verified by Sanger

25 sequencing of plasmid DNA (LGC Genomics, Berlin, Germany).

Monovalent Nanobodies were expressed in *E. coli* TG1 from a plasmid expression vector

containing the *lac* promoter, a resistance gene for kanamycin, an *E. coli* replication origin and a

Nanobody® cloning site preceded by the coding sequence for the OmpA signal peptide. In

frame with the Nanobody® coding sequence, the vector codes for a C-terminal FLAG3 and HIS6

30 tag. The signal peptide directs the expressed Nanobodies to the periplasmic compartment of

the bacterial host.

Expression and purification of NanobodiesGeneric expression of Nanobodies in *E. coli*

E. coli TG-1 cells containing the Nanobody® constructs of interest were grown for 2 hours at

37°C followed by 29 hours at 30°C in baffled shaker flasks containing “5052” auto-induction

5 medium (0.5% glycerol, 0.05% glucose, 0.2% lactose + 3 mM MgSO₄). Overnight frozen cell pellets from *E. coli* expression cultures are then dissolved in PBS (1/12.5th of the original culture volume) and incubated at 4°C for 1 hour while gently rotating. Finally, the cells are pelleted down once more and the supernatant, containing the proteins secreted into the periplasmic space, is stored.

10 Generic expression of Nanobodies® in *P. pastoris*

P. pastoris cells containing Nanobody® constructs of interest were grown for two days (at 30°C,

200rpm) in BGCM medium. On the third day, the medium was switched to BMCM and the

constructs were further grown (at 30°C, 200rpm) and induced with 0.5% v/v methanol after 8 hours. Next day the constructs were induced with 0.5% v/v methanol in the morning, at noon

15 and in the evening. On the fifth day, the cells are spun down and the supernatant (containing the secreted Nanobody®) is collected.

Generic purification of Nanobodies®

HIS6-tagged Nanobodies® were purified by immobilized metal affinity chromatography (IMAC)

on either Ni-Excel (GE Healthcare) or Ni-IDA/NTA (Genscript) resins with Imidazole (for the

20 former) or acidic elution (for the latter) followed by a desalting step (PD columns with Sephadex G25 resin, GE Healthcare) and if necessary, gel filtration chromatography (Superdex column, GE Healthcare) in PBS.

3. Thermal shift assay

25 Thermal stability of the anti-FX Nanobodies® were determined using a thermal shift assay (TSA) performed in a 96-well plate on the LightCycler 480II machine (Roche). Per row, one Nanobody® was analysed according to the following pH range: 3.5/4/4.5/5/5.5/6/6.5/7/7.5/8/8.5/9. Per well, 5 µL of Nanobody® sample (0.8 mg/mL in PBS) was added to 5 µL of Sypro Orange (40x in MilliQ water; Invitrogen cat. No. S6551) and 10 µL of buffer (100 mM phosphate, 100 mM borate, 100 mM citrate and 115 mM NaCl with a pH 30 ranging 3.5 to 9). The applied temperature gradient (37 to 99°C at a rate of 0.03°C/s) induces unfolding of the Nanobodies, whereby their hydrophobic patches become exposed. Sypro Orange binds to those hydrophobic patches, resulting in an increase in fluorescence intensity (Ex/Em = 465/580 nm). The inflection point of the first derivative of the fluorescence intensity 35 curve at pH 7 serves as a measure of the melting temperature (Tm).

4. Analytical size exclusion chromatography

Potential occurrence of aggregation and oligomerization of the Nanobodies® was investigated by analytical size exclusion chromatography (SEC). To this end, 8 µg of Nanobody® sample (0.5 mg/mL in PBS) and 10 µL of the BioRad standard (Cat. No. 151-1901, 1/10 diluted in PBS) 5 were injected via the Dionex Ultimate 3000 equipment on a Waters Xbridge column (particle size: 3.5µm, pore size 200Å, ID 7.8mm). An Arginine buffer [10 mM Phosphate + 150 mM Arginine + 10% 1-propanol + 0.02% NaN₃ (pH7.0)] was used as mobile phase and a flow-rate of 0.5 mL/minute was applied. The overall SEC behavior was determined by considering three 10 parameters: peak area of the main peak (>90% = pass), percentage recovery (>80% = pass) and the retention time versus the 1.35 kDa BioRad standard peak.

5. Competition assay

Antibodies (such as Nanobodies®) binding same or similar epitopes can be characterized using a competition assay which may be performed as follows.

15 25 µL (1 µg/mL) human plasma derived FX (Haematologic Technologies Inc, USA) is immobilised in a microtiter plate (Nunc, Wiesbaden, Germany). After washing and blocking of the wells, the “binning” mAb (mAb 00916) is added at a concentration of 1 µM in buffer containing 50 mM HEPES pH 7.4, 2.5 mM CaCl₂, 1% BSA and 0.05% Tween 20 (Sigma), or a reference with buffer only, and pre-incubated for 30 minutes with the coated human FX.

20 Subsequently test antibodies (here different Nanobodies®) are added and allowed to bind for 1 hour. Unbound test antibody (Nanobody®) and binning mAb are washed away and bound Nanobody® is detected using Horseradish Peroxidase (HRP) conjugated anti-FLAG mAb (Sigma, Cat#A8592) and a subsequent enzymatic reaction in the presence of the substrate esTMB (3,3',5,5'-tetramethylbenzidine) (SDT, Brussels, Belgium).

25 For the “binning” mAb, the % inhibition observed in the presence of each of the test antibody (Nanobody®) is calculated by the below equation.

$$\% \text{ inhibition} = 100 - \left(\frac{\text{OD}_{450 \text{ nm}} \text{ test antibody (or Nanobody) at } 1 \text{ uM}}{\text{OD}_{450 \text{ nm}} \text{ reference}} \right) \times 100\%$$

30 Antibody molecules are generally considered to compete if more than 50 % inhibition is observed.

Examples 1- 5**Example 1: anti-FX Nanobodies[®]**

From the pool of anti-FX Nanobodies, a group of Nanobodies selectively binding the FX zymogen (FX and not FXa) were selected for further studies. The sequences of the Nanobodies 5 are defined by SEQ ID NOs:8-11 and 54-57. A competition experiment with mAb 00916 (IgG1 isotype, variable sequences identified by SEQ ID NO:4 and 5) as “binning” antibody was performed and the Nanobodies Nb 701B09, Nb 701C06, Nb 702C12, Nb 701D07, Nb 721E08, Nb 729A04, Nb 729C08 and Nb 730C03 were all shown to compete with mAb 00916. A control Nanobody[®], Nb 501A02 (SEQ ID NO:12), which binds a different region of FX was also 10 included and no competition with mAb 00916 was observed for this Nanobody[®]. Results are shown in table 1 below and illustrates that all compounds but Nb 501A02 compete with mAb 00916 for binding to FX, i.e. bind to the same or overlapping epitope on FX as mAb 00916.

Table 1: Nanobody[®] (Nb) binding FX zymogen and competing with mAb 00916

Nanobody[®] ID	Competition w. mAb 00916
Nb 701B09 (SEQ ID NO:8)	+
Nb 701C06 (SEQ ID NO:9)	+
Nb 702C12 (SEQ ID NO:10)	+
Nb 701D07 (SEQ ID NO:11)	+
Nb 501A02 (SEQ ID NO:12)	-
Nb 721E08 (SEQ ID NO:54)	+
Nb 729A04 (SEQ ID NO:55)	+
Nb 729C08 (SEQ ID NO:56)	+
Nb 730C03 (SEQ ID NO:57)	+

Example 2: SPR analysis of anti-FX Nanobody® binding to FX

Binding of purified anti-FX Nanobodies (Nb) to human plasma-derived FX (Haematologic Technologies Inc, USA) was probed by Surface Plasmon Resonance (SPR) (Biacore T200). Briefly, anti-His mAb (MAB050 from R&D systems) was immobilised on a CM4 sensor chip 5 using standard amine coupling chemistry. Anti-FX Nanobodies (10 nM), according to Table 3, was injected at a flow rate of 10 μ L/min for 1 minute. Subsequently 4096, 1024, 256, 64, 16, 4, and 0 nM of FX were injected at a flow rate of 30 μ L/min for 4 minutes to allow for binding to anti-FX Nb followed by a 5 minutes running buffer (10 mM HEPES, 150 mM NaCl, 5 mM CaCl₂, 0.05%(v/v) Surfactant P20, 1 mg/mL bovine serum albumin, pH 7.4) injection allowing 10 dissociation from anti-FX Nanobody®. The running buffer was also for dilution of anti-FX Nb and FX samples. Regeneration of the chip was achieved using a regeneration buffer consisting of 3M MgCl₂, 30 seconds contact time, and a 30 μ L/min flow rate. The binding data were collected at 25 °C and were analysed according to a 1:1 model using BiaEvaluation 4.1 supplied by the manufacturer (Biacore AB, Uppsala, Sweden).

15 In all cases, the binding sensograms displayed a fast on and a fast off binding kinetic profile precluding K_D determination based on kinetic analysis. Therefore, the reported K_D values are determined based on steady state analysis. Analysis resulted in the binding constants reported in Table 2. The strongest binder identified is Nb702C12, while the others Nanobodies® tested binds FX with a slightly higher K_D and lower R_{max} .

20

Table 2: Estimated binding constants based on steady state analysis for the interaction of anti-FX Nanobodies® with human plasma-derived FX as determined by SPR analysis

FX binder	K_D	R_{max}
Nb 701B09	2.1 μ M	17
Nb 701C06	0.96 μ M	14
Nb 701D07	2.4 μ M	15
Nb 702C12	1.2 μ M	30

Example 3: Activity of anti-FX Nanobodies in FXa generation assay

The ability of the monovalent anti-FX Nanobody® (Nb) to promote FIXa-mediated FX-activation was determined in the presence of a procoagulant phospholipid membrane according to the principles described by Scheiflinger *et al.* (2008) *J Thromb Haemost*, 6:315-322. A Fab of mAb

5 13F62 (IgG1 isotype, variable sequences identified by SEQ ID NO:6 and 7), also found to bind the activation peptide, were included for comparison. Moreover, anti-FX antibodies as disclosed in US 9,334,331 (J327 and L404-k in said publication), corresponding to the anti-FX arm of ACE910); and more recently in WO2018/021450 (J327 D31H and JYL280 in said publication) and WO2018/098363 (BIIB-12-917 represented by SEQ ID NO:427 and 615 in said publication)

10 are stated to be suitable for use as part of anti-FIX/anti-FX bispecific FVIII mimetic compounds were, furthermore, included for comparison.

Each compound was tested individually in a concentration range from 0-1000 nM, 0-2000 nM, 0-4000 nM or 0-8000 nM by pre-incubation with 1-1.5 nM human plasma-derived FIXa (Haematologic Technologies Inc, USA) and 500 µM 25:75 phosphatidyl serine:phosphatidyl 15 choline phospholipid vesicles (Haematologic Technologies Inc, USA) in assay buffer (50 mM HEPES, 100 mM NaCl, 5 mM CaCl₂, 0.1%(w/v) PEG8000, 1 mg/mL bovine serum albumin, pH 7.3) for 10 minutes. The reaction was initiated by addition of human plasma-derived FX (Haematologic Technologies Inc, USA) to a final concentration of 100 nM and a reaction volume of 50 µL. Following 20 minutes activation at room temperature while agitated (1000 20 RPM), the reaction was quenched by addition of 25 µL quench buffer (50 mM HEPES, 100 mM NaCl, 60 mM EDTA, 0.1%(w/v) PEG8000, 1 mg/mL bovine serum albumin, pH 7.3). The amount of FXa generated was determined by addition of 25 µL 2 mM S-2765 chromogenic substrate for FXa (Chromogenix, Sweden) and chromogenic substrate conversion was followed by measuring absorbance at 405 nm for 10 minutes in a microplate reader. The observed 25 change in 405 nm absorbance (ΔAbs405/min) was fitted to the quadratic binding equation (eq. 1) to obtain the peak stimulatory activity and EC50.

Table 3 lists fitted maximal enhancement of FXa-generation rate (fold increase in FX-activation) and fitted K_D-values. Most of the tested Nanobodies stimulate FIXa-mediated FX-activation (~4 to ~83-fold relative to FIXa alone), whereas a Fab of mAb13F62 showed a 1.5 fold increased 30 activation and Nb 501A02 showed no activation. No fitted EC50 values are provided for the Fab of 13F62 and FIXa alone.

Eq. 1:

$$Y_i = \frac{[FX] + [binder]_i + K_D - \sqrt{([FX] + [binder]_i + K_D)^2 - 4 \cdot [FX] \cdot [binder]_i}}{2 \cdot [FX]} \cdot (Y_{max} - Y_0) + Y_0$$

where Y_i is the observed substrate conversion ($\Delta\text{Abs405}/\text{min}$) at a given FX binder concentration (i), [FX] and [binder] is the total concentration FX and FX binder, respectively, K_D is the apparent dissociation constant of the FX binder, Y_{max} and Y_0 is the maximal and initial signal ($\Delta\text{Abs405}/\text{min}$), respectively.

Table 3: Effect of FX binders on FIXa-mediated FX activation. Estimated K_D (mean \pm SD, n = 3) and increase in FX-activation (mean \pm SD, n = 3) relative to FIXa only.

FX binder	Estimated K_D (nM)	Increase in FX activation (fold)
Nb 701B09	72.3 ± 16.3	83.0 ± 13.1
Nb 701C06	41.9 ± 8.1	26.0 ± 6.7
Nb 701D07	66.1 ± 25.0	17.2 ± 6.2
Nb 702C12	75.4 ± 34.2	18.9 ± 3.0
Nb 721E08	~ 1700	> 25
Nb 729A04	83.2 ± 39.4	4.1 ± 0.1
Nb 729C08	~ 1400	> 32
Nb 730C03	63.9 ± 41.5	9.2 ± 0.3
Nb 501A02	802 ± 505	0.8 ± 0.1
Fab of mAb 13F62	3.1 ± 2.9	1.5 ± 0.1
Fab ACE910 anti-FX (J327/L404-k)*	~ 3900	< 0.6
Mono-valent J327 D31H/JYL280**	62.3 ± 52.7	0.45 ± 0.4
Mono-valent BIIB-12-917***	N/A	No effect
FIXa only	N/A	1.0

N/A refers to the case where no effect on FX activation is observed when comparing absence and presence of FX binder. In cases where FX could not be saturated with a given FX binder, and thus no plateau could be reached, the effect on FX-activation is given as “more than”/“less

than" the maximum observed effect and the estimated KD is marked with "˜". * see US 9,334,331; ** see WO2018/021450; *** see WO2018/098363

Example 4: Effect of anti-FX Nanobodies on FXa amidolytic activity

To exclude that the fold increase in activation observed in example 3 could be due to a positive 5 effect of the Nanobodies on FXa amidolytic activity the ability of the monovalent anti-FX Nanobodies to stimulate FXa amidolytic activity was investigated as follows. 5 nM human plasma-derived FIXa (Haematologic Technologies Inc, USA) was pre-incubated with 50 μ M 25:75 phosphatidyl serine:phosphatidyl choline phospholipid vesicles (Haematologic Technologies Inc, USA) in assay buffer (50 mM HEPES, 100 mM NaCl, 5 mM CaCl₂, 0.1%(w/v) 10 PEG8000, 1 mg/mL bovine serum albumin, pH 7.3) for 10 minutes. Human, plasma-derived FX (Haematologic Technologies Inc, USA) was added to the reaction in a final concentration of 100 nM and a final activation volume of 40 μ L. After 20 minutes of incubation at room temperature while agitated (1000 RPM), the FX-activation reaction was terminated by addition of 25 μ L quench buffer (50 mM HEPES, 100 mM NaCl, 60 mM EDTA, 0.1%(w/v) PEG8000, 1 mg/mL 15 bovine serum albumin, pH 7.3). Hereafter, 10 μ L 25 μ M of the individual FX binder were added to the generated FXa before addition of 25 μ L 2 mM S-2765 chromogenic substrate (Chromogenix, Sweden) and determination of chromogenic substrate conversion by measurement of absorbance at 405 nm (Δ Abs405/min) in a microplate reader. The relative FXa amidolytic activity (a_{rel}) is calculated using Eq. 2:

20

$$\text{Eq. 2: } a_{rel} = \frac{a_{FXa\text{-binder}}}{a_{FXa}}$$

where $a_{FXa\text{-binder}}$ is the amidolytic activity of the FXa/FX binder complex and a_{FXa} is the amidolytic activity of FXa alone.

25 Table 4 shows the relative FXa amidolytic activity for the individual FX binders and it was concluded that increased FX activation could not be due to Nanobodies® having increased FXa amidolytic activity.

Table 4: FXa amidolytic activity (mean \pm SD, n = 2-3) in the presence of FX binders relative to free FXa

FX binder	FXa amidolytic activity (relative to free FXa, fold)
Nb 701B09	1.06 \pm 0.10
Nb 701C06	1.06 \pm 0.15
Nb 701D07	1.05 \pm 0.63
Nb 702C12	1.05 \pm 0.04
Nb 721E08	1.07 \pm 0.01
Nb 729A04	1.11 \pm 0.01
Nb 729C08	1.09 \pm 0.05
Nb 730C03	1.01 \pm 0.03
mAb 13F62	0.94 \pm 0.06
Fab ACE910 anti-FX (J327/L404-k)*	1.02 \pm 0.05
Mono-valent J327 D31H/JYL280**	0.98 \pm 0.004
Mono-valent BIIB-12-917***	0.95 \pm 0.02
Free FXa	1.00 \pm 0.02

* see US 9,334,331

** see WO2018/021450

5 *** see WO2018/098363

Example 5: Binding epitope of anti-FX Nanobodies®

To determine whether the binding epitopes of anti-FX Nanobodies® and mAb 13F62 antibody are located inside the activation peptide (AP) of human FX, an ELISA assay was setup.

41 unique 12-mer peptide fragments spanning the 52 residues of the activation peptide with

5 one amino acid spacing were immobilized in microtiter plate wells followed by incubation with the Nanobody®/antibody to be tested, and detection of bound ligand was performed by addition of a secondary HRP-labelled antibody.

The peptides were C-terminally conjugated to biotin and 50 µL of 1 µg/mL peptide solution was

used for immobilization in discrete wells of the microtiter plate which was pre-coated with 1

10 µg/mL streptavidin. Each well was washed with washing buffer (10mM Tris, 150mM NaCl, 2.5mM CaCl₂, 0.05% Tween 20, pH 8.60) followed by addition of 50 µL of 2 µg/mL FLAG-tagged anti-FX Nanobody® or IgG antibody to be tested. After 1 hour non-bound Nanobody®/antibody was washed off using washing buffer.

Bound anti-FX activation peptide ligand was detected by first binding a HRP-labelled secondary

15 antibody (for FLAG-tagged Nanobodies: Anti-FLAG mAb M2-Peroxidase (HRP) (Sigma Aldrich, US), for antibody: Fcγ Fragment Specific Peroxidase AffiniPure F(ab')₂ Fragment Goat Anti-Human IgG (Jackson ImmunoResearch Laboratories, Inc., US), or Peroxidase AffiniPure Goat Anti-Mouse IgG (Jackson ImmunoResearch Laboratories, Inc., US)) for 1 hour, and then adding 100 µL TMB-1 ELISA substrate (Kem-En-Tec Diagnostics, Denmark).

20 The minimal epitopes were then deduced from the set of peptides giving rise to a signal above baseline by identifying the common sequence covered by the set of peptides (table 5) bond by each FX binder. The first residue of the epitope was defined by the last amino acid in the first consecutive, ELISA-positive peptide, while the last residue of the epitope was defined as the first residue of the last consecutive, ELISA-positive peptide.

25 Thus, table 5 shows ELISA signal from consecutive peptides spanning the entire FX AP for several different anti-FX Nanobodies® (Nb) and an anti-FX mAb 13F62. ELISA signals have been normalized relative to the background signal (bbg). The grey areas marks the positive binding signals used for determining the minimal epitope.

Table 5: Epitope identification

Epitope residues	SEQ ID NO:	13F62	701B09	701C06	701D07	702C12	501A02	721E08	729A04	729C08	730C03
empty		1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
SVAQATSSSGEA	13	2.55	0.76	0.92	0.76	0.96	0.74	2.25	0.92	1.14	1.21
VAQATSSSGEAP	14	2.70	0.73	0.93	0.84	1.02	0.88	2.13	0.99	1.09	1.24
AQATSSSGEAPD	15	1.89	0.75	0.91	0.89	0.97	0.79	1.92	1.08	1.17	1.19
QATSSSGEAPDS	16	1.82	0.77	0.94	0.81	0.96	0.82	1.97	1.08	1.12	1.14
ATSSSGEAPDSI	17	3.20	0.82	0.91	0.86	0.98	0.82	2.27	1.24	1.13	1.19
TSSSGEAPDSIT	18	0.68	0.97	0.87	0.75	0.77	0.76	2.20	1.12	1.06	1.20
SSSGEAPDSITW	19	0.77	0.84	0.90	0.73	0.86	0.82	1.99	1.24	1.10	1.21
SSGEAPDSITWK	20	0.73	0.89	0.89	0.74	0.88	0.71	2.01	0.96	1.06	1.22
SGEAPDSITWKP	21	0.82	0.84	0.88	0.78	0.88	0.76	2.15	0.98	1.07	1.18
GEAPDSITWKPY	22	1.50	0.86	0.90	0.80	0.93	0.94	2.26	1.05	1.15	1.24
EAPDSITWKPYD	23	1.64	0.79	0.89	0.76	0.97	0.76	2.35	1.01	1.11	1.24
APDSITWKPYDA	24	1.59	0.82	0.96	0.90	1.06	0.74	2.29	1.04	1.09	1.16
PDSITWKPYDAA	25	1.89	0.83	0.92	0.84	1.05	0.79	2.40	0.95	1.17	1.24
DSITWKPYDAAD	26	3.61	0.76	0.93	0.89	1.08	0.79	2.18	1.05	1.09	1.22
SITWKPYDAADL	27	7.95	0.84	0.94	1.04	1.08	0.71	2.28	1.13	1.11	1.18
ITWKPYDAADLD	28	4.23	0.83	1.03	0.89	1.10	0.74	2.08	1.28	1.06	1.20
TWKPYDAADLDP	29	1.95	0.92	1.00	0.91	1.13	0.74	2.26	0.99	1.17	1.26
WKPYDAADLDPT	30	1.18	1.14	0.99	0.85	0.89	0.74	1.83	1.20	1.08	1.14

Epitope residues	SEQ ID NO:	13F62	701B09	701C06	701D07	702C12	501A02	721E08	729A04	729C08	730C03
KPYDAADLDPTE	31	0.77	0.88	0.90	0.73	0.80	0.82	1.89	1.33	1.10	1.17
PYDAADLDPTEN	32	0.84	0.88	0.82	0.73	0.83	0.79	2.05	1.06	1.08	1.20
YDAADLDPTENP	33	0.84	0.81	0.85	0.75	0.87	0.71	2.21	1.06	1.09	1.28
DAADLDPTENPFF	34	0.77	0.81	0.85	0.70	0.88	0.88	2.30	1.10	1.18	1.24
AADLDPTENPFD	35	0.77	0.79	0.82	0.69	0.88	0.79	2.22	1.05	1.17	1.21
ADLDPTENPFDL	36	1.25	0.73	0.87	0.77	0.91	0.71	2.34	0.98	1.11	1.25
DLDPTENPFDLL	37	26.45	0.82	0.88	0.74	1.00	0.79	2.48	1.06	1.21	1.26
LDPTENPFDLLD	38	31.00	0.84	0.94	0.80	1.11	0.91	2.29	1.91	1.58	1.30
DPTENPFDLLDF	39	29.75	2.87	1.51	1.39	4.16	0.88	2.27	4.03	1.95	1.68
PTENPFDLLDFN	40	30.11	3.91	1.61	1.29	4.58	0.88	2.35	5.18	2.06	1.62
TENPFDLLDFNQ	41	29.68	4.38	1.74	1.44	4.84	1.09	2.54	9.12	3.14	2.10
ENPFDLLDFNQT	42	28.68	3.43	1.56	1.27	4.00	0.82	2.88	17.83	8.06	6.57
NPFDLDFNQTQ	43	28.61	2.16	1.29	0.96	3.13	0.94	2.28	8.27	3.41	2.82
PFDLLDFNQTQP	44	29.73	3.48	1.50	1.13	4.95	0.79	2.50	1.41	1.18	1.23
FDLDFNQTQPE	45	30.57	3.27	1.41	0.99	4.38	0.85	3.01	1.58	1.15	1.28
DLLDFNQTQPER	46	0.82	1.17	1.13	0.81	3.08	0.76	2.45	1.12	1.22	1.18
LLDFNQTQPERG	47	0.86	1.09	1.03	0.80	1.88	0.79	2.30	1.10	1.13	1.10
LDFNQTQPERGD	48	0.80	0.82	0.93	0.79	0.97	0.74	2.21	0.98	1.12	1.14
DFNQTQPERGDN	49	1.23	0.87	0.87	0.75	0.94	0.71	2.25	0.97	1.10	1.16
FNQTQPERGDN	50	1.77	0.89	0.88	0.82	1.00	0.71	2.16	1.05	1.08	1.16

Epitope residues	SEQ ID NO:	13F62	701B09	701C06	701D07	702C12	501A02	721E08	729A04	729C08	730C03
NQTQPERGDNNL	51	2.45	0.79	0.85	0.87	0.92	0.71	2.02	1.13	1.09	1.22
QTQPERGDNNLT	52	1.95	0.72	0.93	0.79	0.88	0.76	1.96	1.11	1.04	1.10
TQPERGDNNLTR	53	8.86	0.93	0.97	0.88	1.05	0.85	1.97	1.09	1.37	1.06

The minimal epitope was defined as the amino acid sequence in common between the ELISA positive peptides for each FX binder. The determined minimal epitopes within AP is summarized in table 6.

5 Table 6: Minimal epitope sequences for the anti-FX Nanobodies® and mAb13F62

FX binder	Epitope in AP	Minimal epitope sequence
Nb 701B09	33-38	FDLLDF
Nb 701C06	33-38	FDLLDF
Nb 701D07	32-38	PFDLLDF
Nb 702C12	35-38	LLDF
Nb 721E08	33-40	FDLLDFNQ
Nb 729A04	33-37	FDLLD
Nb 729C08	31-37	NPF DLLD
Nb 730C03	31-38	NPF DLLDF
mAb13F62	33-36	FDLL
Nb 501A02	No epitope in AP detected	

By correlating the data of tables 5 and 6 with the data of table 3, it is observed that the ability to stimulate FX activation is observed for FX binders for which the minimal epitope on FX for example is "PFDLLDF".

10

It follows from Table 6 that a common minimal epitope can be identified as 'LL'.

15

While certain features of the invention have been illustrated and described herein, many modifications, substitutions, changes, and equivalents will now occur to those of ordinary skill in the art. It is, therefore, to be understood that the appended claims are intended to cover all such modifications and changes as fall within the true spirit of the invention.

CLAIMS

1. An antibody or antigen-binding fragment thereof capable of binding FX, wherein the antibody or antigen-binding fragment

- a. is capable of stimulating FX activation;
- 5 b. is capable of stimulating FX activation by FIXa;
- c. stimulates FX activation;
- d. stimulates FX activation by FIXa;
- e. is capable of making FX more prone to proteolysis; or
- f. is capable of making FX more prone to proteolysis by FIXa.

10

2. The antibody or antigen-binding fragment thereof according to claim 1, wherein the activation/proteolysis of FX is determined as described in Example 3 herein.

15 3. The antibody or antigen-binding fragment thereof according to claim 1 or 2, wherein the antibody or antigen-binding fragment thereof is capable of binding the activation peptide of FX (amino acid residues 143-194 of SEQ ID NO:2).

20 4. The antibody or antigen-binding fragment thereof according to any of the previous claims, wherein the antibody or antigen-binding fragment thereof is capable of binding the activation peptide of FX and wherein the common minimal epitope, as determined by peptide array, comprises amino acid residues "LL" (amino acid residues 177-178 of SEQ ID NO:2).

25 5. An antibody or antigen-binding fragment thereof capable of binding FX

- a. comprising the heavy chain variable domain (SEQ ID NO:4) and light chain variable domain (SEQ ID NO:5) of mAb 00916;
- b. comprising the three CDRs of the heavy chain variable domain (SEQ ID NO:4) and the three CDRs of the light chain variable domain (SEQ ID NO:5) of mAb 00916;
- c. comprising the heavy chain variable domain (SEQ ID NO:6) and light chain variable domain (SEQ ID NO:7) of mAb 13F62;
- 30 d. comprising the three CDRs of the heavy chain variable domain (SEQ ID NO:6) and the three CDRs of the light chain variable domain (SEQ ID NO:7) of mAb 13F62;
- e. comprising SEQ ID NO:8, 9, 10, 11, 54, 55, 56 or 57; or
- f. comprising the three CDRs of SEQ ID NO:8, 9, 10, 11, 54, 55, 56 or 57.

6. An antibody or antigen-binding fragment thereof according to any of claims 1-4 wherein the antibody or antigen-binding fragment thereof comprises a heavy chain variable domain which is at least 90, 91, 92, 93, 94, 95, 96, 97, 98 or 99% identical to the sequence identified by SEQ ID NO:8, 9, 10, 11, 54, 55, 56 or 57, respectively.
- 5
7. An antibody or antigen-binding fragment thereof capable of binding FX, wherein the antibody or antigen-binding fragment thereof competes with a reference antibody or antigen-binding fragment thereof according to claim 5.
- 10 8. The antibody or antigen-binding fragment thereof according to claim 5 or 7, wherein the antibody or antigen-binding fragment
 - a. is capable of stimulating FX activation,
 - b. is capable of stimulating FX activation by FIXa,
 - c. stimulates FX activation,
 - d. stimulates FX activation by FIXa,
 - e. is capable of making FX more prone to proteolysis or
 - f. is capable of making FX more prone to proteolysis by FIXa.
- 15
9. The antibody or antigen-binding fragment thereof according to any of the previous claims, wherein the antibody or antigen-binding fragment thereof stimulates FX activation by FIXa independently of the presence of a FIXa binder.
- 20
10. The antibody or antigen-binding fragment thereof according to any of the previous claims, wherein the antibody or antigen-binding fragment has a binding affinity determined as the equilibrium dissociation constant (K_D) that is less than 10 μM , such as less than 9 μM , such as less than 8 μM , such as less than 7 μM , such as less than 6 μM , such as less than 5 μM , such as less than 4 μM , such as less than 3 μM or such as less than 2 μM .
- 25
11. The antibody or antigen-binding fragment thereof according to any of the previous claims, wherein the antibody or antigen-binding fragment is monovalent, such as an immunoglobulin single variable domain or antigen-binding fragment thereof, a Nanobody®, a V_HH, a humanized V_HH, a camelized V_H domain, such as a Fab, scFab, Fv or scFv.
- 30

12. The antibody or antigen-binding fragment thereof according to any of the previous claims 1-10, wherein the antibody or antigen-binding fragment thereof is bivalent, such as a full-length mAb or a Fab'₂.
- 5 13. A bi- or multi-specific antibody comprising the antibody or antigen-binding fragment thereof according to any of the previous claims.
14. Use the antibody or antigen-binding fragment thereof according to any of the previous claims for the manufacture of a medicament for use in the treatment of haemophilia, such as haemophilia A or B, with or without inhibitors.
- 10 15. The antibody or antigen-binding fragment thereof according to any of the previous claims for use in the treatment of haemophilia, such as haemophilia A or B, with or without inhibitors.

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2018/081296

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K16/36
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, BIOSIS, Sequence Search, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2007/041978 A1 (HATTORI KUNIHIRO [JP] ET AL) 22 February 2007 (2007-02-22) cited in the application column 3 ----- A SCHEIFLINGER F ET AL: "Enhancement of the enzymatic activity of activated coagulation factor IX by anti-factor IX antibodies", JOURNAL OF THROMBOSIS AND HAEMOST, WILEY INTERSCIENCE, ENGLAND, vol. 6, no. 2, 1 February 2008 (2008-02-01), pages 315-322, XP008122315, ISSN: 1538-7836 cited in the application ----- -/-	1-4,6-9, 11-15 1-15

Further documents are listed in the continuation of Box C.

See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
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"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
1 February 2019	18/02/2019
Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Authorized officer Scheffzyk, Irmgard

INTERNATIONAL SEARCH REPORTInternational application No
PCT/EP2018/081296

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

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